# DOCTORAL THESIS

# AN ARCHITECTURAL INVESTIGATION INTO THE MICROBIOME OF THE BUILT ENVIRONMENT AT TWO SELECTED SOUTH AFRICAN HOSPITALS


## Submitted by

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"In the beginning God created the heavens and the earth."
Genesis 1:1
"In the beginning was the Word, and the Word was with God, and the Word was God."
John 1:2
"The fear of the LORD is the beginning of knowledge: but fools despise wisdom and instruction."
Proverbs 1:1

With humility and Godly fear, praise be to the Lord of Hosts, who has led me into this work, and has given me insight, guidance and perseverance to complete it. Thank you, Jesus.

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# LIST OF PUBLICATIONS RESULTING FROM THE RESEARCH

1. Nice, J. 2014. Air, surfaces and copper halos, interstitial microbial zones. Has it been measured; can it be predicted? *Proceedings of Indoor Air Conference 2014 ISIAQ 7-12 July 2014* Hongkong

2. Nice, J. 2014. Air, surfaces and HAI: An interdisciplinary empirical approach towards architectural design validation, A health care design initiative. *Proceedings of International Union of Architects Conference (UIA) 3-7 August 2014* South Africa

3. Nice, J. 2015. A Microbial design guide to the built environment, designing for Health. *Proceedings of the SAFHE / CEASA, the 11th Biennial Conference & exhibition 11-13 August 2015* South Africa

4. Nice, J & Vosloo, P. 2015. Exploring spatial planning and functional program impact on microbial diversity and distribution in two South African hospital microbiomes. *Proceedings of Healthy Buildings Conference 2015 America 9-22 July 2015* United States

5. Nice, J, & Bole, S. 2016. Investigating the impact of architectural planning and functional program on the indoor microbiome. A health concern. *Proceedings of Indoor Air Conference 2016 ISIAQ 3-7 July 2016* Belgium

6. Nice, J. 2014. Air, surfaces and HAI: Sensing the future of architecture, the microbial paradigm. *Proceedings of the Smart and Sustainable Cities and Transport Seminar (SCC) 12-14 July 2017* South Africa.

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# ABSTRACT

This thesis presents an investigation into the hospital microbiome of the built environment. The researcher characterised the microbial landscape of two Western Cape hospitals through a multi-disciplinary approach. The researcher employed an integrated cross-disciplinary methodology that combined spatial analytics, environmental monitoring and microbial sampling and sequencing. This thesis presents the first South African hospital microbiome classification. Buildings may influence the health and well-being of their occupants through healthcare acquired infection (HAI). HAI contributes to two thirds of all patient readmissions. The researcher suggests a paradigm shift in building ecology to approach this established public health concern.

The relationship between microorganisms and the built environment is much more prevalent than previously recognised. The built environment is a landscape that consists of distinct series of landscapes connected by micro and macro ecosystems. These ecosystems are local and unique, integrated, and dependent on the adjacent environment. Microbiology of the built environment (MoBE) combines built environment studies by merging soft and hard science with seemingly unrelated but systemic dependable study fields. These study fields include engineering, architecture, microbiology, the health sciences, epidemiology, anthropology and sociology. As with all new emerging fields, relationship interplay and interpolation of data parameters in each field dictate the scope of discovery. What constitutes a “healthy” indoor environment is yet to be determined, characterised or defined. One needs to understand the manner in which to process various known and unknown dynamic factors. Indoor environments are complex by nature - extremely integrated, dynamic ecosystems - and require a vast interdisciplinary field of researchers.

This study found that not only do indoor built environment biomes change seasonally, but the indoor conditions of the built environment also experience seasonal variations. Room types and potentially building types, can be distinguished through their microbiomes, as is reflected by the unique biomes associated with each hospital room type investigated. The factors that determine the biome are still unclear but represent possibilities for future research investigation. The researcher considers the following as pertinent findings of the research: 1) Design guidelines for health, in architecture and engineering, are realised where microorganisms are considered. 2) There is confirmation of seasonal variations in the composition of hospital microbiomes. 3) The data provide an indicator list that represents the core species associated with a South African Western Cape hospital biome. 4) This thesis contributes to and confirms the association of known Healthcare associated infection (HAI) pathogens through sequencing and culture, identifying both presence and viability. 5) This thesis contributes to the MoBE research agenda at various levels.

The thesis pursued health and design associated understanding to stimulate public health centred architectural response, and improve indoor building environments for the user. It investigated the spatial relationships of indoor environments and the composition and distribution of the local microbiome. A methodology for infection prevention and control (IPC), building assessment and operational guidance proposes further development.

# DEFINITION OF TERMS

| | | |
|---|---|---|
| Architecture | *"The art and science of designing buildings and (some) non-building structures."* | (Oxford English Dictionary 1993, sv "architecture") |
| Biofilm | *"A thin, normally resistant, layer of microorganisms such as bacteria that forms on and coats various surfaces."* | (Briere & Resnick 2017) |
| Connectivity | *"Number of elements which connect to a certain element. Connectivity is a local measure. It only takes into account the direct neighbours of an element."* | (Schneider 2010) |
| Ecology | *"The scientific study of the relationship between living things and their environments."* | (Olsen, Choffnes & Mack 2012) |
| Eukaryotic | *"One of the three domains of life. The two other domains, bacteria and archaea, are prokaryotes that lack several features characteristic of eukaryotes (e.g. cells containing a nucleus surrounded by a membrane and with deoxyribonucleic acid (DNA) bound together by proteins [histones] into chromosomes). Animals, plants and fungi are all eukaryotic organisms."* | (Olsen, Choffnes & Mack 2012) |
| Fomite | *"A surface or other inanimate object onto which a microorganism can deposit and from which it transfers to a host."* | (Briere & Resnick 2017) |
| Genome | *"The complete set of genetic information in an organism. In bacteria, this includes the chromosome(s) and plasmids (extra-chromosomal DNA molecules that can replicate autonomously within a bacterial cell)."* | (Briere & Resnick 2017, from IOM 2014) |
| Hybrid ventilation | *"A ventilation approach that employs natural and mechanical ventilation systems, potentially using different subsystems at different times of day or seasons of the year."* | (Briere & Resnick 2017, from IEA 2006) |
| Integration | *"The distance of an element to all other elements in relation to the number of elements in the complete system. It is a global measure of the network of space, as it takes into account the relationship of all elements to an element."* | (Al Sayed, Turner, Hillier & Lida 2014) |
| Mean depth | *"Mean depth compares the shortest path though the graph to all other nodes within the graph, summed and divided by all nodes in the graph."* | (Al Sayed *et al.* 2014) |
| Mechanical ventilation | *"The process of moving air into and within a building using ducts and powered fans or blowers, which may include means to filter, cool, heat, humidify, dehumidify, or otherwise condition the air."* | (Briere & Resnick 2017) |
| Metagenome | *"The collection of genomes and genes from the members of a microbiota/microbial community."* | (Marchesi & Ravel 2015) |
| Microbiome | *"Refers to the entire habitat, including the microorganisms (bacteria, archaea, lower and higher eukaryotes, and viruses), their genomes (i.e. genes), and the surrounding environmental conditions. The application of one or a combination of metagenomics, metatranscriptomics, and metaproteomics, together with clinical or environmental metadata characterises the microbiome."* | (Marchesi & Ravel 2015) |
| Microbiota | *"The assemblage of microorganisms present in a defined environment. Lederberg and McCray [1], who emphasised the importance of microorganisms inhabiting the human body in health and disease, first defined the term "microbiota". Using molecular methods relying predominantly on the analysis of 16S ribosomal ribonucleic acid (rRNA) genes, 18S rRNA genes, or other marker genes and genomic regions, amplified and sequenced from given biological samples establishes the microbial census. Performing taxonomic assignments using a variety of tools that assign each sequence to a microbial taxon (bacteria, archaea, or* | (Marchesi & Ravel 2015) |

| | | |
|---|---|---|
| | *lower eukaryotes) at different taxonomic levels from phylum to species."* | |
| Natural ventilation | *"The entry of outdoor air through intentional openings in the building envelope, such as windows, doors and vents, driven by indoor–outdoor air pressure differences due to weather and the operation of the building."* | (Briere & Resnick 2017) |
| Nosocomial infection / HAI | *"A nosocomial infection is strictly and specifically an infection "not present or incubating prior to admittance to the hospital, but generally occurring 48 hours after admittance. Nosocomial infections occur within 48 hours of hospital admission, 3 days of discharge or 30 days of an operation. Healthcare acquired infection (HAI), also known as a nosocomial infection, is an infection that is acquired in a hospital or other healthcare facility. To emphasise both hospital and nonhospital settings, it is also known as a healthcare associated infection (HAI or HCAI) - HAI is defined as an infection occurring in a patient during the process of care in a hospital or other healthcare facility that was not manifest or incubating at the time of admission. This includes infections acquired in the hospital and any other setting where patients receive healthcare and may appear even after discharge. HAI also includes occupational infections among facility staff."* | (Inweregbu & Dave 2005, WHO 2011) |
| OTU | *"Operational Taxonomic Units: "the thing(s) being studied". An OTU is typically defined as a cluster of reads with 97% similarity; the taxonomic level of sampling selected by the user to be used in a study, such as individuals, populations, species, genera, or bacterial strains."* | (Briere & Resnick 2017, from IOM 2014) |
| Pathogen | *"An organism or other agent that causes disease."* | (Alberts, Lewis, Raff, Roberts & Walter 2002) |
| Reads | *"The number of observations of an OTU."* | |
| Sick building syndrome | *"Sick building syndrome is comprised of various nonspecific symptoms that occur in the occupants of a building. "* | (Sumedha 2008) |
| Space Syntax | *"It starts with a certain description of the spatial architecture of buildings and cities. In Space Syntax, spaces are voids (streets, squares, rooms, parks, etc.). Voids are obstructions that might constrain access and/or occlude vision (such as walls, fences, furniture, partitions and other impediments)."* | (Al Sayed *et al.* 2014) |
| Taxa | *"Term used to refer to all the organisms that fall under a particular taxonomic criterion (such as kingdom, phyla, class, order, family, genera, species or subspecies)."* | (Briere & Resnick 2017) |
| 16SrRNA | *"The gene that encodes the ribonucleic acid (RNA) component of the smaller subunit of the bacterial ribosome (16S refers to the rate of sedimentation, in Svedberg units, of the RNA molecule in a centrifugal field). The 16S rRNA gene is present in all bacteria, and a related form occurs in all cells. "* | (Britannica, Science 2017, sv "16SrRNA") |

# ABBREVIATIONS

| | |
|---|---|
| ABC | Airborne bacteria count |
| ACH | Air changes per hour |
| ADMRM | Architectural design microbial risk model |
| A&E | Accident and Emergency |
| BE | Built environment |

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|---|---|
| BIM | Building information modelling |
| BRI | Building-related illness |
| CDC | Centre for Disease Control |
| CEMS | Carbon dioxide evolution monitoring system |
| CFD | Computational fluid dynamics |
| CFU | Colony-forming units |
| CHD | Centre for Health Design |
| CRE | *Carbapenem* resistant *Enterobacteriaceae* - strain *E. coli* |
| CRPA | *Carbapenem*-resistant *Pseudomonas aeruginosa* |
| CSIR | Council for Scientific and Industrial Research |
| DoH | Department of Health |
| DNA | Deoxyribonucleic acid |
| EA | *Enterobacter aerogenes* |
| ESBL | Extended-spectrum beta-lactamase |
| GIS | Geographic information system |
| HAI | Healthcare associated infection |
| HAP | Hospital-associated pathogens |
| HCW | Healthcare worker |
| HIV | Human Immunodeficiency Virus Infection |
| AIDS | Acquired Immunodeficiency Syndrome |
| HVAC | Heating, ventilation and air-conditioning |
| IAQ | Indoor air quality (related to pathogens) |
| IPC | Infection prevention and control |
| ISQ | Indoor surface quality (related to pathogens) |
| KDH | Khayelitsha District Hospital |
| MB | Microbial burden |
| MPH | Mitchells Plain Hospital |
| MoBE | Microbiology of the Built Environment |
| MRSA | Methicillin-resistant *Staphylococcus aureus* |
| NBR | National Building Regulations |
| NHAPS | National human activity pattern survey |
| NIOH | National Institute of Occupational Health |
| NGO | Non-government organisation |
| NTMB | Non-tuberculosis mycobacteria |
| OTU | Operational taxonomic unit |
| PA | *Pseudomonas aeruginosa* |
| PAMP | Pathogen-associated molecular patterns |
| SANS | South African National Standards |
| SBS | Sick building syndrome |
| SS | Space Syntax |
| RNA | Ribonucleic acid |
| TB | Tuberculosis |
| Mtb | *Mycobacterium tuberculosis* |
| MDR-TB | Multidrug-resistant tuberculosis |
| Xdr | Extremely drug resistant |
| Tdr | Total drug resistant |
| Mdr | Multi-drug resistant |
| LTBI | Latent tuberculosis infection |
| UVGI | Ultraviolet germicidal irradiation |
| VRE | Vancomycin-resistant *Enterococcus* |
| WC | Western Cape |
| WHO | World Health Organisation |

## TABLE OF CONTENTS

# LIST OF FIGURES

# LIST OF TABLES

# CHAPTER 1 THE BUILT ENVIRONMENT AND HEALTH

## 1.1 INTRODUCTION

Humans spend up to 90%, the vast majority of their time, indoors (Klepeis, Nelson, Ott, Robinson, Tsang, Switzer, Behar, Hern & Engelmann 2001; Hospodsky, Qian, Nazaroff, Yamamoto, Bibby, Rismani-Yazdi & Peccia 2012.) Global trends in urbanisation are increasing indoor environment living (Höppe & Martinac 1998). Yet our understanding of the indoor environment is limited (Hospodsky, Qian, Nazaroff, Yamamoto, Bibby, Rismani-Yazdi & Peccia 2012). Built environments are complex ecosystems, host to a wide variety of organisms and trillions of microorganisms (Rintala, Pitkaranta, Toivola, Paulin & Nevalainen 2008; Tringe, Zhang, Liu, Yu, Lee, Yap, Yao, Suan, Sing, Haynes, Rohwer, Wei, Tan, Bristow, Rubin & Ruan 2008; Amend, Seifert, Samson & De Bruns 2010). A number of studies investigated this environment with varied approaches and differential focus and research agendas (Rintala *et al.* 2008; Tringe *et al.* 2008; Amend *et al.* 2010, Kembel, Jones, Kline, Northcutt, Stenson, Womack, Bohannan, Brown & Green 2013, Adams, Miletto, Lindow, Taylor & Bruns 2014; Meadow, Altrichter, Kembel, Kline, Mhuireach, Moriyama, Northcutt, O'Connor, Womack, Brown, Green & Bohannan 2014; Ramos, Dedesko, Siegel, Gilbert & Stephens 2015, Lax, Sangwan, Smith, Larsen, Handley, Richardson, Guyton, Krezalek, Shogan, Defazio, Flemming, Shakhsheer, Weber, Landon, Garcia-Houchins, Siegel, Alverdy, Knight, Stephens, & Gilbert 2017. The core focus, however, is to understand this largely unknown ecosystem and indoor environment we call home. There are numerous examples of the health effects of, and links between, the indoor environment and the humans occupying them. Consequently, there is growing interest in the impact that microbiomes have on the health of humans. There are a few researchers (Hospodsky *et al.* 2012; Kembel *et al.* 2013; Dunn, Fierer, Henley, Lef, & Menninger; Ramos *et al.* 2015) exploring the intersection of microbial ecology, building materials and architectural design, to understand microbial diversity and abundance within a building. When considering the application of building design spatial factors, the studies are limited to a total of three (Adams, Bateman, Holly, & Meadow 2015). The literature review in chapter 3 found only four studies considering a form of occupant activity and presence, yet numerous studies consistently confirm the importance of human occupancy and user identification, human activity, space use and spatial relationships.

A primary problem identified in the study is that a large number of people, in excess of 15% in developing countries and 8-10% in developed countries, contract some form of HAI in hospitals (Yates *et al*. 2016; Hamilton 2012). South Africa is suffering from the same burden. Numerous studies and investigations (of which only a few are referenced in chapters 1 and 3) point to the fact that indoor built environments affect the health and well-being of their users. However, little empirical evidence is available on the factors that contribute to this condition (Schweitzer, Gilpin & Frampton 2004; Yates, Tanser & Abubakar 2016; Lax *et al*. 2017). Evidently, there is an understudy of architectural factors, primarily spatial networks in building design. With the research conducted to date on the microbiology of the built environment and building ecology, a lack of understanding and knowledge of the transmission and impacts of infectious microorganisms within the built environment still exists (Lax *et al*. 2017). Unpacking this core problem requires an interdisciplinary approach and by extension a subset of problem statements. Firstly, buildings and dwellings are colonised by pathogenic bacteria – microbes that have adapted to their extreme environmental conditions. Research shows a decline in microbial biodiversity, and a rise in human pathogenic bacteria within engineered

environments when compared to naturally ventilated biome spaces (Kembel *et al.* 2013). The relationship between spatial planning and the distribution and prevalence of microbes is limited and largely unknown. Secondly, the environmental conditions, including but not limited to ventilation and the understudied area of spatial networks in building design and planning of an environment, directly contribute to the spread of various surface-origin bacteria, NTMb and airborne bacteria such as *Tuberculosis* (Nardell, Keegan, Cheney & Etkind 1991). Consequently, they contribute to the high prevalence rate of nosocomial infections (the driver for NTMb, tuberculosis and other infections) in hospitals and other enclosed environments (Basu, Andrews, Poolman, Gandhi, Shah, Moll, Moodley, Galvani, & Friedland 2007; Koenig 2008; Ducel, Fabry, Nicolle, Girard, Perraud, Pruss, Savey, Tikhomirov, Thuriaux & Vanhems 2002). The resources for implementing and maintaining costly mechanical systems are neither affordable nor sustainable in resource-limited settings (Block *et al.* 1999) such as South Africa. The field of architecture, therefore, requires a form of empirical risk validation for building design for healthcare associated infection (HAI).

Due to the interdisciplinary nature of the problem, the author proposes a multi hypothesis approach. The first hypothesis (A) states that building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health architectural design, based on the biome composition (abundance and richness) of indicator organisms. The second hypothesis states that social behavioural science studies considering factors of human movement patterns, occupancy and functional use of space influence the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus the indoor environmental factors of the hospitals (MPH and KDH) influence the composition of both the micro (room level) and macro (building level) biome environments. The first sub-hypothesis states that the source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room. Sub-hypothesis two states that the levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.

To test the hypotheses, the researcher proposes the following five core questions, resulting in a few sub questions to answer the primary question:

1. What is the composition of the South African, Western Cape, Cape flats hospital microbiome?
2. What pathogens are commonly found in South African hospitals, with specific reference to the Western Cape, Cape flats?
3. Which built environment factors contribute to and influence the composition of the built environment microbiome, and how?
4. Is there any correlation between the distribution of the microbes in hospitals and the spatial design of the hospitals (considering user data and design data)? Do design and planning influence the composition of the microbiome?
5. How can built environment data, microbiome data and spatial design data inform IPC processes, with intentional focus on reducing the potential of HAI transmission?

The objective of the investigation was first, to associate environmental built environment (BE) data with microbial communities and building systems for ventilation, surfaces and occupancy, and establish guidance for architectural and engineering design decision making towards

public health centred design outcomes. Secondly, to test if one can utilise spatial analytics, risk and IPC profiling and BE characterisation to support risk assessment and early design analysis, as a guide towards a bio-informed design. Thirdly, to define the microbiome of a hospital environment in the Cape Flats region of the Western Cape and formulate a database, thereby characterising a South African hospital biome which would be representative of the developing world for future meta-data studies. Fourthly, to derive and establish a data set of indicator species for HAI and establish the prevalence of bacteria in the healthcare built environment to support the development of HAI research and a pathogen species list in South Africa and South African hospitals. Lastly, to support the agenda for repeatable, financially viable research methodologies for developing countries in MoBE studies which will enable future research investigations of the collection and generation of data, without compromising accepted and established MoBE and other international standards.

## 1.2 BACKGROUND

Occupational comfort and well-being have been widely documented in the field of architecture. Margaret Campbell (Campbell 2005) mentions a few of the direct impacts that architecture has had on the built environment and the well-being and health of people over the past hundred-and-fifty years. Considering the rate of urbanisation and city densification, the indoor environment is becoming of greater public health concern. Global research investigates healthcare associated infection (HAI), or medically termed nosocomial infection, in various social settings and under various climatic conditions (Ducel, Fabry, Nicolle, Girard, Perraud, Pruss, Savey, Tikhomirov, Thuriaux & Vanhems 2002). HAI transmission occurs primarily in three ways: (1) contact spread, (2) droplet spread and (3) airborne spread. The built environment plays a significant role in all three modes of transmission. Typical organisms associated with contact spread are methicillin resistant *Staphylococcus aureus*, vancomycin-resistant *Enterococci*, extended-spectrum beta-lactamase (ESBL) and *Clostridium difficile.* Organisms associated with droplet spread are *Neisseria meningitides, Streptococcus pneumoniae* and *Mycoplasma pneumoniae*. Organisms associated with airborne spread are *Mycobacterium tuberculosis*, the measles virus and the *Varicella zoster* virus. The two main strategies to control the emergence and spread of antimicrobial resistant microorganisms healthcare acquired infection (HAI) are optimising antimicrobial use and preventing the transmission of resistant organisms (Brink, Feldman, Duse, Gopalan, Grolman, Mer, Naicker, Paget, Perovic & Richards 2006). The role of the built environment directly relates to the second strategy.

The Centre for Health Design (CHD) conducted an extensive systemic evidence-based literature review that included up to a thousand published peer-reviewed papers that considered the built environment and health (Hamilton 2003; 2012). Similarly, Texas A&M and Georgia Institute of Technology conducted a study of six hundred published peer-reviewed papers on the impact of hospital design and measured outcomes (Ulrich 2004). Both studies indicate that sufficient evidence exists on outcomes related to reductions in staff errors and stress, as well as the amount of pain experienced and medication required by patients. Current research indicates that the hospital environment is a contributor in the transmission of pathogens, and a potential incubator of bacteria that cause various illnesses through infection (Yates, Tanser & Abubakar 2016). However, the field of architecture consistently approaches public and human health design outcomes through heuristic social science outcomes that consider behavioural science and psychology. The salutogenic movement in architecture, derived from Antonovsky's theory *Sense of coherence* and the theory on the impact of stress

perception in environments (Antonovsky 1979), led to Alan Dilani postulating the psychosocially supportive design approach, today defined as salutogenic design. Dilani developed and investigated the relationship of psychological impact indicators to design markers, to define the human health response to Comprehensibility, Manageability and Meaningfulness (Dilani 2001). Furrow and Vanderkaay (2013) further developed this social science approach to measure architecture and health outcomes in *Salutogenic spaces: Designed to thrive*. Salutogenic and evidence-based approaches in healthcare architecture are popular mechanisms to gauge health-based outcomes in the built environment. Evans and McCoy (1998) explored the role of architecture in human health through behavioural and psychological social science by measuring stress perception. They conceded… "*[t]here is very little evidence that characteristics of the built environment can affect human health"* (Evans & McCoy 1998:1). Due to these "limited" evidence outcomes, Schweitzer, Gilpin and Frampton (2004) investigate the elements of environmental design that impact on health in an extensive literature study covering four major topics with multiple sub categories. These are: (1) The role of the environment in behaviours, actions, and interactions; (2) Existing research: physical parameters; (3) A survey of healing environment design models; and (4) Elements of spaces and environments that inherently affect health. The research indicates relationships between architectural markers and health; however, of the 78761 published studies only 84 were found to have used adequate methodologies and, furthermore, only 80% of those reported positive links between environmental characteristics and patient health outcomes. They came to a similar conclusion to that of Evans and McCoy: that numerous research reports indicated… "*It is evident that, although the amount of research is steadily growing, there is no sound, directly relevant research yet available for many* healthcare *environmental design questions"* (Schweitzer *et al.* 2004:78).

In a 2009 World Health Organisation (WHO) study in South-East Asia, Europe and the Eastern Mediterranean and Western Pacific regions, the outcome reflected that 8.7% of hospitalised patients suffer healthcare associated infection. The study concluded that, globally, up to 1.4 million people suffer from infectious complications acquired in hospitals. Furthermore, 15.5 people per 100 (15.5%) acquire HAI in developing countries (Brink, Van den Bergh & Kantor 2011); this developing world figure could be far under-reported due to various factors. In South Africa, Tuberculosis (TB) is a driver in nosocomial infection. One such case study, the Tugela Ferry TB outbreak in 2005/2006, recorded eight deaths of hospital staff as a conclusive result of nosocomial infection (Koenig 2008). The increase in HAI in hospitals and the cost burden on government are immense (Eames, Tang, Li & Wilson 2009). This is quantified in various countries but not in South Africa (Klevens, Edwards, Chesley, Horan, Teresa, Robert, Pollock & Cardo 2007; Mendell, Fisk, Kreiss, Levin, Alexander, Cain, Girman, Hines, Jensen, Milton, Rextroat & Wallingford 2002). HAI bears a financial and public health burden (Murray 2004).

Mendell expresses the current state of the United States health cost condition: "*Available data suggest that improving building environments may result in health benefits for more than 15 million of the 89 million US indoor workers, with estimated economic benefits of $5 to $75 billion annually"* (Mendell, Fisk, Kreiss, Levin, Alexander, Cain, Girman, Hines, Jensen, Milton, Rexroat, & Wallingford 2002:430). The following statistics reflect the estimated USA cost burdens and economic impact in 2002: $10-billion-dollar annual healthcare costs, $19-billion-dollar annual work absence costs, and $3-billion-dollar annual reduced performance loss costs (Mendell *et al.* 2002). These figures represent an alarming cost to government due to HAI. It is evident that both surface and air play a defining role in the health and well-being of patients and visitors, and hence good Indoor Air Quality (IAQ) and Indoor Surface Quality (ISQ) are

required to reduce healthcare costs and improve environmental conditions and human health. It is also clear that research based on empirical data correlating health and the built environment is imperative and absent. The need exists for research that goes beyond the conventional sociological methodology, and into an ecological and a microbiological biome paradigm. The ecologist Jessica Green states, "*I am optimistic that well before 2034 we will be collectively designing and managing buildings with intention to promote healthy indoor ecosystems"* (Green 2014:114). This statement implies healthy indoor environments supporting healthy people and moving closer to Florence Nightingale's ideal: "*It may seem a strange principle to enunciate as the very first requirement in a hospital is that it should do the sick no harm"* (Nightingale 1859: preface).

### 1.2.1 HEALTHCARE ASSOCIATED INFECTION (HAI) IN SOUTH AFRICA

Based on international global incidence and prevalence rates, HAI has not received the amount of interest and attention in South Africa that is required. This situation could be the result of an overburdened health sector, due to the epidemic levels and high prevalence rates of TB and HIV and associated nosocomial infections, and it correlates markedly with the current levels of poverty in South Africa (SA 2011; WHO 2009a; Koenig 2008). The expected HAI figures for developing countries as per the WHO indicate a prevalence rate of 15 to 16 people per 100 for hospitalised/healthcare-facility-based patients. As mentioned previously, this figure could be higher. In 2005 Whitelaw and Dramowski conducted the only study on HAI in South Africa to date. The study estimated a prevalence rate of… *9.7% for four major HAI types, with higher prevalence among children (16.5%) and patients in intensive care units (ICUs) (28.5%)* (Dramowski 2017:56). In 2012, South Africa introduced the National Core Standards for Healthcare Establishments, with a patient safety domain mandating HAI surveillance, but lacking recommendations for HAI surveillance methods. (Dramowski *et al.* 2017)

*"There is an urgent need to obtain data on nosocomial transmission"* (Sissolak 2010:423). Tygerberg Academic Hospital in Cape Town conducted studies on their own staff to ascertain the impact of nosocomial infection (Wilson-Eshun, Zeier, Barnes & Taljaard 2008). The studies were done over an 11-year period, and more than 130 healthcare worker infections were identified. Similar studies in KwaZulu-Natal over a period of 5 years, 1999-2004, found that 1133 per 100 000 healthcare workers (HCW) were infected by TB (Naidoo & Jinhabhai 2006). Similar studies that have been conducted globally all point to the same concern: nosocomial infection has major implications for the most important health resource South Africa and other countries have – the healthcare worker. Brink, Feldman, Duse, Gopalan, Grolman, Mer, Naicker, Paget, Perovic, & Richards (2006) note the following patterns in antimicrobial resistance in South Africa, (1) an increase in ESBL production, (2) an increase in *Carbapenem* resistance including multidrug resistance in *Pseudomonas aeruginosa* and *Acinetobacier baumanii,* (3) the emergence of *Carbapenem resistance*, (4) an increase in multidrug-resistant *Escherichia coli,* and (5) emerging resistance among gram positive isolates (Brink *et al.* 2006; SATS 2006). The intention with this thesis is to provide a species classification of the most prevalent bacteria (excluding viruses and fungi) commonly found in the Accident and Emergency (A&E) units of the hospitals under investigation, including both surface and air sources, to potentially set baseline data for future studies and inform current cleaning and infection controls.

### 1.2.2 TUBERCULOSIS (TB) AND HIV/AIDS: AN HAI CASE STUDY

In South Africa, TB is a driver in nosocomial infection. One such case study, the Tugela Ferry TB outbreak in 2005/2006, recorded eight deaths of hospital staff as a conclusive result of nosocomial infection. This indicates… *[h]ospital transmission was a major factor* (Koenig 2008:896). *There is growing evidence that institutional transmission is a critical factor in epidemic HIV-associated TB and MDR-TB. Infection prevention and control (IPC) is only now becoming a feature of the global strategy to control TB. In South Africa, IPC remains the responsibility of individual* healthcare *facilities* (Sissolak 2010:423).

*Mycobacterium tuberculosis* (M.Tb) is the bacterium that causes TB. TB is source-based, hence only a person that produces M.Tb can transmit TB. Being of obligate airborne infection nature, people with TB disease release M.Tb through aerosols called droplet nuclei, produced by coughing. The inhalation of M.Tb droplet nuclei sometimes results in the spread of TB. Tuberculosis is clinically categorised as TB infection, TB transmission or TB disease. TB disease can stay inactive with the presence of M.Tb bacilli due to a healthy immune system, but can become active if one encounters other infectious people through increased droplet nuclei. This state of TB is also known as latent TB infection (LTBI). One in ten people who have LTBI infection develop TB disease (Bock, Jensen & Nardel 2007). TB disease occurs predominantly in the lungs, and a person with TB disease may be an active M.Tb producer. It can, however, also manifest as meningitis and in organs such as the iris, spine, etc. There are strains of TB with differing drug resistance. They are categorised as M.Tb, multidrug-resistant (Mdr) TB, extensively drug resistant (Xdr) TB and, recently, total drug resistant (Tdx) TB. TB is a global problem and an epidemic in South Africa (WHO 2011). The airborne nature of TB infection places all actively infected people with an immune deficiency disease such as HIV, unsuspecting patients, healthcare workers and healthy people at potential risk of contracting TB. Studies seem to indicate that healthcare facilities are contributing to the spread of TB bacteria (Yates, Tanser & Abubakar 2016).

South Africa is the most infected country in the world (per capita) of *Mycobacterium tuberculosis* (WHO 2009b). As far as Mdr and Xdr TB are concerned, *South Africa is the third highest tuberculosis burden country in the world, lagging behind two countries, China and India, who have significantly larger populations than ours* (SA 2011). More than 70% of people that have TB are co-infected with HIV in South Africa (WHO 2009b). The rapid increase of drug resistant strains of TB compounds the heavy burden of TB in South Africa. Numerous organisations such as the WHO, Centre for Disease Control (CDC) and Council for Scientific and Industrial Research (CSIR) in partnership with the South African National Department of Health (NDoH) are contributing to address the epidemic facing South Africa and other parts of the world. In South Africa 768 out of every 100 000 people are TB positive (WHO 2011). The unconfirmed cases may exceed the 70% (as noted above) who also have HIV Aids. In addition, more than 5.5 million people in South Africa have HIV/Aids and are thus highly susceptible to TB due to the immune co-relationship that these diseases share. The statistics indicate the potential exposure and risk for the unsuspecting healthy people, the patients in hospital environments and the healthcare worker. More recent data indicate that the local rate of incidence and prevalence are still of epidemic proportions, but the infection rate does show a slow annual decline (WHO 2013). This decline is a positive change in the fight against TB; however, we are still in excess of epidemic rates (>300), and on the negative spectrum, showing increased numbers of MDR and XDR cases.

### 1.2.3 INTRODUCING THE BUILT ENVIRONMENT MICROBIOME

The notion of buildings influencing the health and well-being of their occupants is well established and, as noted previously, is of marked public health importance. In order to approach this established public health concern, this study and the work of fellow MoBE researchers suggest a paradigm shift in building ecology. In recent years interest has grown in investigating the built environment from an ecological perspective; more particularly, from a microbiological ecosystemic perspective. When one considers complexity theory (a mathematical complexity and aggregate complexity) (Litaker, Tomolo, Liberatore, Stange & Aron 2006), the chaos theory and the interplay of individual elements within a system and the complex behaviour of the system, one is faced with quantitative and qualitative complexity. It argues with this very notion and its systemic interplay and interdependency in MoBE. MoBE combines built environment studies, merging soft and hard science with its seemingly unrelated but systemic dependable factors. It includes engineering, architecture, microbiology, the health sciences, epidemiology and anthropology and social sciences. As with all new emerging fields, relationship interplay and interpolation of data parameters in each field dictate discovery, bringing a distinct level of complexity with much uncertainty and gap research potential. Briere and Resnick (2017:23) note that, "*In-depth studies to explore the connections among microbial communities, different environmental conditions in built environments, and such outcomes as health or illness need to integrate expertise from microbial ecology, building and building system design and operation, epidemiology and human health, materials science, and a number of other fields".*

MoBE research has progressed immensely over the past seven years and has led to heuristic knowledge advances within the field. Originating from international collaborative research studies such as the human gut, the human biome, the home biome, and the space biome projects, there are a number of buildings that have been characterised, sampled and reported. The data, findings and concrete outcomes will only improve with an increased number of building data sets, in different climatic zones, with different contents and in different social development environments. Current building analysis is limited to North America, Europe and parts of Asia, with no data existing for Africa, South America, Central Asia, etc. The rapid progress of study methodologies, sampling methodologies, data analysis, data storage and access, factorisation of qualitative and quantitative data sets, comparability and replicability are some of the main areas of discussion. Replicating uniform sample and analysis methodology is critical (Ramos & Stephens 2014; Ramos *et al*. 2015; Adams, Miletto, Lindow, Taylor & Bruns 2014). Current built environments focused on include office buildings, hospitals, a university residence and schools. The studies comprise short-term and longitudinal studies with overlapping objectives and hypotheses (Kembel, Jones, Kline, Northcutt, Stenson, Womack, Bohannan, Brown & Green 2013; Rintala, Pitkaranta, Toivola, Paulin & Nevalainen 2008; Lax, Sangwan, Smith, Larsen, Handley, Richardson, Guyton, Krezalek, Shogan, Defazio, Flemming, Shakhsheer, Weber, Landon, Garcia-Houchins, Siegel, Alverdy, Knight, Stephens & Gilbert 2017; Ramos, Dedesko, Siegel, Gilbert & Stephens 2015; Frankel, Bekö, Timm, Gustavsen, Hansen & Madsen 2012).

In this thesis, the hospital environment of two public hospitals in South Africa is investigated. The research indicates that this is the first study in Africa and in a developing world environment with social and disease-burden challenges aimed at fully characterising a building by applying BE factors, architectural spatial factors and microbial community composition. In addition, this study is the first study to investigate two hospital environments simultaneously

over two seasons and, lastly, it makes a direct contribution to the field of architecture which to date has received limited focus within the built environment sphere with notable variation in BE factor integration (Adams *et al.* 2015; Ramos *et al.* 2015). Lax *et al.* (2017) conducted a single longitudinal study – microbiology relationships - and Ramos *et al*. (2015) studied built environment effects in the hospital environment and focused on inpatient ward and nursing areas. The current study, however, investigates the accident and emergency units in two Western Cape public hospitals. The areas of investigation of the two studies are vastly different. The wardrooms are semi-static and predictable environments, whereas the A&E is a dynamic environment that in many ways represents the outpatient areas, inpatient wards and surgical environments, with patients receiving a range of services, varying degrees of acuity and varying time stamps; therefore, the A&E would be a good indicator/snapshot of the general hospital environment.

Studies have indicated that the relationship between microorganisms and the built environment (BE) is much more apparent than previously considered. The BE is merely a landscape; in fact, it consists of a distinct series of landscapes connected in micro and macro ecosystems. These ecosystems are both local and unique, integrated, and to some extent dependent on adjacent environments. BE environments (water, air, organic substrates, hosts, etc.) present the core survival needs for organisms. These factors and others are present and quantifiable in the BE. The prevalence, richness and proliferation of organisms and the spread of infectious bacteria, fungi, viruses, prokaryotic and eukaryotic organisms, specifically in hospitals, are widely known to firstly, be through human contamination (Hospodsky *et al.* 2012) and, secondly, are dependent on environmental conditions (Wolfaardt, Bester, Foucher & Porosa 2010; Basu, Andrews, Poolman, Gandhi, Shah, Moll, Moodley, Galvani & Friedland 2007). In other words, specific pathogenic harmful microbes either survive or possibly proliferate in the built environment, or are cultivated in humans and by interaction distributed to and cross infecting other humans, if environmental conditions are favourable; MoBE research indicates that we might have overlooked a key area in the response to non-tuberculosis mycobacteria (NTMB), TB and other invasive pathogenic microbes. The microbial environment in which bacteria survive and live needs to be investigated.

The way we interact in living spaces, the way that we air-seal living spaces, the way that we ventilate and clean living spaces, and the material and methods we use to construct living spaces all play fundamental parts in the microbial make-up that architecture intentionally or inadvertently cultivates. The postulated result is HAI. MoBE-derived bio-informed design brings a new perspective to the built environment in that it is a microbial built environment. Without conscious consideration, architects and engineers have been designing this environment for centuries. Ecologist Jessica Green and fellow researchers at the University of Oregon and the Santa Fe Institute conceived the concept of a microbial landscape or built environment microbiome. To quote from a paper presented by this team of researchers: *Just as we currently manage natural ecosystems to promote the growth of certain species and inhibit the growth of others… An evidence-based understanding of the ecology of the built environment microbiome opens the possibility that we can similarly manage indoor environments, altering through building design and operation the pool of species that potentially colonise the human microbiome during our time indoors* (Kembel *et al.* 2013:1477).

As building occupants, we have adapted and engineered our environment to suit our comfort and needs. The notion of “green” buildings is of extreme relevance to MoBE - on the one hand optimising energy, but on the other impacting BE biomes with unknown health outcomes and

effects. We have neglected to consider the environments invisible to the naked eye that affect our health (Hospodsky *et al.* 2014). Similar to Campbell's deductions (Campbell 2005), researchers from the Environmental Health Department at the National Public Health Institute in Helsinki, Finland, quantify and define these facts in their paper (Rintala *et al.* 2008). For biomes…*as for any other biome, the composition of the built environment microbiome is determined by some combination of two simultaneous ecological processes: the dispersal of microbes from a pool of available species and selection of certain microbial types by the environment* (Kembel *et al.* 2013:1470). Manmade environments, which are in fact unexplored ecosystems that in many ways resemble extreme environmental conditions, would consequently favour the most resilient biota, often found to be human pathogenic microbes, by suppressing competitive exclusion through the various methods of sterilisation. The reported reduction of diversity in indoor environments (Adams *et al*. 2013) as opposed to a natural ecosystem is most likely due to the human removing the diversity of the ecosystem, while forgetting that he himself is a vector to the most harmful pathogens. Architecture and the microbial environment are intimately fused. The interdisciplinary and interrelated nature of the MoBE research is captured in Figure 1. It is often at the nexuses of fields where research boundaries shift and discoveries are made.

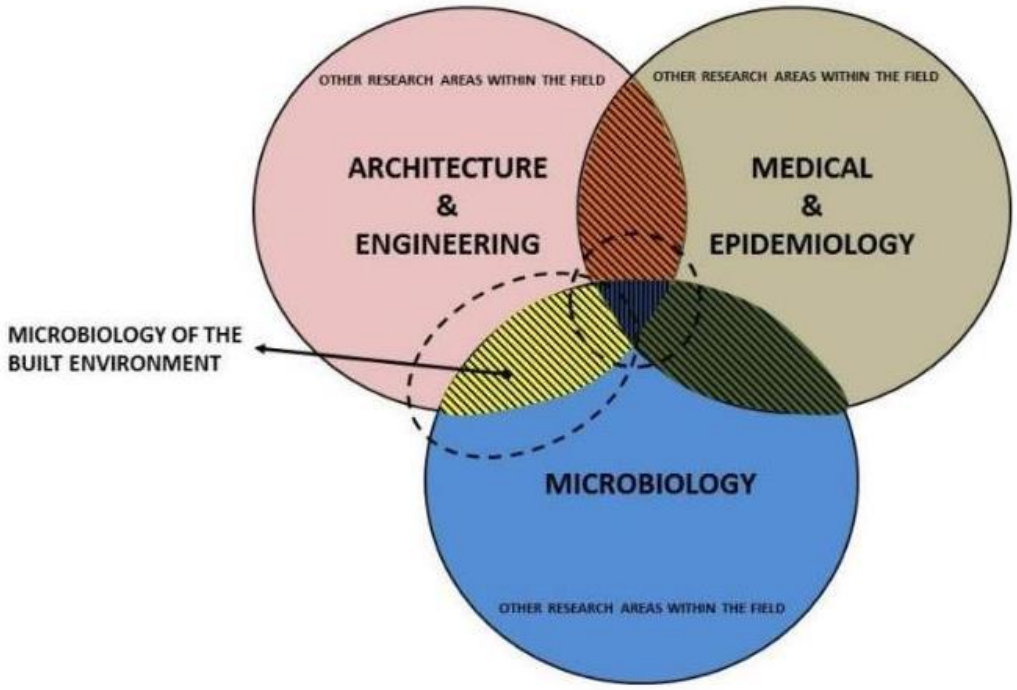



Figure 1: MoBE "ADMRM" research relationship diagram

Architecture plays an important part in this challenge of interdisciplinary studies, not only because of space creation, place making, shelter and human comfort (mostly soft social science investigations in a hard science field) but, as demonstrated in this thesis, by contributing to the study of spatial design. Kembel *et al.* (2014) confirm that the relationship between space use, human flow patterns and functional zones is imperative to understanding and predicting indoor environmental quality. The integration of spatial analytics and microbiome data supports environmental health risk assessment and enables innovative and novel applications in architecture. To understand the research value and current application of spatial metrics and analysis, a literature review on the application and influence of spatial

metrics was conducted and is presented in chapter 3, section 3.3.1: *The microbiology of the built environment for architects: understanding the research field through a review on applied spatial metrics*.

Fundamental to this introduction to the field is the research status quo MoBE report, published in 2017. A brief introduction of pertinent components is supplemented with more detail in chapter 3 under section 3.2. The report *Microbiomes of the Built Environment: from research to application. A research agenda for indoor microbiology, human health, and buildings, was* compiled by the National Academies of Sciences, Engineering & Medicine with contributions from all leading research faculties, units, universities and specialists in the field. It sets out the status of research in MoBE as well as the current research agenda. Publicly presented in October 2017, and officially published as a status document in this emerging field in 2017 (Briere & Resnick 2017), the report is divided into six key sections: 1) Introduction to MoBE; 2) Microorganisms in the built environment: impacts on human health; 3) The built environment and microbial communities; 4) Tools for characterising microbiome–built environment interactions; 5) Interventions in the built environment; and 6) Moving forward: a vision for the future and research agenda. For the purposes of the thesis, it is critical for the reader to be aware of the fact that the state of MoBE research report was published four years after the commencement of this study. It therefore may seem as if many of the findings and approaches the author used were derived from the report; however, the report came after the author had developed the thesis. It is in fact auspicious that the report supports many of this study's goals and objectives, as well as the methodology developed. This is largely because the author was involved in numerous research development discussions with peers through conference special sessions.

The report outlines key global objectives, research gaps and twelve global research focal areas. These have been compiled into three tables referenced here and again for discussion in chapter 3 section 3.2, as well as Chapter 6 under the research investigation methodology (chapter 3 contains the full tables).

Table 1.1: MoBE report: box s-2 and identified knowledge gaps (Briere & Resnick 2017)

| ***MoBE report BOX S-2*** |
|---|
| ***Knowledge gaps identified in this report*** |
| *Improve understanding of the transmission and impacts of infectious microorganisms within the built environment.* |
| *Clarify the relationships between microbial communities that thrive in damp buildings and negative allergic, respiratory, neurocognitive, and other health outcomes.* |
| *Elucidate the immunologic, physiologic, or other biologic mechanisms through which microbial exposures in built environments may influence human health.* |
| *Gain further understanding of the beneficial impacts of exposures to microbial communities on human health.* |
| *Develop an improved understanding of complex, mixed exposures in the built environment.* |
| *Design studies to test health-related hypotheses, drawing on the integrated expertise of health professionals, microbiologists, chemists, building scientists, and engineers.* |
| *Develop infrastructures and practises to support effective communication and engagement with those who own, operate, occupy, and manage built environments.* |
| *Explore the concept of interventions that promote exposure to beneficial microorganisms, and whether and under what circumstances these might promote good health.* |
| ***Knowledge gaps identified in this report, addressed by the thesis*** |

| |
|---|
| *Improve understanding of how building attributes are associated with microbial communities, and establish a common set of building and environmental data for collection in future research efforts.* |
| *Collect better information on air, water, and surface microbiome sources and reservoirs in the built environment.* |
| *Clarify the association of building attributes and conditions with the presence of indoor microorganisms that have beneficial effects.* |
| *Develop means to better monitor and maintain the built environment, including concealed spaces, to promote a healthy microbiome.* |
| *Deepen knowledge on the impact of climate and climate variations on the indoor environment.* |
| *Develop the research infrastructure in the microbiome–built environment–human field needed to promote reproducibility and enhance cross-study comparison.* |
| *Improve understanding of "normal" microbial ecology in buildings of different types and under different conditions.* |
| *Obtain additional data necessary to support the use of a variety of quantitative frameworks for understanding and assessing built environment interventions.* |

(Briere & Resnick 2017:176-177)

In Table 1.1 the knowledge gaps the MoBE identifies are listed, followed by this study's contribution to addressing those gaps. This study's research questions and objectives in Chapter 6 are articulated to produce findings that support the noted gaps and MoBE objectives as identified in Table 1.2. MoBE identifies five core objectives; however, this thesis responds to 1 and 4 and postulates towards 5 (the full table is referenced in chapter 3).

Table 1.2: MoBE: research objectives

| ***MoBE research objectives*** | |
|---|---|
| *1.* | *Characterize interrelationships among microbial communities and built environment systems of air, water, surfaces, and occupants.* |
| *2.* | *Advance the tools and research infrastructure for addressing microbiome built environment questions.* |
| *5* | *Translate research into practise.* |

(Briere & Resnick 2017:78-179)

From the report's twelve focal priority research areas for MoBE captured in Table 1.3, this study examines foci 1, 2, 3, 7, 8, 9 and 12 (the full table is referenced in chapter 3).

Table 1.3: The 12 MoBE focal priority research areas

| ***The 12 MoBE focal priority research areas*** | |
|---|---|
| *Characterize Interrelationships Among Microbial Communities and Built Environment Systems of Air, Water, Surfaces, and Occupants* | |
| **Priority research** | |
| ***1*** | *Improve understanding of the relationships among building site selection, design, construction, commissioning, operation, and maintenance; building occupants; and the microbial communities found in built environments. Areas for further inquiry include fuller characterization of interactions among indoor microbial communities and materials and chemicals in built environment air, water, and surfaces, along with further studies to elucidate microbial sources, reservoirs, and transport processes.* |

| | |
|---|---|
| ***2*** | *Incorporate the social and behavioural sciences to analyse the roles of the people who occupy and operate buildings, including their critical roles in building and system maintenance.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research foci one and two in more detail, with chapter five serving as a precursor to item two. In this thesis the impact that built environment factors have on the microbiome is investigated with the aim to correlate diversity, distribution and proliferation with environmental conditions such as occupancy, space use and flow, and the interdependency of space use, occupancy and flow patterns (the spatial analytics of the indoor environment). | |
| *Assess the Influences of the Built Environment and Indoor Microbial Exposures on the Composition and Function of the Human Microbiome, on Human Functional Responses, and on Human Health Outcomes* | |
| **Priority research** | |
| ***3*** | *Improve understanding of the relationships among building site selection, design, construction, commissioning, operation, and maintenance; building occupants; and the microbial communities. Use complementary study designs - human epidemiologic observational studies (with an emphasis on collection of longitudinal data), animal model studies (for hypothesis generation and validation of human observational findings), and intervention studies - to test health-specific hypotheses.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research focus three in more detail. In this thesis, occupancy and functional space use are investigated through observational methodologies employed in architecture to correlate the spatial analytical findings with the biome findings. Items four and five are not addressed in this study. | |
| *Advance the Tools and Research Infrastructure for Addressing Microbiome–Built Environment Questions* | |
| **Priority research** | |
| ***7*** | *Refine molecular tools and methodologies for elucidating the identity, abundance, activity, and functions of the microbial communities present in built environments, with a focus on enabling more quantitative, sensitive, and reproducible experimental design.* |
| ***8*** | *Refine building and microbiome sensing and monitoring tools, including those that enable researchers to develop building-specific hypotheses related to microbiomes and assist in conducting intervention studies.* |
| ***9*** | *Develop guidance on sampling methods and exposure assessment approaches that are suitable for testing microbiome–built environment hypotheses.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research foci seven, eight and nine. In the thesis a methodology is presented that could be used by multiple studies, that is cost effective, and is viable in developing world environments, as has been learned from various MoBE and related studies accessed through literature reviews. Lastly, a high-level theoretical model that integrates various data sources and fields as introduced in chapter 2 is recommended. | |
| | **Priority research** |
| ***12*** | *Support the development of effective communication and engagement materials to convey microbiome–built environment information to diverse audiences, including guidance for professional building design, operation, and maintenance communities; guidance for clinical practitioners; and information for building occupants and homeowners. Social and behavioural scientists should be involved in creating and communicating these materials.* |

| **Author's comments** |
| --- |
| It is important to note that the subsequent chapters intend to address research applications through providing the first microbiome data set for South Africa. This study aims to implement item 12 by introducing new research to the architecture field. This set is specific to the WC, Cape Flats region in Cape Town, South Africa, and is the characterisation of two public hospitals. |

The fundamental overarching questions asked in the report are: *Which microorganisms are people exposed to in these indoor settings? Which factors control their abundance, diversity, persistence and other community characteristics? And what effects could these organisms have on the health of human occupants?* This report proposes to contribute through a cross-seasonal semi-longitudinal study to the MoBE research agenda and data pool. The need for improved indoor air quality (IAQ) and indoor surface quality (ISQ) in the built environment is evident when addressing public health needs, with particular reference to developing countries like South Africa. The field of architecture is set for a paradigm shift towards becoming an integrated health focus for all building typologies and industries through a microbial perspective, making building design a civic health duty (Brown, Kline, Mhuireach, Northcutt & Stenson 2016). The MoBE research could potentially address the proverbial empirical data gap through bio informed design (Green 2014) in architecture and current architectural health-aligned research. Brown, Kline, Mhuireach, Northcutt and Stenson (2016:2) postulate, *architectural design is poised to undergo a revolution over the next few decades in response to climate change, urbanisation, and population growth. MoBE is a critical juncture of study because humans spend most of their time inside buildings, and the microorganisms encountered there can affect public health… In closing, we reaffirm that architects and other designers are committed to improving occupant health through strategies such as bio-informed design.*

## 1.3 RESEARCH DESIGN

### 1.3.1 RESEARCH METHODOLOGY INTRODUCTION

A medium-term longitudinal study was conducted, spanning two seasons, four days per season. The research investigation included a series of literature reviews and literature summaries with reference to seminal published reviews, which included literature on built environment microbiomes; microbiology sampling, built environment sampling, analysis, sequencing and bioinformatics; ventilation and related models; architecture and engineering, salutogenesis; HAI; building ecology; spatial modelling and analytics; and healthcare architecture (refer to Chapter 3, *Interdisciplinary literature reviews).* The microbiology methodology found in chapter 8 is a structured and integrated literature review, with reference to chapter 3 analysis.

To provide context and background to the field of space syntax and hospital design (in particular Accident and Emergency (A&E) centres, the researcher dedicated two chapters to these topics. They address both the study environment and complexities and the research gap related to spatial metrics and their application in BE MoBE studies. Chapter 4, *Hospitals and Accident & Emergency units,* is the result of normative development by the author on the new Infrastructure Unit System Support (IUSS) healthcare norms and standards for South Africa. Understanding of the complex spatial arrangements and inter and intra departmental relationships is fundamental to the application of spatial analysis for healthcare environments - none more so than those of A&Es. Chapter 5, *Spatial analytics, application for the*

*microbiome,* was developed from the literature review and personal communication with University College London (UCL) staff and GIS specialists. The chapter aims to bring context to the reader on common terminology and methods of spatial measure and analysis, supported by more than 50 documents. The author also investigated complex modelling theory due to the nature of the investigation; this was incorporated into chapter 4. The literature reviewed (including academic papers, theses, dissertations, articles, guidelines, manuals, personal communication and books) exceeded 350 sources.

The researcher composed Chapter 2 at the inception of the study as part of the literature review. This coincided with the early stages of the MoBE research. Personal communications and the attendance of various international conferences, workshops and special sessions provided the author with insight into the development of the field, as well as research gaps and opportunities. Chapter two's framework must be viewed as the author's investigation into, and vision for, a "new" field of research, with specific interest in architecture and risk modelling focused on practical outcomes through design guidance. The framework was updated based on the dynamic stages of MoBE investigation at the time; however, the fundamental systemic approach stays relevant. The framework compares itself to a proposed mechanistic framework derived from leading researchers, as described: *Unites a material-balance approach of engineering with the ecological concept of metacommunities, which both seek to track the sources and sinks of a constituent in a system. A material-balance approach draws on the principle of conservation of mass to track the material (typically a pollutant), entering and leaving a system, while in ecological theory, metacommunities considers sets of local communities linked by the dispersal of organisms. We propose this integrated framework, which combine principles of particle transport and microbial demographics, to inform how microbiomes of indoor environments assemble to generate indoor microbiome patterns observed across a variety of settings* (Adams, Bhangar, Dannemiller, Eisen, Fierer, Gilbert, Green, Marr, Miller, Siegel, Stephens, Waring, & Bibby 2016:225). The Architectural Design Microbial Risk Model (ADMRM) framework and long-term vision agenda has been compared to the research agenda presented in 2017 (Briere & Resnick 2017) by the MoBE community. This included a research map for future work and the development of a core model, intended as design tools for BE professionals and building scientists, and for creating an architectural design microbial risk model (ADMRM). It is imperative that for each field of study in this interdisciplinary research the researcher develops clear and sound methodology, including microbiology, environmental and spatial observation. The methodologies, which are described in detail in Chapter 7, Chapter 8 and Chapter 9, consider the following criteria defined in Table 1.4.

Table 1.4: Methodology criteria

| **Chapter 7 Architectural space modelling by observation** | **Chapter 8 Microbiology** | **Chapter 9 Environmental data collection** |
|---|---|---|
| | Guidance developing a sampling strategy and sampling plan | Mechanical characterisation (sub set of methodologies) |
| Pre-sample testing | Study zones and room types | Pre-sample testing |
| Sample types | Microbiology methodology overview | Sample types |
| Sampling duration | Site sample sterilisation protocol | Sampling duration |
| Sample size | Pre-sample testing | Sample size |
| Analysis | Sample environments | Analysis |
| Delineations of the experiment | Sampling duration and media | Delineations of the experiment |

| Observational questionnaire | Sample size | Observational questionnaire |
|---|---|---|
| | Sample storage | |
| | DNA extraction | |
| | Sequencing and bio-informatics | |
| | Analysis and sequencing processing | |
| | Culture sample analysis | |
| | Delineations of the experiment | |

A rigorous ethics approval process was conducted (refer to addenda 5) for approval by the University of Pretoria's (UP) EBIT and other faculties, the University of Cape Town (UCT), Western Cape Department of Health (WC DoH), the National Research Council and the research and ethics committees of the two hospital sites. All parties granted and approved research access. The investigation affected procurement challenges, resulting in an estimated 10-month delay, rolling over the sampling date from 2016 to 2017.

### 1.3.2 RESEARCH METHODOLOGY MAIN

Literature analysis and peer engagement started in 2014. The observational and environmental methodologies were tested in a pilot study conducted in June 2015 at both hospital sites. In September 2016, a microbial pilot sampling was done for air and surfaces and collected in the CMEG laboratory at Pretoria University to test the equipment, establish protocols and test methodologies. This was followed by a full system mechanical characterisation for both sites in November 2016. During the mechanical system characterisation, a research questionnaire was circulated and completed by the hospital staff at both facilities, forming part of the environmental and observational methodology as finalisation of the methodology development. The first sample set was taken in the summer of January 2017. This included all three data sets. The second set was completed in the winter of June 2017.

The sampling included simultaneous data collections by room sensors ($CO_2$, relative humidity and temperature) at both facilities. Samplers were calibrated externally for 5 minutes and then placed in matching room types with matching room heights. The samplers ran simultaneously for the total duration of the sample period, sampling at 1minute 30second intervals. A once-off illuminance measure for each room was captured per facility. The illuminance sampling was done once consecutively within an hour for both hospitals as only a single Lux meter was available. Two technicians, one per facility, performed the Architectural spatial informatics via observation analysis. A route mapped out for each facility included the same and additional zones as per the environmental samplers. The technician per room took two sampling measures: a *Mental snap shot* for an occupancy measure and a *Movement tracer* for a people flow measure. The technician recorded the instant occupancy value of the space defining user type and position on a drawing plan and thereafter the technical recorded user flow identifying type and flow for a period of three minutes on a drawing plan. The number of observations per hour varied due to practical operational restrictions by the hospital; however, there was an average of 18 sheets over the 12 hours of observation.

Simultaneous microbial sampling for air and surfaces was completed in the same 12-hour period as the observational sampling. Sampling started with a 30 minutes outdoor air sample, approximately 15 meters away from the hospital building in the adjacent garden. This was followed by a 60-minute room sampling placed in the centre of each room approximately

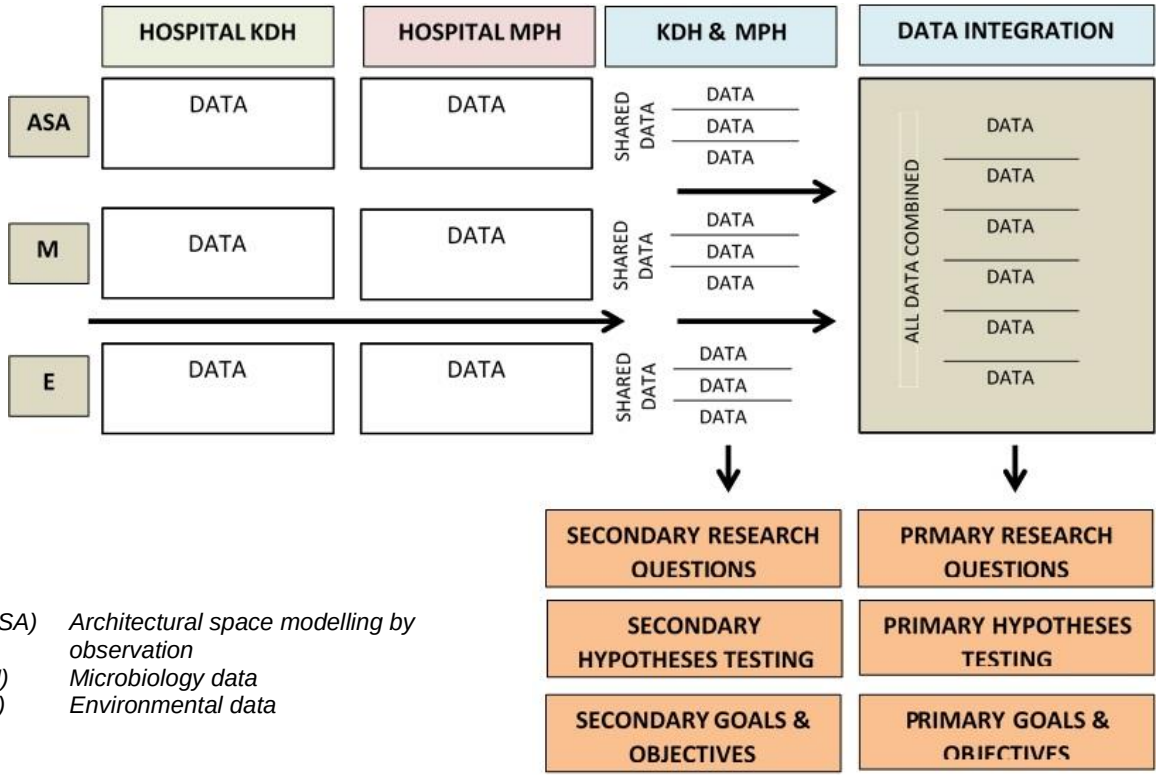
1200mm above the floor for the same eight rooms with environmental samplers and observational sampling, and completed with another 30-min outdoor sample in a different location approximately 15 meters away from the hospital building in the adjacent garden. With every air sample, two surface samples were swabbed on various surfaces, one for culture, the other for sequencing. In addition, one additional air sample was taken per day in a different, matching room location at each hospital for culture analysis. The sequence of rooms was constant unless operational restrictions forced a room order change (this did occur, i.e. death, emergency stabilisation, room occupied). The environmental measures, observational sampling and microbial sampling were done in "near" real time. Samples were stored on site at 0-4 degrees Celsius, subsequently in the freezer at -10 degrees Celsius, and finally in the laboratory at -20 degrees Celsius. This methodology was repeated in both summer and winter for each A&E department simultaneously (one air sampler per hospital and one observational technician per hospital) for the same room types over the same period daily and seasonally. Post sampling, data from loggers, observation data and microbial samples were kept and the data captured and stored on multiple drives and servers.

The air samples were captured in liquid by impingement; it was found that direct DNA extraction yielded to low biomass for PCR or sequencing, consequently samples first had to be filtered and then the filters had to be dissected and DNA extraction performed using a power soil kit. The microbial samples DNA extraction was done, followed by Nanodrop for protein quantification and thereafter, horizontal electrophoresis for 35 minutes to determine an estimate DNA resolution (due to low biomass expected, as reported for indoor environments). One hundred samples were PCR amplified to check acceptable levels of DNA, and then sent to the USA for microbial metagenomics DNA sequencing by 16SrRNA after sampling in the CMEG laboratory. The samples were sent for sequencing in two batches. The author conducted the DNA extraction, PCR viability, electrophoresis, Nanodrop and QIIME processing (supported by CMEG staff and Dr Angel Valverde). The raw sequences were processed using QIIME and further downstream analysis was performed. Statistical analysis was done through the phyloseq package for R.

The architectural observation data were collected on drawing plans through computer-aided design (CAD) software and geographical information system (GIS) software, followed by DepthMap™ (Space Syntax) software for modelling and analysis. Sample sets were recorded on a master data table (addenda AD 1), categorised by sample ID and 40 sub categories of factors for analysis in R. Gaslab™ Software captured and Microsoft™ Excel processed Environmental Logger data (T, RH and $CO_2$). The sample sets were recorded on a master data table (addenda AD 1), categorised by sample ID and 40 sub categories of factors for analysis in R. The analysis for all factors as per the master data set and the microbial data set was performed in R, environmental correlations were performed in Excel, and spatial correlations were performed in Depthmap. The detailed description of the methodologies can be found in Chapter 7, Chapter 8 and Chapter 9.

Figure 2 is a graphical representation of the route for data synthesis for the different fields and hospitals. The dataset for each field is formulated into a single dataset, and categorised. The data are captured for each hospital and analysed individually. The hospital datasets are then compared and findings presented. The findings, or rather the correlations and comparisons of the relevant factors as guided by the research questions, are then tested. Some datasets have been tested and reported for only the individual hospital; however, most of the findings have been presented based on the combination of both hospital datasets. A randomised 175

microbial samples and their related BE factors have been analysed for most findings in chapter 9 and interdisciplinary findings as reported in chapter 10. Finally, the hypotheses are tested based on the answers to the research questions, and the achievement of the research objectives determined.




*(ASA)* *Architectural space modelling by observation*
*(M)* *Microbiology data*
*(E)* *Environmental data*

Figure 2: Applying the research methodology – a process diagram

### 1.3.3 DOCUMENT OUTLINE

Chapter 1 introduces the research investigation and provides context to the research problem statement and hypotheses, along with the primary research questions to test the hypotheses. This is followed by a more detailed background divided into three main sections. 1) HAI in South Africa, 2) TB, HIV AIDS and HAI in South Africa and 3) an introduction to the MoBE field, with reference to the MoBE report. The research design is described per chapter, followed by the methodology followed for the full investigation from inception to submission. The chapter on the research outline is completed by noting the various limitations and delimitations of the study. Chapter 2 steps back and considers the global viewpoint and direction of the MoBE field, by presenting a framework with practical application to BE professionals. This chapter intends to provide the broader perspective and direction of the MoBE field. Chapter 3 delves into the literature reviews on key topics, starting with a more defined summary of the seminal piece, the 2017 MoBE report introduced in chapter 1; this is followed by a critical literature review of MoBE and the BE, with specific focus on spatial metrics for architects. This review with findings, research gaps and future study proposals lays the foundation for the chapter 6 research investigation and chapter 10 conclusions. A further review on sampling in the BE - both environmental and microbial - is reported on. The literature that is considered, reviewed and referenced throughout the thesis completes this chapter.

Chapter 4 investigates the healthcare environment and unpacks the hospital architecture and complexity, specifically the accident and emergency unit. It provides background to the study in support of the findings. Chapter 5 examines spatial analytics in architecture and its novel application in the microbiome study field. It provides background to terminology, methods and spatial analysis in support of the findings. Chapter 6 outlines the detailed research methodologies, expanding on the introduction in chapter 1. Chapters 7, 8 and 9 report individually on each applied study field: observation (spatial analytics), microbiology and environmental factors; these include detailed methodology, analysis and findings.

Chapter 10 brings it all together, reporting not only on individual relevant findings, but also on the synthesis of all three field metrics and the impact on architecture as postulated in the hypotheses for the hospitals investigated. Chapter 11 provides future recommendations and research opportunities.

### 1.3.4 DELIMITATIONS

- The results of this investigation are delimited to hospital environments in the Cape Flats region, Western Cape.
- This study was limited to the A&E departments at both hospitals. The investigator accepted that the fluid nature and varying degree of patient activity are in fact representative of both the outpatient and inpatient, as well surgical and medical, units.
- The mechanical ventilation systems of both hospitals were characterised prior to sampling in November 2016. The data for the characterisation were utilised as normative for all samples. No post-completion characterisation was conducted (refer to section 9.2.1).

### 1.3.5 LIMITATIONS

- Because of on-site equipment failure on the final day of the summer season, sampling for MPH had to be conducted at night, but for the same period and with the same methodologies. This was repeated in the winter season for replicability. In addition, due to equipment failure in the winter sample season, all the sampling, excluding the final day at KDH, was conducted at night. Observation sampling was done in both day and night sample sets.
- Due to the hospital environment being operational at the time of sampling, care needed to be taken to not affect day-to-day activities. This led to occasions on which the sampling order was amended when rooms were not available because of a dead body being held there, severe trauma incidents, psychiatric patient control, etc.
- Owing to funding limitations, this investigation only considered bacteria. Due to the nature of, and challenges in, testing for viruses (using 16S rRNA sequencing) and running separate ITS sequencing for fungi, the investigation was limited to bacteria isolation. The culture samples identified fungi, but these were not included in the bioinformatics results.
- Lastly, due to cost restrictions only 16S rRNA sequencing was conducted.

# CHAPTER 2 TOWARDS AN ARCHITECTURAL DESIGN MICROBIAL RISK MODEL

## 2.1 INTRODUCTION

In a recent review of MoBE studies, Adams *et al*. (2016) propose a framework to deal with interpreting different studies, in particular studies that are interdisciplinary, considering engineering and architecture factors with those in microbiology. They postulate a "mechanistic framework that combines a material-balance approach of engineering with the ecological concept of metacommunities… both seek to track the sources and sinks of a constituent in a system". This framework considers tracking mass, entering and leaving a system, whereas metacommunities are a set of local communities linked by dispersal of organisms. They argue that the demographic parameters in metacommunities have direct similarities to those of the material-balance approach. The similarities in the principles are those of measurable factors entering and exiting a system that directly affect either the community (by birth, death, etc.) or the aerosol (filtration, deposition, etc.). This proposes a manner in which factorisation can occur to predict across fields within a shared framework. In the same way that the researchers identified a common challenge of factorisation, and the dissemination of field data to enable system definition or system modelling for prediction, the author of this thesis considered the need for a framework in which to place architecture and the BE and identify factors and measures within a global framework.

The author postulated a mechanistic theoretical framework in which to place design, planning and architecture as a component of the system, with the end goal to develop a design tool to assist practitioners and researchers towards "bio informed" design and risk factorisation. The interdisciplinary diversity of the field makes this a particularly challenging task. The author by no means suggests that the proposed framework or later version thereof is resolved or fully developed. The wire diagram recommends core inputs and suggests critical paths and practical outputs that it puts forward.

The rate at which the MoBE field knowledge has grown demands a clear roadmap and framework, be this a mechanistic metacommunities-quasi-material balance approach or other. As part of venturing into the MoBE field (2014), the author suggested a micro and macro approach, due to the scale of processes and systems. The framework referenced in Figure 3, Figure 4 and Figure 5 provide a structure for research development and contribution to the MoBE field, but with the focus on health risk in indoor environments.

## 2.2 ORIGINAL PROPOSED THESIS MOBE RESEARCH ROADMAP

At project level for research investigations, the author proposed a macro and micro research process as a means of contributing to the research roadmap.

### 2.2.1 MOBE RESEARCH ROAD MAP THESIS PROPOSAL 2014

The research roadmap (Figure 3) was initially developed to illustrate the potential relationships between parties, within research fields and geographically. It merely structures input variables in the system that either exist or are novel systems yet to be developed. It considers the four core fields of study and the set of variables in the matrix that each field contributes. It recognises the various methodologies for data collection and the central role that they would play. This section covers the matrix for architectural indicators and spatial metrics. The

framework hinges on interdisciplinary study collaboration. This is a rudimentary global study framework conceptualised in 2014, to assist the author in finding context within MoBE, and for architecture. The MoBE research road map offers a broad, inclusive and open approach towards developing public health centred design and bio-informed design. It recognises the critical role of funding and institutional role-players. A feedback process loop is required to generate interest, build confidence, show outcomes, and inform the broader public on emerging findings. The roadmap identifies the need for interdisciplinary research collaboration amongst the disciplines of microbiology, epidemiology, medical archetypes and engineering. Each of these disciplines boasts numerous theoretical models and sample methodologies, and needs metadata studies to disseminate and identify gaps. The research repository for MoBE has been established (as is currently done through (microBEnet). From the metadata studies a matrix of architectural and engineering indicators and variables can be developed.

A variety of broad-based studies, both short-term and mostly longitudinal, will be required, as well as focused studies to test and develop the matrix and identify the nature of the variables. This is a cyclical approach and each study should support the matrix, which informs and develops the ADMRM. In addition, field case studies, model validation, HAI database development and constant methodology improvement and guidelines are necessary to ensure repeatability of studies that could form cross comparisons. To ensure that the findings and applications have an impact on and influence the public health domain and authorities, this roadmap envisions ecological adaptations with continental and intercontinental studies, localised climate studies, localised sub-climate studies, socio-economic diversity studies, and intra-urban and rural data sets. The roadmap (Figure 3), although elementary, considers the complex inter-relationship between disciplines.

Much of what has been described and put forward as a potential road map in this thesis represents research done over the past four years, and is testimony to the shared approach within the MoBE community of the needs and challenges, opportunities and relationships that have to be developed and cultivated.

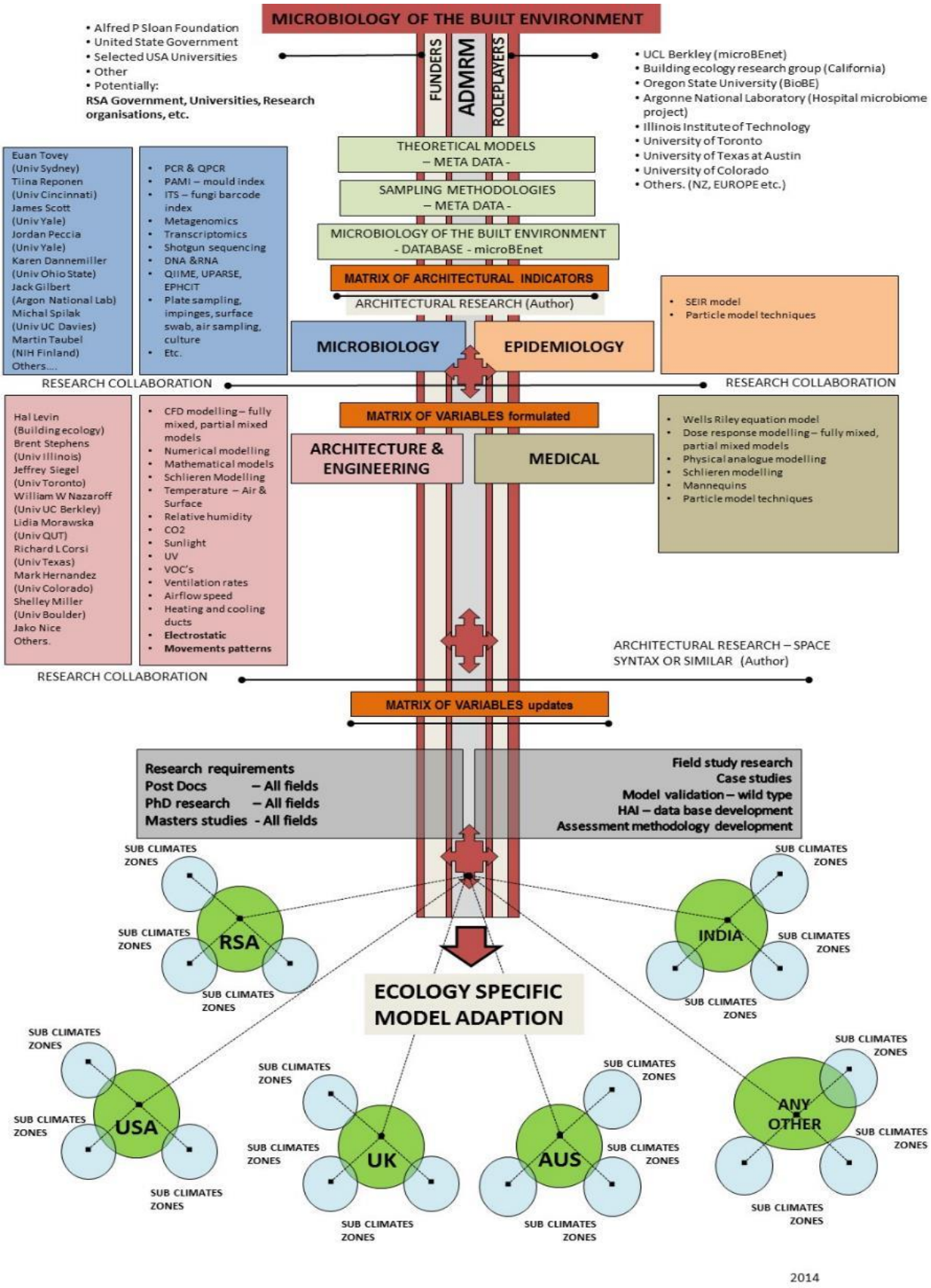



Figure 3: ADMRM framework diagram and MoBE research road map developed in 2014

### 2.2.2 The Architectural Design Microbial Risk Model (ADMRM)

The ADMRM (Figure 4) depicts the central repository of data, research and development for the MoBE research roadmap. It could become the platform for depositing and nurturing findings and data studies, expanding the field of knowledge but making it applicable and implementable. It aims to serve as practical tool to disseminate data that inform BE scientists, BE specialists, architects, engineers, IPC specialists, HCWs, hospital managers, industry, government and other policy makers.

This tool will combine complex data sets and translate indicators into application. The goal is to provide real-time measures for designers to inform decision making before the construction of healthcare facilities. It promotes bio-informed design for healthier indoor environments. The elements discussed in the macro and micro processes are the building blocks for the tool. The platform should be BIM-based to allow for computational modelling in real-time, to afford potential agent-based analysis for typology-specific environments or function-specific programs, not only in the healthcare sector, but also for public buildings, civic centres, sports halls, offices and homes, both temporary and permanent.

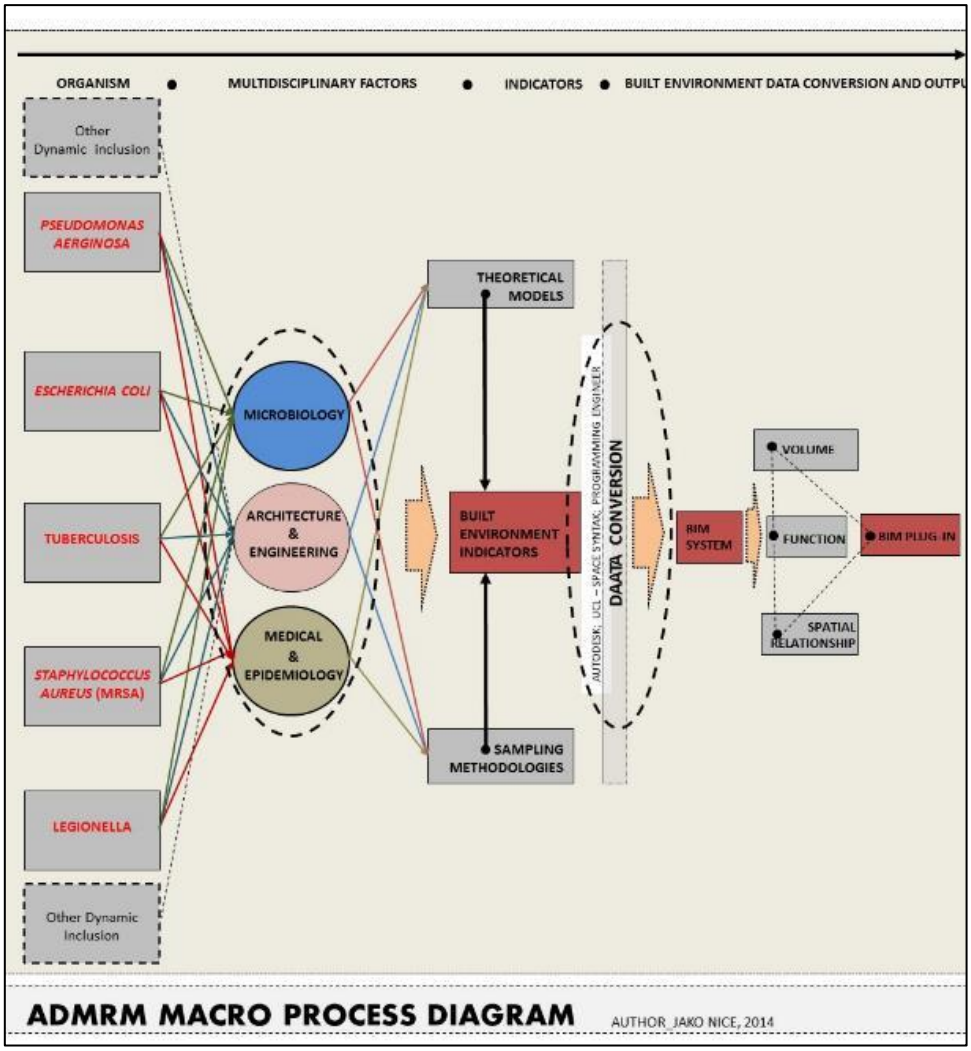



Figure 4: ADMRM macro process diagram developed in 2014

### 2.2.3 MICRO RESEARCH PROCESS PROPOSAL

Figure 5 presents the micro MoBE research diagram that refers to specific BE architectural and engineering components. The flow process considers “input constants” that are found universally in the built environment, i.e. room types, building typologies and building types. This is followed by built environment constants such as volume, function and spatial relationships (note the interrelationship between the macro and micro process feed). These data are disseminated into architecture and engineering “built environment indicators”, i.e. temperature, RH, surface material, UV, climate and others and then combined with interdisciplinary factors (sampling methodologies and models) for microbiology, medical and epidemiology indicators. The conversion of the macro data is then applied and integrated into BIM platforms, as mentioned in the macro process diagram. This process is cyclical, creating fluid boundaries and allowing for novel research approaches and the inclusion of new factors. The process considers the various potential indicators or factors such as temperature, RH, surface material, equipment, $CO_2$, ventilation sunlight, spatial factors, etc. This micro process diagram serves as a theoretical approach to investigate building by room type data for input into BIM applications as a design tool or dissemination of information in developing data for design tools.

## 2.3 NEW PROPOSED RESEARCH ROADMAP

This roadmap considers the ADMRM macro Figure 4 and micro Figure 5 process diagram as data generators for the roadmap. The research findings provided critical direction for further investigation and studies required to expand the MoBE data sets of knowledge and factors influencing the built environment microbiome. The findings of this study and those of other research studies point to a complex relationship between BE factors and microbial ecosystems. The data confirmed that biomes not only change seasonally in the built environment, but that the built environment also experiences seasonal variations. The spatial data indicated factors of spatial change in occupancy, flow patterns and functional use of spaces and the building program. The building climate factors, such as temperature, relative humidity and $CO_2$, showed seasonal variations. The microbial communities present in the air and on surfaces evidenced seasonal variation, and the biomes by room type indicated seasonal variation in genera and their relative abundance; thus one can infer that the complex interrelationship between a “fluid” built environment, a “fluid” spatial environment and a variable ecosystem requires more research. Sampling for the study directed a broader architectural focus by associating spatial patterns, BE factors and microbial community indicators. It is evident from the results that it was of local importance that the study be conducted, as it confirms previous international MoBE study results, as well as methodology applications. But it also indicates that a critical area of investigation is the notion of sample threshold, for both BE factors, microbial samples, and the niche role spatial metrics. The study demonstrates that focused interventional studies are required to understand the complex relationships between BE factors and the microbial environment. It is evident that BE factors do play an influential role, but this study could not determine at which scale, of which type, or how much of each type played an influential role in the composition of the indoor microbiome (excluding ventilation).

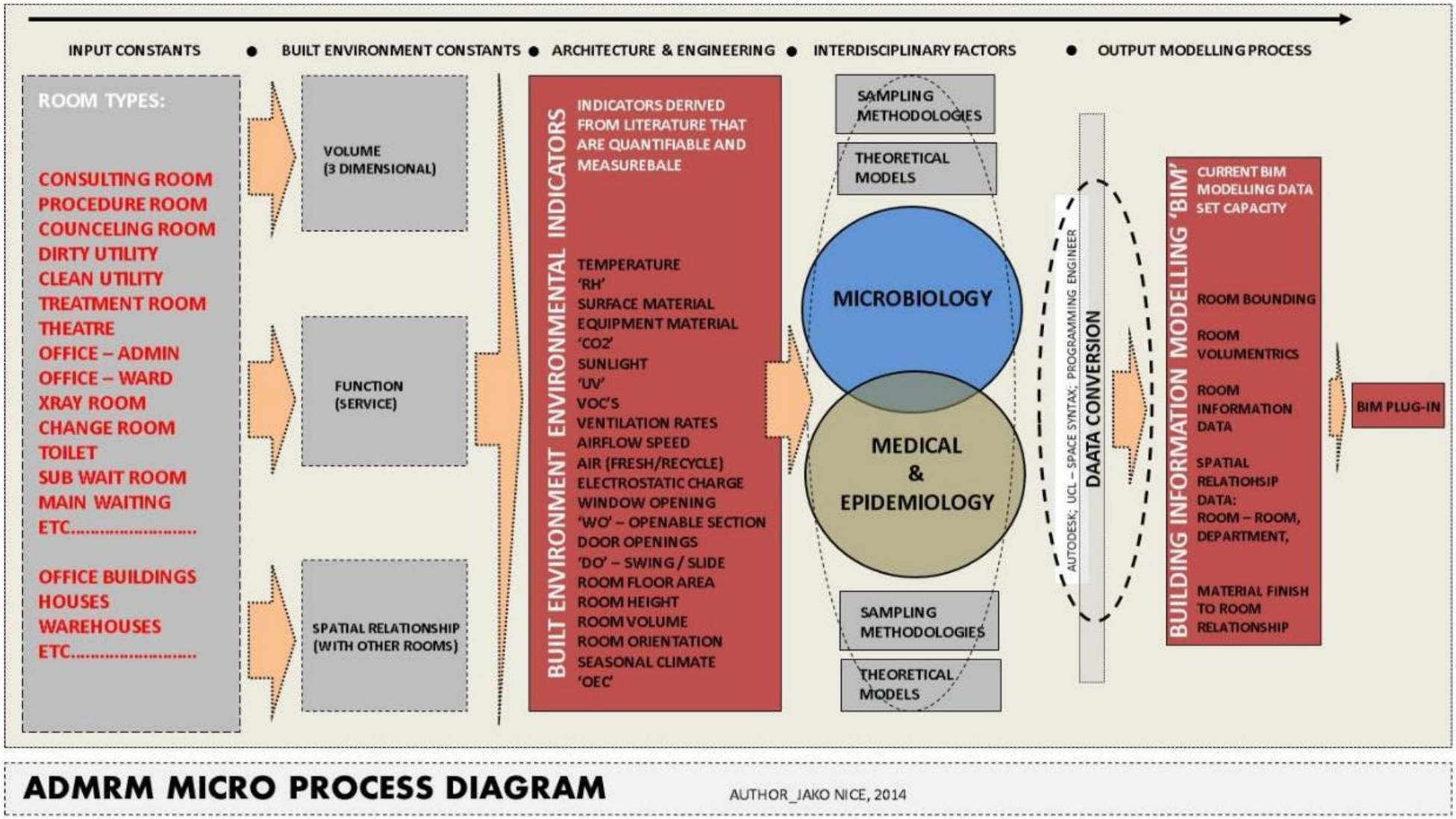



Figure 5: ADMRM micro process diagram developed in 2014

The research indicates that the broad macro-scale investigation is critical, as found by Lax *et al.* (2017), to determine the next level of required data and data thresholds. In the context of the microbiome, the macro spatial planning network indicated spatial core and isolation flow and functional variation; however, it can be inferred from the data that the size of the microbial sample needs to be increased and dynamic temporal factors are at play (spatial analytic findings presented in chapter 10). This study indicates that total hospital or building characterisation is appropriate, but a micro level of investigation should follow. The research findings suggest that one of two studies needs to follow this investigation. The first is a study repeating the same methodologies, but for two different hospitals in two different provinces and climatic zones, that will contribute to the current findings. Conversely, a more in-depth study in the same hospital environments with focused sample collection in limited rooms and with multiple daily microbial samples could provide guidance as to influential BE factors (niche based focus). The number of BE data points will always outweigh microbial data sample collection; however, it is critical to determine the critical mass of MoBE studies. The optimum extent of sample size and BE data is still undetermined. More studies, longitudinal and short-term, micro and macro, will be required to determine this threshold of influence in the indoor environment. The research map requires a balance between focused interventional studies and broad biome studies as presented in this thesis. The micro-focused studies need to isolate factors and determine direct influences, such as investigating the Triage Consult 1 room through multi-point air sampling daily and seasonally, single area swabs with multiple swabs daily and seasonally, and multiple sensors collecting BE data and spatial use and occupancy patterns. This methodology will track localised biome variations over the course of multiple days, combined with a record of BE variations. The macro studies require completion of the same study in two different climate zones at two different hospitals, to inform seasonal variations by climate and total varied design by planning. The value of such a study will only be relevant if focused or multiple-focused intervention studies are conducted at the same hospitals. Areas of investigation should include:

1. Identifying the threshold of the microbial sample size
2. Isolating BE factors and determining singular influence (only temperature, only RH, only surface material, etc.)
3. Extensive comparative studies on varied hospital designs (as in this thesis)
4. Niche environments
5. Hospital design studies in varying climates
6. Diverse social demographic studies
7. Consistent unit-based studies for comparative purposes (wards, A&E or outpatients only)

## 2.4 APPLICATION

Apart from further developing the ADMRM tool for application in the built environment, the thesis presents a potential methodology for IPC assessment that will not only inform potential designs and evaluate existing designs, operational changes and spatial reconfigurations, but also contribute to the data repository for the ADMRM tool. Numerous infection prevention control (IPC) risk assessment tools exist, developed by the Council for Scientific and Industrial Research (CSIR), Centre for Disease Control (CDC), World Health Organisation (WHO), Department of Health (DoH), National Health Laboratory Services (NHLS), National Institute for Occupational Health (NIOH), and non-government organisations (NGOs). These tools address IPC holistically and some are highly focused, such as for TB and airborne infection control; however, the element of spatial assessment is absent in the majority of assessment

methodologies (only four present in all studies - refer to chapter 3) and it is, if included, very rudimentary. The methodology and findings of this study provide evidence to suggest a spatially analytical informed assessment methodology, i.e. the **6 step +1 MoBE analysis tool**. Derived from the thesis methodology and informed by the results, the following steps constitute a framework for this tool:

1. Model the building plan in GIS and DepthMap™ or other spatial relationship syntax programs that consider the factors of integration, connectivity and mean depth
2. Observe in real time the assessment area of the environmental study by count, beam brake, Rfid, heat sensors or other tools of identification
3. Verify the model and note the variations of space use through analysis and observations
4. Overlay the building data for each room within the analysis area
5. Add in the microbial data based on the samples collected (air and surface) of indicator species, OTU abundance for the room and richness of genera, and sample type (source)
6. Apply appropriate IPC methodologies based on the risk factors found to inform maintenance and operational and cleaning policies

   Alternatively, as proposed: +1

7. Make design changes and test these through agent-based simulation modelling, then reassign the sample data to the rooms and review the location variations for factor changes or IPC simplification in application

# CHAPTER 3 INTERDISCIPLINARY LITERATURE REVIEWS

## 3.1 LITERATURE REVIEW METHODOLOGY

A large quanta of literature was reviewed over the course of this investigation. Additional literature concerning spatial analytics, hospital design and A&E departments, microbial fall out and complex modelling literature. The diverse literature reviews started in 2013 and formed part of an ongoing literature data collection and reference document to guide the author on methodologies, practice and analysis.

The disassociation of the current body of literature dedicated to multi-disciplinary work relating to microbiology, architecture and healthcare (medical research and epidemiology) is due to the isolation of each discipline. Each of these fields has focused research groups with specific research objectives. It became apparent during the development of this thesis that an integrated and inclusive multidisciplinary perspective is required. MoBE represents this integration and knowledge sharing. In this chapter there is one report review summary, with two literature reviews and two literature summaries for literature referenced in the thesis. They endeavour to present the current research position of each field and in context to the MoBE study field, identify key concepts and critically look at the gaps presented in each field of study to identify shared interest, which to date has not been reported.

The literature reviews comprised a combination of ”research themes” and “focused methodology” investigations, intended to be both focused identification and investigative. The key topics of the reviews were MoBE, microbiology and medical; engineering; architecture; sampling; space syntax; and complex modelling. The following are key focus areas under each theme, including methodologies:

1. Microbiology:
    - TB, NTM, PCP, microorganisms in the built environment, quorum sensing and biofilm, indoor and outdoor communities
2. Engineering:
    - Ventilation mechanical, ventilation natural, models and methods, CFD, sensing technology, built environment factors, climate
3. Architecture:
    - Nosocomial/HAI, microbial environment, building ecology and materials (CU), spatial planning, healthcare environments, health, MoBE reference architecture studies
4. MoBE:
    - MoBE studies and architecture or building design themes (due to the newness of the field, they are few in number) including the MoBE report
5. Sampling:
    - Microbial and built environment sampling, sequencing, surfaces, air, communities, analysis, bio-informatics
6. Space Syntax:
    - Healthcare, sampling, analysis, programs, building, space
7. Complex modelling:
    - Interdisciplinary research and approaches

The literature search methodology employed made use of the following online research databases: Scopus, ISI and Google Scholar. The architecture research specialists of the University of Pretoria library provided keyword searches and initial research support. In addition, the CSIR and the building ecology workgroup (UC Berkley) made the database

resources available. Books, journal articles, theses, dissertations, papers and personal communications were scrutinised. The following themes and keyword searches were done:

1. Microbiology of the Built Environment (MoBE)
    - MoBE, architecture, bio informed design, building ecology (see section under architecture)
2. Complex modelling
3. Microbiology and Medical
    - TB, NTMb, PCP, Biofilm persistence, microbe aerosolisation, quorum sensing, surfaces, airborne, pathogenic bacteria, competitive exclusion, nosocomial infection, hospital acquired infection, sampling, epidemiology, HIV and Aids, immune-compromised patients
4. Ventilation
    - Mechanical ventilation, natural ventilation, airflow analysis, CFD, air changes, measurement testing, statistical analysis, airborne risk
5. Architecture
    - Hospital design, building ecology, microbial environments, case studies, sick building, HAI, syndrome, sanatorium, pro-biotic environments, regulation, policy, building standard, space syntax, materials
6. Sampling methods
    - Environmental sampling, microbiology sampling, built environment, biome

For this thesis a MoBE based built environment study was undertaken at two hospital buildings in South Africa. The methodologies and findings of similar studies were accessed and explored through literature reviews, conference attendance and peer discussions. In summary, this chapter includes one report review summary, two literature reviews and two literature summaries for literature referenced in this thesis. The literature was formulated by topics into Excel sheets and disseminated to the various reviews. The reviews and knowledge gathered from, but not limited to, the above sources guided the thesis investigation. The index below offers page and section references.

(1) MoBE status report 2017 (pg.43_3.2)

(2) Microbiology of the Built Environment (MoBE) (pg.59_3.3)

(3) Built environment and microbial sampling (pg.75_3.4)

(4) Microbiology and Medical, the built environment and health (pg.75_3.5)

(5) Architecture and Engineering in the built environment (pg.93_3.6)

## 3.2 MoBE STATUS REPORT 2017 (REVIEW 1)

Briere and Resnick's (2017) report is categorised into six key sections: 1) Introduction to MoBE; 2) Microorganisms in the built environment: impacts on human health; 3) The built environment and microbial communities; 4) Tools for characterising microbiome-built environment interactions; 5) Interventions in the built environment; and 6) Moving forward: a vision for the future and research agenda. For the purpose of this thesis, only directly relevant and essential information that will provide context and significance to this study within the greater research agenda is noted. Where applicable, the potential thesis contribution is stated, supported in further detail in later chapters. The MoBE report is essentially a literature summary and critical review by numerous authors in the field; for that reason, the author will only highlight aspects of the report along with a the specific literature review of MoBE.

### 3.2.1 MoBE REPORT IN REVIEW

We cannot yet characterise or define a "healthy" indoor environment, or fully understand how to process the various known and unknown dynamic factors involved. Indoor environments are complex by nature, are extremely integrated, dynamic ecosystems, and require a vast interdisciplinary field of researchers: microbial biologists, ecologists, chemists, building scientists and human psychologists. The more we understand these environments, the closer we get to improving, operating and designing indoor environments that enhance human health. Essentially, as the report suggests and in accordance with the author's deductions, these are the questions we face: 1) Which microorganisms are people exposed to in these indoor settings? 2) Which factors control their abundance, diversity, persistence and other community characteristics? 3) What effects could these organisms have on the health of human occupants? The MoBE research community identified the need to collect a core set of building, environment, and occupant data when studying indoor microbiomes, which does, however, still require further development, consensus and agreement. The balance between sufficient information, financial resources and time is yet to be achieved. Complex models that represent the various factors, i.e. environmental inputs, social inputs and health outcomes, still have to be developed. The complex social and medical data associated with health-related concerns, such as the burdens of microbial diseases, energy costs and united health effects, need to be considered and incorporated; an important area of sub-study is the social and behavioural sciences. This thesis has set out to address this research gap, along with other related opportunities noted under the research knowledge gaps as shown in Table 3.1 below. The table is an excerpt from the report. Items that are identified and responded to in this thesis are noted under the heading: *MoBE knowledge gaps identified in this report, addressed by the thesis*.

Table 3.1: MoBE report: box s-2 and identified knowledge gaps (Briere & Resnick 2017)

| ***MoBE report BOX S-2*** |
|---|
| ***Knowledge gaps identified in this report*** |
| *Improve understanding of the transmission and impacts of infectious microorganisms within the built environment.* |
| *Clarify the relationships between microbial communities that thrive in damp buildings and negative allergic, respiratory, neurocognitive, and other health outcomes.* |
| *Elucidate the immunologic, physiologic, or other biologic mechanisms through which microbial exposures in built environments may influence human health.* |
| *Gain further understanding of the beneficial impacts of exposures to microbial communities on human health.* |

| |
|---|
| *Develop an improved understanding of complex, mixed exposures in the built environment.* |
| *Design studies to test health-related hypotheses, drawing on the integrated expertise of health professionals, microbiologists, chemists, building scientists, and engineers.* |
| *Develop infrastructures to support effective communication and engagement with those who own, operate, occupy, and manage built environments.* |
| *Explore the concept of interventions that promote exposure to beneficial microorganisms, and whether and under what circumstances these might promote good health.* |
| ***Knowledge gaps identified in this report, addressed by the thesis*** |
| *Improve understanding of how building attributes are associated with microbial communities, and establish a common set of building and environmental data for collection in future research efforts.* |
| *Collect better information on air, water, and surface microbiome sources and reservoirs in the built environment.* |
| *Clarify the association of building attributes and conditions with the presence of indoor microorganisms that have beneficial effects.* |
| *Develop means to better monitor and maintain the built environment, including concealed spaces, to promote a healthy microbiome.* |
| *Deepen knowledge on the impact of climate and climate variations on the indoor environment.* |
| *Develop the research infrastructure in the microbiome-built environment-human field needed to promote reproducibility and enhance cross-study comparison.* |
| *Improve understanding of "normal" microbial ecology in buildings of different types and under different conditions.* |
| *Obtain additional data necessary to support the use of a variety of quantitative frameworks for understanding and assessing built environment interventions.* |

The report that follows describes the complexity of the indoor biome: *The built environment interacts with the indoor microbiome in multiple ways that affect humans. Microbial exchange between indoors and outdoors, microbial growth and persistence in indoor settings, and human exposures to indoor microbial communities are affected by building design, operation, and maintenance. Research that focuses only on one microbe, on a specific aspect of building design, or on a single human health outcome will not be sufficient to understand these multifactorial relationships (*Briere & Resnick 2017:8*).*

#### 3.2.1.1 MoBE REPORT MULTIDISCIPLINARY RESEARCH AGENDA

It is evident that integrated, interdisciplinary and cross-disciplinary research is required. The MoBE report in *Box S-3: A Research agenda for moving to practical application,* suggests the future agenda and focus areas for cross-disciplinary research. In Table 3.3, items that are identified and responded to in this thesis are noted under *Research Agenda for Moving to Practical Application*. The MoBE report provided focused insight into specific research areas. Derived from the identified gaps and shortcomings in the research, and for the advancement of the research, twelve focused research areas were identified that are priorities in progressing MoBE research. Table 3.2 presents the five principal objectives of the MoBE research committee and the larger research community that guided the development of the twelve research focus areas.

Table 3.2: MoBE: research objectives

| ***MoBE research objectives*** | |
|---|---|
| *1.* | *Characterise interrelationships among microbial communities and built environment systems of air, water, surfaces, and occupants.* |

| | |
|---|---|
| *2.* | *Assess the influences of the built environment and indoor microbial exposures on the composition and function of the human microbiome, on human functional responses, and on human health outcomes.* |
| *3.* | *Explore non-health impacts of interventions to manipulate microbial communities.* |
| *4.* | *Advance the tools and research infrastructure for addressing microbiome built environment questions.* |
| *5.* | *Translate research into practice.* |

(Briere & Resnick 2017:78-179)

The author collated the 12 MoBE priority research areas set out by the larger research community in Table 3.3 taken from the summary table BOX S-3 in the report, identifying each research study area with the research focus areas listed. The author provided, where relevant, a key quote or finding with direct relevance to this thesis investigation.

Table 3.3: The 12 MoBE focal priority research areas

| ***The 12 MoBE focal priority research areas*** | |
|---|---|
| *Characterize Interrelationships Among Microbial Communities and Built Environment Systems of Air, Water, Surfaces, and Occupants* | |
| **Priority research** | |
| ***1*** | *Improve understanding of the relationships among building site selection, design, construction, commissioning, operation, and maintenance; building occupants; and the microbial communities found in built environments. Areas for further inquiry include fuller characterisation of interactions among indoor microbial communities and materials and chemicals in built environment air, water, and surfaces, along with further studies to elucidate microbial sources, reservoirs, and transport processes.* |
| ***2*** | *Incorporate the social and behavioural sciences to analyse the roles of the people who occupy and operate buildings, including their critical roles in building and system maintenance.* |
| | Key quote/finding<br>The MoBE report and, by association, the greater MoBE community by consensus outline a critical research suggestion that is very relevant to this thesis investigation:<br>*… [I]dentifying key building attributes that are critical to the survival, activity, or death of bacterial, viral, and eukaryotic microbial communities, and discovering how variations in indoor environmental conditions, such as air temperature, humidity, and the condition of water in premise plumbing and other indoor water systems, affect these communities. The level of detail needed to capture and analyse these relationships will be substantial given the variations in these attributes in current and future built environments, compounded by occupant behaviours and facility managements* (Briere & Resnick 2017:180) |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research foci one and two in more detail, with chapter 5 serving as a precursor to item two. In this thesis, the impact that built environment factors have on the microbiome is investigated, with the aim to correlate diversity, distribution and proliferation with environmental conditions such as occupancy, space use and flow, and the interdependency of space use, occupancy and flow patterns (the spatial analytics of the indoor environment). | |

| | |
|---|---|
| *Assess the Influences of the Built Environment and Indoor Microbial Exposures on the Composition and Function of the Human Microbiome, on Human Functional Responses, and on Human Health Outcomes* | |
| **Priority research** | |
| ***3*** | *Improve understanding of the relationships among building site selection, design, construction, commissioning, operation, and maintenance; building occupants; and the microbial communities. Use complementary study designs - human epidemiologic observational studies (with an emphasis on collection of longitudinal data), animal model studies (for hypothesis generation and validation of human observational findings), and intervention studies - to test health-specific hypotheses.* |
| ***4*** | *Clarify how timing (stages of life), dose, and differences in human sensitivity, including genetics, affect the relationships among microbial exposures and health. These relationships may be associated with protection or risk and are likely to have different strengths of effect, parameters that are important to understand further.* |
| ***5*** | *Recognise that human exposures in built environments are complex and encompass microbial agents, chemicals, and physical materials. Develop exposure assessment approaches to address how combinations of exposures influence functional responses in different human compartments (for example, the lungs, the brain, the peripheral nervous system, and the gut) and downstream health outcomes at different stages of life.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research focus three in more detail. This thesis investigates occupancy and functional space use through observational methodologies employed in architecture to correlate the spatial analytical findings with the biome findings. Items four and five are not addressed in this study. | |
| *Explore Non-health Impacts of Interventions to Manipulate Microbial Communities* | |
| **Priority research** | |
| ***6*** | *Improve understanding of energy, environmental, and economic impacts of interventions that modify microbial exposures in built environments, and integrate the relevant data into existing built environment–microbial frameworks for assessing the effects of potential interventions, understanding of the relationships among building site selection, design and construction.* |
| **Author's comments** | |
| - | |
| *Advance the Tools and Research Infrastructure for Addressing Microbiome–Built Environment Questions* | |
| **Priority research** | |
| ***7*** | *Refine molecular tools and methodologies for elucidating the identity, abundance, activity, and functions of the microbial communities present in built environments, with a focus on enabling more quantitative, sensitive, and reproducible experimental design.* |
| ***8*** | *Refine building and microbiome sensing and monitoring tools, including those that enable researchers to develop building-specific hypotheses related to microbiomes and assist in conducting intervention studies.* |
| ***9*** | *Develop guidance on sampling methods and exposure assessment approaches that are suitable for testing microbiome–built environment hypotheses.* |
| ***10*** | *Develop data commons with data description standards and provisions for data storage, sharing, and knowledge retrieval. Creating and sustaining the microbiome–built environment research infrastructure would promote transparent and reproducible research in the field, increase access to experimental data and knowledge, support* |

| | |
|---|---|
| | *the development of new analytic and modelling tools, build on current benchmarking efforts, and facilitate improved cross-study comparison.* |
| ***11*** | *Develop new empirical, computational, and mechanistic modelling tools to improve understanding, prediction, and management of microbial dynamics and activities in built environments.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address priority research focus seven. In this thesis a methodology is presented that could be used by multiple studies, that is cost effective and is viable in developing world environments, as has been learned from various MoBE and related studies accessed through literature reviews. Lastly, chapter 2 recommends a high-level theoretical model that integrates various data sources and fields. | |
| | **Priority research** |
| ***12*** | *Support the development of effective communication and engagement materials to convey microbiome–built environment information to diverse audiences, including guidance for professional building design, operation, and maintenance communities; guidance for clinical practitioners; and information for building occupants and homeowners. Social and behavioural scientists should be involved in creating and communicating these materials.* |
| **Author's comments** | |
| It is important to note that the subsequent chapters intend to address research into applications through providing the first microbiome data set for South Africa. This thesis endeavours to support item 12, introducing new research to the architecture field. This set is specific to the WC, Cape Flats region in Cape Town, South Africa, and is the characterisation of two public hospitals. | |

In MoBE report addenda provide information on current sampling and sequencing tools, open- and closed-format tools, specificity, taxonomic resolution, sensitivity and organism coverage, organism viability, biological activity, functional coverage, toxicological potential, quantification, reproducibility and data sharing, as well as metadata on buildings and building systems. These addenda have not been summarised, but will be incorporated into the appropriate chapters where they are of important reference value.

The substantial amount of time people spend indoors necessitates a better understanding of indoor environments. The US National Human Activity Pattern Survey (NHAPS) revealed that people spend between 85% and 90% of the day in various indoor environments (Briere & Resnick 2017). The microbial communities in these environments are complex and diverse, consisting of bacteria, viruses and microbial eukaryotes. The advent of DNA and RNA sequencing and bioinformatics has moved the study of organisms way beyond the culture and microscopy generation, allowing for full community investigation and identification, to explore abundance and complexity. Reference data of microbial genomes have grown tremendously. The challenge of viability is still a reality. Sequencing indicates dead and live organisms, but it does indicate their presence in the ecosystem and biome. Both culture dependent and independent techniques will be necessary to gauge the status of the biomes, i.e. which species are present, what they are doing and how they are affecting other species.

The number and diversity of built environment studies limit the MoBE report, as it mainly focuses on residential and office environments, but does refer to studies done in hospitals, public spaces and transit environments. It is also restricted to the environments of study, and does not directly respond to and, as noted… *Does not draw detailed comparisons among microbiomes and their impact in nations with more widely varying climates and levels of*

*economic development. It will also be important to consider challenges facing residents living in poor housing stock and of lower socioeconomic status, who may have less control over environmental conditions, may not be able to improve their residences, or may need information and resources to address indoor microbiome–built environment issues (*Briere & Resnick 2017:15). It is evident that this study, because of its South African siting and context, should address the country's developing socio-economic environments, diverse climate and developing-world disease burdens, allowing for further comparisons with current studies conducted in developed economic environments. Indoor built environment spaces can be categorised as resident and transitory spaces. The degree to which occupants can change or control their building environment directly relates to these environmental categories, with residential (the most), office and public spaces (less) and transport environments (the least). A building must be seen as a systemic environment that has strong ecological relationships within different environments, *The resident community of microbes in a building will be amplified by colonization, modulated by in situ population dynamics, and depleted by extinction or depletion to below detectable levels (*Briere & Resnick 2017:17). The fabric, systems, occupancy use and flow patterns of and in a building all contribute to and function eco-systemically. Figure 6 below depicts this relationship.

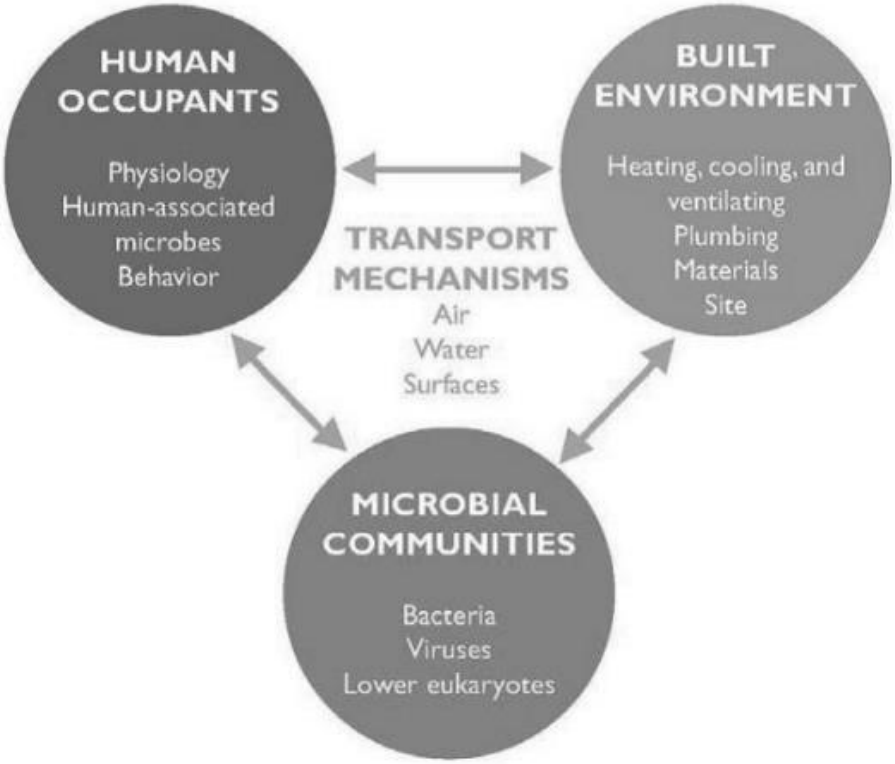



Figure 6: Building ecosystems (Briere & Resnick 2017)

The MoBE report presents three core equations gathered from ecology, microbiology and building science. These have been integrated and developed to describe theoretically the community composition of the built environments and the factors that affect them. These equations intend to elucidate the key ecosystemic processes involved, i.e. entry portal, generation processes, death, inactivation and evolution, and exit portal. The equations are:

Equation 1) The **mass balance equation** below (flow of material into and out of a system) refers to the built environment ecosystem. This very simplified equation does not consider the complex nature of each of the variables (proliferation, desecration, hibernation, susceptible environment, growth, etc., but is meant to be a concept for further development.

$$dN/dt = B + I - D - E$$

| | |
|---|---|
| *N* | Abundance |
| *B* | Births |
| *D* | Deaths |
| *E* | Emigration |
| *I* | Immigration |
| *dN/dt* | Change in specie abundance over time |

Equation 2)The **mass balance equation variation** (mass balance equation – contaminant specie balance concepts) is a variation of the above. *All of the parameters that affect a representative microbial population in the built environment can be spatially heterogeneous and temporally variable…there may be multiple spatial "compartments" in a building, whose microbial populations are linked as organisms are transported between them and as microorganisms deposit and are re-suspended* (Briere & Resnick 2017:21).

$$C_{in} = PC_{out} + G^* - L^*$$

| | |
|---|---|
| $C_{in}$ | Steady-state microbial concentration indoor |
| $PC_{out}$ | Penetrative indoor from outdoor |
| *G** | Indoor generation |
| *L** | Loss |

Equation 3) **Material balance equation simplified** *(for a single-zone space and steady-state contaminant concentration, with no internal loss due to deposition or an engineered control system*). (Briere & Resnick 2017)

$$C_{in} = PC_{out} + \frac{G}{Q_o}$$

| | |
|---|---|
| $C_{in}$ | Mass/number steady-state indoor contaminant concentration microbial concentration indoor |
| $C_{out}$ | Mass/number outdoor concentration |
| *P* | Penetration factor outdoor contaminants |
| *G* | Mass/number over time indoor contaminant generation rate |
| $Q_O$ | Volume per time outdoor airflow rate into the building |

In summary, it is important to state that questions have arisen from the MoBE report concerning population models and the associated factors and variables. Many of these questions will be long-standing and very complex to solve, and will require focused research, as well as whole biome identification studies. Below, Table 3.4 references these complex questions and those that the thesis responds to, with findings discussed in chapters 7, 8 and 9.

Table 3.4: Modelling built environment ecology research questions (Briere & Resnick 2017)

| ***BOX 1-2*** | |
|---|---|
| ***Modelling research questions on the ecology of the built environment*** | |
| *1.* | *What is known about the kinds of resources available in the built environment?* |
| *2.* | *What is known about the death, persistence, and removal rates of different types of microorganisms in the built environment?* This requires a microbiologically specific investigation. |
| ***Modelling research questions on the ecology built environment, addressed by the thesis*** | |
| *3.* | *Where do the colonists come from? What is known about the sources that populate the microbiome of a particular building?* This thesis attempts to answer this in the specific environments that were studied. |
| *4.* | *To what extent are local microbial communities and the individual species within those communities determined by dynamics within a building or by coupling to the external environment?* This thesis attempts to answer this in the specific environments that were studied. |
| *5.* | *How well described are the environmental gradients that can define the "ecological niches" available for microbes in the built environment?* This thesis attempts to answer this in the specific environments that were studied; however, a microbiologically specific investigation is required. |

#### 3.2.1.2 MICROORGANISMS IN THE BUILT ENVIRONMENT: IMPACTS ON HUMAN HEALTH

This section refers to the MoBE report on *Microorganisms in the built environment: Impacts on human Health*, pages 27-74 (Briere & Resnick 2017). Reference is made to pertinent portions of the report. The MoBE report presents the following issues and postulates hypotheses based on the current findings and research gaps with reference to human health:

1. *In developed areas of the world, in indoor environments do people inhabit the primary ecosystems?*
2. *The environments people inhabit may influence the human microbiome, which may in turn impact human health.*
3. *A wide array of microbial components and characteristics are known to impact human health.*
4. *A number of sources of microorganisms within indoor environments affect human health.*

The MoBE report offers discourse on the impact that the built environment microbiomes have on the diversity of the human biome. The predominant biome/habitat that a person functions in daily has a significant impact on the constitution of that individual's personal human biome and hence virulence, immunity and general health condition. If we spend the majority of our time indoors, then that biome will affect our biome, be it negative or positive. Diversity then becomes significant with reference to microbial diversity indoors versus outdoors. Presumably, in developing countries people are more exposed to outdoor- than indoor-associated organisms than in developed countries. The lack or abundance of diversity and the impact on human health are still unknown. Reduction in diversity in the human biome could be environmentally associated.

*Yet, there is no concrete evidence that the human microbiome can be colonized by bacteria that originate from a building* (Briere & Resnick 2017:30). Lax *et al.* (2017) found that the building microbiome did not appear to influence the microbial structure or composition of the skin of the occupants (Lax *et al.* 2017). It has, however, been proved that pathogenic bacteria found indoors via various transmission modes impact and infect the resident. Numerous mechanisms exist through which microorganisms can affect human health. The MoBE report describes these mechanisms as pathogen-associated molecular patterns (PAMPs): *Microorganisms can affect human health through a variety of mechanisms. The dominant microbial components linked to human health include pathogen-associated molecular patterns (PAMPs). PAMPs are molecules such as endotoxin and lipopolysaccharide (LPS) (a component of bacterial cell membranes), flagellin (from bacteria), (1–3)-β-D glucans (also referred to as triple helical glucans, from fungi wall membranes). These molecules are associated with groups of microbes (bacteria or fungi) that may influence human innate immune system responses, interact with airway epithelial cell or irritant receptors [...] A large respiratory and allergy literature that has evolved over two decades suggests complex positive as well as negative associations of various PAMPs with allergy and respiratory outcomes* (Briere & Resnick 2017:30). The degree of infection varies based on virulence, immune status, etc. (Lax *et al.* 2017). The hospital biome study of this thesis notes the following pertinent areas for future research and consideration post this investigation:

- Additional South African hospitals must be studied to test and understand the reproducibility and generalisability of the findings of the study.
- Further focused research is required to understand how temperature, humidity, building materials, and the integrity of the building structure affect the interchange between the indoor and human bacterial microbiomes as suggested in the report.
- According to recent literature and similar study findings, the predominant source of microbes is from the outside via ventilation systems, doors, windows and from indoors via the occupants (human and non-human). Chapters 7, 8 and 9 present the thesis findings in relation to the MoBE report findings. The MoBE report refers to numerous studies indicating both source and transmission in indoor environments, with the majority of these studies originating from the USA and Europe and none from Africa and in particular South Africa.

Infection transmission in the indoor environment has received increased interest in recent times. Most of the research focuses on infectious organisms; however, fomites are well documented to spread infectious disease through aerosol transmission of pathogens. *Some viruses, bacteria, fungi, protozoa, and algae in the indoor environment have long been known to be pathogens, with the potential to cause infectious disease or allergic illness* (Burge 1980 in Briere & Resnick 2017:32). Organism transmissibility, mode of transmission and virulence are critical factors in transmission and the effectiveness of infection control strategies. For context, the author refers to the TB epidemic in South Africa as a case study (Basu *et al.* 2007; Yates *et al.* 2016). Other organisms include influenza and Aspergillus. Figure 7 presents the different modes of transmission.

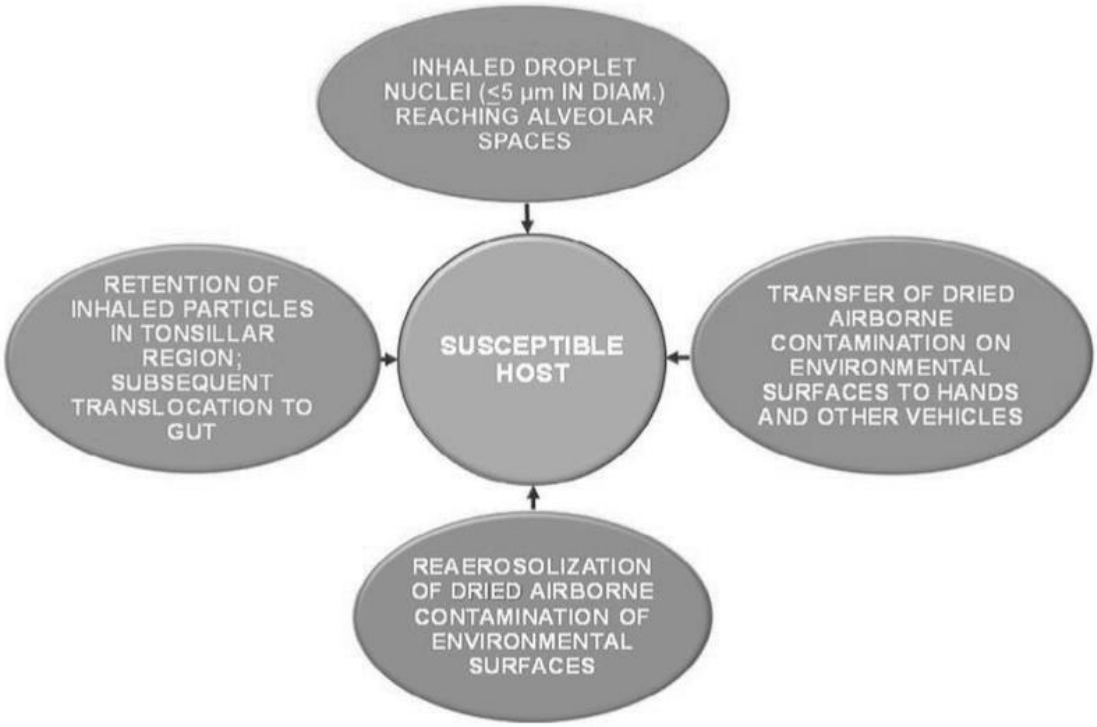



Figure 7: Modes of transmission (Briere & Resnick 2017)

Table 3.5 displays the transmission modes of various pathogens and source organisms. This table along with other tables developed in this thesis through literature studies will be used as reference to assess the Western Cape (WC) hospital Accident and Emergency (A&E) microbiome. *Transmission of microorganisms within the built environment is a complex process that is contingent not only on the class of microorganism itself but also the state of the building (for example, its humidity or ventilation) and the number and behaviour of building occupants* (Briere & Resnick 2017:34).

Table 3.5: Source, mode and pathogen (Briere & Resnick 2017)

| ***Super kingdom*** | ***Mode of transmission*** | ***Examples*** |
|---|---|---|
| Bacteria | Inhalation | *Bacillus anthracis, Coxiella burnetii, Chlamydia psittaci, Legionella, Mycobacterium tuberculosis,*Atypical *mycobacteria* |
| | Fomites | *Clostridium difficile, Staphylococcus aureus, Enterococcus* |
| Fungi | Inhalation | *Cryptococcus neoformans, Histoplasma capsulatum Aspergillus fumigatus* |
| | Fomites | *Trichophyton mentagrophytes, Trichophyton rubrum* |
| Protozoa | Inhalation | *Acanthamoeba spp.* |
| Viruses | Inhalation | *Variola* (smallpox), *Rubella, Norovirus, Rotavirus Adenovirus, Coxsackie virus, Influenza, Rhinovirus Coronaviruses* (Middle-East respiratory syndrome [MERS], Severe acute respiratory syndrome [SARS]) |
| | Fomites | *Variola* (smallpox), *Rubella, Norovirus, Rotavirus Adenovirus, Coxsackie virus,* Influenza, *Rhinovirus Coronaviruses* (MERS, SARS) |

Indoor sources can include piping and ventilation systems, walls, wet areas, humidifiers and the general condition of the building environment, i.e. temperature, humidity and $CO_2$ levels, cleaning and hand-washing, and occupant patterns. Numerous associated HAI pathogenic infections have been studied and recorded. Persistent biofilms on surfaces become hosts and reservoirs for colonisation and communities for these pathogens. Various studies have been conducted over the last decade linking bacteria, viruses and fungi to human health, and sources directly associated with or suggested by the BE. These studies include, but are not limited to, asthmas developing and worsening, rhinitis, microbial metabolic compounds, eczema, hyper-sensitivity pneumonitis, TB and NTB, endocrine disruption and child development, brain health and neurological outcomes, moisture damage in buildings, poor quality housing and brain health, as well the investigation into beneficial microbes and links with “green” buildings and “green” spaces. Table 3.6 indicates the knowledge gaps that have been identified by the research community and reported in the MoBE report with regards to exposure and health effects.

Table 3.6: Knowledge gaps on indoor microbial exposure and health effects

| ***Knowledge gaps*** | |
|---|---|
| ***Knowledge gaps concerning indoor microbial exposure and health effects*** | |
| *1.* | *Elucidate the immunologic, physiologic, or other biologic mechanisms through which microbial exposures in built environments may influence human health.* |
| *2.* | *Clarify the relationships between microbial communities that thrive in damp buildings and negative allergic, respiratory, neurocognitive, and other health outcomes.* |
| *3.* | *Gain further understanding of the beneficial impacts of exposures to microbial communities on human health.* |
| *4.* | *Develop an improved understanding of complex, mixed exposures in the built environment.* |
| ***Knowledge gaps concerning indoor microbial exposure and health effects, addressed by the thesis*** | |
| *5.* | *Improve understanding of the transmission and impacts of infectious microorganisms within the built environment.* This thesis attempts to contribute towards closing this gap. |
| *6.* | *Design studies to test health-related hypotheses, drawing on the integrated expertise of health professionals, microbiologists, chemists, building scientists, and engineers.* This thesis attempts to contribute to filling the knowledge gaps through architectural spatial analytic integration. |

#### 3.2.1.3 THE BUILT ENVIRONMENT AND MICROBIAL COMMUNITIES

This section refers to the MoBE report on the built environment and microbial communities, pages 75-111 (Briere & Resnick 2017). Reference is made to pertinent portions of the report. Table 3.6 shows the knowledge gaps that have been identified for this focus area in the MoBE report:

Table 3.7: Knowledge gaps concerning the built environment and microbial communities

| ***Knowledge gaps*** |
|---|
| ***Knowledge gaps concerning the built environment and microbial communities*** |

| | |
|---|---|
| *1.* | *Develop means to better monitor and maintain the built environment, including concealed spaces, to promote a healthy microbiome.* |
| *2.* | *Deepen knowledge on the impact of climate and climate variations on the indoor environment.* |
| ***Knowledge gaps concerning the built environment and microbial communities, addressed by the thesis*** | |
| *3.* | *Improve understanding of how building attributes are associated with microbial communities, and establish a common set of building and environmental data for collection in future research efforts.* This thesis attempts to contribute towards closing this gap. |
| *4.* | *Collect better information on air, water, and surface microbiome sources and reservoirs in the built environment.* This thesis attempts to contribute towards closing this gap. |
| *5.* | *Clarify the association of building attributes and conditions with the presence of indoor microorganisms that have beneficial effects.* This thesis attempts to contribute towards closing this gap. |

#### 3.2.1.4 TOOLS FOR CHARACTERISING MICROBIOME BUILT ENVIRONMENT INTERACTIONS

This section refers to the MoBE report on the tools for characterising microbiome–built environment interactions, pages 119-144 (Briere & Resnick 2017). Reference is made to pertinent portions of the report. There is a critical need for longitudinal studies; the report refers to two recent studies of this nature: the home biome and the hospital biome study. The hospital biome study was a yearlong study with environmental, social and microbial sampling. It provided a fruitful source for comparisons with the current study based on outcomes and results. *Through longitudinal investigation of microbial exposure and exchange across different building codes and buildouts, it might be possible to discern how these differences influence exposures and hence affect health outcomes* (Briere & Resnick 2017:123). Some pertinent findings from the hospital microbiome longitudinal study include: 1) *Data from sampling of surfaces and occupants in 10 patient rooms and 2 nursing stations, daily for 365 consecutive days (Lax et al. 2017:*2); 2) Hospitals are found to exercise more control, and maintain more uniform environmental conditions over time*;* 3) There is a dynamic microbial exchange between patients and their rooms/spaces*. Patients entering a room acquire microbes from the room environment, but after 24 hours, the room is filled with the patient microbes* (Briere & Resnick 2017:122); 4) Among other factors affecting microbial distribution, the entry and activities of visitors and staff, along with the cleaning regime, had an impact. Lastly, the study provided dynamic occupancy data and *amplicon and metagenomics sequence data that can be used to help construct a platform for statistical analysis of the dynamic turnover of the microbial community in the built environment* (Briere & Resnick 2017:122).

The report refers to numerous core tools for data collection that have been employed in various studies, but not in a consistent manner. The nature of this emerging research field implies that teasing out methodologies and appropriate techniques is part of the development of quality replicable research. The MoBE report describes the core tools and assessments applied to date. The areas of data collection and guides required are listed below:

*1.* Measuring occupancy and human activities *(Briere & Resnick 2017:124)*
*(The role of humans and human activities in the built environment is complex and combines with building characteristics to affect microbial communities. The density of occupants in the environment affects not only microbial shedding but also such variables as room temperature, humidity, and CO2 content, which in turn may affect the operation of building systems designed to maintain environmental parameters and occupant comfort.)*

2. Identifying and quantifying the microorganisms present in a built environment *(Briere & Resnick 2017:129.*
*(Improving sensitivity may be a particularly important challenge for the built environment because biomass collected from indoor samples, especially air samples, often is very low. Sample biomass generally is much lower, for example, than that obtained in other types of microbiome sampling for which tools and analysis platforms have been developed. Such samples are taken from the human gut and a practical result is that microbial information from air samples often represents community integration over space and time, because common sampling methods rely on pumps to pull large volumes of air across a filter or analyse samples of dust that has settled over extended periods.)*

3. Relative and absolute quantification *(Briere & Resnick 2017:130)*
*(It is useful to know not only which types of microorganisms are present in the microbial communities sampled from a built environment but also how abundant they are. The genomics information obtainable from most studies provides relative quantification, reflecting the abundance of a type of microorganism relative to the total microorganisms measured in the sample (as a fraction of the total). Information on relative abundance can be useful in some characterization studies. However, having information on absolute abundance is also important to enable knowledge to move toward practical application.)*

*4.* Understanding the viability and functions of microorganisms *(Briere & Resnick 2017:131)*
*(Yet, while culture-based approaches remain an important complementary technology to such tools as genomics, suitable culture conditions for many microorganisms are not known, or do not account for the range of environments that prompt microbial metabolic activity and reproduction, or may miss the activity of less abundant taxa. Culture-based measures thus, are limited as to the information about microbial communities they can provide; metagenomics can provide a "snapshot" of the diversity of a microbial population. Thus, there is some information on functional potential in a community, but this DNA-based information does not reveal whether the microorganisms are actively engaged in metabolic activity.)*
*5.* Reproducibility and development of reference materials *(Briere & Resnick 2017:132)*
*(However, understanding the strengths and limitations of existing studies will enable comparisons across study results and given the high community complexity and potentially dynamic nature of microorganisms, natural biologic variation can prevent two laboratories from producing the same results even when they control for technical variation.)*

6. Elucidating causal connections between microbial exposures and human health outcomes *(Briere & Resnick 2017:133-134)*
*(Supporting or promoting health is a key motivation for understanding indoor microbiomes and using that knowledge to inform how buildings are designed, built, maintained, and operated. To make progress toward such practical applications, researchers will need to build on the*

*existing base of studies to develop and test hypotheses. The general steps summarised below involve the collection and analysis of data in a manner aimed at demonstrating relationships in a clinically relevant framework.)* The sub list is not referenced here; however, the relevant page number within the report is noted above.

Table 3.8: Knowledge gaps concerning core tools and assessment techniques

| ***Knowledge gaps*** | |
|---|---|
| ***Knowledge gaps concerning core tools and assessment techniques*** | |
| *1.* | *Useful suites of tools exist with which to characterise building and occupant factors and microbial communities.* |
| ***Knowledge gaps concerning core tools and assessment techniques, addressed by the thesis*** | |
| *2.* | *Further efforts in foundational areas that support the research infrastructure for built environment–microbiome studies are needed.* This thesis attempts to contribute towards closing this gap. |
| *3.* | *Both experiments and modelling will help the research community better understand the interrelationships among buildings, microbial communities, and human occupants, and this understanding will support eventual application of the knowledge gained through research.* This thesis attempts to contribute towards closing this gap. |
| *4.* | *Interest in connecting microbial characterisation of the built environment to an improved understanding of human health impacts will benefit from studies designed to address health-relevant hypotheses.* This thesis attempts to contribute towards closing this gap. |
| *5.* | *Many groups are involved in conducting microbiome–built environment research and moving the knowledge thereby gained toward practical changes in such areas as building and indoor air quality codes and standards develop the research infrastructure in the microbiome–built environment human field needed to promote reproducibility and enhance cross-study comparison.* This thesis attempts to contribute towards closing this gap. |
| *6.* | *Develop infrastructures to support effective communication and engagement with those who own, operate, occupy, and manage built environments.* This thesis attempts to contribute towards closing this gap. |

#### 3.2.1.5 INTERVENTIONS IN THE BUILT ENVIRONMENT

This section refers to the MoBE report on *Interventions in the Built Environment*, pages 151-169 (Briere & Resnick 2017). Reference is made to pertinent portions of the report. Table 3.8 shows the knowledge gaps identified in the MoBE report on the built environment and microbial communities.

Table 3.9: The Interventions in the built environment

| ***Knowledge gaps*** | |
|---|---|
| ***Knowledge gaps concerning the interventions in the built environment*** | |
| *1.* | *Further, explore the concept of interventions that promote exposure to beneficial microorganisms, and whether and under what circumstances these might promote good health.* |

| ***Knowledge gaps concerning the interventions in the built environment, addressed by the thesis*** | |
|---|---|
| *2.* | *Improve understanding of "normal" microbial ecology in buildings of different types and under different conditions.* This thesis attempts to contribute towards closing this gap. |
| *3.* | *Obtain additional data necessary to support the use of a variety of quantitative frameworks for understanding and assessing built environment interventions.* This thesis attempts to contribute towards closing this gap. |

#### 3.2.1.6 MOVING FORWARD: A VISION FOR THE FUTURE AND RESEARCH AGENDA

This section refers to the MoBE report on the *Interventions in the Built environment*, pages 175-207 (Briere & Resnick 2017). Reference is made to pertinent portions of the report and the long term and current research opportunities and agenda. *Since knowledge about the interactions among indoor microbiomes, human occupants and built environments is not yet at an actionable level, this chapter of the MoBE report lays out a vision for the future of buildings informed by microbial understanding and provides a research agenda. A desire to design, construct, and operate buildings that support occupant health and well-being while promoting sustainability and resilience drives this vision. The vision also takes into account several trends that will continue to impact building design and operation, including climate change, aging building stock, increasing urbanisation, the adaptive reuse of existing buildings, and the increasing use of chemicals indoors, including antibiotics and antimicrobials*. With reference to the report: *To this end, partnerships are needed across scientific disciplines, bridging U.S. and international research expertise with communities in clinical medicine and in the design, reinvention, and operation of buildings…and provide greater understanding of microbial functional activities and to clarify whether and how built environment microbiomes impact human health* (Briere & Resnick 2017:178).
*Researchers have not agreed on which standardised microbial and building data to collect; on sampling and analytical protocols; and on data-sharing, which would facilitate cross-comparison of results. And providing solid evidence of health effects connected to indoor microbial exposures will require additional studies that contribute more quantitative and reproducible exposure and response data* (Briere & Resnick 2017:178). Table 3.10 presents the future vision identified in the MoBE report:

Table 3.10: Future vision of the MoBE research committee

| ***Future vision of the MoBE research committee*** | |
|---|---|
| *1.* | *Researchers will have a much deeper understanding of the effects of indoor microbial communities on human health, and the connections among exposure, response, and health outcomes will be established.* |
| *2.* | *The growth, establishment, and evolution of indoor microbiomes will be better understood.* |
| *3.* | *The sources of microorganisms in buildings that affect human health and wellbeing positively or negatively will have been identified and understood.* |
| *4.* | *Advanced technologies that facilitate indoor environmental quality and energy efficiency will have been developed, installed, and embraced in building operations.* |
| *5.* | *People will be informed about and engaged in maintaining healthy indoor environments.* |

| | |
|---|---|
| *6.* | *The benefits of connections to the outdoors will be better understood and where useful, incorporated into the design and operation of buildings.* |

(Briere & Resnick 2017:176-177)

With this thesis, the author proposes to contribute through a cross-seasonal semi- longitudinal study to the MoBE research agenda and data pool. The need for improved indoor air quality (IAQ), and indoor surface quality (ISQ) in the built environment is recognised when addressing public health needs, with particular reference to developing countries, e.g. South Africa. The field of architecture is set for a paradigm shift that can be seen as an integrated health focus for all building typologies and industries through a microbial perspective. The MoBE research could potentially fill the proverbial empirical data gap in current architectural health-aligned research. In a recent paper Brown, Kline, Mhuireach, Northcutt and Stenson (2016:2) postulate: *Architectural design is poised to undergo a revolution over the next few decades in response to climate change, urbanization, and population growth. MoBE is a critical juncture of study because humans spend most of their time inside buildings, and the microorganisms encountered there can influence public health. In closing, we reaffirm that architects and other designers are committed to improving occupant health through strategies such as bio-informed design.*

## 3.3 MICROBIOLOGY OF THE BUILT ENVIRONMENT (MOBE)(REVIEW 2)

Chapter 8 of the thesis, under section 8.2: Microbiology methodology, contains an integrated literature review for application to sampling, sequencing and analysis. The review is integrated into the microbiology methodology. However, due the relevance to microbiology and MoBE, it will again be summarised under the relevant literature review Built environment and microbial sampling. This literature review will only make reference to the current MoBE status report (status quo summary review of the research field) published in August 2017, as this report is a standalone review summary. (It is important for the purposes of this thesis for the reader to be aware of the fact that the state of MoBE research, published through the 2017 MoBE report, was presented four years after the commencement of this thesis. It will therefore seem that many of the findings and approaches used by the author were derived from the report; however, the report came after the author had developed the thesis. It is in fact auspicious that the report confirms many of this study's goals and objectives, as well as methodology approaches. This is largely due to the author's involvement in numerous research development discussions with peers through conference special sessions.) This review considers the most pertinent MoBE literature and provides context to the MoBE research field with specific reference to architecture and building design, discussing the potential contribution and impact of the research outcomes now and in future on building design, user health and well-being.

### 3.3.1 THE MICROBIOLOGY OF THE BUILT ENVIRONMENT FOR ARCHITECTS: UNDERSTANDING THE RESEARCH FIELD THROUGH A REVIEW ON APPLIED SPATIAL METRICS

Topic:

- Microbiology of the built environment, providing insight into the research field and elucidating the contribution, presence or absence of building design investigation in MoBE

Literature review hypothesis:

- Architecture - in particular spatial metrics such as human use and activity - influences the microbial environment

Literature review research questions asked with reference to known and new contributions in BE; agreement or disagreement with peers; the knowledge gaps identified; key concepts identified by the thesis author; and the context provided to the MoBE research field:

- Did the study investigate building and microbial relationships?
- Which engineering and architectural factors were considered?
- Was reference made to architecture and spatial planning and how was this applied?
- Was reference made to building ecology and microbial environments and how was this applied?
- The study period: short term (- 2 days) or longitudinal (+ 3 days)?
- The study site: single study site or multiple sites?
- What sampling methods were utilised for the BE and how were they applied?
- What sequencing methods were used?
- Which indicator microbes were identified in the BE?

- What sampling methods were utilised for microbiology and how were they applied?
- Did the study consider an interdisciplinary approach by different fields?
- What were the challenges?
- Did the study discuss or make reference to health and/or IPC in the built environment?

#### 3.3.1.1 INTRODUCTION

Humans spend the vast majority of their time indoors, up to 90% (Klepeis *et al.* 2001). Global trends in urbanisation are increasing indoor environment living (Höppe & Martinac 1998). Yet our understanding of the indoor environment is limited (Hospodsky *et al.* 2012). Built environments are complex ecosystems, host to a wide variety of organisms and trillions of microorganisms (Rintala *et al.* 2008; Tringe *et al.* 2008; Amend *et al.* 2010) share these spaces with us. This collective environment is known as the built environment microbiome. A number of studies have been conducted to investigate this environment with varied approaches and differential focus and research agendas (Rintala *et al.* 2008; Tringe *et al.* 2008; Amend *et al.* 2010, Kembel *et al.* 2013; Adams *et al.* 2014; Meadow *et al.* 2014; Ramos *et al.* 2015; Lax *et al.* 2017) The core focus, however, is to understand this largely unknown ecosystem and indoor environment we call home. There have been limited studies in the MoBE field, and of those studied the methodologies varied considerably. Adams *et al.* (2016) report that there has been a sharp increase in interest in the built environment microbiome, yet in comparison to any other environment studied, the built environment is in its infancy. Furthermore, Ramos notes, *microbial components to indoor air are receiving increased attention, but the sources of the microbial communities and the processes that affect them are not well understood* (Ramos *et al.* 2015:1264; Corsi 2012). There are numerous examples of the health effects of, and link between, the indoor environment and humans occupying them. Consequently, there is growing interest in the impact that microbiomes have on the health of humans. There are a few researchers (Hospodsky *et al.* 2012; Kembel *et al.* 2012; Dunn *et al.* 2013; Ramos *et al.* 2015) who explore the intersection of microbial ecology, building materials and of particular interest to this review, architectural design, to understand microbial diversity and abundance within a building. There have been a number of reviews, reports and commentary published, aimed at collating the work and raising the status of research in the MoBE field. This is most likely due to the rapid pace at which the field is growing and progressing, the interdisciplinary nature of the studies, and the “newness” of the field. Peers in the field (Larsen, Hamada & Gilbert 2012; Kelley & Gilbert 2013; Ramos & Stephans 2014; Adams *et al.* 2015, 2016) conducted five key and critical literature reviews. They have exhaustively summarised various aspects within the MoBE field. These include modelling approaches and culture analysis, sequencing and sampling, built environment tools for data collecting and meta-analysis of various datasets for various fields in various studies identifying challenges and similarities aimed at identifying patterns and the connections between studies.

#### **3.3.1.2** METHODOLOGY

This literature review does not intend to copy and repeat what has already been disseminated; it intends to identify the contribution to architecture and the research gaps thereof in current MoBE investigations. There has been a specific focus on spatial planning in considering human activity and space use to date, with possibilities for future studies. This study

hypothesises that architecture and in particular spatial metrics such as human use and activity, influence the microbial environment, yet limited research into architectural spatial factors have been incorporated into MoBE studies. Literature was critically surveyed within the MoBE field and its related study fields. Literature search methodology employed made use of the following online research databases: Scopus, ISI and Google Scholar. The architecture research specialists of the University of Pretoria library provided key word searches and initial research support. In addition, the CSIR and the building ecology workgroup (UC Berkley) made database resources available. A critical review was performed on journal articles, papers and personal communications. The following thirteen research questions were posed to assist the analysis and categorisation, mainly due to the large variation in architectural factors, combination of architectural factors, and the combination of architectural factors and microbiology factors employed. Ramos *et al.* (2013) in their comprehensive review on BE tools, put it succinctly: *unfortunately there are no standardised methods for measuring and recording human occupancy in indoor environments, but there are several helpful options from which to choose* (Ramos *et al.* 2013:249).
1). Did the study investigate building and microbial relationships? 2) Which engineering and architectural factors were considered? 3) Was reference made to architecture and spatial planning and how was this applied? 4) Was reference made to building ecology and microbial environments and how was this applied? 5) The study period: short term (- 2 days) or longitudinal (+ 3 days)? 6) The study site: single study site or multiple sites? 7) What sampling methods were utilised for the BE and how were these applied? 8) What sequencing methods were used? 9) Which indicator microbes were identified in the BE? 10) What sampling methods were utilised for microbiology and how were these applied? 11) Did the study consider an interdisciplinary approach by different fields? 12) What were the challenges? 13) Did the study discuss or refer to health and/or IPC in the built environment?

The literature was critically reviewed and categorised under these issues (some of which were absent): identifying the known and new contributions in BE; research finding agreements or disagreements; the knowledge gaps identified; key concepts identified; and the context provided to the MoBE research field by the published article. It was found that only a limited number of studies have included spatial factors and there were few spatial related studies, even though numerous investigations have shown the impact of human occupancy as major driver of indoor microbial communities through a combination of direct human shedding, resuspension from flooring, and emission from respiratory activities (Ramos & Stephens 2014). Our activities and the way in which we utilise spaces through touch (surfaces) breathing (air quality) and travel, are all critical determinants of microbial diversity (Oberauner, Zachow, Lackner, Högenauer, Smolle, & Berg 2013; Dunn *et al.* 2013; Flores, Scott, Bates, Knights, Lauber, Stombaugh, Knoght, Fierer 2011; Chen 2009; Taubel, Rintala, Pitkaranta, Paulin, Laitinen, Pekkanen, Hyvarinen & Nevalainen, 2009; Kembel *et al.* 2013). Architecture design indirectly and by extension the user directly, impact on the microbial diversity and community composition of the building microbiome through factors of building design, planning, occupancy and use patterns in different spaces and places.

#### 3.3.1.3 ARCHITECTURAL **FACTORS IDENTIFIED**

Kembel *et al.* (2014) suggest that network analysis, or simply put, analysis of the relationship of indoor spaces of a building, could be a potentially powerful tool for applying indoor ecology and biogeography in the future for building design. The literature identified a number of factors.

This study separates the building environmental factors and building spatial factors identified. The influence of the collective of these factors is difficult to determine as they vary in quantitative and qualitative data. Some studies have merely listed factors for information or conducted minimal qualitative observations versus studies that performed quantitative data measurements. First, the qualitative factors are discussed, followed by the quantitative.

*Qualitative factors*
*Building environmental factors*

Adams *et al.* (2014) in a study on airborne bacterial and fungal communities in residence in the United States of America (USA), utilised questionnaires that were "self-reported" on factors of: unit floor plan (rooms and room types), inhabitants and their behaviour, houseplants and the use of humidifiers. Due to the nature of the data collection, the following topics were invariant and unfortunately excluded: air treatment, daily occupancy, cleaning regime and opening of windows. The building typology was also factored, defined as matching residential units. There were references to the factors they reported as found in surfaces in variant locations. Rooms also differed in bacterial communities based on a common source or a different source, or supported the growth of different microbial communities. Building design spatial factors were not studied, only geographic distance of samples which indicated that bacteria as fungi samples separated by a few hundred meters *tended to have greater compositional differences than samples closer together in space*. Of spatial interest was that D*einococci, Alphaproteobacteria, Cyanobacteri, and Cytophagia decreased from their greatest relative abundance outdoors as you entered the indoor spaces, whereas Gammaproteobacteria, Clostridia, Bacilli, Flavobacteria, and Actinobacteria increased in abundance as you moved to the more central rooms of the dwelling* (Adams *et al.* 2014:3). This community changed by room type with outdoor and indoor bacteria found in the building, indicating the influence of spatial layout and human activity, confirmed by the fact that bacterial composition varied by residential unit and room type. *Human-associated bacterial genus, Corynebacterium,* represented 11% of indoor sequences, making humans a source of indoor microbes.Other studies with qualitative BE data include Adams *et al.* (2013) for airborne fungal communities at a university housing facility using a questionnaire by self-assessment for BE and limited spatial factors and analysis. Hospodsky *et al.* (2012) sampled a university classroom for resuspension (this was only for a single room) and averaged the occupancy for BE and limited spatial factors and analysis; Horner, Worthan & Morey (2004) sampled 50 detached single-family homes in metropolitan Atlanta using a questionnaire and visual assessment for BE and limited spatial factors and analysis.

*Quantitative factors*
*Building environmental factors*

Only two healthcare typology studies, the latter from 2015 and 2017 (Ramos *et al. 2015;* Lax *et al. 2017),* were reported as part of the hospital microbiome project; this study reports on the first MoBE healthcare study. Kembel *et al.* (2013) investigated the *airborne bacterial community structure and environmental conditions in patient rooms exposed to mechanical or window ventilation and in outdoor air* at the Providence Milwaukie Hospital. The BE factors considered included ventilation source and related metrics, temperature and humidity. Specific ventilation metrics studied included air changes per hour calculated for patient rooms taking into account room volume, air speed and volume flowing into the room through the window (window-ventilated rooms) or diffuser (mechanically ventilated rooms). To account for the

different ventilation sources, variance in community dissimilarity was measured explained by each environmental variable after accounting for the ventilation source. No consideration of building design spatial factors was reported or studied. The study found that *building attributes, specifically the source of ventilation air, airflow rates, relative humidity and temperature, were correlated with the diversity and composition of indoor bacterial communities.* Similar to the findings of Adams *et al*. (2014) the relative abundance of bacteria closely related to human pathogens was higher indoors; in addition, the composition of the indoor airborne communities differed based on ventilation source. The mechanical source communities were distinct from outdoor air communities, and accounted for the major difference in community composition among rooms in the study. The factors humidity and temperature (environmental conditions) had a significant relationship in the airborne bacterial community composition. A distinct change in the indoor air community was observed from mechanical to hybrid to natural ventilated spaces. These finding are supported by previous studies (Tang *et al*. 2009; Rintala *et al*. 2008; Qian, Hospodsky, Yamamoto, Nazaroff & Peccia 2012). In a positional piece Brown *et al*. (2016) affirm the impact of BE and architectural factors such as ventilation on microbial communities indoors.

In the first of two extensive architectural MoBE studies, Kembel *et al*. (2014) investigated a multi-use classroom and office buildings in the USA, the other studies being those of Ramos *et al. (2015)* and Lax *et al.* (2017). They considered factors related to space type, building arrangement, human use and movement, and ventilation source. Further spatial and architectural attributes of each space were factored: floor level, East wing versus West wing, floor area, air handling unit (AHU), ventilation type (natural or mechanical), human use patterns per space, ambient air temperature and relative humidity per space. The data were obtained by field observation (data sampling), a building information model and building plans. Building design spatial factors included design attributes of each space: function, form and organisation. The human use patterns for each space were estimated values based on a qualitative assessment of expected patterns of human diversity based on annual occupied hours in each space. This was the only study that referenced network analysis. Factors considered were, 1) spatial connectedness of space: immediate and between pairs of spaces in the building; 2) measures of network centrality for each space in the building: betweenness and degree. They found that space size, relative humidity, and occupancy varied less across offices than across all rooms at the building-scale, suggesting the dynamic nature of shared indoor environments. Statistically, the ventilation air source in offices had the greatest effect on bacterial community structure. Two pertinent findings from the study are the room type factor and spatial relationship factors: room types contained highly distinct communities, e.g. restrooms versus all other rooms, and spatial factors, noting *spaces with high human occupant diversity and a high degree of connectedness to other spaces via ventilation or human movement contained a distinct set of bacterial taxa when compared to spaces with low occupant diversity and low connectedness* (Kembel *et al*. 2014:1). In addition to the Kembel *et al*. (2014) paper, Meadow *et al*. (2014) reports on the same project with more focused BE findings related to ventilation, occupancy, and outdoor air source. Additional factors noted are weather data, the flooring of classrooms (sheet linoleum flooring; none were carpeted) and specific occupancy regimes (by direct observation). Sampling was conducted over the same time frame as occupancy observation. The ventilation system was altered for the study to test the influence of flushing and standard mechanical operation. No building design spatial factors besides occupancy variations were studied. Human source bacteria indoors, the impact of ventilation on microbial community composition and the impact of occupancy and ventilation

strategies on microbial environments were aligned with other studies (Adams *et al*. 2014; Kembel *et al*. 2013; Kembel *et al*. 2014; RInatala *et al*. 2008; Adams *et al*. 2016; Lax *et al*. 2017).

The second healthcare typology study, first reported by Ramos *et al*. in 2015 followed by Lax *et al*. in 2017, was for 10 patient rooms and 2 nearby nurse stations at a new hospital pavilion at the University of Chicago hospital. The study, which was designed as part of the Hospital microbiome project through development workshops, was reported by Smith *et al.* (2012) and Benjamin *et al.* (2013). In the workshops the following BE factors were noted for inclusion in the study: the total building design; spatial metrics that include occupancy, space use, user types and user interactions in space (facilitated by the proposed RFID system); the measuring of $CO_2$ concentrations used to estimate the percentage of recycled air; recording and measuring various ventilation metrics of the HVAC system (airflow and filtration system for both pressure, CO2 and microbial/viral community structure); and finally, project scope and sample size. In the follow up and final workshop Benjamin, Smith, Packman, Kelley, Landon, Bhangar, Vora, Jones, Keegan, Stephens, Ramos, Kirkup, Levin, Rosenthal, Foxman, Chang, Siegel, Cobey, An, Alverdy, Olsiewski, Martin, Marrs, Hernandez, Christley, Morowitz, Weber & Gilbert, (2013) added to the previous factors the cataloguing of surface materials and to the initial spatial metrics, the use of real time sensors and beam break sensors at indoor walkways for occupancy measures, as well as inpatient stay and associated clinical data. The need for spatial metrics was again emphasised, with reference to high spatial and temporal resolution observation of microbial and human occupant dynamics which were to be incorporated to enable more specific identification of the routes of transmission between building occupants and building infrastructure.

Ramos *et al*. (2015) report on the findings of the hospital microbiome study. The BE factors that were used included environmental conditions: *indoor dry-bulb temperature, relative humidity, humidity ratio, and illuminance in the patient rooms and nurse stations; and differential pressure between the patient rooms and hallways and outdoor air fractions in the heating, ventilating, and air-conditioning systems serving the sampled spaces*. The 10 patient rooms *were nearly identical, single-occupancy, west-facing perimeter adult inpatient rooms, classified as neutral pressure rooms on the mechanical plans. Their floor plans were flipped such that their sinks and bathrooms were installed along shared wa*lls. Detailed room metrics and detailed HVAC data were provided per room and nurse station. The built environment data collection campaign and corresponding analysis included long term characterisations of indoor environmental conditions. *The findings indicated that indoor temperature, illuminance and human occupancy/activity were all weakly correlated between rooms, while relative humidity, humidity ratio and outdoor air fractions showed strong temporal (seasonal) patterns and strong spatial correlations between rooms*. All room comparisons generated significant correlations for relative humidity values; stronger correlations existed between rooms on the same floor. The findings indicated clear variations in the factor metrics pre and post opening. An exhaustive data set on environmental metrics was recorded. *These strong correlations between humidity in sample locations indicate that the largest influence on room relative humidity values was the common HVAC system, with little effect from environmental conditions, occupancy, or occupant activity* (to the extent that it was measured). The building design spatial factors and metric data were measured for human occupancy and activity for the patient rooms; this was achieved by indoor $CO_2$ concentrations and infrared (IR) beam-break counters installed at the patient room doorways. The investigative studies (Kembel *et*

*al*. 2014; Hospodsky *et al*. 2012; Qian *et al*. 2012; Lax *et al*. 2014) support the selection of spatial metrics and occupancy measures. The data gaps noted by the researchers were the identification of user type and time or frequency and user activity, as well as user medical data. These metrics factors were noted and considered in the preceding workshops. When considering the beam break and $CO_2$ concentration the two surrogate measures in the patient rooms were fairly well correlated and the researchers suggest that both can serve as reasonable indicators of human occupancy. Other methods of assessing human occupancy need to be identified.

Lax *et al*. (2017) report on the bacterial dynamics found correlating microbial sampling data in the BE findings reported by Ramos *et al*. (2015) with noted correlation between the BE factors. Again, the same BE and spatial factors are relevant for this study and will not be repeated. As per previous studies mentioned, similar findings are reported concerning human source; however, surface material metrics and skin biota are noted. The bacteria in patient rooms, particularly on bedrails, consistently resembled the skin microbiota of the patient occupying the room. The bacterial communities on patients and room surfaces became increasingly similar over the course of a patient's stay. From a building design spatial perspective the follow findings are noteworthy: *Dynamic Bayesian network analysis suggested that hospital staff were more likely to be a source of bacteria on the skin of patients than the reverse but that there were no universal patterns of transmission across patient rooms (*Lax *et al*. 2017:1). *Network analysis revealed an almost complete shift in operational taxonomic unit (OTU)–level composition… Well beyond these dominant general skin samples from patients and nurses were generally the least diverse of all sample types by both metrics, whereas sample sites most likely to interact with the outdoors, such as shoes, floors, and recirculated indoor air from outdoor air (*Lax *et al*. 2017:3) as reported by Ramos *et al.* (2015) were the most diverse*.* The researchers reported a change in the community composition of patient rooms over time; it suggests that patients initially acquired room-associated taxa that predated their stay but that their own microbial signatures began to influence the room microbiota over time. Ramos and Stephens (2014) conducted an extensive literature review related to MoBE studies aimed at developing and recommending tools to improve built environment data collection for indoor microbial studies. Their review identified the following building factors: air and surface temperatures, relative and absolute humidity, outdoor air ventilation rates, HVAC particle filtration efficiency, human occupancy, human contact frequencies with surfaces, and several others. They suggest a categorisation of measures as suggested by Glass, Dribinsky, Yilmaz, Levin, Van Pelt, Wendel, Wilke, Eisen, Huse, Shipanova, Sogin, Stajich, Knight, Meyer & Schriml (2013) in the development review of the MIxS-BE package for BE and BE data fields and factors. (1) building characteristics and indoor environmental conditions, (2) HVAC system characterisations and ventilation rate measurements, (3) human occupancy measurements, (4) surface characterisations, and (5) air-sampling and aerosol dynamics. Ramos *et al.* strongly suggest (and the author firmly agrees) that more standardised building operational and environmental measurements will improve extrapolation or translation between indoor environments and studies. Adams *et al.* (2015) confirm this notion as they experienced the outcome of this very challenge in their meta-data analysis, *Microbiota of the indoor environment: a meta-analysis,* performed on a number of MoBE studies. *Lastly, as this field matures, standardized data collection and description methods of operational building characteristics will allow for more meaningful comparisons across disparate studies* (Adams *et al.* 2015:14).

Their analysis of the literature indicated the following fundamental building data factors to consider and measure: age of construction, floor areas and volumes, material descriptions, type of use, typical occupancy, history of water damage, occupant complaints, HVAC system type and operation, ventilation method and source, the use of humidifiers, and many others, as many of these have already been shown to influence microbial communities and are well known to influence other aspects of indoor air and building operation; important indoor environmental conditions, including air temperature, relative humidity, absolute humidity, and light levels in the sample space; HVAC system characterisations and ventilation rate measurements: airflow rates and ventilation rates for each sampled space, system operation and ventilation performance; ventilation modes for performance prediction with meteorological conditions; surface characterisations: porosity, composition, and environmental conditions immediately adjacent to materials can all affect microbial community structure, growth, and survival (Hota 2004; Tringe *et al.* 2008; Kolter & Greenberg 2006, 2010; Adams *et al.* 2016); and cleaning regime for surface (Dancer 2006, 2010).

From the various studies reviewed the following building design spatial factors and metric data were identified: human occupancy measurements, human activity measures and the related contact surfaces, similar to the studies already mentioned in this review. Ramos *et al. (2015)* offer a few options for occupancy measures, noting that environment specific appropriateness, ethics and cost are important factors in determining the best approach. These include: doorway break sensors for presence quanta only (uni or multi directional); video camera system (a collection of both systems); RFID and Bluetooth tracking systems (require pre-screening, but can be anonymous); proximity sensors (lack accuracy as they require movement); and $CO_2$ sensors with appropriate mass balance equations (Riley 1934) - these lack sensitivity and other data requirements and are potentially costly. The review concludes that *the number of studies collecting robust, long-term data using standardised methods to characterise building operation, human occupancy, indoor environmental conditions remain limited (*Ramos & Stephens *2014:244)*. Furthermore, the consequences of insufficient or inadequately described building operational and environmental characteristics will limit our ability to compare results from microbial ecology investigations, as noted earlier. Finally, Dedesko, Stephens, Gilbert, & Siegel (2015) investigated multiple measures of occupancy and occupant activity in the hospital microbiome study of 10 patient rooms. Predictably, occupancy would have a prominent effect on indoor microbial communities. Four methods were used for occupancy: (1) Beam-break, (2) CO2, (3) Lagged CO2, and (4) Combined methods. The method of determining occupant activity was the beam-break method (in this study activity was defined as crossing the room threshold). *Although a number of approaches have been analysed, there is still a gap in the literature. The majority of existing methods have focused on estimating occupancy. Much less attention has been given to detecting occupant activity (i.e., occupant movements), despite evidence indicating that such movements have a stronger effect than occupancy on certain aspects of IAQ, including increasing bio aerosol concentrations (*Dedesko *et al.* 2015:137)*.* Dedesko *et al.* present correlation findings with other BE factors and conclude that patient room temperature, RH, and humidity ratio are not suitable indicators of occupancy in this study, and for occupant activity measures. They postulate that this is *most likely due to the very small changes in each of these parameters (caused by low levels of occupancy), as well as the homogenizing effect of the hospital HVAC system in this relatively tightly controlled environment (*Dedesko *et al.* 2015:143)*.* Ramos *et al.* (2015) discuss findings of the effect of the HVAC.

A number of studies have investigated the microbiome of the built environment, but with far less rigour concerning BE factors than the studies mentioned (Frankel *et al.* 2012; Rintala *et al.* 2008; Tringe *et al.* 2008; Amend *et al.* 2010; Hospodsky *et al.* 2012; Horner *et al.* 2004) and more. The omission of BE factors co-studied results in under reporting on potential factors that influence the microbial community and limits the characterisation of the microbiome of building indoors. Unfortunately, they are far more in number than investigations that do provide BE data, as confirmed by Ramos and Stephens (2014). However, they still fundamentally contributed to the understanding and development of core theories of MoBE as we know it today. Adams emphasises the potential of BE data sets: *It would be powerful to be able to predict the microbiome of indoor spaces and their community dynamics based on knowledge of building factors* (Adams *et al.* 2016:231). The application of building design spatial factors are even fewer in number. Adams *et al.* (2015) in their literature reviews only identify four studies that consider a form of occupant activity and presence; this presents a far greater discrepancy - by spatial factors we infer more than only occupancy per space, yet numerous studies have consistently confirmed the importance of human occupancy and user identification, human activity, space use and spatial relationships. Levin and Corsi (2012) confirm this position: *Human activities and patterns and building operation seem to have the greatest impact on indoor microbial ecology (*Levin & Corsi 2012:4). Whereas Kembel *et al.* (2014) confirm the application of "spatial analytics" and *network analysis as a potentially powerful tool for applying indoor ecology and biogeography to the future of building design* (Kembel *et al.* 2014:9).

#### 3.3.1.4 BE DATA SAMPLING APPLICATIONS

As reported in the previous section, the application of building design spatial factors in most studies was invariant or omitted. However, the studies that did apply a form of spatial analysis or considered a form of spatial metrics are discussed here. Adams *et al.* (2013) only report the use of questionnaires for self-reporting by residents. Kembel *et al.* (2014) reviewed building plans, conducted field observations and developed a building information model (BIM), collected data on human use patterns and performed network analysis (spatial analytics) based on estimated qualitative assessments of expected patterns of human occupancy and diversity in space. Kembel *et al.* (2013) report no spatial data collection. In a position piece Brown *et al.* (2016) refer to a current investigation of the Bullitt Centre in Seattle, WA, which is the only office building to have attained Living Building Challenge certification; this building is currently being used to investigate relationships among design, occupant health, and microbial dynamics. Amend *et al.* (2010) in their study of 61 buildings of various typologies for fungal growth only considered a potential spatial metric of geographic distance between samples to correlate phylogenetic dissimilarity. Hospodsky *et al.* (2012) in their study of floor dust and resuspension only considered the internal movement of a single room and only recorded occupancy. Similarly, Qian *et al.* (2012) quantified size-resolved emission rates of airborne biological particles in a university classroom measuring occupancy. Meadow *et al.* (2014) report only on the collection of occupancy data by "technicians on site". In one of two papers on the hospital microbiome project Lax *et al.* (2017:9) report on the collection of $CO_2$ concentrations, and infrared doorway beam breaks used continuously as proxies for human occupancy/activity (*although neither of our methods could distinguish between hospital staff and non-staff visitors)* in their paper, *Methods to assess human occupancy and occupant*

*activity in hospital patient rooms.* Dedesko *et al.* (2015) investigated multiple measures of occupancy and occupant activity in the hospital microbiome study of 10 patient rooms. Predictably, occupancy would have a prominent effect on indoor microbial communities. The four methods were used for occupancy: Beam-break, $CO_2$, Lagged $CO_2$, and Combined methods. The prime method for determining occupant activity was the raw beam-break count, as the value for occupant activity by measuring doorway movements at 5min intervals; the second method comprised the $CO_2$ and Lagged $CO_2$ methods. *The $CO_2$ method and Lagged $CO_2$ method assumed that a change in direction and magnitude of the respective occupancy estimates between consecutive time intervals indicated a doorway movement* (Dedesko *et al.* 2015:138). Manual visual occupancy measures for multiple patient rooms by a single observer for five hours twice to test the two other methods suggested that the gold standard for true value occupancy and activity measures was manual observation. When comparing the occupancy methods to the manual count values the manual count for occupancy was accurate, but less so for activity (in this study defined as crossing the door threshold). The sensor was more accurate than the manual count of multiple spaces simultaneously. They conclude that for short term (activity) $CO_2$ applied methods are invariable, but not for long term (occupancy); the methods that incorporate $CO_2$ data (i.e., the $CO_2$, Lagged $CO_2$, and Combined methods) were preferred to estimate occupancy. For activity the preferred methods that utilize beam-break sensor data are the beam-break method and the combined method ($CO_2$ and beam break). When considering the applications for building design spatial factors in sampling, Kelley and Gilert (2013), in their literature on culture-independent analysis of microbial diversity in the BE and the dynamics and distribution of bacteria and fungi in indoor environments, note a critical research gap in the successful characterisation of the indoor environment. *In saying that, studies need to follow and sample the human inhabitants as they enter and move through the BE over time. To do this, it will be necessary to define the rate of change in the microbiome to sample at the appropriate temporal and spatial resolution* (Kelley & Gilbert 2013:4). It can then only be assumed and maybe accepted that the literature review by the authors indicated a lack of focused spatial data reported. Kelley captures the dynamic essence of microbial environments and the intra discipline data collection that is required in space and real time. Ramos and Stephens (2014) note that *insufficiently or inadequately described building operational and environmental characteristics can limit our ability to compare results from microbial ecology investigations* (Ramos & Stephens 2014:244). Finally, in their impressive literature review Adams *et al.* (2015) reflect on findings by Glass *et al.* (2014) and Ramos *et al.* (2015) *in that as this field matures, standardised data collection and description methods of operational building characteristics will allow for more meaningful comparisons across disparate studies* (Adams *et al.* 2015:4).

#### 3.3.1.5 ARCHITECTURAL **TYPOLOGIES INVESTIGATED**

Typology refers to the study of types defined by the comparative analysis and classification of structural or other characteristics into types (Guney 2007). When one considers typology in architecture, one classification is by its function versus its aesthetics and form. This does, however, initiate the theoretical supposition of universality, in many ways a modernist ideal. When referring to typology this review defines it as the functional type identified by the commonly accepted use pattern. From the literature reviewed within MoBE and studies on the periphery of microbial BE investigations the following types are amongst the few that have been part of initial characterisation - initial, due to the large quanta of unknowns in BE

microbiomes and the dynamic rate of knowledge gathering and new technologies and approaches being developed. Typologies include:

- Residential homes and flats: USA, Finland, Denmark, Australia, Canada, Indonesia, Mexico, South Africa, Micronesia, Netherlands, United Kingdom, Uruguay
- University classrooms: America
- Old-age home: Finland
- Hospitals: America
- Shopping centres and shops: Singapore, Mexico
- School class rooms: America, Denmark
- Office buildings: Indonesia, Micronesia, South Africa
- International space station
- Airplanes

A number of studies suggest the need to gather data seasonally, and in various climatic regions, identifying seasonal variation and climatic variation in microbial communities. Adams *et al.* (2013) and Amend *et al*. (2010) in their global fungi studies noted the variation in communities seasonally and climatically, as did Hospodsky *et al.* (2012) and others. Furthermore, the difference in cultural and social behaviour globally will by extension impact on the way in which the indoor built environment is used, and as a result of the large influence human occupancy and activity have on community composition (shown early in this review), will vary from culture to culture. Of the numerous MoBE or peripheral MoBE studies noted by typology and country, only two studies (hospital and university classroom) have applied architectural building design spatial analysis on building spatial factors sampled. Most studies have applied a form of spatial measures, but much less thorough.

#### 3.3.1.6 ARCHITECTURAL FACTORS AND HEALTH IN MoBE STUDIES

The large percentage, up to 90% (Klepeis *et al*. 2001) we spend indoors in our life time, will invariably mean that the manner in which we design, use, interact with and shape our indoor environments will impact on our health. Numerous studies reveal the presence of human associated biota in indoor spaces (Lax *et al*. 2017), indicating that we leave behind our microbial signature for the next occupant (in hospital environments and by extension other environments). It is not surprising that Rutala and Weber (2013) recommend room decontamination between inpatients to mitigate the risk of patient-to-patient transmission.

HAI estimates indicate that 9-10% (Brink, Van den Bergh & Kantor 2011; Rosenthal 2011) of hospital admissions are readmitted in the developed world and in excess of 15% in the developing world (Durlach, Mcllvenny, Newcombe, Reid, Doherty, Freuler, Rodriguez, Duse & Smyth 2012; Alvarez-Moreno, Perez-Fernandez, Rosenthal, Quintero, Chapeta-Parada, Linares, Pinilla-Martinez, Martinez-Saleg, Sierra & Mindiola-Rochel 2014; Brink *et al*. 2006)
Magill *et al*. (2014) conducted a large HAI prevalence study to ascertain the HAI rate in American hospital environments across 10 states. This study intended to update the National HAI data sets and prevalence rate statistics. Data from 183 hospitals showed that out of 11 282 patient samples, 452 had some form of healthcare associated infection (4.0%). The most common in ranking order: pneumonia, surgical site infection and gastrointestinal infections. *Clostridium difficile* was the most commonly reported HAI pathogen. Device-associated infections accounted for 25% of total HAIs (Magill *et al*. 2014). These statistics

indicate that in 2011 in the USA, out of 6.6 million patients, 720 000 had HAI infections in hospitals. Brown *et al.* (2016) argue that quality architecture should be a public health service considering the potential impact of BE on our health. However, to implement this health conscious approach and design *"bioinformed" buildings that foster well-being, architects need scientific knowledge that addresses the conditions and constraints of their work. Microbiology of the built environment* (MoBE) *research represents a prime opportunity for such design science collaboration* (Brown *et al.* 2016:1). Adams *et al.* (2016) report that current research highlights the potential connection between the indoor microbiome and health, although many of the recently published connections (with a few notable exceptions) are based on correlation, not causation. There are numerous examples of a direct link between specific microbes in the indoor environment and acute infections, the most noteworthy being Mycobacteria Tuberculosis in indoor environments (Yates, Tanser & Abubakar 2016). The indoor ventilation system can serve as a transmission route for pathogens including influenza, and the *fungus Aspergillus.* Kelley recommends *a deeper understanding of indoor microbial diversity to help inform public health policy, particularly in settings with many immune-compromised individuals such as hospitals, intensive care units and nursing homes* (Kelley & Gilbert 2013). The data from MoBE research could greatly contribute to a baseline index of air microbiota, which will be valuable for improving designs for the surveillance of natural or man-made release of virulent pathogens, as suggested by Tringe *et al*. (2008). Hospodksy *et al.* (2012) report that the inhalation of resuspension or shed organisms (from human skin biota) has the potential for current or previous occupants of a room to contribute substantially to inhalation exposure of bioaerosols. Kembel *et al*. (2013) state that the sequencing of samples from a hospital found in mechanically ventilated patient rooms were closely related to the facultative human pathogens *Staphylococcu sepidermidis, S.haemolyticus* and *Ralstonia pickettii.* The presence of pathogens was also reported in other studies – however, it must be noted that high-throughput DNA sequencing identifies full community but not viability, and thus sampling methods that consider viability such as more traditional culture methods need to be incorporated into study designs. Lax *et al.* (2017) report an instant increase on the floor and nurse station surfaces in the relative abundance of human skin–associated genera *Corynebacterium, Staphylococcus*, and *Streptococcus* and a decrease in previously dominant genera *Acinetobacter* and *Pseudomonas,* when a new hospital opened. Their study considered the microbial environment before and after the commissioning of a new hospital. They conclude that the *potential link between hospital-associated microbial communities and hospital-acquired infections, a leading cause of patient death, needs further investigation* (Lax *et al.* 2017:1).

#### 3.3.1.7 RESEARCH GAPS AND FUTURE INVESTIGATIONS

Various studies identify a number of research gaps. Dispersal and niche-based studies will be required to define and promote healthy indoor microbiomes (Kembel *et al.* 2014; Brown *et al*. 2016); these bring a more pragmatic and realistic approach, greatly under-expressed, in that scientific research can (and does) fail to inform architectural practice in three ways. *First, research results may not reach practitioners. Second, the research may not address questions that seem important or relevant to architects. Finally, researchers can fail to synthesize their findings into design tools or guidelines* (Brown *et al*. 2016:1); here the development of spatial analytic tools and design guidance models are paramount. The gaps in research are due to the neglect of BE factors and for this review spatial (both space and time) research remains

limited (Ramos & Stephens 2014). The BE represents a unique context and under-explored ecosystem; as in other microbial fields (soil, marine…), the built environment requires the development of standards for use in microbial studies (Glass *et al*. 2013; Gilbert *et al*. 2012) with reference to spatial data activity and occupancy. According to Desdeko *et al*. (2015), *one needs to understand occupant behaviours and their effect on the indoor air and surface parameters in a hospital environment. Although a number of approaches have been analysed, there is still a gap in the literature*. The majority of existing methods are based on estimations of occupancy whereas real-time rates could prove to be of greater value in dynamic microbial community characterisation; similarly, much less attention has been given to detecting occupant activity (movement in space), despite evidence indicating that such movements have a stronger effect than occupancy on certain aspects of IAQ (Desdeko *et al*. 2015). The limited measure of occupant activity (at most only by gate crossing/threshold crossing) presented in the various studies indicates an opportunity for new approaches in spatial syntactical measures. Considering niche space in microenvironments as noted by Keley and Gilbert (2013) and Kolter (2006, 2010), implies the need for finer detail studies in human activity and conversely the spatial function or probable activities in space in real time. A modelling tool for consideration for future studies could be the novel application of Space Syntax.

#### **3.3.1.8** CONCLUSION

It is clear from literature that the BE factors are critical in defining and understanding the composition of the indoor microbiome. What is more evident is the absence or limited number of spatial metrics actively applied in MoBE research investigations. Understanding the complexity of the indoor building ecology requires spatial metrics which include occupancy, occupancy type, activity in space and relationships between spaces in the built environment. *We unintentionally shape indoor microbial ecosystems through choices about human occupancy* (Green 2014:1). Architectural design decisions affect microbial community diversity and composition.

### 3.3.2 An overview of MoBE

As an addition to the main literature review in section 3.3.1, this summary intends to provide further insight into the MoBE interdisciplinary research. Kembel *et al.* (2013) researched the relationship between building design, biodiversity and human health in the first of two studies investigating a healthcare facility. Air samples were taken to characterise the airborne community in patient rooms. The rooms were distinguished by having either mechanical ventilation or natural ventilation via windows. The samples were sequenced for bacteria by 16S rRna. They found that the indoor environment had a lower abundance of microbes than the outdoor environment and that the mechanically ventilated rooms were less diverse in community than the naturally ventilated rooms. They established that the indoor microbial communities were closely related to human pathogens. They also defined factors that correlated with diversity and composition of the community, source of ventilation, airflow rate, relative humidity and temperature. The rooms that had low airflow and low humidity had bacteria more closely related to human pathogens. The relative abundance of bacteria associated with humans was higher indoors than outdoors. They observed a relationship between building design and bacteria diversity. In the second study, published in 2014, additional factors of function, form and organisation of space were included to understand the impact of design choices on the biogeography of the built environment. The same sample and sequencing methodology was followed: In total 2750 OTUs were sampled (Kembel *et al.* 2014), the most dominant being Proteobacteria, *Firmicutes* and Deinococci. The factors that influenced the bacteria community structure such as space type, building arrangement, human use and movement and ventilation source were as found in the previous study. Through spatial analysis, they found that spaces with a higher degree of connectedness and high human diversity connected through ventilation had a distinct set of bacteria. The weighing factor was ventilation; they concluded that human occupancy and use patterns had an effect on the communities in different spaces (Kembel *et al.* 2013).

Following on from the initial two papers, Brown *et al.* (2016) put forward a position based on the previous findings that building scientists need to make MoBE more practical for real world applications, to address both health and sustainability. Brown *et al.* suggest practice-based research with evidence-based design (EBD) could be a viable approach to translating indoor biome knowledge to architecture (Brown *et al.* 2016). Adams, Miletto, Lindow, Taylor and Bruns (2013) investigated the indoor environment at a university student housing building. They conducted a longitudinal study that considered bacterial and fungal identification, for indoors and outdoors. Five dust samples were collected monthly at each unit, which provided seasonal investigation. These samples were sequenced for the 16SRrna gene. Both fungi and bacteria were found. The fungi and bacteria OTU richness was higher outdoors than indoors. The samples were invariant across different rooms; however, the fungal abundance was only seasonal. Human taxa were more abundant indoors than outdoors, with abundant outdoor taxa found indoors but not the opposite. The authors found a partial correlation between the distance between sample sites on the composition of the sample community; this was true for bacteria but not for fungi.

Building on the work of Kembel *et al.* (2013, 2014), Meadow *et al. (*2014) conducted a study in a high-traffic university building. The objective of the study was to understand the factors that shape the diversity of bio-aerosols across space and time in the built environment. The aim was to test whether ventilation, occupancy and the outdoor environment influenced the indoor environment. They collected air samples from mechanically and naturally ventilated

sources and tracked outdoor air communities. The findings were similar to those of Kembel *et al.* (2013, 2014) and Adams *et al.* (2013), in that the human-associated bacteria were almost twice as abundant indoors as outdoors. They concluded that occupancy patterns and ventilation shape the indoor microbial community (Meadow *et al.* 2014). In a position piece, Jessica Green (2014) puts forward three reasons why society will embrace bio-informed design well before 2034. *Firstly, there is an explosion of research and public interest focused on host microbe interactions and in particular the human Microbiome. The second reason, I believe we will embrace bio-informed design is due to the rich history of examples where an ecosystem has been managed to achieve some desired result…this brings me to the third reason I believe we will embrace indoor bio-informed design. We're designing indoor microbial ecosystems right now, but we're doing it unintentionally* (Green 2014:113-114). Her position paper was based on the investigations (which she was part of) by Kembel *et al.* (2013) and Meadow *et al.* (2014). She closes with the thought that designers will…*collectively be designing and managing buildings with intention, to promote healthy indoor ecosystems* (Green 2014:113-114).

In a second hospital typology building study, Lax *et al. (*2017:1) hypothesise that…*microorganisms that inhabit hospitals may influence patient recovery and outcome.* This yearlong longitudinal study investigated surfaces, patients and staff as well as clinical outcomes in a new hospital before and after it opened. They found that the bacteria on touch surfaces and wardrooms resembled the skin biota of the patient that occupied the room. They also found that new patients acquired the biota of the room but eventually left their own microbial signature. Using Alpha and Beta diversity analysis, clinical factors were incorporated into the study but showed no correlation. What they did find through metagenomics analyses was the gene conferring antimicrobial resistance which was commonly and consistently found on room surfaces, but not on the skin of patients. Persistent unique genotypes of *Staphylococcus* and *Propionibacterium* were consistently identified in the rooms. They concluded that there was no universal pattern of biota transmission across patient rooms, but postulated that it could be related to the nursing staff.

Because of the availability of more sampling and metadata, due to an increased number of investigations, it is evident that the need exists to compare the various sample methodologies, sequencing types, environmental data loggers and sensors. The MoBE field is still in its infancy and the development of accepted standards and processes is becoming critical for comparability between studies. The author's literature review identified six unique studies addressing these requirements, each providing recommendations or selection options with advantages or disadvantages for selection. The review will refer to them briefly, as most of the data have been incorporated into the microbiology sampling literature for appropriate sampling types, sequences, and indoor loggers and sensors based on the elected study methodology applied as guidance for this study. Frankel *et al.* (2012) compare sampling methods and sequences assessment and Ramos and Stevens (2014) provide a detailed guide to the best tools to use for indoor microbial studies for all environmental and sampling categories. Ramos and Stephens (2014) and Adams *et al.* (2015) review methodology and approaches with outcomes and research gaps, and they provide insight and guidance to study designs and confirm broad factors such as geography, building structure, microbiota types and community variants. Adams *et al.* (2015) and Glass *et al.* (2013) present the development of a dedicated MiXS-BE MiXS extension platform for built environment sequencing studies in order to provide a standard sequencing set for comparability between MoBE studies. Marchesi and Ravel

(2015) recommend a standardised microbiome vocabulary to remove confusion, misinterpretation and misrepresentation between studies and enable accurate reporting. Lastly, Kelley and Gilbert (2013) investigated, through an extensive literature review on culture-independent analysis of microbial diversity, what the dynamics and distribution of bacteria and fungi are in indoor environments. They suggest that the outcomes could help inform public health policy and improve indoor environments that host immune-compromised people. From their review, they developed a table of signature microbes per site type, which is of particular relevance to the hospital focus of this thesis. They also found evidence suggesting that microbial interactions exist between humans and their indoor spaces; however, the mechanistic relationship enabling this interaction remains poorly characterised. Their review produced two core guides: a review of molecular studies indicating advantages and disadvantages of sequence selection, and the type by site list of the signature microbes (Kelley & Gilbert 2013). Leading up to the 2017 MoBE research agenda report, microbial sampling and analysis received the greatest attention compared to the limited attention paid to architecture and spatial programming, which were reviewed in Chapter 3.

## 3.4 BUILT ENVIRONMENT AND MICROBIAL SAMPLING IN MoBE STUDIES (REVIEW 3)

This literature review is integrated into chapter 8 of the thesis under Microbiology methodology. The basis of the sampling discussed originates from various literature reviewed for microbial sampling for surface and air cross compared as applied by various studies. The literature informed chapter 8 and was integrated into the methodology section. As an addition to chapter 8, a brief comparator extrapolated from key large literature reviews considering sampling, analytics and sequencing in the BE is presented below. These reviews are current and exhaustive, negating reapplying this process. Reference is made to 71 accepted and relevant reviewed literature articles. Note that some articles overlap in review sections due to the interdisciplinary nature of the studies, but were specifically reviewed in reference to this topic. A number of literature reviews were conducted by peers in the field during the course of this thesis development; they include: MoBE review on sampling and sequencing, MoBE literature review on sampling, analysis and sequencing, MoBE literature meta-analysis and sampling review, MoBE review on built environment sampling and equipment (Kelley & Gilbert 2013; Adams *et al.* 2016; Adams *et al.* 2015; Ramos & Stephens 2014). The author also conducted a critical analysis of sampling, sequencing and analysis options for microbiology to gain an understanding of the complexity of microbial studies, which was critical.

### 3.4.1 MICROBIAL SAMPLING

Chapter 8: microbiology, the methodology section includes an integrated sampling review. Previous MoBE literature reviews guided the development of a repeatable and tested methodology, that will enable the incorporation of the data set with other MoBE data sets, for future meta data analysis and studies.

**Microbial sampling analysis**

An analysis was conducted on microbial sampling. The literature was reviewed and analysed through a cross comparative Excel spreadsheet. Sampling was categorised into the broad categories of 1) air and 2) surface, with subcategories for important factors as per Table 3.11 The following literature and university microbiology and ecology departments were referenced in Table 3.12.

Table 3.11: Microbiology sampling analysis categories

| | **Air** | **Surface** |
|---|---|---|
| 1 | Type | Type |
| 2 | Target | Target |
| 3 | Sequencing applicable | Sequencing applicable |
| 4 | Appropriate environment | Appropriate environment |
| 5 | Flow rate | Flow rate |
| 6 | Aero diameter | Sample collection |
| 7 | Sampling media | Sampling media |
| 8 | Detection level | Detection level |
| 9 | Organism | Organism |
| 10 | Challenges | Challenges |
| 11 | Other comments | Other comments |
| | | Viability |

Table 3.12: Microbiology sampling reference list

| | **Air** (19 options) | **Surface** (16 options) |
|---|---|---|

| | | |
|---|---|---|
| 1 | Yale University | Frankel *et al.* (2012) |
| 2 | UC Oregon University | Buttner *et al.* (2004) |
| 3 | UC Berkeley | Lax *et al.* (2004) |
| 4 | Mui *et al.* (2008) | Hewitt *et al.* (2012 |
| 5 | Wichham *et al.* (2015) | Rintala *et al.* 2008 |
| 6 | Kembel *et al.* 2012) | Hormer *et al.* (200) |
| 7 | Frankel *et al.* (2012) | Kembel *et al.* (2014) |
| 8 | Horner *et al.* (2004) | Hospodsky *et al.* (2012) |
| 9 | Chung Yang Dai *et al.* (2015) | Adams *et al.* (2013) |
| 10 | Tringe *et al.* (2008) | |
| 11 | Meadow *et al.* (2013) | |
| 12 | De Boer *et al.* (2006) | |

Critical for the consideration of sampling of surfaces and particularly air, is sufficient biomass. It is accepted by literature that biomass levels in indoor environments are generally low (Kelley & Gilbert 2013) compared to other “natural” ecosystems. Selecting the appropriate sampler that can sample the required size, at relatively high volumes, in relatively short periods, with relatively low noise and still provide microbial samples that can be sufficiently sequenced (i.e. the cell walls have not been broken) and cultured for potential viability, is the goal. From the literature, information was also extracted to determine the appropriateness of the sampler for collecting in the required environments for the study time constraints. Adams *et al.* (2016) note a very important factor in sampling, namely spatial and temporal resolution. This relates to location and quantity of sample of that location and the change or stability in the microbial community. The temporal variability of microbes in buildings is due to a number of factors (environmental, movement, and ecological) directly related to time in space. The data analysis was critical in guiding the sampling selection process for this study. This summary and analysis for each factor considered are further developed in the methodology section of chapter 8 with the central goal of conducting a repeatable study with comparable data for this and future studies whilst considering current technologies and developments in microbiology. For this study both surface and air communities were sampled to determine the community composition of each hospital as representation of the hospital environment in the Cape Flats, South Africa.

In very simple and rudimentary terms, the analysis of microbial samples is a multi-step process and depends on the sample media and sample type. The process includes DNA extraction followed by DNA, RNA and protein quantification by NanoDrop™, followed by horizontal electrophoresis and selective PCR and then quantitative sequencing. Once the data have been extracted/sequenced from the samples, analytics follow via QIIME and green genes or other platforms and databases and then analytics normally performed by the statistical program *R*. These factors all require critical consideration to ensure that the study achieves the required goals, as microbial sequencing and sampling is a very costly and time consuming exercise. In the literature review *Studying the microbiology of the indoor environment* Kelley and Gilbert (2013) review the literature on culture-independent analysis of microbial diversity in the BE aimed at understanding the dynamics and distribution of bacteria and fungi in indoor environments. Extracted from this concise review is Table 3.13, which compares the various sequencing techniques for the analysis of microbial communities. This work is reviewed and accepted by peers and thus would not require further literature analysis.

Table 3.13: Comparison of different techniques for analysis of microbial communities (Kelley & Gilbert 2013)

| | *Description* | *Advantage* | *Disadvantage* |
|---|---|---|---|
| **Amplicon sequencing** | *The amplification and sequencing of a single gene from a broad selection of the microbiome. Traditionally applied to 16S rRNA for bacteria, but now being applied to a wide range of targets* | *Primarily cost and depth of analysis. Amplicon sequencing is very cheap and enables a rapid and deep characterization of the varying structure of microbial life under changing environmental gradients* | *This approach provides a narrow field of view, targeting a single gene, be it taxonomic or functionally informative, and only gives information about that one gene. It also can be affected by primer and amplification biases* |
| **Genomic sequencing** | *Sequencing of the genome of representatives of a community, ideally resulting in a single sequence, but more often resulting in 100s of genomic fragments* | *The genome enables a defined link between potential function and phylogeny, so that one can deduce that species x performs process y. When linked to a cultured cell, it can also be used to define gene function through targeted biochemical tests* | *Throughput is a problem. Sequencing the genome of isolated organisms has become rudimentary, but few can be isolated. Screening sorted cells from a community, followed by sequencing, is becoming viable, but often results in limited coverage of the genome owing to amplification bias* |
| **Metagenomic sequencing** | *Sequencing of a random sample of the genomic DNA from the cells of a microbial consortium* | *This technique enables broad observation of the taxonomic and functional genes from an entire community, without the bias associated with amplicon sequencing. With sufficiently deep sequencing, it is also possible to reassemble microbial genomes and other genetic elements* | *Current sequencing platforms require extensive starting material, although this is changing. Cost can be prohibitive, leading to only shallow characterization of the most dominant microbial taxa. The output only describes potential function, and it is often difficult to link function and phylogeny definitively. Also has the potential to sequence DNA from dead cells* |
| | *This techniques was applied in the thesis for the purpose of full community identification.* | | |
| **Metatranscriptomic sequencing** | *Random sequencing of the messenger, small and other RNAs from a microbial community that define the mechanism and response of microbial gene expression* | *As with metagenomics, this technique enables broad taxonomic and functional characterization, but of expressed genes, which enables deeper analysis of the community and targets the active members of the community. Sequence data can be mapped to known genomes to help identify phylogenetic-specific functional responses* | *Cost is prohibitive as the steps required to remove the 90-95% of ribosomal RNA to enable deeper characterization of the mRNA are expensive and time consuming, which also limits throughput. RNA is sensitive to degradation, and the half-life of mRNA is very short, which creates biases from sampling the community.* |
| **Metaproteomic sequencing** | *Random sequencing of the amino acid sequences that represent the protein material in a microbial communitysequences that represent the protein material in a microbial community* | *The primary advantage is the ability to identify proteins that have not only been expressed as mRNA but have also been folded and have potentially formed active proteins - for example, enzymes - in a cell. When combined with genomics and metatranscriptomics, it is possible to define protein isoform s and map protein function to phylogeny* | *The primary disadvantage of cost and throughput, which is still higher than metagenomics or metatranscriptomics. By itself, it is complicated to assign taxonomy* |
| **Metabolomic sequencing** | *Random characterization of the metabolic products present in a sample that might have been generated by a microbial community* | *This is the zenith of microbial activity, and when compared with that of other samples, the relative change in metabolite concentration can explain a lot about the functional consequence of genomic potential, or transcript and protein abundance* | *As with proteomics, metabolomics is limited by cost and throughput but also by identification of products. It also currently has a limit of detection, with very rare metabolites being hard to detect.* |

Due to the quantity of factors that are required in considering the appropriate sampling methodology and sampler, the data are presented in six tables, with the factors in no particular order of importance. They are found in Table 3.14, Table 3.15 and Table 3.16 for air, followed by Table 3.17,

Table 3.18 and Table 3.19 for surface. Further to these tables Adams *et al*. (2015) in a meta data analysis of numerous studies in different locations also provide a supporting table (Table 1, Adams *et al.* 2015:6-8) of sampling, sequencing and analysis used in various studies, which provides good insight and guidance for future work and application..

Table 3.14: Air sample analysis (part 1 of 3)

| Air sampling (Portion 1 of 3 of Air sampling table) | | | | | |
|---|---|---|---|---|---|
| **No** | **Reference** | **Sample type** | **Target** | **Sequencing applicable,** | **Environment** |
| 1 | Yale University | Anderson non-viable 8 stage cascade impactors | Size resolved (8 sizes) | PCR (Both quantitative and amplification sequencing) | Indoor – Human occupied |
| 2 | Yale University | SKC , Personal Environmental Monitors (PM 10, PM2.5) | Respirable or fine matter | PCR (Both quantitative and amplification sequencing) | Indoor – Human occupied |
| 3 | Yale University | ECO-HVS3000 with PM 10 inlet | | | |
| 4 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 filters | | | |
| 5 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 liquid impingers | | | |
| 6 | UC Oregon University | Two Welch 2425B-01 pumps, connect in series to 1 liquid impinger (SKC biosampler) | Respirable and fine particle | PCR (amplicon sequencing) | Indoor – Human occupied |
| 7 | UC Oregon University | AirCheck 2000 pump (SKC) one button Aerosol SampleR | Respirable and fine particle | PCR (amplicon sequencing) | Indoor – Human occupied |
| 8 | UC Berkeley | AirCheck XR 5000 pump (SKC) button Aerosol Sampler | | PCR (amplicon sequencing) | Indoor – Human occupied |
| 9 | Mui *et al*. (2008) | Anderson Impactor (single stage) | | | Indoor – Human occupied |
| 10 | Wichham *et al*. (2015) | Harvard impactors, Inc., Naples, Maine, USA | | | Indoor – Human occupied |
| 11 | Kembel *et al*. 2012) | Liquid impingers (BioSamplers) | Respirable and fine particle | PCR (amplicon sequencing) & 454 pyro-sequencing | Indoor - Human occupied<br>Outdoor – Adjacent HVAC unit |
| 12 | Frankel *et al.* (2012) | GSP samplers (CIS by BGI, Inc., Waltham, MA, USA) | | | Indoor – Human occupied |
| 13 | Frankel *et al*. (2012) | The BioSampler (SKC Inc.) | | | Indoor – Human occupied |
| 14 | Horner *et al*. (2004) | Surface Air System (SAS) High Flow air sampler (Bioscience International, Rockville, Md.) | Genera requiring cultivation on diagnostic media, subcultures for identification. | | Indoor - Human occupied<br>Outdoor – 15m from entrance |
| 15 | Chung Yang Dai *et al.* (2015) | fluorescent particle counter (BAC-6825, Institute of Optical Precision Machinery, Anhui, | | | Indoor - Human occupied |
| 16 | Chung Yang Dai *et al.* (2015) | Impactor air sampler (Anderson Air Sampler; PSW 6-level mesh air impactor | | | Indoor - Human occupied |
| 17 | Tringe *et al.* (2008) | Indoor air filters | | PCR using bacterial 16S specific primers16S rDNA PCR analysis | Indoor - Human occupied<br>Outdoor – River side |
| 18 | Meadow *et al.* (2013) | SKC Button Samplers & AirChex XR5000 pump (SKC Inc.) | Respirable and fine particle | PCR (amplicon sequencing) & 454 pyro-sequencing | Indoor - Human occupied<br>Outdoor – At pump house |

| | | | | | |
|---|---|---|---|---|---|
| 19 | De Boer *et al.* (2006) | Gil Air sampler pumps, sensidyne | | PCR (amplicon sequencing) | Indoor - Human occupied and unoccupied |

Table 3.15: Air sample analysis (part 2 of 3)

| **Air sampling (Portion 1 of 3 of Air sampling table)** | | | | | |
|---|---|---|---|---|---|
| **No** | **Reference** | **Sample type** | **Flow rate** | **Aero diameter** | **Sampling media** |
| 1 | Yale University | Anderson non-viable 8 stage cascade impactors | 28.3 L/min or 3.5 L/min per stage | Stage 1: 0.4-0.7<br>Stage 2: 7-1.1<br>Stage 3: 1,1-2.1<br>Stage 4: 2,1-3,3<br>Stage 5: 3.3-4.7,<br>Stage 6: 4.7-5.8<br>Stage 7: 5.8-9.0<br>Stage 8: >9/0 um | Polycarbonate filters, 0.2 um pore size, 81 mm diam / Glass fibre 81 mm diam |
| 2 | Yale University | SKC , Personal Environmental Monitors (PM 10, PM2.5) | 10.0 L/min for PM10, 4L/min for PM2.5 | Respiratory PM: da <10um<br>Fine PM: da <2.5um | Polycarbonate filters, 0.2um pore size 37 mm diam |
| 3 | Yale University | ECO-HVS3000 with PM 10 inlet | | | |
| 4 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 filters | | | |
| 5 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 liquid impingers | | | |
| 6 | UC Oregon University | Two Welch 2425B-01 pumps, connect in series to 1 liquid impinger (SKC biosampler) | 12.5L/min | 0.4-10um | Liquid impinger sterile water, filtered & 0.22um pore size cellulose nitrate filter |
| 7 | UC Oregon University | AirCheck 2000 pump (SKC) one button Aerosol SampleR | 4L/min | <100um | SKC filter, mix cellulose ester membrane, 1.2 um pore size, 25mm filter diam |
| 8 | UC Berkeley | AirCheck XR 5000 pump (SKC) button Aerosol Sampler | 4.0 L/min, 24 hrs | d<100 um | SKC filter, mix cellulose ester membrane, 1.2 um pore size, 25mm filter diam |
| 9 | Mui *et al*. (2008) | Anderson Impactor (single stage) | | | Suitable agar, Tryptocase Soy Agar (TSA) |
| 10 | Wichham *et al.* (2015) | Harvard impactors, Inc., Naples, Maine, USA | | | |
| 11 | Kembel *et al*. 2012) | Liquid impingers (BioSamplers) | 1hr at 12.5 l min | | molecular-grade water |
| 12 | Frankel *et al.* (2012) | GSP samplers (CIS by BGI, Inc., Waltham, MA, USA) | 6hr at 3.5 l min | | polycarbonate filters (37 mm, pore size 1.0 lm, or teflon filters (37 mm, pore size 1.0 lm; and Polycarbonate filters (N = 129) & Teflon filters (N = 129) |
| 13 | Frankel *et al*. (2012) | The BioSampler (SKC Inc.) | 5hr at 12.5 l min | | |

| | | | | | |
|---|---|---|---|---|---|
| 14 | Horner *et al*. (2004) | Surface Air System (SAS) High Flow air sampler (Bioscience International, Rockville, Md.) | 1x 20 sec & 1x 60 sec, | | Media used were those described by Pitt and Klich |
| 15 | Chung Yang Dai *et al*. (2015) | fluorescent particle counter (BAC-6825, Institute of Optical Precision Machinery, Anhui, | 5hr at 1.0 l min, UV current 1.46 A, tube voltage 550 V, Particles per minute. | | |
| 16 | Chung Yang Dai *et al*. (2015) | Impactor air sampler (Anderson Air Sampler; PSW 6-level mesh air impactor | 28.3 L/min for 5 minutes. | | The collected air samples were plated onto blood agar |
| 17 | Tringe *et al*. (2008) | Indoor air filters | | | The suspension was filtered through WhatmanH filter paper (#114) to remove big particles. |
| 18 | Meadow *et al.* (2013) | SKC Button Samplers & AirChex XR5000 pump (SKC Inc.) | 8hr at 4.0 l per min | | 25 mm-diameter cellulose ester filters (1.4 lm pore diameter) |
| 19 | De Boer *et al*. (2006) | Gil Air sampler pumps, sensidyne | 8hr at 2.0 l per min | | Glass fiber filter |

Table 3.16: Air sample analysis (part 3 of 3)

| | | **Air sampling (Portion 1 of 3 of Air sampling table)** | | | | |
|---|---|---|---|---|---|---|
| **No** | **Reference** | **Sample type** | **Detection level** | **Organism** | **Challenges** | **Comments** |
| 1 | Yale University | Anderson non-viable 8 stage cascade impactors | 2,000 to 3,000 bacterial cells, 10 to 25 fungal cells | Study specific | low flow rate, no detection & limitations on sampling times | |
| 2 | Yale University | SKC, Personal Environmental Monitors (PM 10, PM2.5) | | | | |
| 3 | Yale University | ECO-HVS3000 with PM 10 inlet | | | | |
| 4 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 filters | | | | |
| 5 | UC Oregon University | GAST 1023 -V102, vacuum pump, 12 liquid impingers | | | | |
| 6 | UC Oregon University | Two Welch 2425B-01 pumps, connect in series to 1 liquid impinger (SKC biosampler) | <106 cells | Study specific | Noisy to operate in indoor environments & refill of impingers | |
| 7 | UC Oregon University | AirCheck 2000 pump (SKC) one button Aerosol SampleR | <106 cells | Study specific | Low biomass, long length of time, and no detection | |
| 8 | UC Berkeley | AirCheck XR 5000 pump (SKC) button Aerosol Sampler | enough DNA recovered for 16S | Study specific | Low biomass, long length of time, and no detection & noise | |
| 9 | Mui *et al*. (2008) | Anderson Impactor (single stage) | | Study specific | | |
| 10 | Wichham *et al*. (2015) | Harvard impactors, Inc., Naples, Maine, USA | | Study specific | | |
| 11 | Kembel *et al*. 2012) | Liquid impingers (BioSamplers) | | Study specific | | |
| 12 | Frankel *et al*. (2012) | GSP samplers (CIS by BGI, Inc., Waltham, MA, USA) | | Study specific | day-long airborne measurements may | GSP found to be better than the biosampler, higher sampling |

| | | | | | | |
|---|---|---|---|---|---|---|
| 13 | Frankel *et al*. (2012) | The BioSampler (SKC Inc.) | | Study specific | adequately represent longer-term exposure of at least 2-month periods (the age of the vacuumed dust was unknown). | efficiency, yet higher TIP values found in the biosampler. Comparing airborne vs settled dust the EDC correlated more significantly with both GSP and the biosampler than for the DFC fungal |
| 14 | Horner *et al*. (2004) | Surface Air System (SAS) High Flow air sampler (Bioscience International, Rockville, Md.) | | Study specific | | cultureable airborne fungi |
| 15 | Chung Yang Dai *et al*. (2015) | fluorescent particle counter (BAC-6825, Institute of Optical Precision Machinery, Anhui, | | Study specific | air samples onto culture plates using impaction or natural sedimentation, followed by incubation for 2-3 days, is time consuming and laborious for routinely monitoring air quality. It is widely believed that developing a real-time method to measure airborne microorganisms is essential | demonstrated that fluorescent particle counters can be used to precisely measure a variety of laboratory generated biologic particles |
| 16 | Chung Yang Dai *et al*. (2015) | Impactor air sampler (Anderson Air Sampler; PSW 6-level mesh air impactor | | Study specific | | Real-time monitoring function and the detection interval can be chosen according to different real-time monitoring purposes & It provides the ability of simultaneous counting of bioaerosols and nonbioaerosols, |
| 17 | Tringe *et al*. (2008) | Indoor air filters | | | | |
| 18 | Meadow *et al*. (2013) | SKC Button Samplers & AirChex XR5000 pump (SKC Inc.) | | Study specific | | |
| 19 | De Boer *et al*. (2006) | Gil Air sampler pumps, sensidyne | Genotyping of Pneumocystis isolates was performed | | Of the 6 samples from the pump filters no Pneumocystis organisms were detected by real-time PCR | |

Table 3.17: Surface sample analysis (part 1 of 3)

| | **Surface sampling (Portion 1 of 3 of Surface sampling table)** | | | | | | |
|---|---|---|---|---|---|---|---|
| | **Reference** | **Type** | **Sample type** | **Target** | **Sequencing applicable** | **Environment** | **Flow rate** |
| 1 | Other | Wipe | Woven polyester rayon, cotton / non woven: polyester, sponge | spores and pathogens | Molecular methods, PCR | Indoor – porous, non porous surfaces, dry, wet surfaces | |
| 2 | Frankel *et al*. (2012) | Wipe | EDC: polypropylene folder with electrostatic cloths, DFCs was collected by vacuuming | Dust | | Indoor - floor | Electrostatic cloth surface exposure area of 0.0209 m2 (19 · 11 cm) & polycarbonate filters (76 mm, pore size 1 lm; |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 3 | Buttner *et al*. (2004) | Wipe | Heavy Wipe | | culture and QPCR | Indoor - surfaces | volume 1.0 to 1.5 ml |
| 4 | Lax *et al*. (2014) | Wipe | | Bacteria | 16S rRNA | Indoor – body and home | |
| 5 | Hewitt *et al*. (2012 | Swab | dual tip sterile cotton swabs | Bacteria | 16S Rrna & 454 pyrosequencing | Indoor - touch surfaces various | |
| 6 | Buttner *et al*. (2004) | Swab | a swab sample processing (SSP) kit | | | Indoor - surfaces | volume 1.0 to 1.5 ml |
| 7 | Buttner *et al*. (2004) | Wipe | a swipe | | analyzed by culture and QPCR. | Indoor surfaces | volume 1.0 to 1.5 ml |
| 8 | Other | Swpte | Cotton, polyester, Rayon, Sponge, Nylon flocked, calcium alginate | spores and pathogens | Molecular methods, PCR | Indoor – porous, non-porous surfaces, dry, wet surfaces | |
| 9 | Other | Vacuum | HEPA socks: 0.1um, 3M Trace evidence collection filters | | Molecular methods | | |
| 10 | Rintala *et al*. (2008) | Vacuum | vacuum cleaner | Dust | 16S Rrna & 454 pyrosequencing | Indoor - surfaces | |
| 11 | Frankel *et al*. (2012) | Vacuum | vacuum cleaner | Dust | | Indoor - furniture surfaces | |
| 12 | Horner *et al*. (2004) | Vacuum | Vacuum | Dust | | | |
| 13 | Kembel *et al*. (2014) | Vacuum | Shop-VacH 9.4L Hang Up vacuum | Dust | 16S Rrna & 454 pyrosequencing | Indoor - surfaces | |
| 14 | Hospodsky *et al*. (2012) | Vacuum | high-volume vacuum sampler fitted with a Mitest adapter and dust filter | | 454 GS-FLX pyrosequencing | Indoor – floor 1.5m Outdoor – window ledge | duct supply air and HVAC filter dust collected on a 0.8-mm pore-sized, 37-mm diameter sterile polycarbonate track etched (PCTE) filter that was |
| 15 | Other | Contact | Adhesives, contact/ RODAC plates, dipslides | | Not available for Molecular methods | Indoor | Contact plates most widely used, limited information on tape and adhesives |
| 16 | Adams *et al*. (2013) | Settling plates | suspending sterile, empty, 9cm petri dish, 0.3m from the ceiling | wipe the surface. | 16S Rrna & 454 pyrosequencing | Indoor - surface | This petri-dish sampler with a cotton swab moistened with sterile water |
| 17 | Other | Bulk collection | Visible material collection by scoop, card, scissor, packaged and transported | | Molecular methods, PCR | Non-porous surface by card procedure | |

Table 3.18: Surface sample analysis (part 2 of 3)

| | | Surface sampling (Portion 2 of 3 of Surface sampling table) | | | |
|---|---|---|---|---|---|
| | **Reference** | **Type** | **Sample type** | **Sampling media** | **Challenges** |
| 1 | Other | Wipe | Woven polyester rayon, cotton / non woven: polyester, sponge | Wet: PBS, water, saline, syringers solution, Copa SRK formula, rinse solution, neutralising buffer | Good for: large area, various surfaces, easy use, low cost. The bad for: Operator efficiency impact, extraction from sponge requires stomacher procedures, recovery efficiency based on collection and extraction conditions |
| 2 | Frankel *et al*. (2012) | Wipe | EDC: polypropylene folder with electrostatic cloths, DFCs was collected by vacuuming | onto polycarbonate filters (76 mm, pore size 1 lm | |
| 3 | Buttner *et al*. (2004) | Wipe | Heavy Wipe | The Heavy Wipe was folded, placed in a sterile bag with 40 ml of PBT. | |
| 4 | Lax *et al*. (2014) | Wipe | | | |
| 5 | Hewitt *et al*. (2012 | Swab | dual tip sterile cotton swabs | | |
| 6 | Buttner *et al*. (2004) | Swab | a swab sample processing (SSP) kit | moistening the surface material section with 20 drops of the supplied buffer | |
| 7 | Buttner *et al*. (2004) | Wipe | a swipe | moistening the sponge in a sterile bag with 30 ml of 0.01 M phosphate buffer with 0.05% Tween (PBT; pH 7.0). The swipe was squeezed to remove the excess buffer and then used to sample surface | |
| 8 | Other | Swipe | Cotton, polyester, Rayon, Sponge, Nylon flocked, calcium alginate | Wet: PBS, water, saline, syringers solution, Copa SRK formula, rinse solution, neutralising buffer | The good: small localised area, hard to reach areas, various surfaces, easy use, low cost. The bad: Operator efficiency impact, Small localised areas requires many swabs, recovery efficiency based on collection and extraction conditions, recovery efficiency highly variable based on previous point |
| 9 | Other | Vacuum | HEPA socks: 0.1um, 3M Trace evidence collection filters | | The good: Large surface areas, porous or carpeted areas, filters in expensive, ease of use. The bad: difficult to process filters, high risk of cross contamination in lab, filters become clogged |
| 10 | Rintala *et al*. (2008) | Vacuum | vacuum cleaner | | |
| 11 | Frankel *et al*. (2012) | Vacuum | vacuum cleaner | | strong correlation with the EDC, and moderate with the DFC dust for fungi. Comparing airborne vs settled dust the EDC correlated more significantly with both GSP and the bio-sampler than for the DFC fungal measures |
| 12 | Horner *et al*. (2004) | Vacuum | Vacuum | | |
| 13 | Kembel *et al*. (2014) | Vacuum | Shop-VacH 9.4L Hang Up vacuum | manually extracted from filters | |

| | | | | | |
|---|---|---|---|---|---|
| 14 | Hospodsky *et al*. (2012) | Vacuum | high-volume vacuum sampler | | |
| 15 | )ther | Contact | Adhesives, contact/ RODAC plates, dipslides | | The good: low cost, direct observation, preserve deposition distribution, contact plates preserve viability, reduce organism loss due to various processing steps, ease of use. The bad: limited collection areas, contaminants and other may mask organisms of interest, requires direct observation method/growth to evaluate |
| 16 | Adams *et al*. (2013) | Settling plates | suspending sterile, empty, 9cm petri dish, 0.3m from the ceiling | | collecting settled dust, which is accumulative. Although the placement of the sampler at a particular height has the potential to introduce bias because the dynamics of particles are known to vary depending on their size (Nazaroff, 2004). |
| 17 | Other | Bulk collection | Visible material collection by scoop, card, scissor, packaged and transported | | The good: Large quantity for analysis, ease of use, low cost. The bad: must be visible material, Lab constraints the number of collected material, contaminants in bulk samples could inhibit downstream analysis methods. |

Table 3.19: Surface sample analysis (part 3 of 3)

| | **Surface sampling (Portion 3 of 3 of Surface sampling table)** | | | | | |
|---|---|---|---|---|---|---|
| | **Reference** | **Type** | **Sample type** | **Comments** | **Viability** | **Organism** |
| 1 | Other | Wipe | Woven polyester rayon, cotton / non-woven: polyester, sponge | | based on wetting agent/transport conditions/ extraction processing | |
| 2 | Frankel *et al*. (2012) | Wipe | EDC: polypropylene folder with electrostatic cloths, DFCs was collected by vacuuming | day-long airborne measurements may adequately represent longer-term exposure of at least 2-month periods (the age of the vacuumed dust was unknown). strong correlation with the EDC, and moderate with the DFC dust for fungi. Comparing airborne vs settled dust the EDC correlated more significantly with both GSP and the biosampler than for the DFC fungal measures | | |
| 3 | Buttner *et al*. (2004) | Wipe | Heavy Wipe | | | |
| 4 | Lax *et al*. (2014) | Wipe | | | | OTUs sourced from humans were mainly Actinobacteria and Proteobacteria. opportunistic human pathogens *Pantoea agglomerans* and *Acinetobacter baumannii* |
| 5 | Hewitt *et al*. (2012 | Swab | dual tip sterile cotton swabs | | | high proportion of bacterial genera associated with human skin, |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | particularly *Propionibacterium.* High number of *Corynebacterium, Lactobacillus, Staphylococcus, and Streptococcus,* |
| 6 | Buttner *et al*. (2004) | Swab | a swab sample processing (SSP) kit | | | |
| 7 | Buttner *et al*. (2004) | Wipe | a swipe | | | |
| 8 | Other | Swpte | Cotton, polyester, Rayon, Sponge, Nylon flocked, calcium alginate | | based on wetting agent/transport conditions/ extraction processing | |
| 9 | Other | Vacuum | HEPA socks: 0.1um, 3M Trace evidence collection filters | | function of vulnerability to air transport during collection, storage transport and processing conditions | |
| 10 | Rintala *et al*. (2008) | Vacuum | vacuum cleaner | | | |
| 11 | Frankel *et al*. (2012) | Vacuum | vacuum cleaner | day-long airborne measurements may adequately represent longer-term exposure of at least 2-month periods (the age of the vacuumed dust was unknown). | | |
| 12 | Horner *et al*. (2004) | Vacuum | Vacuum | | | water indicator fungi: *Chaetomium spp., Ulocladium spp., and Stachybotrys spp.* |
| 13 | Kembel *et al*. (2014) | Vacuum | Shop-VacH 9.4L Hang Up vacuum | | | |
| 14 | Hospodsky *et al*. (2012) | Vacuum | high-volume vacuum sampler fitted with a Mitest adapter and dust filter | | | |
| 15 | Other | Contact | Adhesives, contact/ RODAC plates, dipslides | | viable by contact plates, and only by some adhesives | |
| 16 | Adams *et al*. (2013) | Settling plates | suspending sterile, empty, 9cm petri dish, 0.3m from the ceiling | | | Fungi |
| 17 | Other | Bulk collection | Visible material collection by scoop, card, scissor, packaged and transported | | Function of storage, transport and processing procedures | |

The application of these summary tables are found in the integrated review and sampling selections made in chapter 8 microbial methodology.

### 3.4.2 A REVIEW OF SEMINAL WORKS IN MoBE ON BUILT ENVIRONMENT METRICS, TOWARDS IMPROVING FUTURE ARCHITECTURAL DESIGN

In the preceding sections on the MoBE literature review with emphasis on spatial metrics, a number of BE environmental factors were defined and extrapolated from the literature; in addition to the literature already reviewed and reported on, the author has reviewed in excess of 90 literature pieces on architecture and engineering. The collective input from each of these assessments enabled the development of the chapter 9 environmental methodology and other aspects of this thesis. Finally, three seminal literature reviews produced by Ramos and Stephens (2014) *Tools to improve built environment data collection for indoor microbial ecology investigations;* Adams *et al. (*2015) *Microbiota of the indoor environment: a meta-analysis* and Adams *et al.* (2016) *Ten questions concerning the microbiomes of buildings* in and for the MoBE field are discussed. They offer a succinct and very relevant set of BE approaches valid for the fields of architecture and engineering, but tailored to MoBE in critical review of interdisciplinary investigations.

Topic:

- Microbiology of the built environment, providing insight into the research field and elucidating the contribution, presence or absence of building design investigation in MoBE

Literature review hypothesis:

- Architectural design considers built environment factors in building design; these factors influence the composition of the microbial environment

Literature review research questions asked with reference to: known and new contributions in BE; agreement or disagreement with peers; the knowledge gaps identified; key concepts identified by the thesis author; and the context provided to the MoBE research field.

- Did the study investigate building and microbial relationships?
- Which engineering and architectural factors were considered?
- What sampling methods were utilised for the BE and how were these applied based on the factors identified?
- The study period for BE factors: short term (- 2 days) or longditudal (+ 3 days)?
- What were the challenges?
- Did the study discuss or make reference to health and/or IPC in the built environment?

**Built environment factors and sampling**

The effect of building design and operations, the indoor environmental conditions and the users and their activity on the structure of building microbiomes has been well reported. Ramos and Stephens (2014) and Lax *et al*. (2017) reported that basic environmental parameters such as temperature, relative humidity and human occupancy patterns are influential in the structure and dynamics of building microbiomes. Yet there are few studies collecting full BE data. Ramos and Stephens (2014) in their review of BE tools for application in building microbiology studies categorised studies based on the number of BE metrics utilised. They conclude that the ideal would be to report on the full suite of factors (which will

be described later); however, the absolute minimum metrics would require temperature, relative humidity and lux or lighting source (all factors related to ecological processes) (Adams *et al.* 2016). The indoor environment can be categorised as the new frontier in ecosystem exploration; it is a complex and unique environment of which we know and understand very little. Characterising the factors of the ecosystem, i.e. BE metrics, provides insight into the ecology of the indoor environment. Building characteristics that are fundamental to capture are building age, construction type, floor areas and volumes, materials, functional use classification, occupancy ventilation sources and building systems. These factors influence both the air and surface environments in building. Broad categories to be considered are the indoor conditions, HVAC system and/ or natural ventilation, human occupancy and surface characteristics and the cleaning regime. Each of these categories has subsets of parameters and methods with tools to characterise and measure them (Ramos & Stephens 2014). One such parameter worth mentioning is $CO_2$ measures. $CO_2$ is used in the fundamental calculation of airflow, air quality and occupancy determinants. It is used as a surrogate for detecting increased occupancy and measuring IAQ and reported in most ventilation studies emanating from the Wells and Rilley (1934) mass balance equation. Adams *et al.* (2015) from their meta data study report that *The factors with the largest explanatory power for bacterial communities were: individual study, geolocation, and specific sampling matrix … source of the sequenced material differentiating air, surfaces, dust, and water; and the use of the building.* The dynamic nature of ecosystems and by extension the built environment ecosystems requires both space and time consideration in all metrics (Kelley & Gilbert 2014*).* The influence of season and climatic and geographic location is equally important, as reported in numerous studies (Hospodsky *et al.* 2012; Amend *et al.* 2010 …). Increased attention is given to not only the presence of biota in spaces, but also their viability. Approaches to studying the active portion of microbial community, while still culture independent, are beginning to be applied to indoor environments, and future work is likely to inform the extent of microbial activity and persistence in the indoor environment. An area of future development is sensors (Adams *et al.* 2016). The development of real time environmental sensors and even microbial sensors would add tremendous value and insight into building ecology.

Ramos and Stephens (2014) developed a matrix of BE tools available for future MoBE studies. It comprises the various BE parameters, the measurement or collection method and key considerations in application. This matrix was developed from an exhaustive review of a number of leading researchers' contributions. The author accepts the soundness of the data and does not see the value in a repeat exercise. Most of the referenced literature and collection methods were reviewed by the author. However, the table is inserted here for reference and in confirmation and support of parametric choices made in this thesis (note: before this table was published).

Table 3.20: Tools for improved collection of built environment data, taken from Ramos and Stephens (2014)

| **BE parameters and collection methods** | | | |
|---|---|---|---|
| **1** | Parameter | Measurement/collection method | Important considerations |
| | **Building characteristics and environmental conditions** | | |
| | *Basic building characteristics* | *Surveys, visual assessments* | *Age of construction, floor areas and volumes, material descriptions, type of use, typical occupancy, history of water damage, occupant complaints, HVAC system type and operation,* |

| | | | |
|---|---|---|---|
| | | | *ventilation method and source, the use of humidifiers, etc.* |
| | *Indoor T/RH, absolute humidity, and artificial/ natural light* | *Portable, off-the-shelf, battery-powered sensors with data loggers* | *Storage capacity, accuracy, precision, battery power* |
| | *Outdoor T/RH, absolute humidity, and light* | *Publicly available meteorological data or local weather station installations* | *Data availability, installation location* |
| **2** | Parameter | Measurement/collection method | Important considerations |
| | **HVAC system characteristics and ventilation rates** | | |
| | *Spot measurements of airflow rates at AHU* | *Correlate pressure readings to fan curve data by the fan manufacturer* | *Requires knowledge of fan manufacturer and in-situ verification* |
| | | *Traverse velocity with pitot tubes or hot-wire anemometers (multiplied by duct area)* | *Requires knowledge of duct areas, high uncertainty* |
| | | *Pressure matching with powered, calibrated fan* | *Typically greater accuracy than capture hood, limited to smaller systems, requires clear access to AHU* |
| | | *Airflow metering plates* | *Requires modifications for larger AHUs* |
| | *Spot measurements of airflow rates at individual supply diffusers or return grilles* | *Airflow capture hood* | *Limited accuracy under some conditions* |
| | | *Air velocity or pressure readings correlated to diffuser characteristics* | *May not accurately reflect in-situ performance, requires knowledge of specific manufacturer* |
| | | *Traverse velocity with pitot tubes or hot-wire anemometers (multiplied by duct area)* | *Requires knowledge of duct areas, high uncertainty* |
| | | *Pressure matching with powered, calibrated fan operating as flow hood* | *Typically, greater accuracy than capture hood* |
| | *Continuous flow measurements* | *Flow meters installed directly into HVAC system (e.g. venturi meters, flow nozzles, orifice meters, rotameters)* | *Invasive, requires HVAC access, data logger, and power* |
| | | *Duct pressure correlations with spot flow measurements* | *Simple and cost-effective, requires data logger and power* |
| | *Outdoor air (OA) fraction in mechanical HVAC systems* | *Tracer (e.g., temperature, CO2, or SF6) in RA, SA, and OA* | *Accuracy issues at low concentration changes, high costs for accurate sensors, requires injection, data logger, and power* |
| | | *Zone tracer testing (e.g., CO2, SF6) coupled with room volume* | *Costly, labor intensive, requires assumptions for mixing* |
| | | *Building automation system (BAS) readings, including economizer settings* | *Often low accuracy, sensor reliability, requires access to facility data, typically only present in large buildings* |
| | *Air change rates (ACH)* | *Active tracer gas (e.g., CO2 or SF6)* | *Costly, labor and equipment intensive* |
| | | *Passive tracer gas (e.g., PFT)* | *requires injection and well mixed environment Passive tracer gas (e.g., PFT) Limited to longer-term time-averaged air change rates* |
| | *Natural ventilation rates through windows* | *Pitot tube array* | *Labor intensive, invasive* |
| | *HVAC on/off* | *Current draw on AHU fan or AC compressor* | *Requires HVAC access and data logger* |
| | | *Supply temperature measurements* | *Inexpensive and simple, but issues with averaging times; only works for heating or cooling modes* |
| | | *Vibration or magnetic field* | *Requires equipment training period, inexpensive field sensors are commercially available* |
| | *Duct leakage fractions/ flows* | *Fan pressurization, delta-Q, or nulling tests* | *Time intensive* |

| | | | |
|---|---|---|---|
| | *Particle removal efficiency of HVAC filters* | *Upstream/downstream particle concentrations* | *Expensive instrumentation, requires HVAC access* |
| | | *Whole-zone elevation and decay* | *Expensive instrumentation, time-consuming, requires mixing assumptions and knowledge of HVAC airflow rates, but can also be gathered from long-term time-resolved data* |
| **3** | Parameter | Measurement/collection method | Important considerations |
| | **Human occupancy/ activity measurements** | | |
| | *Number of occupants* | *Manual observational* | *Not feasible for long-term, continuous sampling* |
| | | *Uni-directional IR beam break people counting* | *Better for small environments with limited number of entrances/exits, limited accuracy* |
| | | *Directional beam break or thermal people counting* | *Higher accuracy, costlier, limited number of entrances/exits, requires power* |
| | | *Video þ people counting software* | *Costly in larger environments, requires power* |
| | | *Movement sensors based on IR proximity, light, or acoustics* | *May not represent true occupancy* |
| | | *CO2 mass balance* | *Costly, variable emission rates, requires well-mixed environment, well characterized ventilation, and power* |
| | | *Pressure sensors in HVAC systems* | *Requires high-resolution data loggers, accuracy unknown* |
| | | *RFID tags or Bluetooth tracking* | *Pre-screening/ID required, provides continuous monitoring among people and between locations* |
| | *Occupant profiles* | *Survey questions: age, gender, culture, socioeconomics* | *Requires careful survey design* |
| | *Non-human occupants Survey questions: pets,* | *Non-human occupants Survey questions: pets,* | *Non-human occupants Survey questions: pets* |
| | *Cleaning activities Visual observation* | *Cleaning activities Visual observation,* | *Cleaning activities Visual observation* |
| | *Activity/resuspension* | *Optical particle counters* | *Expensive instrumentation, requires power* |
| **4** | Parameter | Measurement/collection method | Important considerations |
| | **Surface characterisation** | | |
| | *Surface temperature* | *Thermistors or thermocouples* | *Data logging capabilities preferred over spot measurements* |
| | *Water activity (or equilibrium relative humidity* | *Approximated as relative humidity in a sealed chamber installed on sample surface* | *Only provides surrogate measure, few commercial devices* |
| | *Porosity, water vapor permeance, moisture content, and other moisture properties* | *Vacuum saturation tests, SEM, NMR, capacitance methods, water uptake experiments, and others* | *Difficult to measure in-situ, some are costly and destructive techniques* |
| | *Cleaning strategies/details* | *Records of cleaning products and schedule, or microbial loads* | *Potential data quality issues with surveys, issues with standardization on microbial loads* |
| | *Building material/ composition assessment and survey of moisture events* | *Qualitative descriptions, surveys, and quantitative material analysis* | *Potential data quality issues with surveys, material survey is time consuming* |
| | *Identification of highly touched surfaces* | *Visual assessment or proximity IR* | *Time-consuming for visual assessment, inaccuracies in proximity sensors* |

## 3.5 MICROBIOLOGY, MEDICAL, THE BUILT ENVIRONMENT AND HEALTH (REVIEW 4)

### 3.5.1 MICROBIOLOGY

Various literature was considered and analysed under this topic (the MoBE literature review is under section 3.3). HAI referencing is limited to a brief summary below. The author conducted an extensive review of the literature in the course of this thesis (59 accepted and relevant reviewed literature articles); however, this is not presented but only referred to in summary. Note that some articles overlap in review sections due to the interdisciplinary nature of the studies, but were specifically reviewed with reference to this topic.

### 3.5.2 HAI (HEALTHCARE ASSOCIATED INFECTION)

A much larger number of articles than the few summarised below for reference were reviewed over the course of this thesis. The author recognises the need for study and investigation to curb HAI in healthcare buildings. MoBE research outcomes and future investigations could provide potential methodologies to address HAI in hospitals and in public and civic environments. HAI estimates indicate that 9-10% (Brink, Van den Bergh & Kantor 2011; Rosenthal 2011) of hospital admissions are readmitted in the developed world and in excess of 15% in the developing world (Durlach, Mcllvenny, Newcombe, Reid, Doherty, Freuler, Rodriguez, Duse & Smyth 2012; Alvarez-Moreno, Perez-Fernandez, Rosenthal, Quintero, Chapeta-Parada, Linares, Pinilla-Martinez, Martinez-Saleg, Sierra & Mindiola-Rochel 2014; Brink *et al.* 2006). The lack of HAI surveillance and indicator species lists, based on specific environments in South Africa, is of great concern. The report by Dramowski and Whitelaw (2017) on the current state of HAI in South Africa indicates a lack of policy but more importantly, that there is no implementation of any kind of policy. They recognise that there is a gap in standard methodology for HAI reporting and measuring. Only three studies between 1995 and 2008 were published in Africa through the WHO, and none in South Africa, until 2017. The data that do exist categorise all Gauteng hospitals in the same pool and report that 9.7% of patients have HAI illnesses, and that two out of three inpatient mortalities are associated with HAI. The direct cost is estimated at R5,4m (Dramowski & Whitelaw 2017). Their study presents a table of HAI environmental factors and HAI patient factors, information very useful for downstream MoBE data factors association. The authors conclude that a prevention strategy and supporting data are urgently required.

Magill *et al.* (2014) conducted a large HAI prevalence study to ascertain the HAI rate in American hospital environments across 10 states. This study was intended to update the National HAI data sets and prevalence rate statistics. Data from 183 hospitals showed that out of 11 282 patient samples, 452 had some form of healthcare associated infection (4.0%). The most common in ranking order are: pneumonia, surgical site infection and gastrointestinal infections. *Clostridium difficile* was the most commonly reported HAI pathogen. Device-associated infections accounted for 25% of total HAIs. These statistics indicate that in 2011 in the USA, out of 6.6 million patients, 720 000 had HAI infections in hospitals. This study indicates the potential for a reduction in prevalence rate in the US when compared to the WHO and other studies (Magill *et al.* 2014). It does, however, point to the need for a healthier built environment and the need for microbial surveillance. In a focused metadata study on decontamination and cross infection, Rutala and Weber (2013:36) confirm the association of environmental contamination with several healthcare associated pathogens and the need for

effective cleaning and disinfection. This study, through an environmental questionnaire on cleaning regimes as part of the pre-sampling methodology, found the following results on infection perception: 70% of respondents felt unsafe and at risk of contamination, and 55% felt that the surfaces were not sufficiently cleaned, as was evident from the samples data (see chapter 8). Rutala and Weber (2013) recommend room decontamination between inpatients to ameliorate the risk for patient-to-patient transmission. Multiple studies have demonstrated that environmental service workers frequently fail to decontaminate “high-risk objects”. The “no-touch” systems have reduced contamination numbers (Rutala & Weber 2013). Refer to Table 8.2 developed by the author from the literature, for further reference.

## 3.6 ARCHITECTURE AND ENGINEERING IN THE BUILT ENVIRONMENT (REVIEW 5)

Various literature was considered and analysed under this topic and found under the MoBE literature review is under section 3.3). A brief summary of theoretical models and methodologies is found in Table 3.21 and reference is only made to limited articles in the table. The author conducted an extensive review of the literature during the course of this thesis (91 relevant and reviewed literature articles and a further 73 spatial analytics and complex modelling articles); however, it is presented but only referred to in summary. Note that some articles overlap in review sections due to the interdisciplinary nature of the studies, but were specifically reviewed with reference to this topic.

Table 3.21 displays an overview of models and methodologies available to measure indoor air and surface quality as well as risk of infection, and identify microbial communities and relevant building environmental factors that are measurable. The table was developed from numerous literature reviewed over the course of the investigation. It does not claim to be exhaustive, but provides some information and guidance on available resources for consideration to the architect.

Table 3.21: Theoretical models and methodologies

| TABLE OF THEORETICAL MODELS AND METHODOLOGIES | | | | | |
|---|---|---|---|---|---|
| | **AIR QUALITY & RISK** | | **MICROBIOLOGY** | | **ARCHITECTURE & ENGINEERING** |
| | **List of common theoretical models that investigate relationships between air quality and risk, and epidemiology models** | | **List of common theoretical models, databases and sampling methodologies that investigate microbiology** | | **List of common measurable architectural and engineering indicators** |
| 1 | Wells Riley equation model & stochastic models | 1 | PCR – Polymerasa chain reaction | 1 | In-room and external temperature of air and at surface |
| 2 | Epidemiological models – SEIR (Noakes, Beggs, Sleigh & Kerr 2006) | 2 | QPCR – real time Polymerasa chain reaction (quanta of specie or taxa) | 2 | In-room and external relative humidity |
| 3 | Computational fluid dynamics modelling (fully mixed and partially mixed models) | 3 | PAMI – Mould index | 3 | In-room CO2 levels |
| 4 | Dose response modelling (fully mixed and partially mixed models) | 4 | ITS index – barcoding for fungi | 4 | In-room sunlight/lux levels |
| 5 | Mathematical models (Mui, Wong & Hui 2008) | 5 | Metagenomics (shotgun sequencing, etc.) | 5 | In-room UV levels |
| 6 | Numerical modelling (version of CFD) (Tang, Noakes, Nielsen, Eames, Nicole & Settles 2011) | 6 | Transcriptomics – set of RNA & mRNA, rRNA, tRNA & non-coded RNA | 6 | In-room dry bulb temperature |
| 7 | Physical analogue modelling (Tang *et al.* 2011) | 7 | DNA & RNA sequencing | 7 | In-room VOC emission |
| 8 | Schlieren imaging – thermal plumes and exhalation | 8 | QIiME, UPARSE, EPHCIT – Microbiological taxa and specie databases (OTU – Operational taxonomic unit) | 8 | In-room ventilation rates |
| 9 | Mannequins, etc. | 9 | Surface – plate sampling, impingers, surface swab, Anderson air sampling, etc. | 9 | Internal and external air flow speed |
| 10 | Particle model techniques (Tang *et al.* 2011) | 10 | Realtime particle counters | 10 | HVAC ducts |
| | | | | 11 | Electrostatic characteristic of the indoor surfaces |
| | | | | 12 | Movement patterns of building users |

# CHAPTER 4 HOSPITALS AND ACCIDENT & EMERGENCY UNITS

## 4.1 HOSPITAL

A hospital environment was chosen as the study site for this thesis since it has the highest potential for healthcare associated infection. It also represents one of the most complex – if not the *most* complex – architectural design typologies. The core function of a hospital is to provide health services over the full life cycle of the asset (the building), which implies that hospitals have a long life span. In South Africa, the estimated life cycle is 40 years, and most of the public hospitals are now in excess of that cycle. What does that mean for the building, standards, the indoor environment, and condition of the building and material finishes? This is not intended to be an exhaustive analysis of the hospital environment, but merely an overview of the critical elements that constitute a healthcare facility. The intention is to create a better understanding of the complexities of space, function, service, interrelationship, IPC and clinical layers of a health facility, and provide a context to stimulate an interest in hospital assessment and microbial analysis.

To provide appropriate care to the client patient, the facility must provide an extensive array of services, functional spaces, specialised equipment, climate, and conditioned environments. The layers of administration, back of house services, clinical services and public domain add levels of complexity. The design and planning, form and function, flow and access, and interrelationships of spaces and, lastly, engineering services will either provide an effective health service or impede it. *Hospitals are built around a complex interrelationship of systems that together enable the people, equipment, supplies into a defined environment at the right time to enable a specific* healthcare *activity to be performed and, after completion, for the space to be recycled for the next activity* (NDoH 2015). Refer to Figure 8 below.

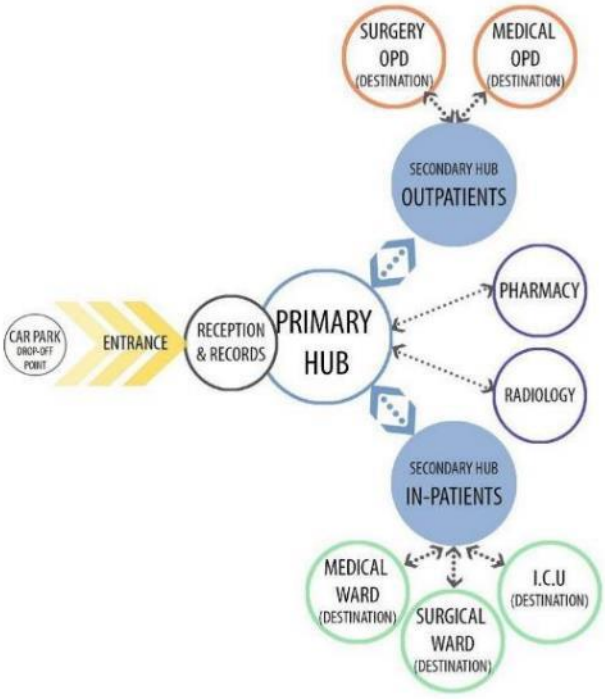



Figure 8: Hospital hub and inter-relationships (IUSS 2015)

The hospital is an integrated system of services that provide many functions simultaneously. These are connected by circulation routes that are either shared, public or public-private, or of a clinical or service nature. Each department is a unit within the system. The units are integrated, depending on the service platform they provide. In the case of an A&E, this unit is highly integrated; it is connected to the emergency entrance for staff, EMS and ambulant patients; the internal overnight wards for critical cases; the diagnostic radiology for emergency X-ray services; the pharmacy for medication collection; the main entrance for public access; the theatres for emergency operations; and the wards for long-term admissions. The relationships and flow between these areas are of critical importance. The hospital layout is built around primary service clusters. These could be on ground level for outpatient services and 24-hour service, or hypothetically on the first floor for the surgical services, also known as the hot floor. Multiple routes and flow patterns function simultaneously, as seen in Figure 9, Figure 10, and Figure 11. These include patient routes, staff routes, routes for collection and waste removal, routes for delivery and supply distribution, and emergency evacuation and circulation routes.

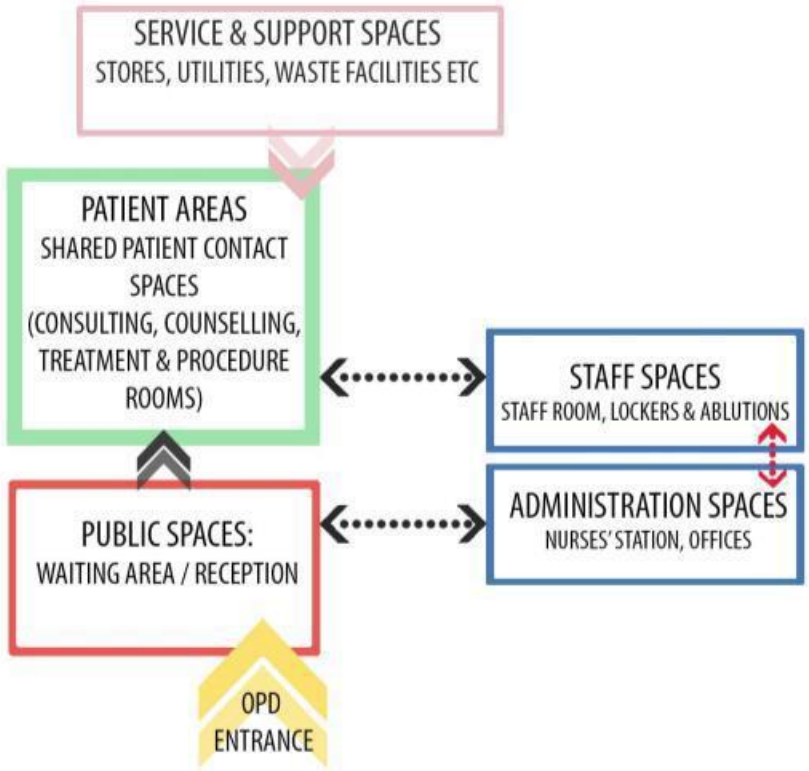



Figure 9: Functional zone relationships (SA 2015)


Figure 10: Patient flow diagram (SA 2015)

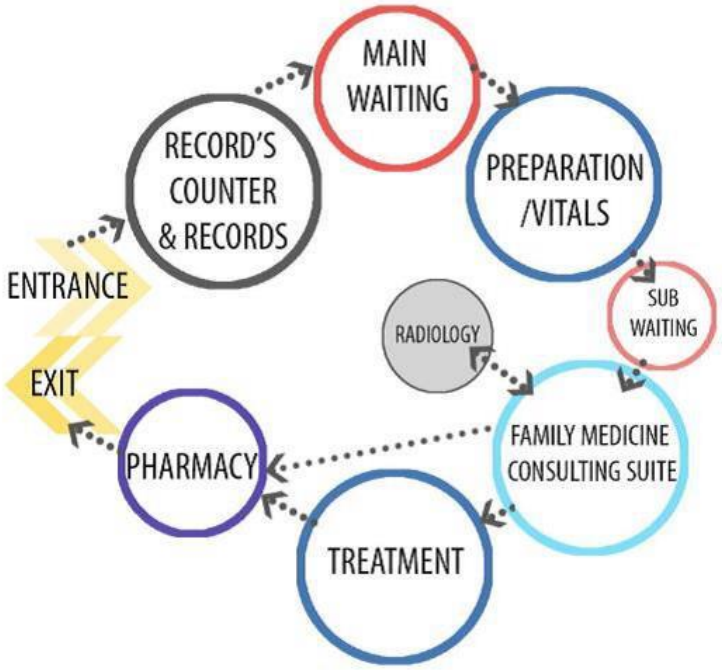



Figure 11: Staff flow diagram (SA 2015)

This information relates to findings that MoBE researchers and the author have referred to, namely that 65% of the bacteria indoors are human-sourced – thus the relevance to this study. Human-sourced bacteria are known to be commonly pathogenic of the *Proteobacteria* genus origin. When one considers hospital flow patterns, a complex IPC condition emerges. As much as hospitals have open and free flowing access, they do in fact have barriers of separation and restrictions. The way in which those activities are managed is essential in transmission control. There is no typical hospital morphology; there are, however, tested planning typologies that provide flexibility in design and functionality in layout. For example, the A&E department at both KDH and MPH have a linear planning layout that is centrally connected. In many ways, they represent the same layout as a church nave with a central main corridor and a secondary interconnecting passage, forming a central core area, which would then be the nurses' station that centrally manages the unit. When ward planning layouts are considered, there are two to three accepted types: a linear layout that is double loaded (services on either side of the passage) with importance given to the "access ability" zone; or the central service space with a ward corridor running around it and with ward rooms on the outside wall, also known as a "race track" plan; and historically the "Florence Nightingale" ward layout – a large rectangular open plan ward with beds on either side, and the nurses' station on the edge or central. In many ways it resembles the modern double loaded corridor layout, but with an open plan.

A hospital is a system of spatial layering, from large units with multiple departments to departments with multiple sub-departments with specific room types and individual rooms fit for purpose. The patients that would be attended to will be vastly different from one department to the next (here purposely excluded are outpatients, pharmacy and emergency). The patient type and human biome going to gynaecology would be different to those in a renal unit. What this alludes to is the possibility of varying biomes within a single building. The user defines the

biome, as Lax *et al.* (2017) reported on patient rooms: the rooms take on the signature of the patient; so too will different departments. Adding a layer of pathogenicity to the different biomes, one can postulate that a standard IPC for infection risk protocol might not work. As our understanding and knowledge of the indoor microbiome grow, so too will the effectiveness of our HAI prevention planning. The complex nature of hospital planning, form and function affords opportunities for studying the indoor microbiomes with direct health outcomes and measurable impacts.

## 4.2 ACCIDENT & EMERGENCY UNITS

The selection of the A&E unit as subject for this investigation was informed by the fluidity of the A&E environment. The A&E unit does not have a typical patient. It serves patients in all clinical categories for 24 hours daily. It was selected because it could potentially reveal a very diverse microbiome, due to the variety of patients and variety of cultures, illnesses, origins and levels of acuteness. Architecturally and spatially speaking, it cannot be regarded as a stable environment. The A&E unit fluctuates seasonally with space and functional use. For example, in MPH the winter season had more patients present with air tract conditions, to the extent that the nebulisation room was moved to a larger room to support the increase in cases. In summer MPH showed a 50% reduction in patient load and needed to move the unit back to its assigned space. The fluid nature of this environment presented an ideal opportunity to investigate the microbiome. The A&E units in the Western Cape are high-risk TB environments. Most HCWs that have contracted TB are from the WC region, where the population TB incidence rates are 1100+ per 100 000 people. Combined with the long period of exposure in indoor environments of a HCW, 12-hour shifts and longer increase the potential risk exponentially.

The emergency department works on a classification system to triage patients and provide the required medical service, as seen in Table 4.1.

Table 4.1: A&E triage priority levels and times (WCGH 2012)

| Priority colour | Target time | Management / Stream |
|---|---|---|
| Red | Immediate | Take to Resusciation room for emergency management |
| Orange | < 10 min | Refer to majors for very urgent management |
| Yellow | < 1 hour | Refer to majors for urgent management |
| Green | < 4 hours | Refer to designated minors area for non-urgent cases |
| Blue | < 2 hours | Refer to doctor for certification |

The triage grading system grades patients on acuity at the point of triage. Their length of stay will be determined by their acuity. Consider the triage area in relation to MoBE: the triage area in an A&E unit is the most fluid space, but could also be the most stable. The author has observed patients entering being graded orange, fast tracked to Resuscitation, stabilised and admitted to the trolley area for observation, and released 3 hours later, while at the same time a patient is coded blue or green and has to wait as low-risk, in some cases for more than 12 hours. The process flow of this sub-unit is very relevant to the spatial logic for analysis – see

Figure 12 and Figure 13. Patients are passed through four spaces in KDH and three in MPH before they are taken “deeper” into the unit. This implies that time spent in this triage zone is far higher than in other areas. It also implies crossing between rooms that allows for increased “bio-fouling” or contamination, depending on the host as well as the signature that is left behind for other patients to come into contact with. The A&E unit requires a far deeper investigation in order to recommend effective protocols for infection prevention and health biomes. For an explanation, refer to Figure 12. The figure shows a very simple process flow; in reality, however, the theory and clinical process are linear, but the route on plan is not.


Figure 12: One-way patient flow (SA 2015)

Figure 13 and Figure 14 show the interrelationships between the A&E and other departments. This unit is potentially a source tracker for hospital microbial surveillance.

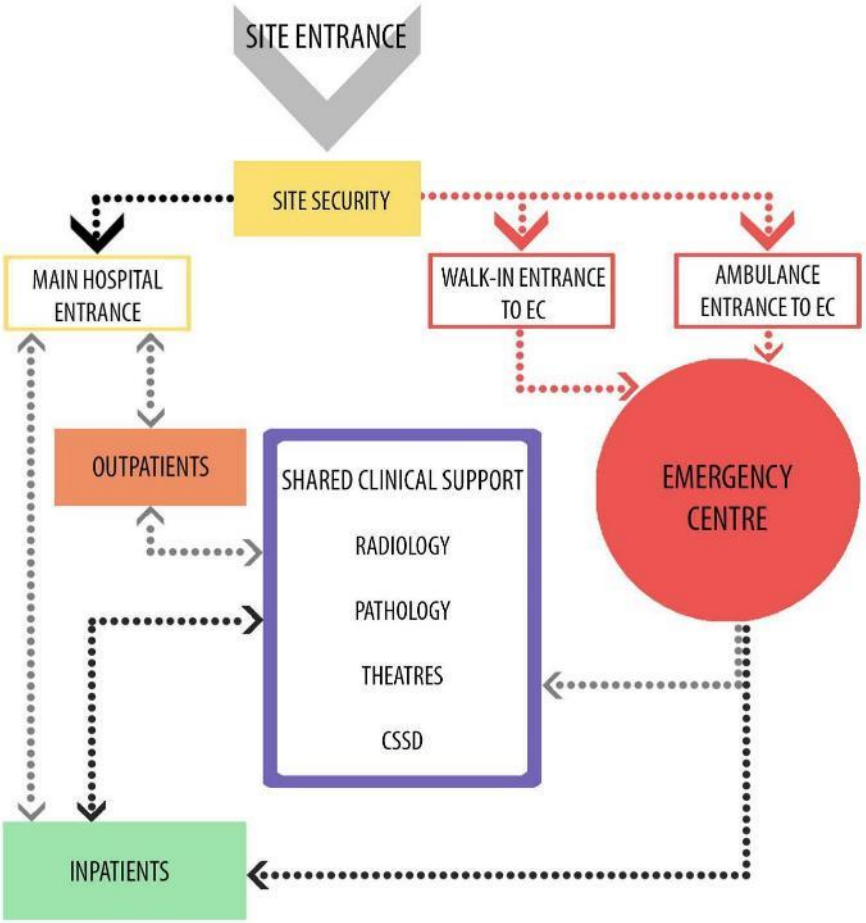



Figure 13: The relationships between departments (SA 2015)

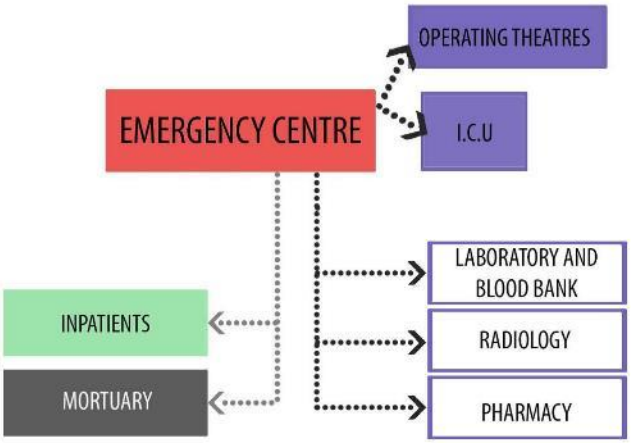



Figure 14: The relationships between critical departments (SA 2015)

The number of variations in access and departure patterns makes this unit a destination and a pass-through zone. Figure 15 illustrates the complex nature of spatial modelling for this zone. In Chapter 7 and Chapter 8, the departmentalisation of space and of ventilation sources to manage microbial dispersal is discussed. The sampled data indicate that the indoor biota were evenly distributed throughout the entire unit, which points to the HVAC unit as vehicle. Depending on the composition of that biome, this is either good or bad, but based on further investigation it revealed that 65% of the biota were human-sourced, which is mostly pathogen based. In MPH and KDH the majority was *Proteobacteria* followed by the *Firmacute* phylum.

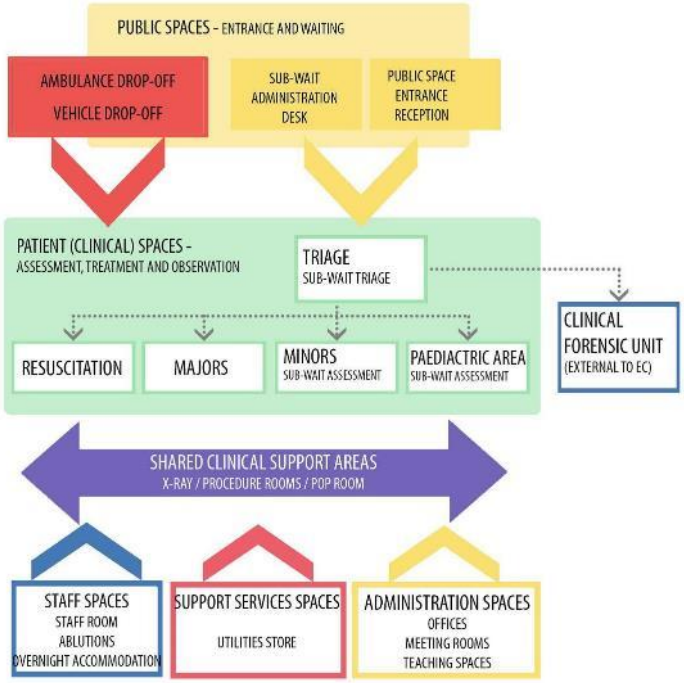



Figure 15: Intradepartmental zones (SA 2015)

Figure 15 shows the relationships within the unit. The level of activity is very dependent on the status and acuity of the patient. The flow patterns can vary within the hour or within days. The

spatial observation study did show stable core and cluster areas, but there were some seasonal variations in the way the space was used. It is interesting that Williams and Crouch (2014:162) noted that, due to challenges experienced in the assigning of the patient classification system (PCS) related to the constant changes in space in the A&E unit, they could not accurately predict nurse staffing needs: *It has been recognised that there are difficulties in developing PCSs for use in the emergency department (ED) setting. The nature of the constant changes in the flow of patients and illness severity within emergency departments has been recognised as a potential problem in being able to accurately predict nurse staffing needs.* The above provides testimony to the fluid nature of emergency units.

Hospitals and A&E departments are complex environments that are functionally driven. The space use and services rendered in an A&E unit require spatial mapping which could benefit from informed spatial analytics. The social knowledge of space imbedded in highly fluctuating and fluid environments requires further investigation. These environments can benefit from MoBE studies to respond to the prevalence of HAI.

# CHAPTER 5 SPATIAL ANALYTICS, APPLICATION FOR THE MICROBIOME

## 5.1 BACKGROUND

Architectural design is the configuration and relationship of spaces associated with function and constructed for control or freedom. Design in many ways is a learned act that becomes intuitive by experience. Schon (1987, cited in Dursun 2007:2) explains: *Designing in its broader sense involves complexity and synthesis. In contrast to analysts or critics, designers put things together and bring new things into being, dealing in the process with many variables and constraints, some initially known and some discovered through designing. Almost always, designers' moves have consequences other than those intended for them. Designers juggle variables, reconcile conflicting values and manoeuvre around constraints – a process in which, although some design products may be superior to others, there are no unique right answers. … Beginning with the situations that are at least in part uncertain, ill defined, complex and incoherent, designers construct and impose a coherence of their own. Subsequently they discover consequences and implications of their constructions – some unintended – which they appreciate and evaluate. Analysis and criticism play critical roles within their larger process. Their designing is a web of projected moves and discovered consequences and implications, sometimes leading to the reconstruction of initial coherence – a reflective conversation with the materials of a situation.*

The fluid and in many ways organic nature of the intuitive learned response would benefit from empirical foundational knowledge, and would guide the acceptable "no unique right answers…" and "less superior" response to at least a minimum acceptable health-centred standard.

Nichersu and Lacoboaea (2011:67) define spatial planning as: *the change of the distribution of activities in space and the change of the links between them by converting forms of land use and property.* Spatial planning is equally relevant at building and urban scale. Hillier and Hansen (1984) describe the social logic of space and argue that a building can be seen as an artefact or object, but is in fact a collection of spaces imbedded with function and social meaning; *the ordering of space is really about the ordering of relations between people (*Hillier & Hansen 1984:144). The relational characteristics of spaces and human behaviour are imbedded in the social knowledge of space. Spatial analytics consider the interrelationship of spaces, measuring the configurational properties of a layout, floor plan, urban plan, etc.

## 5.2 SPACE SYNTAX

*Space Syntax starts with defining movement and occupation as the fundamental functions of a layout, where permeability of all spaces is the priority* (Al Sayed *et al.* 2014).

The architectural concept of Space Syntax, developed by Bill Hillier and Julienne Hanson in 1983 (Hillier & Hansen 1984), with more recent involvement by Philip Steadman and colleagues at the Bartlett Faculty of the Built Environment of University College London, assesses spatial use based on function, user behaviour and distribution to provide a platform for evidence-based research design. Space Syntax was developed for urban planning but has evolved into the development of internal space relationship design and applications for hospitals and other indoor environments (Dursun 2007; March 2002). Space Syntax has

developed methods to configure and describe mathematically, present visually, and state by coefficient correlation the underlying social meaning of space networks and the potential for human behaviour. According to Hillier and Hanson (1984, in Durson 2007b:4)*… [s]pace syntax is theory of space and a set of analytical, quantitative and descriptive tools for analysing the spatial formations in different forms: buildings, cities, interior spaces or landscapes*. A floor plan can be analysed for its spatial characteristics to determine the relationships that spaces have to each other and the manner in which they are interconnected. Visual observations of these same said spaces can then be imported and analysed to compare the topological factors of the base plan and the utilisation of that space in real-world conditions. The result will determine whether the space utilisation matches the planned design potential. Space Syntax can also test the validity of the simulation when experimenting with new methods of analysis, and confirm through the correlation coefficient of $R^2$ 0.65 => for a selected design, or a design comparator. The accepted coefficient for spatial analysis is $R^2$ => 0.65. The correlation value defines the achieved level of integration, connectivity or intelligibility of a design and/or an observed measure of the design. Numerous studies indicated poor correlation at below 50%; personal communication with SS UCL lecturers indicate 65% as acceptable R2 correlation, and for social science in general (including architecture) with regards to regression analysis, factors matching by more than 60%, is an acceptable confidence level for correlations, where 100% represents the observed dependant variable perfectly matching (hard science - this value must be in excess of 90 – 99%). Space Syntax, through various ways of graph mapping, creates a representation of spatial structure. Table 5.1 describes the various graph syntax tools available in Space Syntax DepthMap™ for the purposes of spatial analysis. Table 5.2 describes the topological factors that can be applied for analyses.

Table 5.1: Space Syntax classification

| | |
|---|---|
| 1 | Axial line analysis (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | 1. Space is expressed as a series of interconnected axial lines, where each line is recognised as a node and each nodal intersection as a link. Depth of connectedness is defined by change in direction (at node intersections). Axial lines are theoretical syntactic representations. Drawing the axial lines is critical to accurate analysis. Sailer (2010) argued for a variation in the methodology of axial mapping to achieve a more relevant representation of spatial relationships by considering the known social relationships of a given environment (e.g. a hospital).<br>2. In Space Syntax analysis, the axial plan does not consider the function of spaces, but merely the layout and mathematical spatial relationships. It provides insight into the most visually integrated spaces, which is relevant for hospital environments.<br>3. Axial and visibility graphs are representations of layouts. They correspond to the way people take cognisance of space (are aware of space). |
| 2 | Segment analysis (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | Similar to axial lines, segment analysis considers not the lines but the segment between intersecting lines. The analysis considers the angles between intersecting points, and not the steps, as they are removed from one another. Segment analysis in fact is better correlated with movement analysis. |
| 3 | Visibility Graph Analysis (VGA) (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | 1. VGA is a graph of mutually visible points in space. It considers the set of vertices in the graph and the sets of edge connections joining the pairs of vertices.<br>2. Axial and visibility graphs are representations of layouts; they correspond with the way people take cognisance of space (are aware of space) |
| 4 | Convex space analysis (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |

| | |
|---|---|
| | 3. Represents adjacency relationships by reducing the spatial complexity of a layout to the fewest and fastest convex spaces, based on a visibility graph. Within the convex space all points are inter-visible and depth is graded by levels of separation (step depth), i.e. the least number of syntactic steps. |
| 5 | Agent-based modelling (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | This entails a virtual analysis of "people" released in an environment that make decisions on where to move, based on constraints imposed on them. They operate within the constraints of VGA. |

From the various graphs (convex, axial, visibility and segment) a topological analysis can be performed, with an appropriate topology factor for each graph type – see Table 5.2.

Table 5.2: Space Syntax topological analysis variation

| | |
|---|---|
| 1 | Connectivity (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | 1. The number of elements that are connected to a certain element. Connectivity is a local measure; this means it only takes into account the direct neighbours of an element (local = relations within a certain distance of each element).<br>2. VGA connectivity: the number of points in space connected with one point. |
| 2 | Integration (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |
| | 1. This is a topologically based measure indicating topological accessibility, and aimed at correlation with movement patterns. Spaces are either integrated or segregated.<br>2. The distance of an element to all other elements in relation to the number of elements in the complete system (the to-movement and centrality). It is a global measure of the network of space, as it takes into account the relationship of all elements to a certain element.<br>3. VGA integration: the visual distance from one point to all other points in the system, i.e. how deep each location is in relation to all others.<br>4. VGA clustering coefficient: measure of the extent to which all lines of sight could exist within the neighbourhood of a location in the visibility graph (the more you see the higher the coefficient).<br>5. Segment integration: the angular distance of an element to all other elements in relation to the number of elements in the complete system (the centrality of that segment). |
| 3 | Choice (Turner & Pinelo, 2010; Schneider 2010; Turner 2004) |
| | Segment choice: indicates how often an element is passed when calculating the shortest paths between elements (through movement). |
| 4 | Control (Turner & Pinelo 2010; Schneider 2010; Turner 2004) |

The level of spatial connectivity and integration with neighbouring spaces, termed spatial intelligibility (SI), provides insight into potential social interactions. The functional use of spaces affects the required level of integration and connectivity. Clustering of core functional spaces theoretically provides a high level of connectivity and correlates strongly with spatial integration. The level of intelligibility represents how easy it is to comprehend a local position within a global structure (Al Sayed *et al.* 2014).

Figure 16 presents the method of measuring for each topological analysis as described in Table 5.2. The illustration represents the same plan with varying degrees of measures and outcomes. It is imperative that the appropriate research question is asked to test the spatial characteristic that is desired for the functional use pattern of the spatial network.

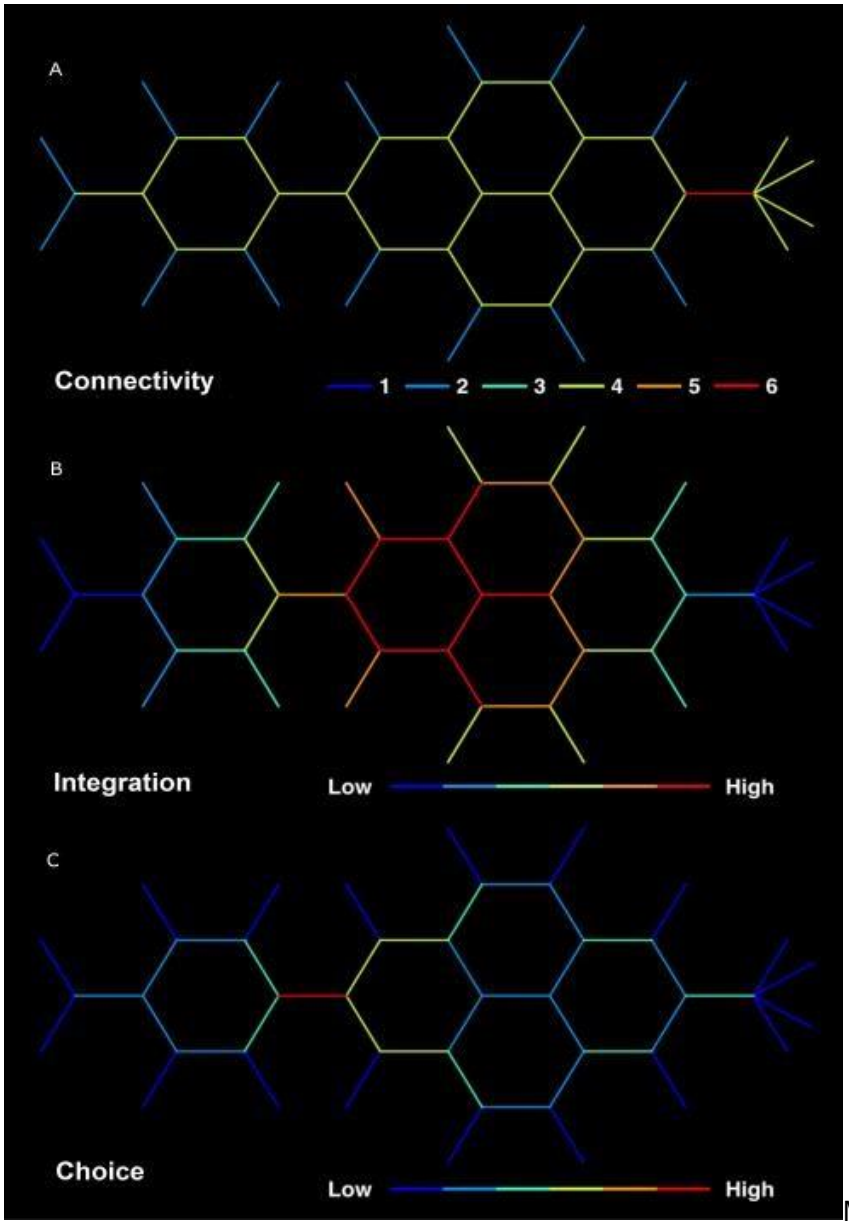



Figure 16: Topological measures (Javadi, Emo, Howard, Zisch, Yu, Knight, Silva & Spiers 2017)

Multiple Space Syntax case study investigations, at both urban and building scale, over the past thirteen to twenty years have reported evidence that utilising Space Syntax to model potential human movement patterns has high correlation coefficients with actual observed flow patterns (Orellana & Al Sayed 2013; Penn & Turner 2001; Patterson 2016, etc.)

## 5.3 GIS INTEGRATION

Utilising GIS for Space Syntax analysis through DepthMap™ software enables the researcher to correlate observational data with simulated graph data. GIS enables data layering with multiple subsets, incorporating numeric data into graphical representation. Having made manual observations of flow patterns and recorded occupancy counts, the data can be imported into GIS creating a database of data points. These points and axial lines are categorised by date and time, by type and function, or by any other identification (ID) that could be required. The database can be analysed in statistical programs, manipulated in Excel

or similar, and the visual graphics can be imported into DepthMap™ and analysed. GIS allows for data sets and visual axial graphic exporting.

Because GIS is a database systems tool (MSAccess), it allows for data filtering and sample set exporting through query building. For example, when analysing multiple day data, exporting can be single days, full set days or other. When working with floor plans, polygons that act as boundaries can be assigned to each room. When drawing movement lines, the query builder application can perform counts of threshold crossing and total/mean average or other measures to count flow lines within the selected space and the entire project space. GIS enables the integration of numeric and abstract data sets into vectors (to become object based), and/or regular tessellation (spatial grid or raster), or irregular tessellation (triangulation or Voronoi) diagrams. For this thesis occupancy counts and movement flows by “snapshots” and “movement traces” (Sailer & Pachilova 2013; Grajewski & Vaughan 2001) were drawn and assigned to spaces, and abstract IDs were assigned to the points and lines through data tables. The IDs included people type, direction by angle reference and activity. Colour-graded plans were produced that indicate spaces with the most and least “gate crossing” that imply connection to other spaces and connection by functional value to the entire network as a function of total gate crossing. In addition, an “internal flow” count was measured, indicating accessibility and the function value within the space based on the number of gate crossings. When these two factors where correlated, they indicated a 90% correlation, but when the room occupancy was correlated with either factor, it provided no significant correlation.

For this study a room grading approach by flow and by gate crossing was utilised to compare with the Space Syntax analysis of VGA, axial mapping for integration, connectivity, and mean depth. Significant correlation was found between the data sets. The findings and conclusions are referred to in cChapter 7 and Chapter 10

The observed flow lines were exported and imported into DepthMap™ software to run an analysis on the “observed” axial plan. Topological factors were measured, i.e. integration/connectivity for intelligibility, integration/choice and integration/mean depth for accessibility and spatial cognisance. The outcome presented a poor result for choice, but a good coefficient for mean depth and an acceptable (0.1-0.2) lower correlation coefficient than the base plan for intelligibility, even though the base was marginally (by 0.05) unintelligible. The observed axial factored plan indicated reduced levels of integration/connectivity, but matching values of integration/mean depth. Refer to cChapter 7 findings.

## 5.4 SPATIAL ANALYTICS AND THE HOSPITAL ENVIRONMENT

Ulrich, Zimring, Zhu, Dubose, Seo, Choi, Quan and Joseph (2008) and Ulrich, Quan, Zimring, Joseph and Choudhary (2004), published comprehensive systematic reviews of research on evidence-based healthcare design. Pachilova and Sailer (2013) reviewed the studies by Ulrich *et al.* (2004, 2008) in a recent paper, and identified a “major gap” in the evidence-based design (EBD) concerning the configuration of buildings and its impact on staff and patients. They point out that very few of the EBD studies considered spatial configuration as a factor of influence on the relationship of health in healthcare buildings and human behaviour (Pachilova & Sailer 2013). Consequently they refer to the limited few but recent studies on spatially based investigations for healthcare environments, which include Lu and Hignett (2009); Heo, Choudhary, Bafnam, Hendrich and Chow (2009); Cai and Zimring (2012); Koch and Steen

(2012b); Koch and Steen (2012a); and Sailer, Pachilova, Kostopoulou, Pradinuk, MacKinnon and Hoofwijk (2013).

The interest shown in this thesis in spatial networks and their syntax relationships is based on the premise that spatial configuration positively or negatively generates or segregates social interaction. The extent of these interactions is premised in the social knowledge of space. Hillier and Hanson (1997:1) state: *Space Syntax research is reason based, and more rigorous than most, but it has effectively led to the study of architectural intuition through its creations. In practise design proceeds by mixing intuition and reason. Space Syntax makes the deployment of non-discursive intuition more rational and therefore more discursive.* Space Syntax (SS) engages the relationship between people and space and predicts user flow patterns based on the planning constraints (the floor plan). In a paper titled *How strongly programmed is a strong programme building: a comparative analysis of outpatient clinics in two hospitals,* Sailer *et al.* (2013) conduct an exhaustive literature analysis to identify indicators that would define a building to have either a weak program or a strong program. It is generally accepted or assumed that hospitals have strong programs. However, the analysis indicated that buildings do in fact shift between both. A weak program is defined by the configuration of space, whereas a strong program is defined through the rules and policies enforced on the configuration of space. The analysis by Sailer *et al.* (2013) is based on the function performed by the users in the building and then compared to the configuration and topological measure of the space.

Table 5.3: The criteria for buildings with strong and weak programs (Sailer *et al.* 2013)

| Proceedings of the Ninth International Space Syntax Symposium, Seoul, 2013 | | |
|---|---|---|
| | **STRONG PROGRAMME** | **WEAK PROGRAMME** |
| **THEORY ORIGIN**<br>Hillier, Hansen, Peponis, Penn) | *1. More complex and segregated layout*<br>*2. Low ratio of bounded spaces to convex space*<br>*3. Low ratio of axial lines to convex spaces*<br>*4. Smaller buildings*<br>*5. Strong control of inhabitant – visitor interface*<br>*1.1 Separate non-interchangeable entrances*<br>*1.2 Easily controlled spaces for visitors, shallow in the building – close proximity to visitors*<br>*1.3 Independent routes*<br>*2. Strong control of inhabitant – inhabitant interface:*<br>*2.1 Strong division of categories of users by division of spaces used*<br>*3. Preserved professional status with more segregated spaces*<br>*4. Activities follow programme*<br>*5. Correspondence model*<br><br>*Example of building types: courts, prisons, hospitals, airports* | *1. Simpler and more integrated layout*<br>*2. High ratio of bounded spaces to convex space*<br>*3. High ratio of axial lines to convex spaces*<br>*4. Larger buildings*<br>*5. No control of inhabitant – visitor interface*<br>*5.1 Same entrance for inhabitants and visitors*<br>*5.2 No control over visitors*<br>*5.3 Shared routes*<br>*6. No control of inhabitant – inhabitant interface:*<br>*6.1 No division of spaces, therefore categories of users are mixed*<br>*7. No status expressed with spatial properties*<br>*8. Activities follow configuration*<br>*9. Non-correspondence model*<br><br>*Example of building types: offices, museums, galleries* |

| | | |
|---|---|---|
| **CONTRIBUTIONS** (Sailer, Koch/Steen, Heo *et al*, Lu *et al*, Cai/Zimring | 10. *Attractors placed in segregated areas without configurational logic (Sailer)*<br>11. *Time restriction of space usage (Sailer)*<br>12. *Activities follow programme: no influence of spatial factor on different roles and tasks*<br>13. *Spatial practises (tasks and roles) are realised in space and time (durations) similarly (Koch and Steen)* | 6. *Attractors placed in integrated areas according to configurational logic (Sailer)*<br>7. *No time restriction of space usage (Sailer)*<br>8. *Activities follow configuration: different spatial factors influence difference roles and tasks*<br>8.1 *Targeted visibility (Lu, Peponis & Zimring)*<br>8.2 *Visual connectivity / generic visibility (Lu, Peponis & Zimring, Heo et al.)*<br>8.3 *Axial integration (Heo et al.)*<br>8.4 *Distance (Heo et al; Cai & Zimring)*<br>9. *Spatial practises (tasks and roles) are realised in space and time (durations) differently (Koch & Steen)* |

Table 5.3 was developed by Sailer *et al.* (2013) from literature describing the characteristics of weak and strong programmed spaces based on SS theory and recent studies in SS, and related to SS and building space programming. The research by Sailer *et al.* (2013) is of great value, as it adds another layer of logic to building spatial analytics. Sailer *et al.* (2013) suggest that *Spatial configuration needs to be investigated as an influential factor on behaviour in parallel to a systematic analysis of the logistical pathways taken by professional or other building inhabitants.* Their research indicates that the functional program of a building has the potential to influence the configuration. It is evident that future studies in spatial analytics require both 1) analytics by topological methods of building configuration, and 2) social behaviour. Without applying both of these analyses, it could be argued that a portion of the social logic of space will not be accounted for.

Considering these findings, one could argue that layering infection prevention and control (IPC) policies and protocols onto a building system in effect makes the program stronger than the configuration; however, it would be of much greater value if the configuration were aligned with IPC methodologies and guidance, so that when the program is not followed, the fall-back position is still an informed configuration. The prediction of user flow is of particular relevance in hospital environments. It could provide insight into epidemiological outbreaks, HAI prevalence, design applications for conscious infection prevention, etc. The intention with this thesis is to propose a novel utilisation of predictive spatial network syntax analysis to support the designer, hospital manager and healthcare worker to gauge the highest risk spaces through most integrated indoor spaces, potential core environments, and segregated space data. This will guide the prediction of high-risk zones.

The author proposes that a data matrix be developed, and populated to include:

- the room type and function;
- risk factors based on the most common HAI pathogens potentially room specific or hospital site specific (now derived from this study);

- biome indicators associated with site (room type);
- Space Syntax spatial integration and connectivity grading per room type; and
- Current environmental factors applicable to the room function.

Table 5.4 is a theoretical example scenario developed within the parameters mentioned above for application in a potential TB healthcare environment.

Table 5.4: Theoretical risk matrix using spatial analytics

| **Scenario** | **TB patient** |
|---|---|
| Environments | 1) Common rooms include: Triage Waiting, Triage Consult, Nebulisation |
| Risk factors | 2) Occupancy numbers, time spent, ventilation rate, ventilation type, $CO_2$ as indicator of IAQ |
| Strategies | 3) Ventilation |
| Biome indicator | 1) Predominant organisms: air or surface; refer to abundance, as this will inform active ventilation factors<br>2) Indicator organisms derived from localised seasonal biome study |
| Spatial grading | 1) Room types graded based on integration values (global measure of room space accessibility to all other spaces in entire network, thus core prediction)<br>2) Room type graded by connectivity (local measure or predicted movement pattern relationship to immediate neighbours) |
| Environmental factors per room type | 1) Ventilation, $CO_2$, area $m^2$ |
| Response | 1) Appropriate room selection for patient; localised IPC intervention; known general risk factors per room. If redesigning or opting for reconfiguration, consider appropriate placement of clinical services in space. |

## 5.5 SPATIAL ANALYTICS AND THE MICROBIOME IN CONCLUSION

The human being contributes to the majority of associated microbes in the indoor biome. The research found this contribution to be 65%, which differs from outdoor sources. In addition, people also spend most of their time indoors – up to 85% (Briere & Resnick 2017). With people being the primary users of indoor environments, the study of how people use and program space is necessary and paramount to the understanding of the indoor microbiome. HAI by touch, air and droplet has a strong correlation with human social interaction in indoor environments, as has been established in various studies including Sternberg (2009); Robinson, Drossinos and Stilianakis (2013); Fisk (2000); Wargocki, Wyon and Fanger (2000); Hospodsky *et al.* (2012); Rintala *et al.* (2008); Ulrich *et al.* (2008) and Mendell *et al.* (2002). Spatial analytics through Space Syntax methodology describes potential social interaction through core and global integration, local connectivity from one space to the next, spaces that resemble main movement passages, shortest routes that are most likely travelled, and gate count for room use frequency. These mathematical model analyses have, through various case studies, been verified with high correlation confidence concerning the observed spatial activity; thus the potential analytical means is provided to quantitatively determine interactions and thereby enable the grading of rooms for risk. The fluid nature of social factors, strength of program and spatial relationships contribute to the complexities in spatial planning analysis. It is believed that an outcome of this research will be an increased understanding of social and spatial relationships and their impact on and within the microbiome of the built environment. Spatial analytics and indoor microbiome data create opportunities to assess possible IPC associated risks for hospital environments.

# CHAPTER 6 RESEARCH INVESTIGATION

A threefold approach has been taken with regard to the research questions and objectives for this thesis: firstly, to investigate methodologies and conclusions drawn from built environment studies with an eye to the replicability of the methodology. This included considering climatic and regional diversity. Secondly, to develop a methodology that is replicable and viable in a developing world setting in order to develop a data set of BE biome data for South Africa, while simultaneously capturing a typical BE HAI index for healthcare environments. Thirdly, to investigate and define the BE factors that shape the microbiome of the built environment – including current known factors, and introducing understudied or new spatial factors relating to human movement flow and distribution, as well as space use and function in buildings, in particular healthcare typologies, i.e. hospital environments known to be HAI-conducive. Healthcare infrastructure is an understudied field in South Africa and arguably globally; the prevalence rates of HAI in these settings demand more focused and intentional research with particular attention paid to building design and planning.

## 6.1 MoBE REPORT RESEARCH GAPS

The document *A research agenda for indoor microbiology, human health, and buildings,* compiled by the National Academies of Sciences, Engineering & Medicine outlines the status of research in MoBE, as well as the current research agenda. It was publicly presented in October 2017, and officially published as a status document in this emerging field in 2017 (Briere & Resnick 2017). The report contains six key categories: 1) Introduction to MoBE; 2) Microorganisms in the built environment: impacts on human health; 3) The built environment and microbial communities; 4) Tools for characterising microbiome–built environment interactions; 5) Interventions in the built environment; and 6) Moving forward: a vision for the future and research agenda. For the greater MoBE research agenda it is imperative that the needs of the current MoBE research agenda are addressed. This thesis is positioned to make a contribution to the current international research agenda by providing foundational data for future investigations.

It is critical for the purposes of the thesis for the reader to be aware of the fact that the state of MoBE research, published in the report, was presented four years after the commencement of this thesis. It will therefore seem that many of the findings and approaches used by the author were derived from the report; however, the report was published after the author had developed the thesis. It is in fact auspicious that the report confirms many of the thesis goals and objectives, as well as methodology approaches. (This is largely because the author was involved in numerous research development discussions with peers through conference special sessions.) The Table 1.1 MoBE report: box s-2 and identified knowledge gaps (Briere & Resnick 2017), Table 1.2 MoBE: research objectives and Table 1.3 The 12 MoBE focal priority research areas presented in Chapter 1 in part and in Chapter 3 in full have been integrated into the research problem statements, questions, hypotheses, goals and objectives, thereby responding to the broader research agenda.

## 6.2 PROBLEM STATEMENTS

From the outset of this investigation the author proposed to address the impact of the built environment on user and public health. The healthcare environment has been shown, through numerous studies (refer to Chapter 1 and Chapter 3), to be a source of HAI. This in part is due to the health condition and levels of immunity of the users, the unknown status of infections,

and potential cross infection, but also the indoor air quality (IAQ) and indoor surface quality (ISQ) - principally, the quality of the indoor built environment.

#### 6.2.1.1 THE PRIMARY PROBLEM STATEMENT

A large number of people, in excess of 15% in developing world countries and 8-10% in developed world countries, contract some form of HAI in hospitals (Yates *et al.* 2016; Hamilton 2012). South Africa suffers the same burden. Numerous studies and investigations (of which only a few are referenced in chapters 1 and 3) point to the fact that indoor built environments affect the health and well-being of their users, however little empirical evidence might be available on the factors that contribute to this condition (Schweitzer *et al.* 2004; Yates *et al.* 2016; Lax *et al.* 2017). There is an apparent oversight or understudy of architectural factors, with spatial networks in building design and planning being one such factor. With the research conducted to date on the microbiology of the built environment and building ecology, there is still a lack of understanding and knowledge of the transmission and impacts of infectious microorganisms within the built environment (Lax *et al.* 2017).

#### 6.2.1.2 THE SECONDARY PROBLEM STATEMENT

The interdisciplinary nature of the research, with particular reference to microbiology and architecture, requires focused statements for each field; collectively they share overlapping problems and approaches to solve them.

1. Microbiology: Buildings and dwellings are colonised by pathogenic bacteria – microbes that have adapted to their extreme environmental conditions. Research has shown a decline in microbial biodiversity, and a rise in human pathogenic bacteria within engineered environments when compared to naturally ventilated biome spaces (Kembel *et al.* 2013). The relationship between spatial planning and the distribution and prevalence of microbes is largely unknown.

2. Architectural, engineering and spatial analytics: The environmental conditions, including but not limited to ventilation and the understudied area of spatial networks in building design and planning of an environment, directly contribute to the spread of various surface-origin bacteria, NTMb and airborne bacteria such as *Tuberculosis* (Nardell *et al.* 1991); as a result they contribute to the high prevalence rates of nosocomial infections (the driver for NTMb, tuberculosis and other infections) in hospitals and other enclosed environments (Basu *et al.* 2007; Koenig 2008; Ducel *et al.* 2002). South African hospitals and the national health system suffer from a lack of HAI data sets even though this is mandated by the National Core Standards for Healthcare Establishments (Dramowski & Whitelaw 2017). As a result, hospital staff, recovering TB patients, HIV patients, unsuspecting patients and the public at large are at risk in nosocomial environments. Secondly, implementing and maintaining costly mechanical systems are neither affordable nor sustainable in resource-limited settings (Block *et al.* 1999) such as South Africa. The field of architecture therefore requires a form of empirical risk validation for building designs to prevent healthcare associated infection (HAI) and support sustainable approaches to infection control and healthcare design.

## 6.3 PRIMARY RESEARCH QUESTIONS AND SUB QUESTIONS

Understanding the micro environments we live, work and play in on a daily basis can lead to creating safer indoor microbial environments that not only prevent illness but also promote health and wellness, i.e. salutogenic environments. The constant human interaction with surfaces, enclosed space and other humans will continuously cause contamination (Hospodsky *et al.* 2012; Ducel *et al.* 2002). The solution lies in understanding the contaminated environment and engineering it to develop healthy ecosystems that are naturally self-regulating and generative rather than the current status quo that promotes pathogenic colonisation of bacteria (Kembel *et al.* 2013; Klevens, Edwards, Chesley, Horan, Teresa, Robert, Pollock & Cardo 2007). The primary research questions therefore are:

**Primary research questions 1) What is the composition of the South African, Western Cape, Cape flats hospital microbiome?**

**Secondary research questions**

1.1 Is there a link between the indoor and outdoor communities of both researched hospitals?
1.2 Are the rooms in the hospitals more representative of human-sourced bacteria or outdoor-sourced bacteria?
1.3 Is there a seasonal variation in the built environment biomes of both hospitals?
1.4 Is there a correlation between the communities of the biomes of the two hospitals, indicating a similarity or variation between and within hospitals?
1.5 Is there a link between the air samples and the surface samples at each hospital, inferring that the air-sample fall-out to the surface will represent the surface biome environment?

**Primary research questions 2) What pathogens are commonly found in South African hospitals, with specific reference to the Western Cape, Cape flats**

**Secondary research questions**

1.6 What are the indicator species prevalent in the hospital indoor environments in the Cape Flats region of the Western Cape?
1.7 Do variations exist between indicator species based on room type?
1.8 How do the prevalent microbes found correlate with international HAI data lists?

**Primary research questions 3) Which built environment factors contribute to and influence the composition of the built environment microbiome, and how**

**Secondary research questions**

1.9 What are the BE factors that can be attributed to influence the BE microbiome and test the factor of influence?
1.10 What are the scientific environmental monitoring methodologies and technologies available for indoor built environment sampling?
1.11 Is there a statistically significant relationship between the organism present and the building ventilation system?

**Primary research questions 4) Is there any correlation between the distribution of the microbes in hospitals and the spatial design of the hospitals (considering user data and design data)? Do design and planning influence the composition of the microbiome?**

**Secondary research questions**

1.12 Have spatial analytical tools been applied to MoBE investigations?

1.13 Does a room type (and its associated function) host a unique biome? If so, are there overlaps in room type biomes within a hospital and between the two hospitals?

1.14 How do the spatial data of human movement patterns and space use correlate with microorganism distribution and richness?

**Primary research questions 5) How can built environment data, microbiome data and spatial design data inform IPC processes, with the intentional focus on reducing the potential of HAI transmission?**

**Secondary research questions**

1.15 What are the known theoretical models and tools available for BE characterisation regarding risk, transmission and microbiome identification?

1.16 Can BE factors be converted into indicators utilised for microbial risk in buildings?

1.17 Can the building form and spatial planning unique to the hospital typology influence IPC outcomes?

## 6.4 HYPOTHESES

From the premise that all environments are ecosystemic and that each constitutes a unique biome, it is postulated in the thesis that the built environment microbiome is shaped by both ecological processes and interrelationships (Martiny *et al*. 2006; Kembel *et al.* 2013), but also by key factors within the BE, unique to indoor building environments. Furthermore, it is postulated in this thesis that the hospital environment would present a unique composition by nature of its use, with each composition being unique in different climates, environments, countries and social conditions.

The architectural layout of a building and its associated engineering aspects will impose differences in the biomes from one building to the next; the source/user would, as is the case with hospitals, be constant, but vary with burden of disease. By characterising the BE aspects and overlaying these with spatial analytics trends, the patterns of use, assemblies, and voids can be derived. In theory, this should lead to variations in the microenvironments of a building. With all ecosystems, both macro- (department and whole building level) and microenvironments (room, table, keyboard) exist within, which also holds true for the built environment. In this thesis the macro biome environment of two A&E departments in the same region and climate are investigated with insight into the micro environment at room level only.

### THE PRIMARY RESEARCH HYPOTHESES

Hypothesis A: Building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health

architectural design, based on the biome composition (abundance and richness) of indicator organisms.

Therefore…

Hypothesis B: Social behavioural science studies which consider factors of human movement patterns, occupancy and functional use of space influence the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus, the indoor environmental factors of hospitals MPH and KDH influence the composition of both the micro (room level) and macro biome (building level) environments.

SECONDARY RESEARCH HYPOTHESES

Sub-hypothesis A: The source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room;

&

Sub-hypothesis B: The levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.

## 6.5 GOALS AND OBJECTIVES

1. To associate environmental BE data with microbial communities and building systems for ventilation, surfaces and occupancy.
   a. Objective: To guide architectural and engineering design decisions for a public health centred outcome.

2. To investigate whether spatial analytics, IPC risk profiling and BE characterisation can support risk assessments in early design analysis.
   a. Objective: To support BE risk assessment and early design analysis, as a guide towards bio-informed design.

3. To define the microbiome of a hospital environment in the Cape Flats region of the Western Cape and formulate a database.
   a. Objective: To characterise a South African hospital biome, which would be representative of the developing world for future meta data studies.

4. To derive and establish a data set of indicator species for HAI and establish the prevalence of bacteria in the healthcare built environment.
   a. Objective: To support the development of HAI research and a pathogen species list in South Africa and South African hospitals.

5. To support the agenda for repeatable and financially viable research methodologies for developing countries in MoBE studies which will enable future research investigations in collection and generation of data, without compromising accepted and established MoBE and international standards.
   a. Objective: To enable future research investigations in collection and generation of data, without compromising accepted and established MoBE and international standards.

## 6.6 ASSUMPTIONS

1. The results of a questionnaire circulated to the hospital unit staff prior to conducting the research indicated the most and least busy days. It was decided to take measurements for four days that included busy, quiet and “normal” days; this was assumed to represent a working week in summer and in winter.
2. Due to lack of HAI data information for hospitals in South Africa as set out in Chapter 3, the most common sources of HAI in hospitals internationally will be considered and compared to the findings in this thesis.

# CHAPTER 7 ARCHITECTURAL SPACE MODELLING BY OBSERVATION

## 7.1 INTRODUCTION

The research methodologies applied in the thesis are intended to be viewed as both a guide to sample collection, sample processing and analysis, and a contribution to new knowledge and processes in data gathering in architecture. The methodology brings together interdisciplinary research fields, each with its own unique paradigms and factors of influence, and collates the findings to produce insight into architectural design and planning and IPC risk management. The methodologies referred to in the following three chapters (7,8 and 9) are derived from various literature sources and supervisor consultations that have been critically reviewed and critically compared. The methodologies presented, and followed in chapters 7, 8 and 9, make direct reference to comparative literature from which the final methodologies were derived. The three methodologies that have been developed for data collection for this thesis are: microbiological sampling in Chapter 8; environmental sampling in Chapter 9; and architectural space modelling observation sampling in this Chapter 7). For reference purposes, this summary will not be repeated in Chapter 8 and Chapter 9. To reduce repetition for each methodology, mutually shared information that includes the study site; study area; and experiment limitations are presented in this chapter and will not be repeated in Chapter 8 and Chapter 9

### 7.1.1 STUDY SITE

The site selection for the thesis investigation was based on the following: First the need for the highest probable HAI source environments – thus a hospital environment was selected. Second, the value in comparing two environments which would inform potential design variations and microbiome uniqueness – thus two hospitals were selected. Third, hospitals based on the same original design brief, but with very different building designs and planning, would provide insight into design selection and probable HAI factors. Fourth, hospitals that serve a similar disease burden and social environments and are situated in the same climatic region would enable comparisons between functional use, occupancy, planning, microbiomes and organism prevalence. Fifth, the cost and time required to study each department at each hospital would not be viable; however, selecting the same department and matching room types in each hospital would enable comparison. Sixth, selecting the appropriate department is critical, as it needs to represent the particular hospital as far as possible. The selection of the A&E unit for this investigation was informed by its fluidity. The A&E unit does not have a typical patient; it serves patients in all clinical categories, for 24 hours daily, and provides inpatient associated services. It therefore represents the variety of patients, length of stay, and service that could be found within the larger facility.

The sites selected for this investigation are Mitchells Plain District Hospital (a public hospital) referred to as MPH and Khayelitsha District Hospital (a public hospital), referred to as KDH. Both hospitals are situated in the Cape Flats, Western Cape, in South Africa. They are within a 10km radius of each other. Refer to Figure 17 and Figure 19.


Figure 17: Hospital study sites – Cape Flats, Western Cape, South Africa (Google maps 2018)

Figure 18: Mitchells Plain district hospital (MPH) (Google maps 2018)

Figure 19: Khayelitsha district hospital (KDH) (Google maps 2018)

### 7.1.2 STUDY AREA

The study investigated the A&E units of two public district hospitals in Cape Town. The A&E represents high travel zones with the highest throughput of patients, HCWs and visitors. A route map of each unit was drafted, with appropriate room and zone annotations. Refer to Figure 20 and Figure 21 for the route maps, and refer to Table 7.1 for room and zone classification. Figure 20 and Figure 21 indicate the thesis study zones for KDH and MPH. The investigation was limited to the A&E core area due to the number of sensors and air sampling duration and equipment required, which was influenced by cost and time. This area represented the highest use of, and variation in, traffic and functional spaces. Cost and time considerations informed the study limitations. Hospital zones were matched for both hospitals (excluding zone 9 that varies in function). The zones are listed in Table 7.1, and graphically presented.

Table 7.1: Room zone classification

| | |
|---|---|
| Z1 | Triage Consult 1 |
| Z2 | Triage Consult 2 |
| Z3 | Triage Waiting |
| Z4 | Procedure 1 |
| Z5 | Passage Main |
| Z6 | Nurses' Station |
| Z7 | Resus [Resuscitation] |
| Z8 | Nebulisation |
| Z9 | Passage Secondary |
| Z10 | Trolley |
| Z11 | (Not indicated) refer to external sampling area 1 |
| Z12 | (Not indicated) refer to external sampling area 1 |

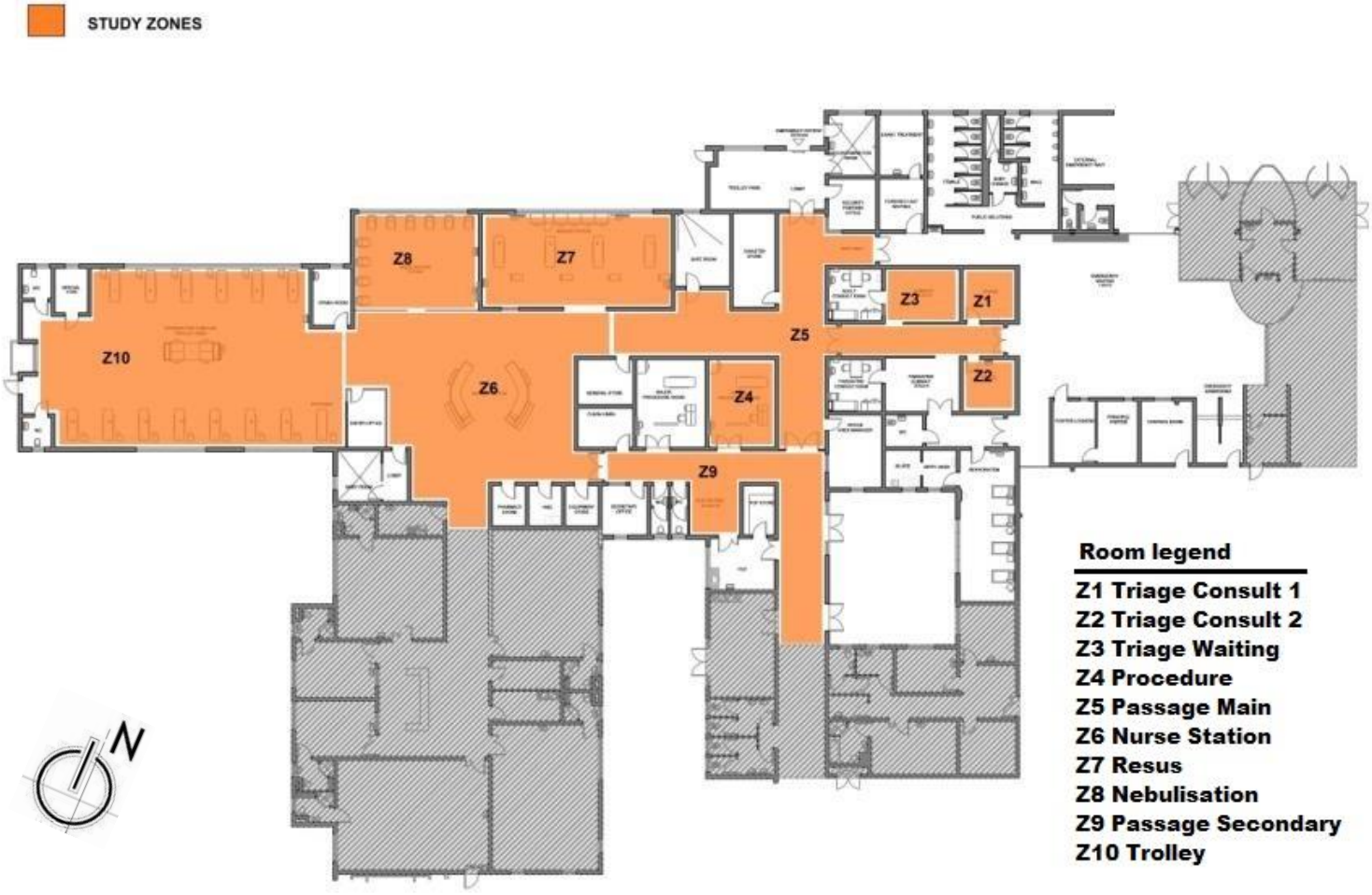



Figure 20: KDH A&E study zones

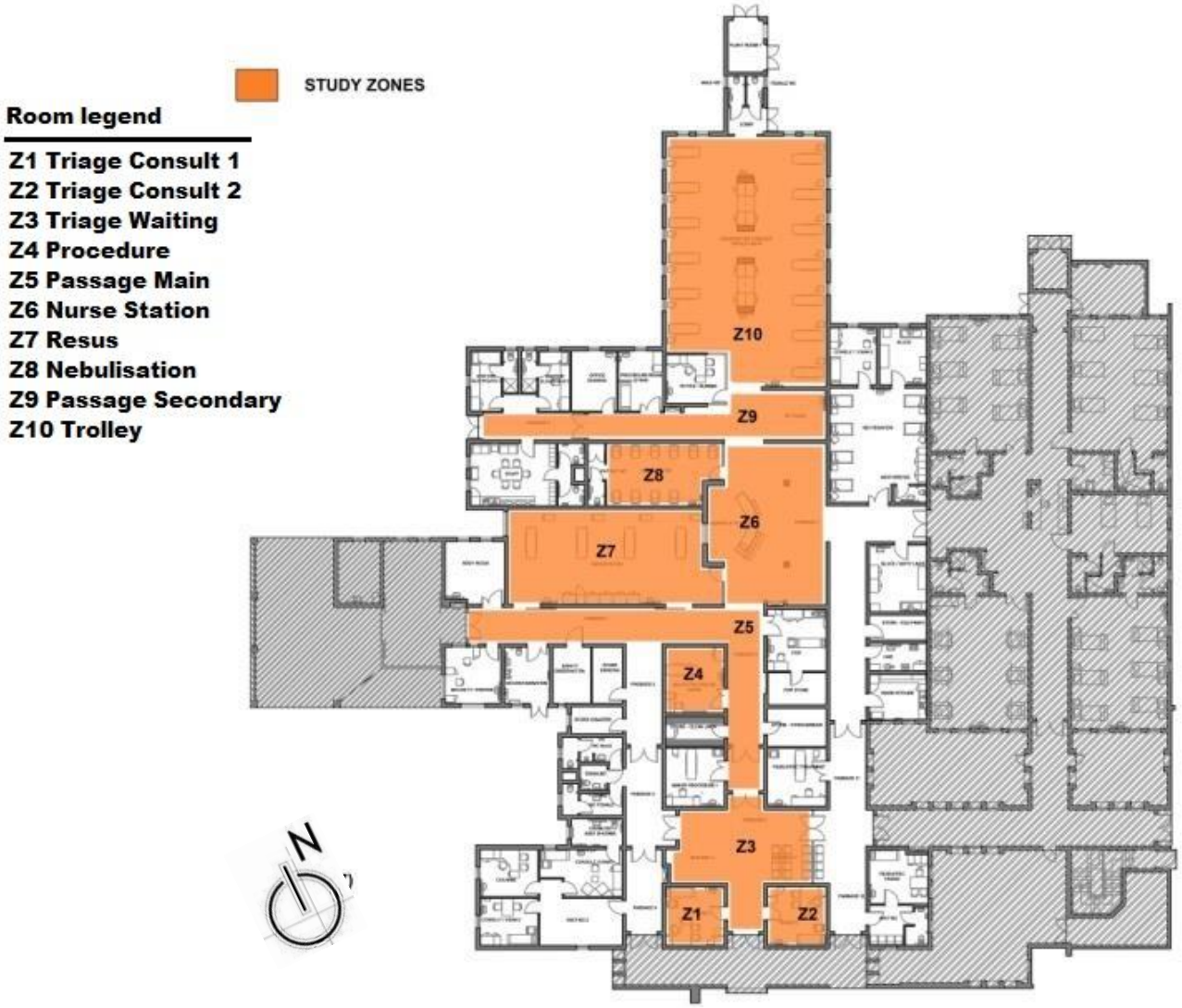



Figure 21: MPH A&E study zones

### 7.1.3 Experiment limitations

#### 7.1.3.1 Sampling equipment

Due to equipment failures during both seasons, adjustments had to be made to the allocated sampling period within the study experiment. This did not reduce the number of observations or sampling time, but merely the period during which the observations and sampling occurred. The number or operational duration of the data loggers was also not reduced. January 2017, summer season: the mechanical failure of the air sampler occurred on the final day (day four, Monday) at the MPH site, irrespective of which a full day of observation was still conducted. The air sampling was restarted and continued from 21:00 to 07:00 the following morning, with observation measures performed simultaneously. Due to this change in the study, it was repeated in the winter season (June). June 2017, winter season: mechanical failure of the air sampler occurred on the first day at the KDH site, which forced a change in the study design time. All observations were still conducted during the daytime and at night on the final day at MPH, as per the study design. However, three days of observation were added during the night at the KDH site. The air sampling was restarted and continued from 21:00 to 07:00 for days one, two and three, and day sampling was conducted on day four as per the planned study. Observations were measured and data logging continued over the same period.

#### 7.1.3.2 Operations

Due to the critical emergency status and fluid/unplanned operational nature of a hospital environment, in particular the A&E, instances arose when the planned route of observation and/or microbial air sampling had to be changed or stopped to be restarted midway. This required completion of the route and returning to the unavailable room, and/or stopping air sampling and returning to the unavailable room later during the day. The following unforeseen circumstances occurred at both sites: holding of a dead body, grieving families, emergency medical and/or surgical treatment, and unruly psychiatric patients. Nonetheless, the observation routes and microbial sampling were completed.

## 7.2 METHODOLOGY

The observation methodology for spatial analytics is based on the Space Syntax Software manuals of the Architecture Department at the University College London (UCL), such as the Space Syntax observational manual developed by Tad Grajewski in 1992 and updated by Laura Vaughan in 2001. The concept of Space Syntax was developed for urban planning network studies; however, subsequent studies have been conducted on building networks (plans), and are now widely accepted in this built environment typology – as discussed in Chapter 5 in more detail. Space Syntax developed, tested and correlated multiple observation data collection methods, each relevant and applicable based on the required investigation, as referenced in various papers and outlined in the Space Syntax manual. For this study, a two-task process was selected and executed. As previously indicated, observations were done for a 12-hour period at each facility, conducted by an assigned single observer per hospital site. See Figure 22 and Figure 23 for the routes covered by the observer. The detailed methodology is provided below. Note: Due to the sensitive privacy nature of the hospital environment, care was taken to ensure appropriate etiquette at all times, including reporting to the ward nurse before the study day commenced, keeping valid identification and a letter of authorisation, and considering patients and their needs.

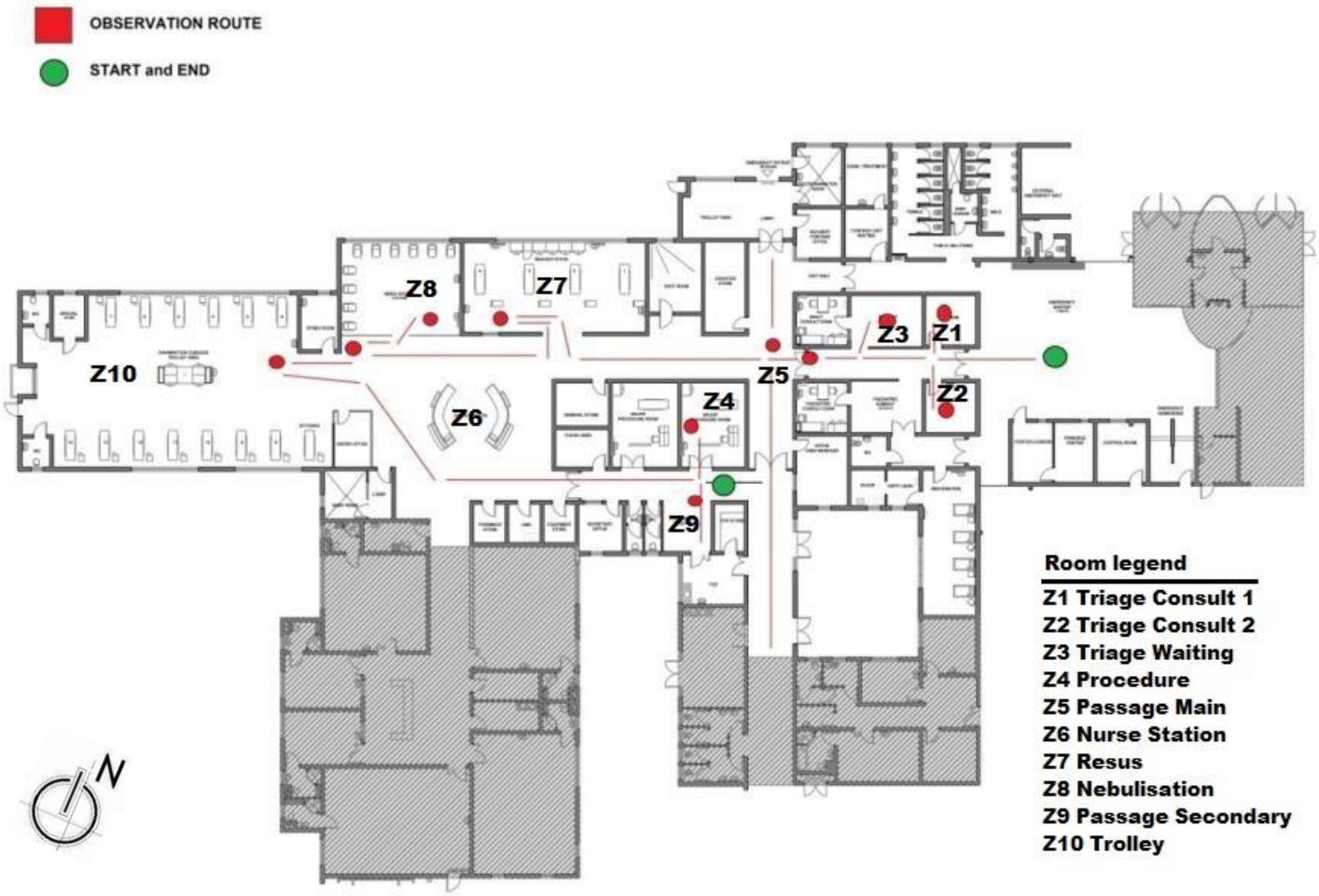



Figure 22: KDH observation route for tasks 1 and 2

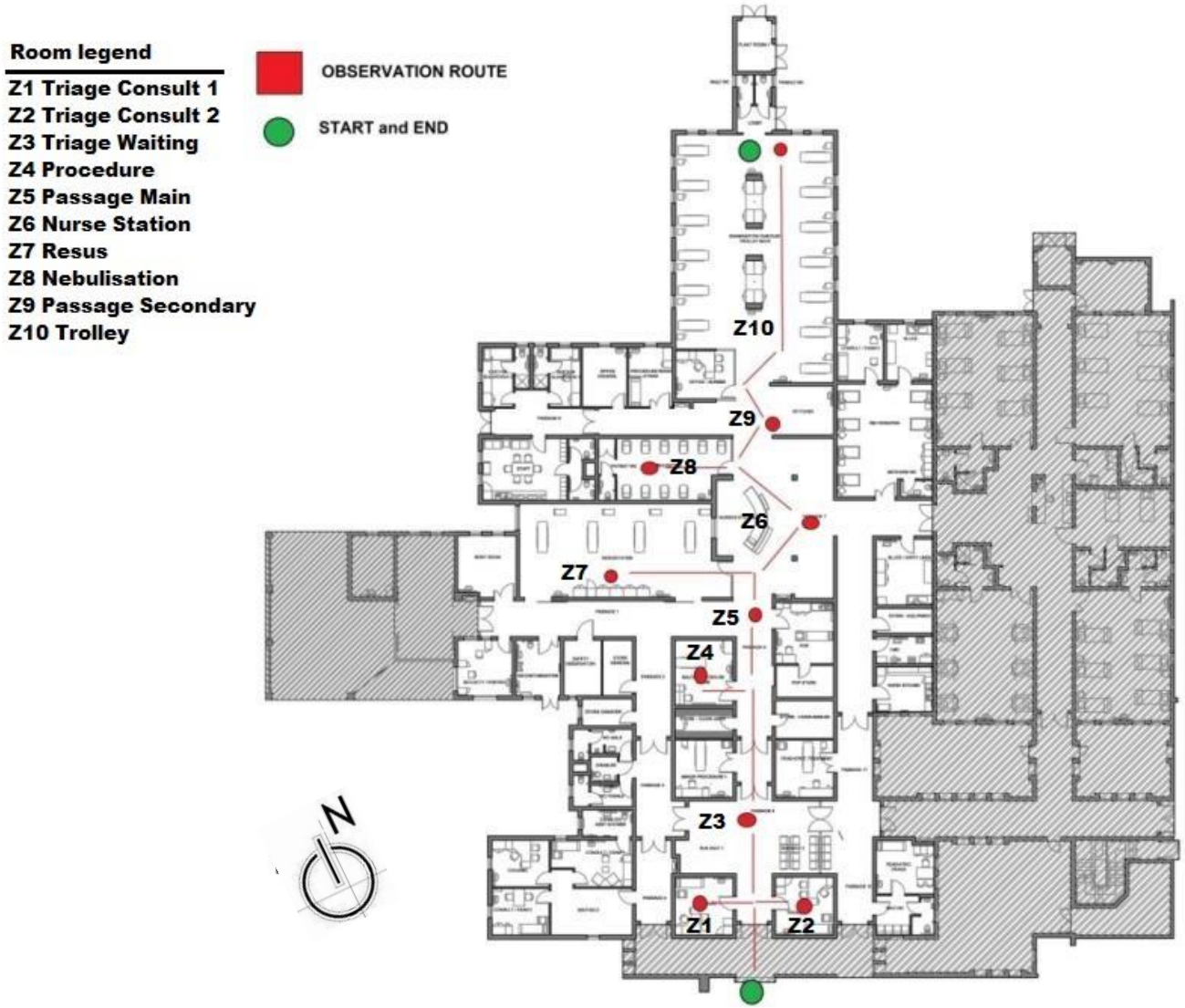



Figure 23: MPH observation route for tasks 1 and 2

### 7.2.1 Pre-sampling test

Prior to the observation study a questionnaire was circulated to the staff at the A&E units of both hospitals, to determine the peak low and peak high times, patient load and active spaces, and individual perceptions of personal safety, healthcare-acquired infection and cleaning regimes. The purpose of this data was to determine the most appropriate four days for analysis for appropriate correlation with environmental data collection, as well as the personal perceived status quo of HAI. Furthermore, a “dry run” of the route was conducted prior to the study which enabled the observers to familiarise themselves with the requirements and pathways.

### 7.2.2 Sample types

The Space Syntax methodology for spatial analytics employs various observation techniques. Each technique is appropriate for the research context and question. For example, the gate method for stationary people and vehicles; the static snapshot for user movement - both stationary and moving - in buildings; following people that disperse from a specific movement distributor such as a train station or shopping mall for observing movement; and directional splits suitable for observing people or vehicles to record the split in movement flows at a point or junction. The data are applied for most cases using DepthMap™ and GIS-based software. The various observation procedures are outlined in the Space Syntax methodology guide (Grajewski & Vaughan 2001; Al Sayed *et al.* 2014). The procedures included the gate method, static snapshots, people following, directional splits, movement traces and others. For this investigation, two observation tasks were selected and observed: the mental snap shot, and the movement tracer technique. Some variations were introduced as required by the specific research strategy and sample design. The data collected allowed for the gate method information to be produced through GIS analyses.

#### 7.2.2.1 Observation task 1: Mental snap shot

Floor plans at scale (A3 paper size) of the selected A&E departments of both KDH and MPH were produced and printed. The data provide insight into patterns of space use. A route was mapped covering all rooms that were frequently used (the core zone of the A&E). Route development ensured that all influential spaces (excluding storage areas) were observed (based on the pre-observation test and the questionnaire). Furniture and divisional changes were marked on the plans prior to commencing with the study. If a single space was too large, it was divided into smaller zones that were individually assessed. The route was walked twice hourly, as far as operationally possible at the time (refer to 7.1.3: Experiment limitations). The number of people occupying each space (zone) was marked on the drawing and the coding system was utilised as per Table 7.2. The occupancy number in the space at that moment was recorded. Rooms that were locked or where entry was prohibited, were marked with an X. Data from each room (zone) were recorded twice hourly, as far as operationally possible at the time (refer to study limitations). A blank sheet plan was used for each round. (Due to hospital operations, the number of observations per hour varied; an average of 18 sheets per day during the 12-hour period was achieved and is considered to be within acceptable sample size limits).

Table 7.2: Observation coding task 1: mental snap shot technique

| No. | Colour | Observation type |
|---|---|---|
| 1 | | Seated |
| 2 | | Standing |
| 3 | | Walking * |
| 4 | | Talking, |
| 5 | | Doctor |
| 6 | | Nurse |
| 7 | | Other |
| 8 | | Patient |
| * (use an arrow indicating the direction) (do not count people behind you, or any one that enters the zone after your snapshot) | | |

#### 7.2.2.2 OBSERVATION TASK 2: MOVEMENT TRACER

This technique noted the precise routes observed of people moving through the spaces (zones). When these data traces were combined with the mental snap shot technique, the space use and through flow of each zone were determined. Similar to task one, the observer had to spend three minutes in each of the rooms (zones), marking observations of the movements of people entering or exiting the space. This was done on a blank floor plan and indicated by flow direction lines. The flow lines were traced with a pen on the plan, each pen colour representing a person type – refer to Table 7.3: Observation coding task 2: movement tracer technique. All the movements through the space were recorded with the flow lines ending with an arrow where the person exited the space. The space use coding system was used in combination with the colour assignment used in task 1 for the mental snapshot technique (refer to Table 7.2 and Table 7.3). Each room (zone) and passage were recorded twice hourly, as far as operationally possible at the time (refer to study limitations). A blank sheet plan was used for each round. (Due to hospital operations, the number of observations per hour varied; an average of 18 sheets per day during the 12-hour period was achieved and is considered to be within acceptable sample size limits).

Table 7.3: Observation coding task 2: movement tracer technique

| No. | Colour | Observation type |
|---|---|---|
| 1 | | Through |
| 2 | | Towards |
| 3 | | From |
| 4 | | Within |
| 5 | | Doctor |
| 6 | | Nurse |
| 7 | | Other |
| 8 | | Patient |
| * (use an arrow indicating the direction) (do not count people behind you, or any one that enters the zone after your snapshot) | | |

### 7.2.3 SAMPLING DURATION

Observations were made over a four-day period (the specific days were determined by the questionnaire response - refer to Table 7.5). The assigned days were Friday, Saturday, Sunday and Monday. The period was largely determined by the time required to complete a

full day microbial sampling of an air sample per room, as well as two outdoor samples. Study times: daily from 08:00 to 20:00 (a 12 hour-period) per hospital, which in effect correspond to a single HCW shift on most days.

### 7.2.4 Sample size

For gate counts, the literature indicated one to three days of observation of a single area for eight hours per day (USA and UAE) (Raford & Ragland 2005; Kubat, RAB, Guney, Ozer & Kaya 2012). For the direct observation, movement tracer and snapshot methods, one to ten days for up to eight hours on consecutive days are required (France and the UK) (Kubal *et al.* 2012; Ozbil *et al.*; 2007; Sailer *et al.* 2013; Orelana *et al.* 2013). When comparing the sample sizes, the research study was larger than most Space Syntax studies, with a total of 144 data sheets per hospital depicting flow patterns and occupancy counts, and representing an average of 18 sheet sets of flow and 18 sheet sets of occupancy observations, collected daily over a period of 12 hours, for four consecutive days during two seasons. Due to the equipment failures and subsequent study design amendments, an additional 72 sheets of both task 1 and task 2 were collected as described in section 7.1.3.1.

### 7.2.5 Analysis

The collected data were processed and analysed in GIS and re-analysed through DepthMap™ Space Syntax software (Al Sayed *et al.* 2014). This was compared to the original design layouts captured in as-built plan CAD format initially analysed in DepthMap™ in Chapter 7. Reference is made to the original design layouts as **"base plans"** and the observation overlays plans as **"observed plans"**. Graphical axial representations and percentage flow indicating spatial distribution were derived; refer to the Space Syntax methodology and DepthMap™ software authors Al Sayed *et al.* (2014) *Space Syntax Methodology*. Details of this process and analysis are provided in Chapter 5. *Observations can be used to generate numerical data on space use and movement in urban areas and this data can be correlated with the spatial variables. We can use the results of observation studies to research social variables: This is because integration is an independent measure – "it is the integration value of a space that can produce the people (or the shops and other functional variables) but the presence of more people cannot make space more integrated* (Grajewski & Vaughan 2001:17). Analysis assessment as described in Chapter 5 and correlations and findings are presented in Chapter 7 and Chapter 10: Findings and conclusions.

### 7.2.6 Delineation of the experiment

1. This study only considered spatial observation data for a period of four days in two seasons as a representation of an average seven-day week over a calendar year.
2. The hourly observation over twelve hours per day is assumed to represent the daily average usage pattern of the studied environment, aligning with the Space Syntax methodology and sample sets in similar published studies.
3. Observations for the study are limited to the two selected hospitals, KDH and MPH, and represent the average space use of high-burden healthcare facility A&E units in South Africa. De Vries *et al. (*2011) compared bed occupancy rates in the Cape Town Metro district. At both KDH and MPH these are 78% and 100% respectively, with an average of 82%. However, since the closure of the GF Jooste hospital in 2015 which had an occupancy rate of 138%, that of KDH increased to over 130%. It can thus be accepted

that they are representative of high-burden district hospitals, situated in an area with the highest gang-related violent crime statistics in South Africa.

4. This study accepts the Space Syntax methodology and DepthMap™ software (peer reviewed and used extensively) for modelling collected data, as they are considered to be appropriate for space use prediction and analysis.
5. The A&E core area within each unit was delineated as the investigation study zones. These areas experience the highest traffic levels and contain the highest number of functional spaces within the hospital. Cost and time considerations informed the study limitations.

### 7.2.7 Observational questionnaire

Ten questionnaires - five per hospital site - were distributed and received back. The author requested a representation of all HCW types per function in the facility; the participants were represented by cleaning staff, doctors and nurses (see questionnaire below in Table 7.4: Observation questionnaire). The data results include staff from both MPH and KDH.

Table 7.4: Observation questionnaire

| No | QUESTION | RESPONSE | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Section A** | | **Yes** | | **Unsure** | | | **No** | |
| **1** | Confirm if you are a hospital staff healthcare *w*orker at this facility? | | | | | | | |
| **2** | In which department do you work? | | | | | | | |
| **3** | Do you feel safe in your work environment from acquiring airborne disease? (such as TB) | | | | | | | |
| **3.1** | If yes response to point 3 - Why? | | | | | | | |
| **3.2** | If no response to point 3 - Why? | | | | | | | |
| **3.3** | If unsure response to point 3 - Why? | | | | | | | |
| **4** | Do you feel that the surfaces in your department are sufficiently cleaned for infection and you are at no risk? | | | | | | | |
| **4.1** | If yes response to point 4 - Why? | | | | | | | |
| **4.2** | If no to response point 4 - Why? | | | | | | | |
| **4.3** | If unsure response to point 4 - Why? | | | | | | | |
| **Section B** | | **Monday** | **Tuesday** | **Wednesday** | **Thursday** | **Friday** | **Saturday** | **Sunday** |
| **5** | Which week days do you work? | | | | | | | |
| **6** | How long is your work shift? | | | | | | | |
| **7** | What time does you shift start and end? | | | | | | | |
| **8** | Which week days are busiest in your department? | | | | | | | |
| **9** | Which week days are the quietest in your department | | | | | | | |
| **10** | What times of the day (of the full 24 hrs) do you perceive are the busiest during a busy day? | | | | | | | |
| **11** | What times of the day (of the full 24 hrs) do you perceive are the busiest during a quiet day? | | | | | | | |
| **Section C** | | | | | | | | |
| **12** | Which rooms in your department do you perceive to have high activity spaces? | | | | | | | |
| **13** | What is the average total recorded number of patients in your department on a busy day (as stated in point 10) over 24 hours? | | | | | | | |
| **14** | What is the average total recorded number of patients in your department on a quiet day (as stated in point 11) over 24 hours? | | | | | | | |

#### 7.2.7.1 SUMMARY OF HCW RESPONSES AND OBSERVATIONS

Table 7.5 is a summary of the findings in the HCW respondent questionnaire. From the questionnaire, the following deductions and sampling methodology decisions were made and corroborated:

1. The average work shift was 10hrs - 12hrs; the thesis sample collection time was 10hrs - 12hrs per day, and was incorporated into the methodology.
2. The busiest days occurred over weekends; the thesis collection days were Friday to Monday, an acceptable representation of both the busy and quiet days in the A&E, and were incorporated in the methodology.
3. The thesis sample time included the quiet and busy times during the day as per the respondents, and was an acceptable representation of both the busy and quiet times in the A&E and incorporated into the methodology.
4. The majority perception of the respondents was that they were at risk of acquiring airborne infection, that the surfaces were not sufficiently cleaned and that they were at risk of cross infection by touching surfaces. This perception is addressed quantitatively in Table 7.5.
5. The perceived busiest zones/rooms in the A&E included: Trolley (Majors & Minors), Triage Consult, Resus, and Nebulisation, which corroborated the room selection for the sampling study and are discussed in Chapter 8, where the observation measures are compared with the perceptions of the HCWs, as are the number of perceived patients on busy and quiet days in the A&E.

Table 7.5: Results of the observation questionnaire (addendum 5)

| Q no. | Average response | Comments |
|---|---|---|
| 1 | 90% | Resident hospital staff |
| 2 | 100% | Accident and Emergency unit |
| 3 | 70% | Do not feel safe in hospital A&E work environment from acquiring airborne diseases such as TB |
| 3.1 | - | |
| 3.2 | No PPE, perception of poor ventilation and high disease burden, and concern about patient mix | |
| 3.3 | - | |
| 4 | 55% | Do not feel that the surfaces in their department are sufficiently cleaned for infection; they feel at risk |
| 4.1 | 45% | Feel they are safe; however, as all “yes” responses came from the cleaning staff, one can assume a bias |
| 4.2 | 55% | Do not feel that the surfaces in their department are sufficiently cleaned for infection; they feel at risk |
| 4.3 | - | |
| 5 | Rotation | Majority of the staff work on a rotational basis, with a minimum of 5 days a week |
| 6 | 10hrs - 12hrs | Majority of the staff work 12hr shifts |
| 7 | 07:00 - 19:00 | Majority of the cleaning staff shifts are 07:00 – 19:00. Majority of the clinical staff shifts are 08:00 – 21:00/20:00 – 08:00 |
| 8 | Friday, Saturday, Sunday | Weekends are the busiest time in the A&E department |
| 9 | Wednesday | Midweek is perceived to be the quietest time in the department, followed by no quiet days |
| 10 | - | |
| 11 | 16:00 – 18:00 | These are the perceived busiest times in the A&E unit |

| | | |
|---|---|---|
| | 16:00 – 19:00<br>22:00 – 00:00 | |
| 12 | 60% = Trolley<br>50% = Triage Consult<br>40% = Resus<br>30% = Nebulisation | Of a total of six rooms mentioned, the Trolley area is perceived to be the busiest, followed by the Triage, Resus and Nebulisation rooms |
| 13 | 99 patients | The perceived average number of patients on a busy day in the A&E |
| 14 | 49 patients | The perceived average number of patients on a quiet day in the A&E |

## 7.3 FINDINGS

The response of the built environment to public health, amidst a rapid rate of urbanisation globally and specifically in South Africa, must be addressed. In this thesis, a public health focused response to the architecture and engineering of buildings is proposed. This response cannot be viewed in isolation, but requires a multivariate approach. The interdisciplinary nature of this investigation supports the approach. A vast number of people contract a form of healthcare associated infection (HAI) in hospitals, in excess of 15% in developing world countries and 8-10% in developed world countries (Dramowski & Whitelaw 2017:56). It is evident that the indoor environments of buildings negatively affect the health and well-being of their users, with little empirical evidence available on the factors that contribute to this condition. The results presented in this thesis offer new knowledge and guidance that will be of use to the research agenda of the built environment microbiome, providing insight and empirical data on building factors that contribute to and affect human health. Architectural design is founded on the notion of place making. Christopher Alexander describes this in his book *A Pattern Language* (Alexander *et al.* 1977). Similarly, Broady (1968, in Gutman 2009:181) draws attention to the human element in the built environment. He states, *Built form is only a potential environment since it simply provides possibilities or clues for social behaviour*. *Instead of monuments, architecture creates instruments*. The hospital is one such instrument. It serves a core function as an environment in which healthcare services are provided to the public. In doing so, it must not do any harm, but merely facilitate the process with optimum efficiency and effectiveness, and is often subject to its human counterparts' ability to perform the required actions.

In this study, the findings on a built environment microbiome investigation of two hospital sites in the Western Cape, South Africa, are presented. The two hospitals, conceived from the same design brief, serving a similar disease burden, and situated within 10kms of each other in the Cape Flats region, vary greatly in design and planning. This section is the first of three dealing with BE and microbiology findings of the investigation. The findings presented in this section refer to the architectural space modelling by observation investigation, a data field that is under-studied in the MoBE context and microbial community structure (section 3.3). The results are described separately for each hospital, after which visual and statistical analyses are reported. The analysis was done in three sequences. Sequence one was the base plan analysis. Sequence two consisted of overlaying observation data onto the base plan analysis, and sequence three comprised comparing GIS processed observational data with the base plan and overlay analysis. Lastly, the conclusions are measured against the research questions and presented in Chapter 10

Table 7.6: Spatial analytics analysis index

| | KDH | MPH |
|---|---|---|
| **1** | **Base plan (Operational design analysis)** | **Base plan (Operational design analysis)** |
| | **Observational base floor plan**<br>1. VGA: connectivity<br>2. VGA: metric mean shortest-path angle<br>3. VGA: visual integration<br>4. Axial analysis: map integration<br>5. Axial overlay segment analysis, total depth<br>6. VGA of axial overlay<br>**Plot graph** | **Observational base floor plan**<br>1. VGA: connectivity<br>2. VGA: metric mean shortest-path angle<br>3. VGA: visual integration<br>4. Axial analysis: map integration<br>5. Axial overlay segment analysis: total depth<br>6. VGA of axial overlay<br>**Plot graph** |

| | | |
|---|---|---|
| | 1. VGA of axial overlay: integration over choice (graph)<br>2. VGA of axial overlay: integration over connectivity (graph)<br>3. VGA of axial overlay: integration over mean depth (graph) | 1. VGA of axial overlay: integration over choice (graph)<br>2. VGA of axial overlay: integration over connectivity (graph)<br>3. VGA of axial overlay: integration over mean depth (graph) |
| **2** | **Observation overlay analysis** | **Observation overlay analysis** |
| | 1. Axial analysis integration, summer<br>2. Axial analysis integration, winter<br>**Plot graph**<br>1. VGA of axial overlay: integration vs choice, summer<br>2. VGA of axial overlay: integration vs choice, winter<br>3. VGA of axial overlay: integration vs connectivity, summer<br>4. VGA of axial overlay: integration vs connectivity, winter<br>5. VGA of axial overlay: integration vs mean depth, summer | 1. Axial analysis integration, summer<br>2. Axial analysis integration, winter<br>**Plot graph**<br>1. VGA of axial overlay: integration vs choice, summer<br>2. VGA of axial overlay: integration vs choice, winter<br>3. VGA of axial overlay: integration vs connectivity, summer<br>4. VGA of axial overlay: integration vs connectivity, winter<br>5. VGA of axial overlay: integration vs mean depth, summer |
| **3** | **GIS gate and flow count analysis** | **GIS gate and flow count analysis** |
| | 1. Entry and egress, summer<br>2. Entry and egress, winter<br>3. Occupancy, summer<br>4. Occupancy, winter<br>5. Internal flow, summer<br>6. Internal flow, winter | 1. Entry and egress, summer<br>2. Entry and egress, winter<br>3. Occupancy, summer<br>4. Occupancy, winter<br>5. Internal flow, summer<br>6. Internal flow, winter |

### 7.3.1 TESTING THE HYPOTHESES

For reference, the hypotheses from Chapter 6 are repeated prior to discussing the investigation findings.

Primary research hypotheses:

Hypothesis A: Building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health architectural design, based on the biome composition (abundance and richness) of indicator organisms.

Therefore…

Hypothesis B: Social behavioural science studies which consider factors of human movement patterns, occupancy and functional use of space influence the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus, the indoor environmental factors of hospitals MPH and KDH influence the composition of both the micro (room level) and macro biome (building level) environments.

Secondary research hypotheses:
Sub-hypothesis A: The source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room;

&

Sub-hypothesis B: The levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.

### 7.3.2 BASE PLAN ANALYSIS

This section consists of four parts: 1) Graphical analysis of the base plan by VGA and Axial mapping reported with findings. 2) An overlay graphical analysis of both the VGA and Axial mapping. 3) Regression analysis of the graphical base plan overlay, reported with findings. Laslty, 4) Summary of correlations. Further deductions are presented in the concluding chapter 10, under section 10.1

### 7.3.2.1 GRAPHICAL ANALYSIS OF BASE PLAN MODELLING KDH AND MPH

A visibility graph represents mutually visible points in space (vertices and edge connectors). The level of connectivity refers to the number of points in space that can be connected to a single point – refer to Chapter 5. The visual analyses represent points of connectedness, colour banded from red to blue (red = most connected, dark blue = the least). From the analysis in Figure 24, it is possible to gauge the zones that are connected and most central within the whole KDH A&E unit, the Nurses' Station (mostly red and yellow) being the most connected, followed by the Trolley area and Main Passage. The Resuscitation and Nebulisation rooms are less connected to the whole, while the Triage Consult areas are the least connected.

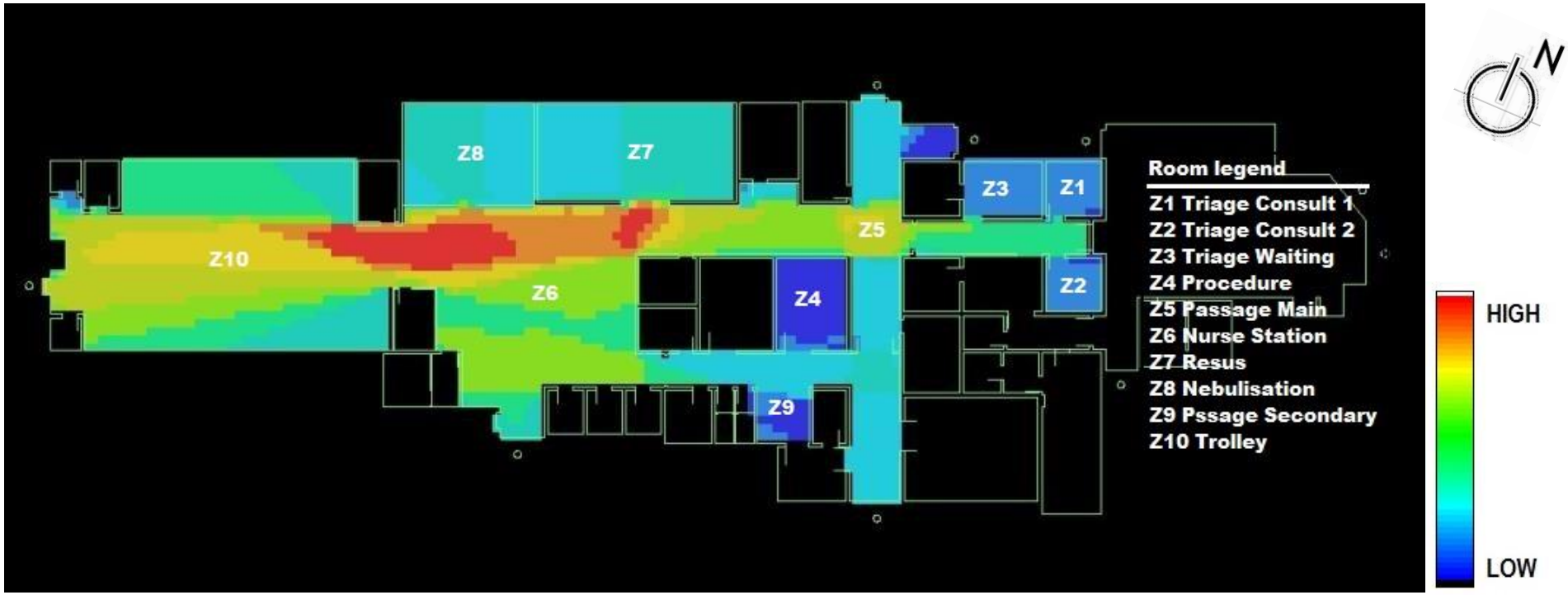



Figure 24: VGA of KDH base plan: connectivity

From the graphical analysis in the Figure 25 visibility graph, it is possible to gauge the rooms/zones that are connected and most central within the whole MPH A&E unit. At MPH we find that the Trolley area is the most connected, followed by the Nurses' Station and Main Passage region. The Resus room is more connected than the Nebulisation room. Two distinct variations exist: The Triage Waiting and Resus rooms are much more connected than their matching rooms at KDH.

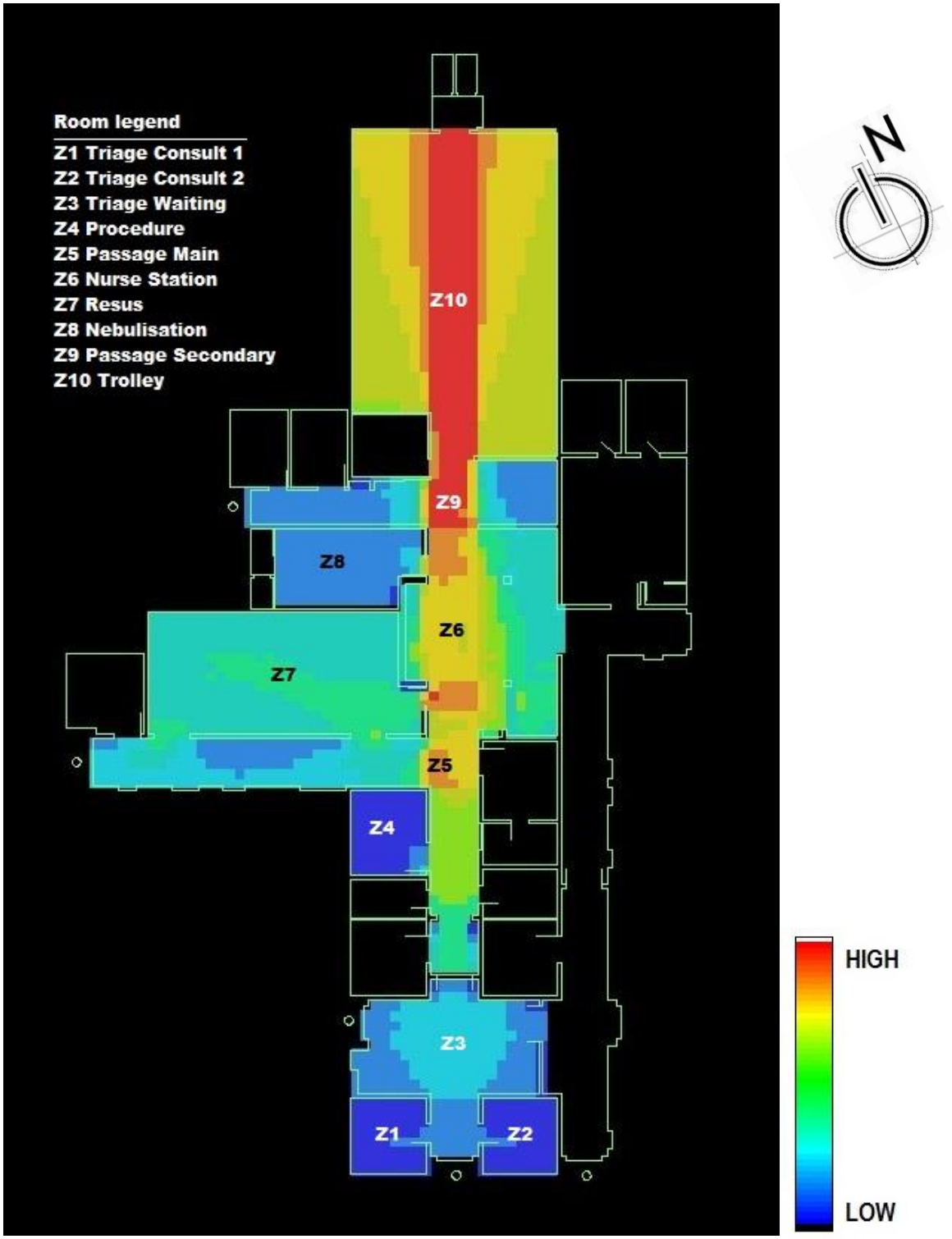



Figure 25: VGA of MPH base plan: connectivity

A visibility graph metric analysis is a derivative by metric step depth. *The shortest metric paths through the visibility graph to other locations are calculated and weighted, and indicated by a colour assignment. These are summed and the mean (also known as the metric mean) is calculated. The graph represents the number of times a location is encountered on a path from origin to destination*, thus anywhere within the zone of analysis, as is the case in this study of KDH and MPH. The metric mean shortest path angle (MMSPA) is a next level of analysis that includes not only the metric distance but also the angular deviation to the short path route. *The angular inclusion refers to the number of turns between nodes in the visibility graph*, as seen in the staggered effect on the base plan drawings in Figure 26 and Figure 27. From the graphical analysis in Figure 26, the Nurse's Station, Trolley room/zone and Main Passage reflect the shortest and most direct route through the unit. One can see clusters of potential connection along the passage network. Secondly, the Resus room/zone and sub wait at the Procedure rooms/zones share the same level of MMSPA. It is noticeable that the Triage Waiting area reflects angular inclusion, but compared with the VGA visual connectivity analysis more accurate levels of interaction are proposed, as confirmed by the observed analysis data.


Figure 26: VGA of KDH base plan: metric mean shortest path angle

From the graphical analysis in Figure 27, a similar finding is noted. The Nurses' Station, Main Passage and the Triage Waiting rooms/zones reflect the shortest and most direct route through the unit, followed by the Trolley and Resus rooms/zones. Secondly, the Triage Waiting and Triage Consult rooms/zones reflect high levels of angular inclusion, but compared with the VGA visual connectivity analysis more accurate levels of interaction are proposed, as confirmed by the observed analysis data.

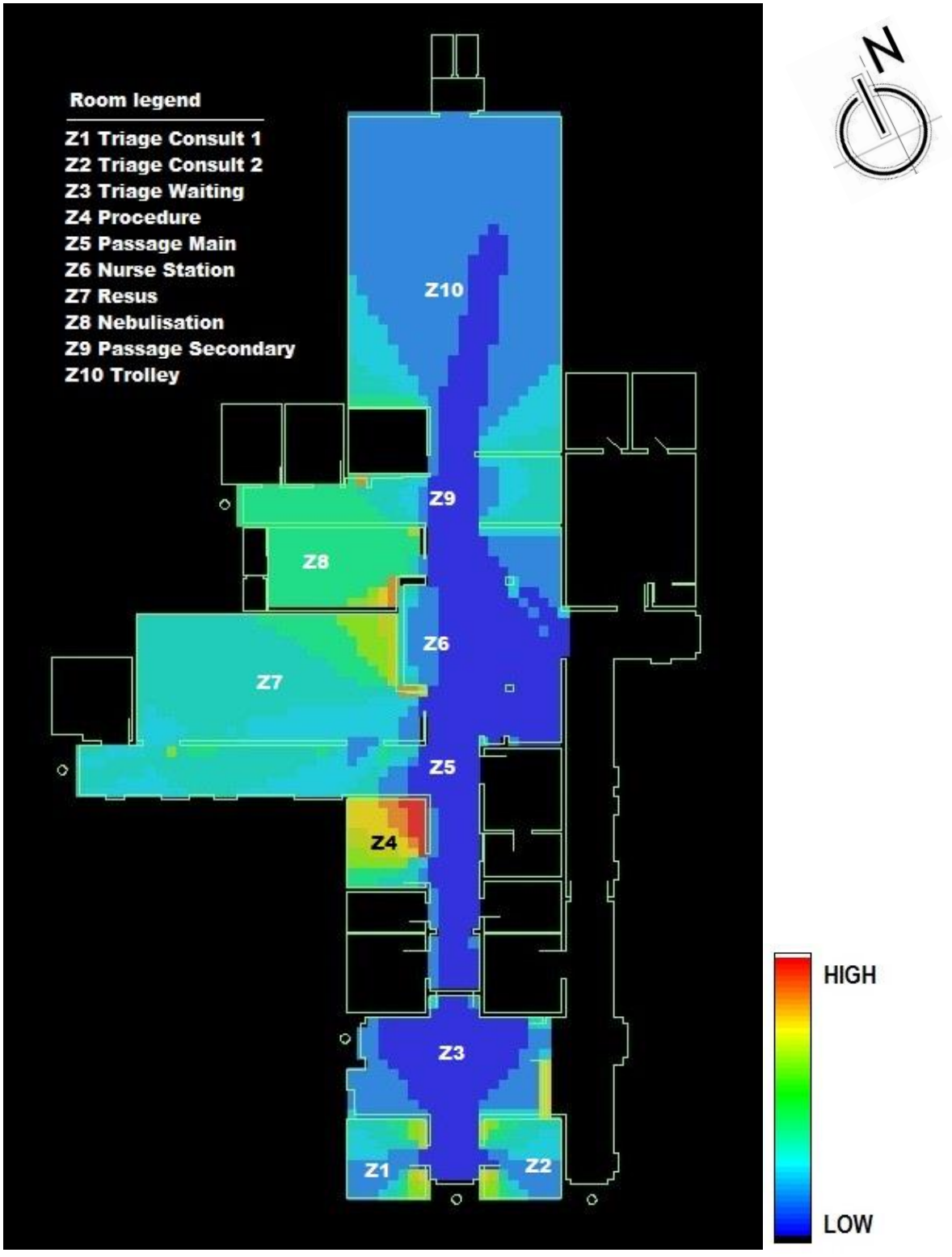



Figure 27: VGA of MPH base plan: metric mean shortest path angle

A visibility graph integration measure indicates the global measure (*prepares the shortest path from each node and through the entire graph to all other nodes*). It is strongly related to the axial maps as seen in Figure 30 and Figure 31. The measure of integration is the normalised mean depth (see Chapter 5). The level of integration has been strongly correlated with gate counts and pedestrian movement discussed later on in this chapter (refer to Figure 52 to Figure 57, and Figure 58 to Figure 63, as well as correlation Table 7.16 to Table 7.19.) From the graphical analysis in Figure 28, it is clear that in KDH, the most integrated spaces are the Nurses' Station, Trolley and Main Passage rooms/zones, followed by the Resus and Nebulisation rooms/zones. The Triage Consult rooms and Procedure room are the least integrated.


Figure 28: VGA of KDH base plan: visual integration

From the graphical analysis in Figure 29, it is clear that the most integrated spaces in MPH are the Trolley zone, Nurses' Station, Triage Waiting and Main Passage rooms/zones, followed by the Resus zone. The Nebulisation room and Triage Consult rooms/zones are less integrated, with the Procedure room the least integrated at MPH (refer to Figure 52 to Figure 57, and Figure 58 to Figure 63, as well as correlation Table 7.16 to Table 7.19). It is evident that a variation in spatial planning exists between the two A&E units at KDH and MPH. Much greater integration, MMSPA and connectivity exist at MPH than at KDH.

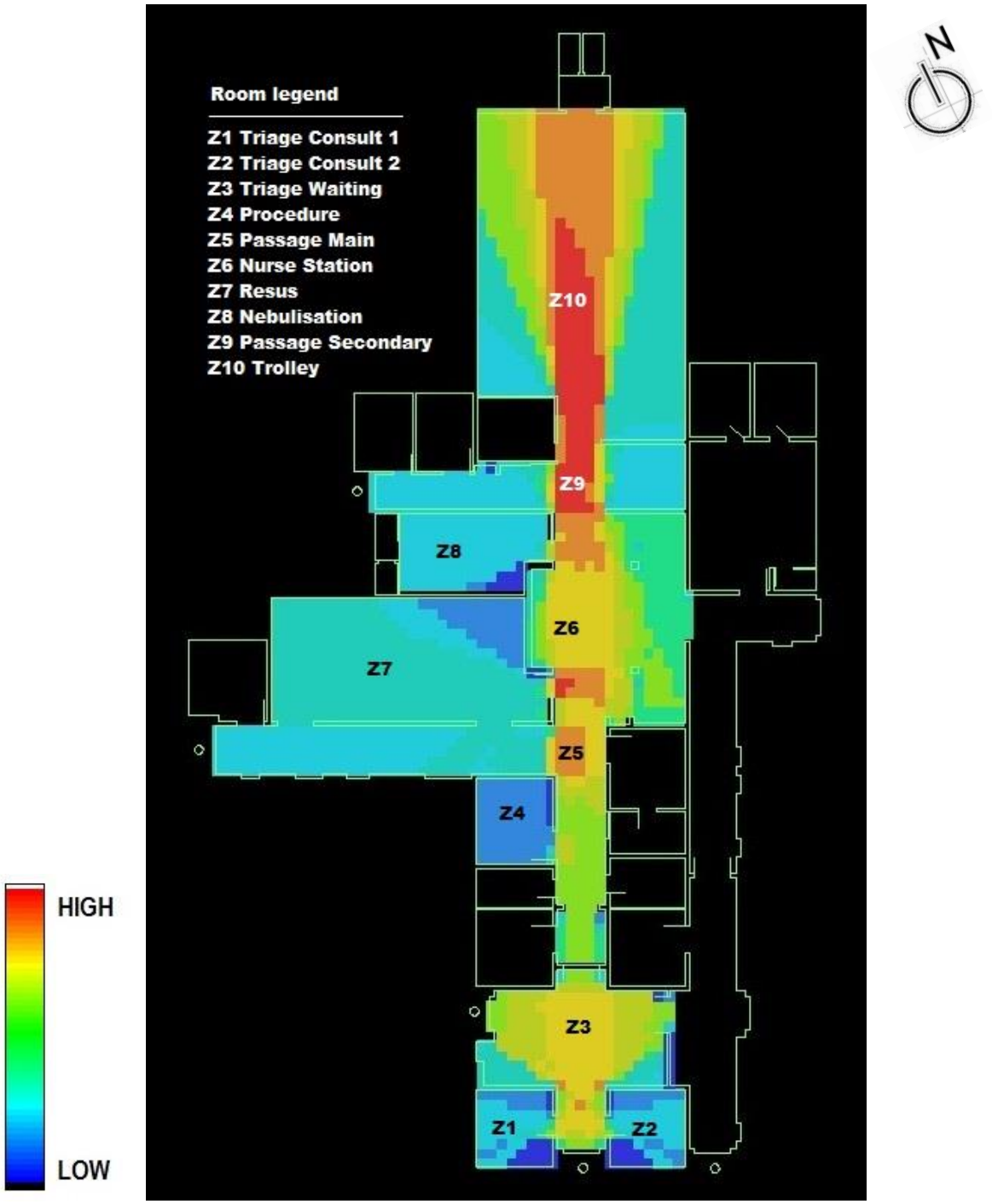



Figure 29: VGA of MPH base plan: visual integration

Figure 24 to Figure 29 visibility graphs are graphic analyses of planning layouts; they correspond with the way people take cognisance of space (their potential awareness of space). The analysis is graded for the levels of spatial awareness form high (red) to low (blue). The planning for KDH and MPH is visually analysed through metrics of connectivity, mean shortest path and integration. Each metric presented a different analysis based on its parameters. From the data, KDH planning indicates higher potential connectivity than MPH, similar with the mean shortest path even though the layout does have similarity. Finally, MPH presents a greater global measure of integration than KDH. Considering similar rooms in each hospital, similar findings are observed. Matching room function and type with interdisciplinary microbial findings in chapter 10 will give more insight into biome composition (clearly there is a micro and macro logic of space, with main and sub clustering of space occurring).

The manually drawn axial map methodology is derived from Sailer (2010): *Lines are considered nodes in the axial graph network, and intersections between the lines are the links that connect these nodes. Each line is considered connected to other lines that it intersects. The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, and is measured by the number of steps it takes from one line to any other line in the map/plan/graph*. The axial line relates strongly to the flow diagram of the observation plan found in Figure 42 to Figure 45. From the analysis in Figure 30, it is clear that the most integrated spaces for human flow and movement are potentially the Nurses' Station, Main Passage and a portion of the Trolley rooms/zones. The potential flow integration does extend into the Triage Consult and Waiting rooms/zones. Secondary flow zones are the Trolley, Resus and Nebulisation rooms/zones. Noteworthy is the relationship between the Triage Consult rooms. Refer to the graph analyses in Figure 39 to Figure 41 for R-value coefficients of the global integration.

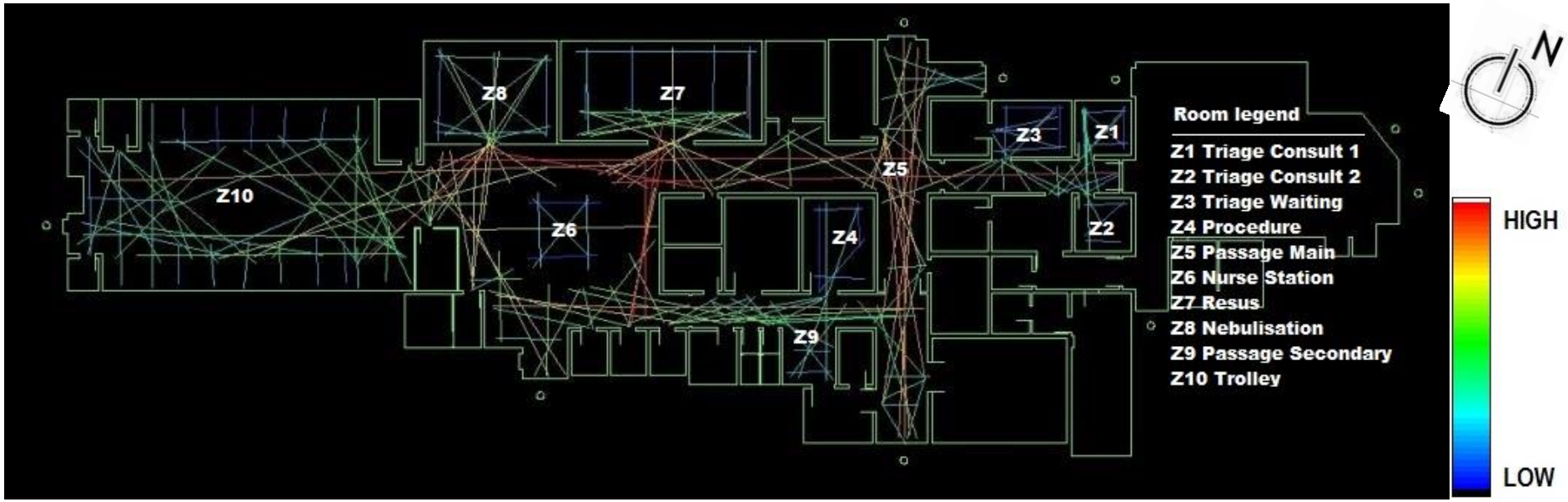



Figure 30: Axial analysis map of KDH base plan: integration

From the analysis in Figure 31, it is clear that the most integrated spaces for human flow and movement are potentially the Nurses' Station, Trolley rooms/zones, Main Passage and the Triage Waiting rooms/zones. Secondary flow zones are the Resus and Nebulisation rooms/zones. Noteworthy is the relationship between the Triage Consult rooms, similar to KDH. Refer to the graph analyses in Figure 39, Figure 40 and Figure 41 for R-value coefficients of the global integration. Again, it is evident that a variation in spatial planning exists between the two units. Much greater integration, MMSPA, connectivity, and axial flow integration exist at MPH than at KDH.

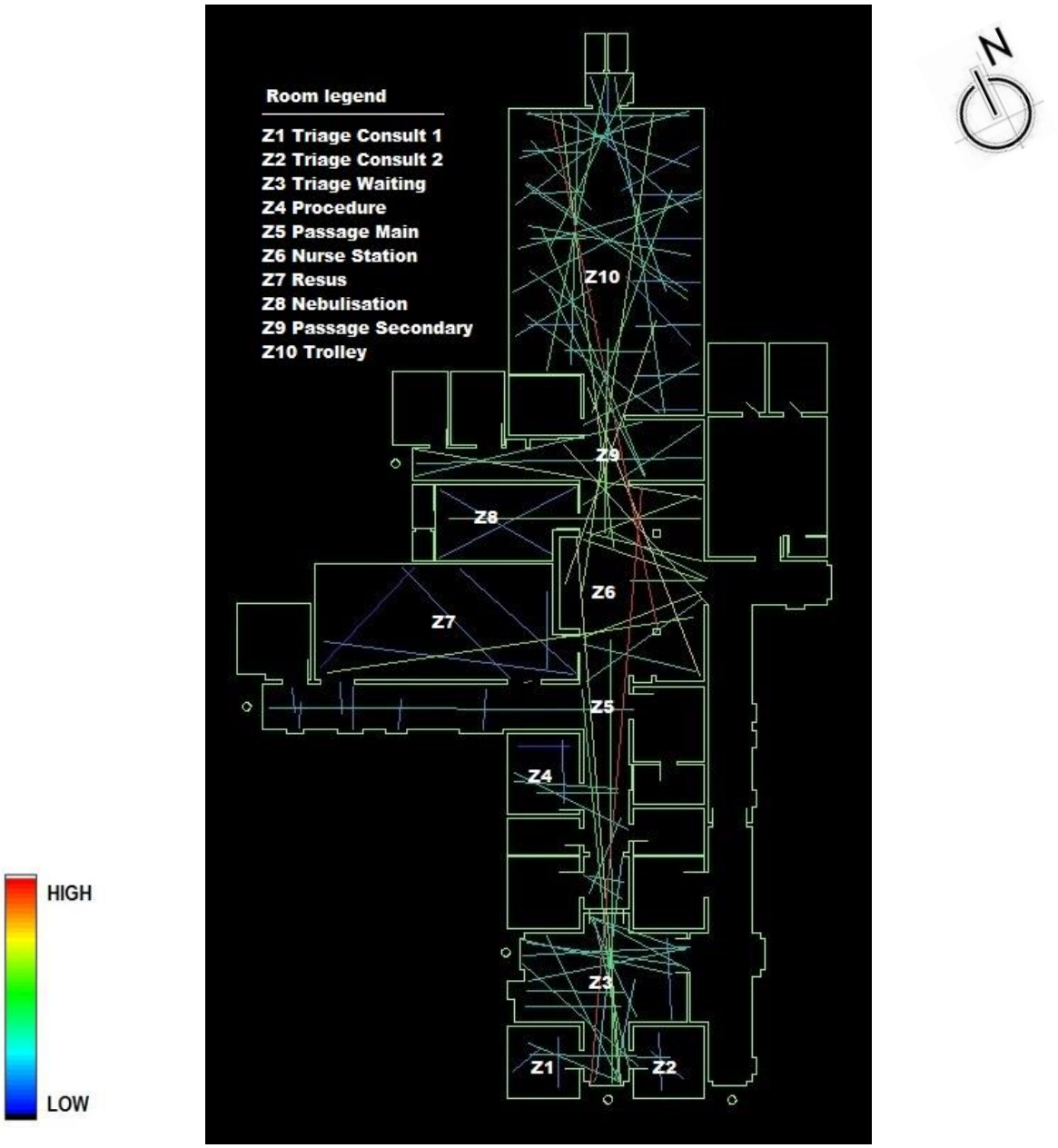



Figure 31: Axial analysis map of MPH base plan: integration

From the analysis in Figure 32, it is clear that the most integrated spaces for human flow (activity) movement are potentially the Nurses' Station, Main Passage and a portion of the Trolley rooms/zones. The potential flow integration does extend into the Triage Consult and Waiting rooms/zones. Secondary flow zones are the Trolley, Resus and Nebulisation rooms/zones. Noteworthy is the relationship between the Triage Consult rooms. Refer to the graph analyses in Figure 39 to Figure 41 for R-value coefficients of the global integration.

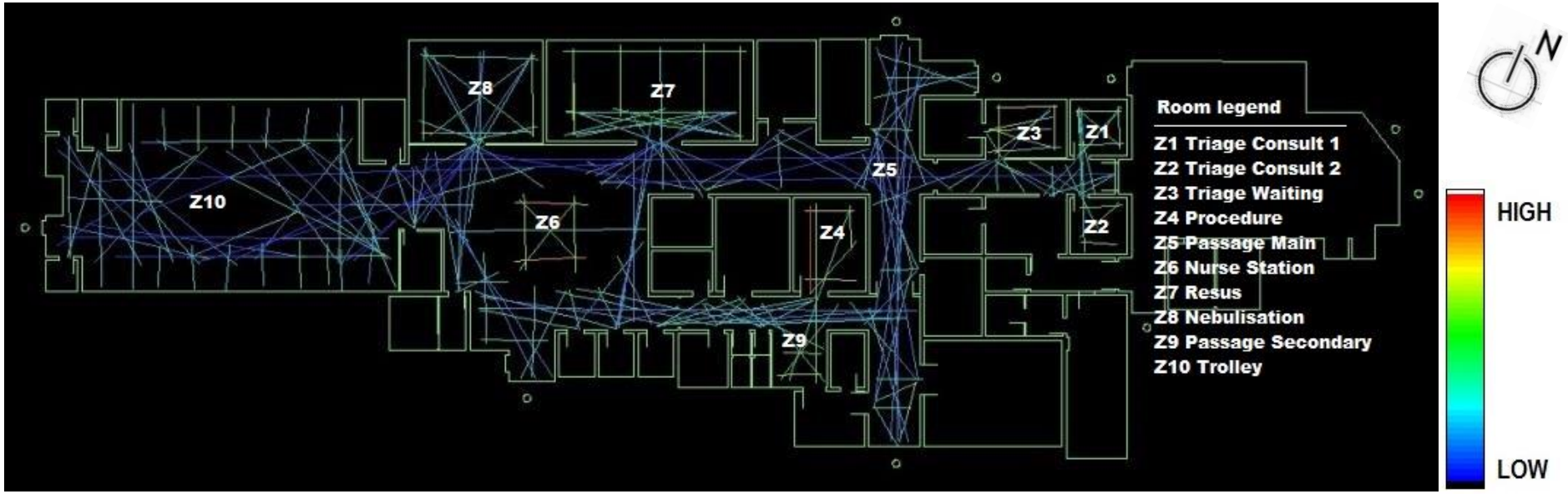



Figure 32: KDH segment analysis of base plan overlay: total depth

From the analysis in Figure 33, it is clear that the most integrated spaces for human flow and movement are potentially the Nurses' Station, Trolley rooms/zones, Main Passage and the Triage Waiting rooms/zones. Secondary flow zones are the Resus and Nebulisation rooms/zones. Noteworthy is the relationship between the Triage Consult rooms, similar to KDH. Refer to the graph analyses in Figure 39, Figure 40 and Figure 41 for R-value coefficients of the global integration. Again, it is evident that a variation in spatial planning exists between the A&E units at MPH and KDH. Much greater integration, MMSPA, connectivity and axial flow integration exist at MPH than at KDH.

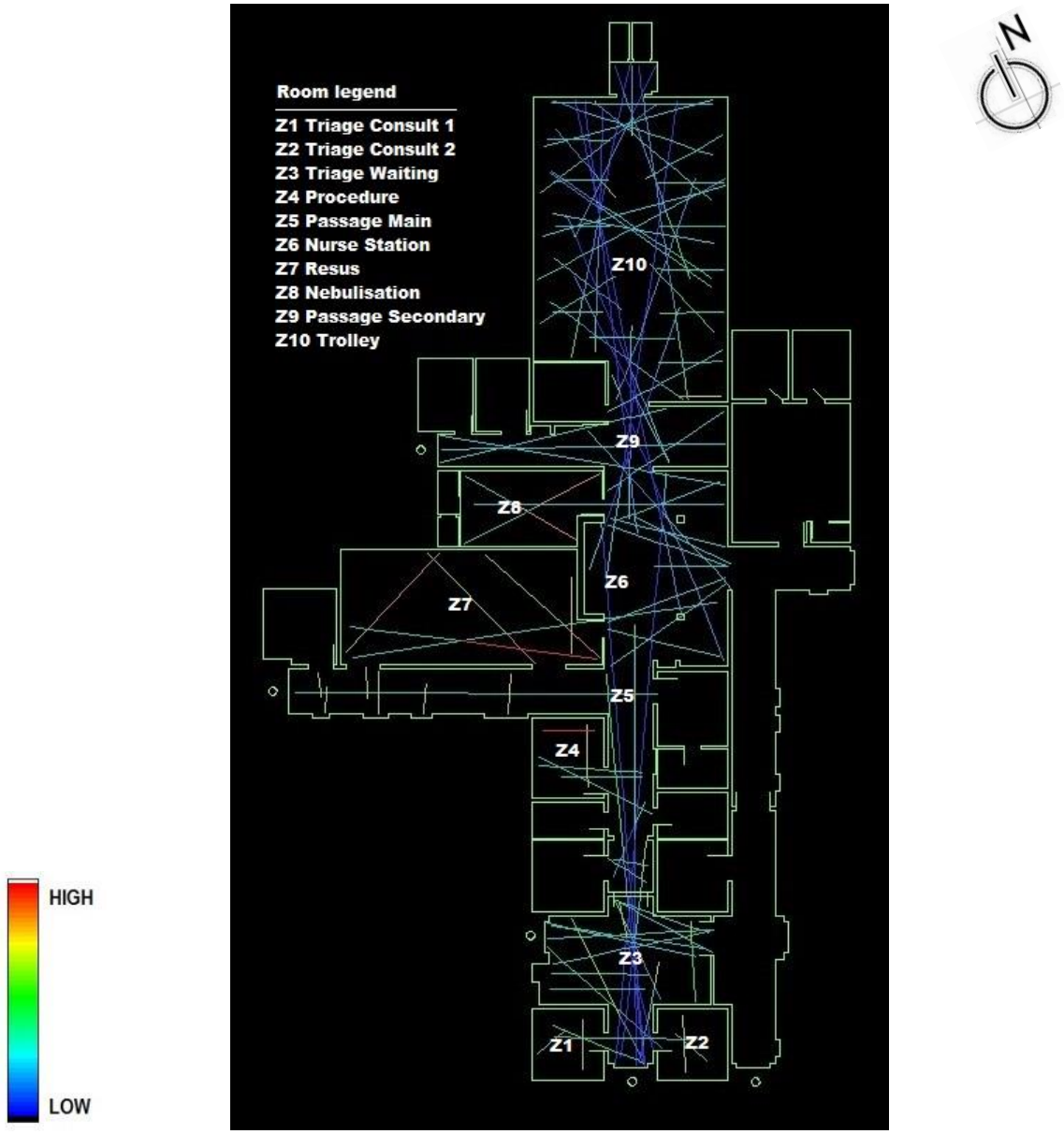



Figure 33: Segment analysis of MPH base plan overlay: total depth

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Overlaying the axial map and VGA visual analysis compares the “potential flow” and the “potential gate cross” of the unit. In addition, it compares the potential flow with the visual perception of space. A strong correlation is often found between spatial perception as it is understood, and the most commonly used areas. From the analysis in Figure 34, similarities exist between the most integrated zones and the visually most connected zones. One should therefore find similar values from Figure 52 to Figure 63, based on actual observation (which was found to be true; refer to Table 7.20, no 3). Both analyses indicated core zones of interaction.

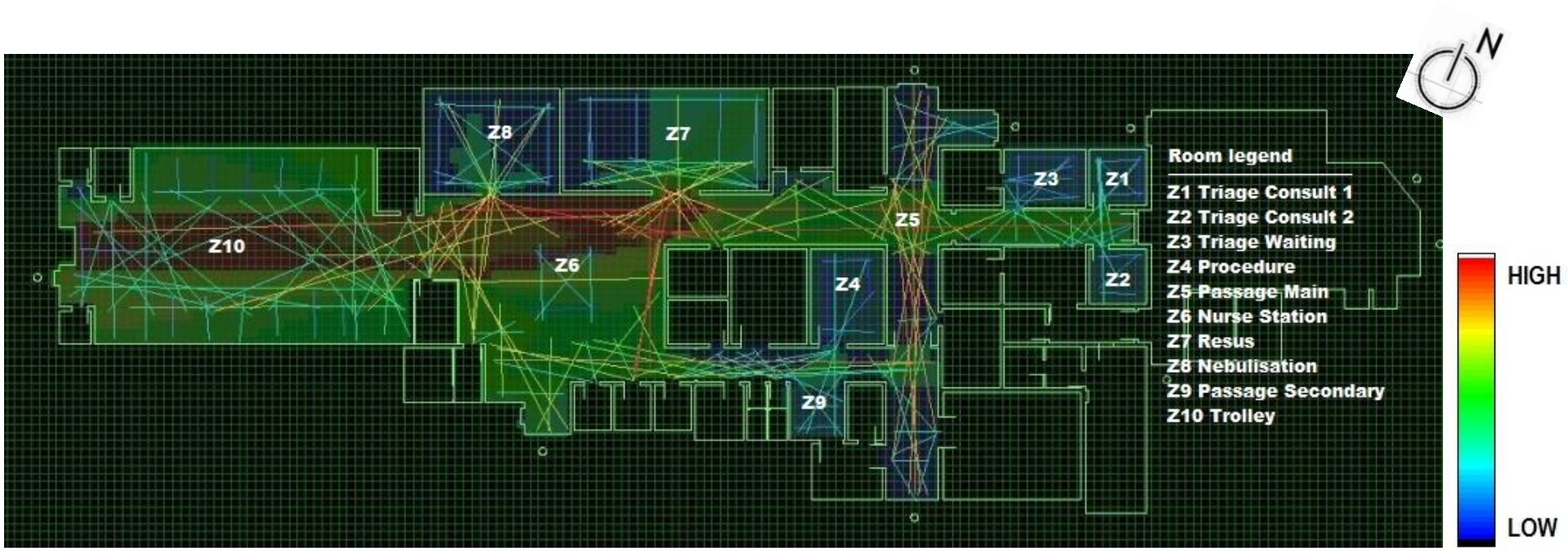



Figure 34: Axial overlay of KDH base plan: VGA

From the analysis in Figure 35, it can be seen that similarities exist between the most integrated zones and most visually connected zones; however, at KDH the VGA analysis indicated lower connectedness than the axial mapping, i.e. the Trolley and Triage Waiting rooms/zones were indicated to be less visually connected, but the axial mapping showed strong integration. To corroborate the simulation one must find similar values from Figure 52 to Figure 63, based on actual observation (which was found to be true; refer to Table 7.20, no 3). Both analyses indicated core zones of interaction. Again, it is evident that a variation in spatial planning exists between the A&E units at MPH and KDH.

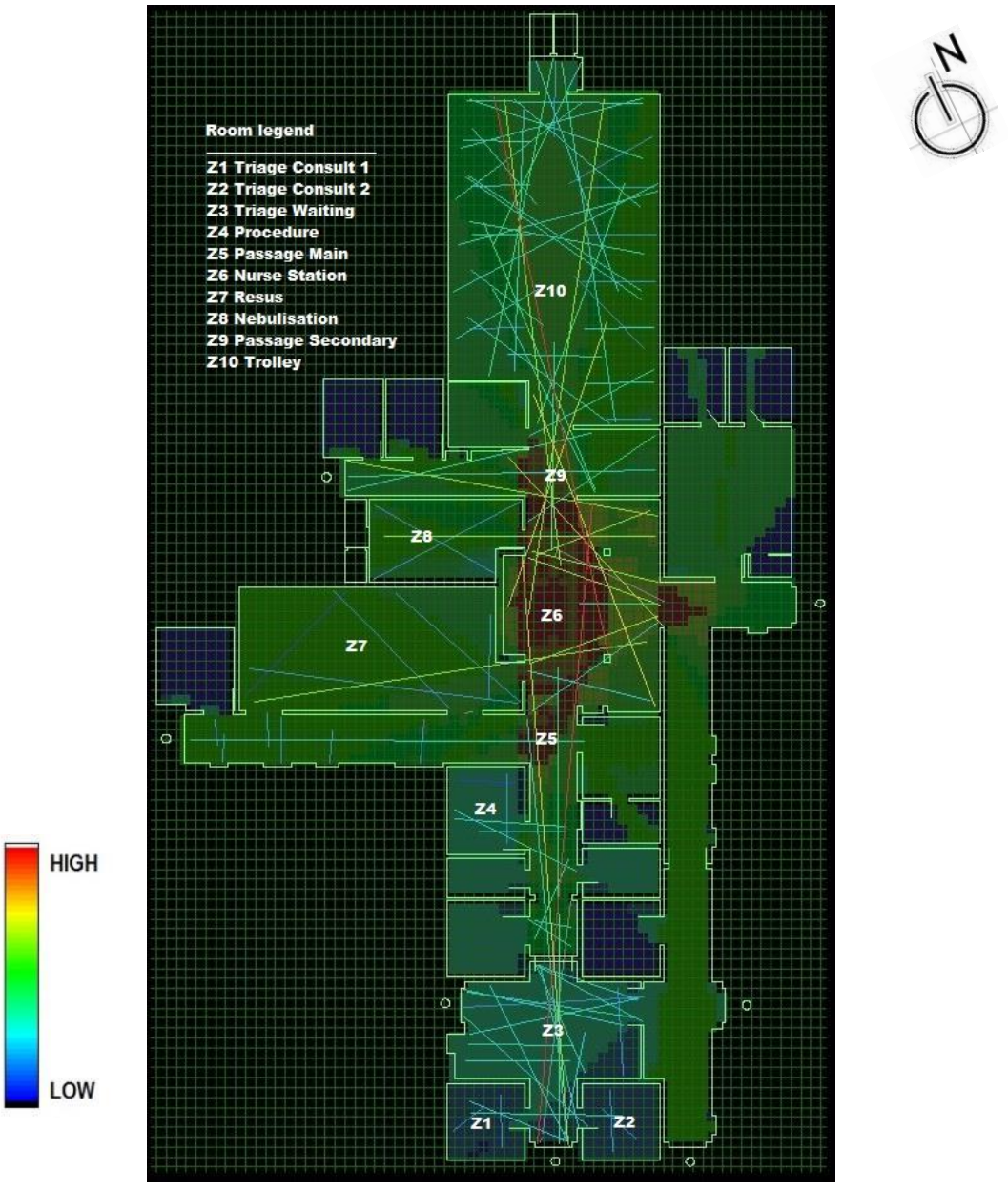



Figure 35: Axial overlay of MPH base plan: VGA

### 7.3.2.2 Regression analysis on base plan modelling of KDH &MPH

A regression analysis of the graphical base plan was performed, considering the planned space use in factors of integration over choice/mean depth and connectivity. An acceptable $R^2$

coefficient correlation value for spatial analytics is 0.65: *Numerous SS studies indicated poor correlations at below 50%; personal communication with SS UCL lecturers indicate 65% as acceptable $R^2$ correlation; and as for "soft" social science in general (including architecture) with regards to regression analysis, two or more variables matching by more than 60% is considered an acceptable confidence level for correlations, where 100% represents the observed dependant variable perfectly matching (for "hard" science this value must be in excess of 95% – 99%*). Note1: *The axial integration denotes the number of times a node (Space Syntax [SS] lines) connects to other nodes (SS lines) that intersect and create links*. Note 2: *The axial graph denotes the number of times a node connects to other lines that it intersects. The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, thus creating potential destinations or cores*. Refer to Chapter 5.

KHAYELITSHA DISTRICT HOSPITAL (KDH)

Regression analysis KDH set one: Applying regression analysis for the variables integration versus choice in the axial & VGA graphs for KDH base plan (un-observed), the following correlation is reported for KDH (Figure 36): an **$R^2$** value of **0.26.** Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. Applying the variable choice refers to through movement in a spatial network and is comparable to the level of axial integration. Choice over integration refers to the measure of freedom of access versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.26 indicates a poor correlation.

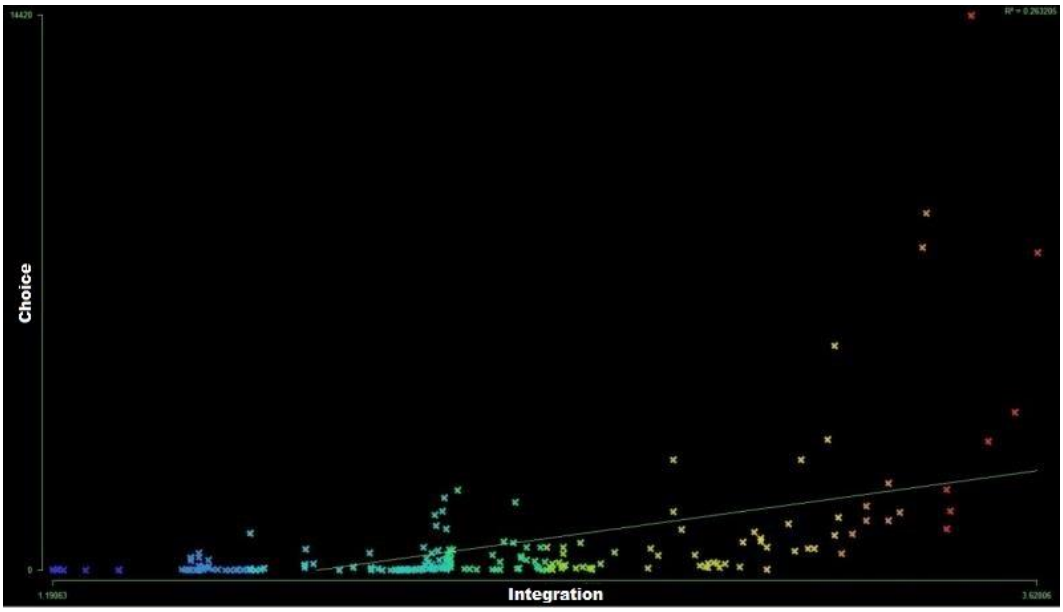



Figure 36: KDH graph – VGA of axial overlay: integration over choice

Regression analysis KDH set two: Applying regression analysis for the variables integration versus mean depth in the axial & VGA graphs for KDH base plan (un-observed), the following correlation is reported for KDH (Figure 37): an **$R^2$** value of **0.90.** Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. Applying the variable mean depth refers to the shortest path through the VGA graph compared to all other nodes (SS lines) within the graph, summed and divided by all nodes in the graph, and compared to the level of axial integration (*mean depth over integration refers to the measure of sight lines versus a measure of potential flow patterns*). The base plan spatial coefficient of $R^2$ 0.90

indicates a high confidence correlation. This finding implies a highly visually (open plan) connected network planning with clear sightlines and functions.

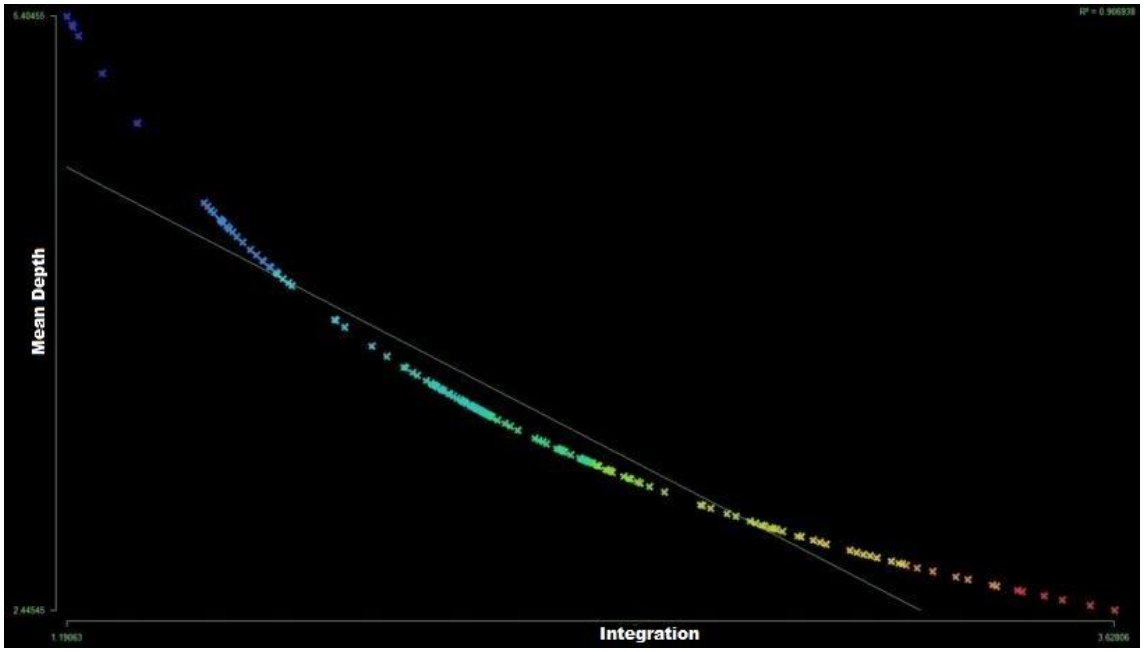



Figure 37**:** KDH graph axial overlay VGA analysis – integration over mean depth

Regression analysis KDH set three: Applying regression analysis for the variables integration versus connectivity in the axial & VGA graphs for KDH base plan (un-observed), the following correlation is reported for KDH (Figure 38): an $R^2$ value of 0.58. Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. The number of points in space that can be connected to a single point in the VGA graph, is compared to the level of axial integration in the axial graph (number of times a node connects to other lines that it intersects). The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, thus potential destinations or cores. The higher the correlation, the more integrated the spatial system is. In summary: *Connectivity indicates the number of lines that are directly connected to a specific line. Integration is an indicator of how easily one can reach a specific line. Mathematically it is the average number of spaces that one needs to pass through to reach a specific line from all the axial lines/segments in the system. These values suggest the extent to which a selected space in the system is more integrated (can be easily reached from other spaces), or more segregated (one has to travel through many spaces in order to reach that selected space)* (Nubani & Wineman 2005). Similarly, when utilising VGA and axial mapping a correlation is drawn between the visual sight connectivity and the movement lines/segments in the spatial system. This represents the measure of sight lines with the potential flow patterns or movement segments making the space spatially intelligible or unintelligible. The base plan spatial coefficient of $R^2$ 0.58 indicated that KDH (like MPH) has been designed spatially intelligible (noting that the planning layouts do vary but the observed use does not). The base plan non-observation analysis indicates that the planning had high potential for core integration - acceptably close to 0.65.

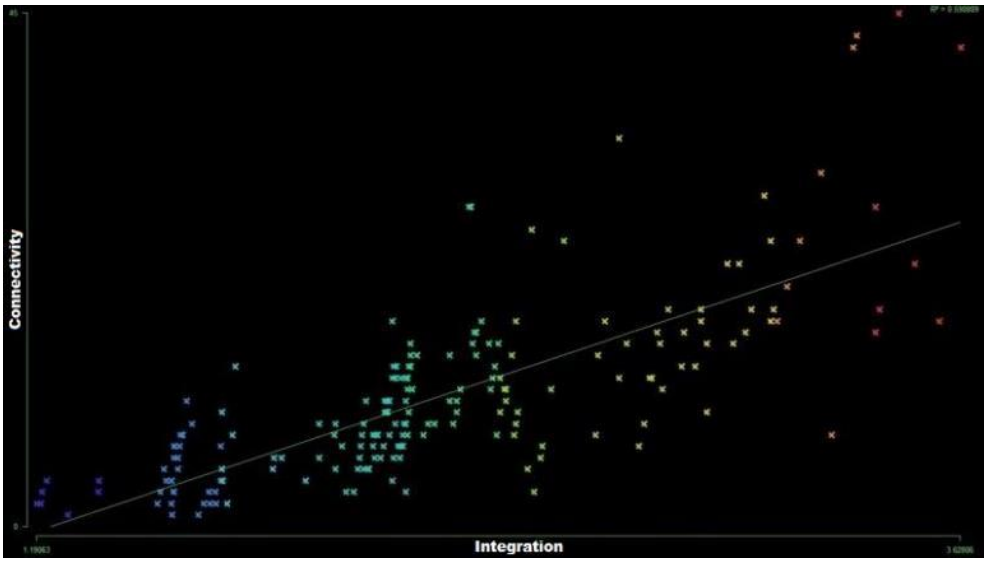



Figure 38: KDH graph – VGA of axial overlay: integration over connectivity

### MITCHELLS PLAIN DISTRICT HOSPITAL (MPH)

Regression analysis MPH set one: Applying regression analysis for the variables integration versus choice in the axial & VGA graphs for MPH base plan (unobserved), the following correlation is reported for KDH: (Figure 39) an **$R^2$** value of **0.43** Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. Applying the variable choice refers to through movement in a spatial network and is comparable to the level of axial integration. Choice over integration refers to the measure of freedom of access versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.43 indicates a poor correlation.

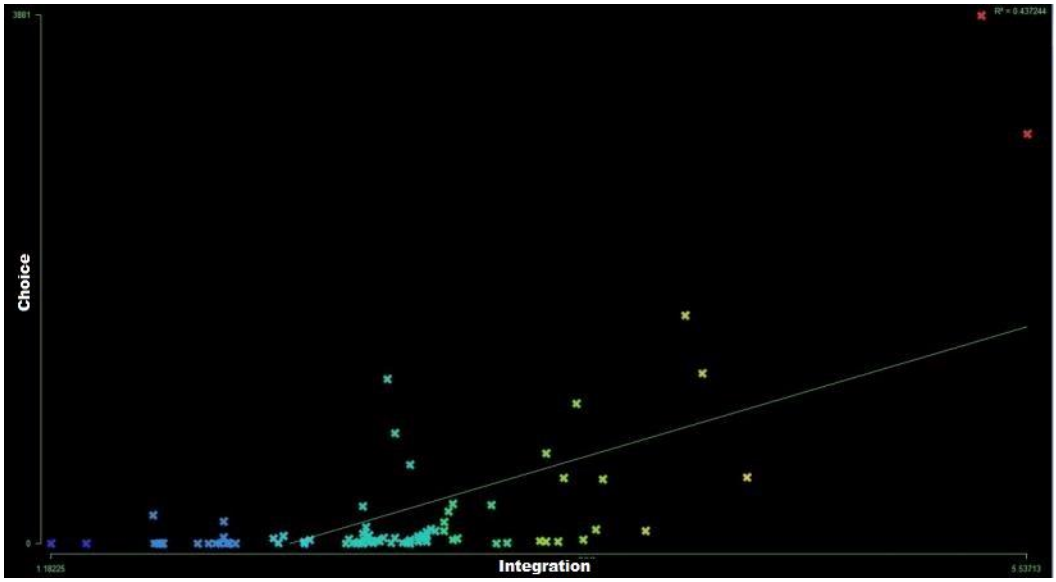



Figure 39: MPH graph – VGA of axial overlay: integration over choice

Regression analysis MPH set two: Applying regression analysis for the variables integration versus mean depth in the axial & VGA graphs for KDH base plan (unobserved), the following correlation is reported for MPH (Figure 37): an **$R^2$** value of **0.83.** Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. Applying the variable

mean depth refers to the shortest path through the VGA graph compared to all other nodes (SS lines) within the graph, summed and divided by all nodes in the graph, and compared to the level of axial integration (*mean depth over integration refers to the measure of sight lines versus a measure of potential flow patterns*). The base plan spatial coefficient of $R^2$ 0.90 indicates a high confidence correlation. This finding implies a highly visually (open plan) connected network planning with clear sightlines and functions.

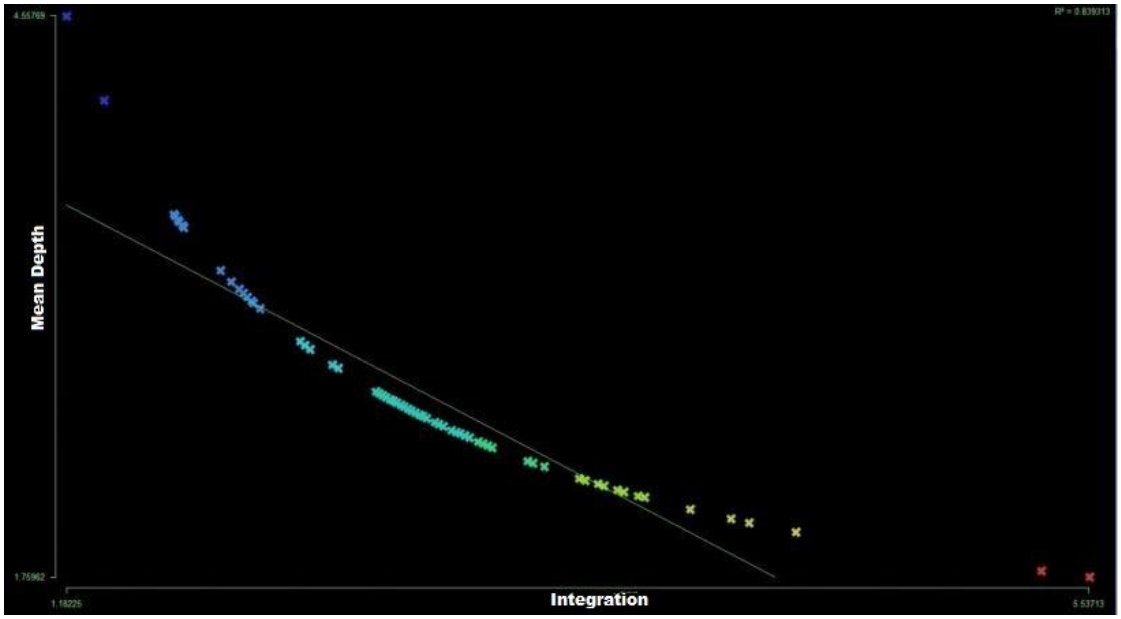



Figure 40: MPH graph – VGA of axial overlay: integration over mean depth

Regression analysis MPH set three: Applying regression analysis for the variables integration versus connectivity in the axial & VGA graphs for MPH base plan (unobserved), the following correlation is reported for MPH (Figure 38): an $R^2$ value of 0.58. This value matches KDH. Correlations are drawn with the base plan by manual axials flow lines overlaid on a VGA analysis. The number of points in space that can be connected to a single point in the VGA graph is compared to the level of axial integration in the axial graph (number of times a node connects to other lines that it intersects). The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, thus potential destinations or cores. The higher the correlation, the more integrated the spatial system is. In summary: *Connectivity indicates the number of lines that are directly connected to a specific line. Integration is an indicator of how easily one can reach a specific line. Mathematically it is the average number of spaces that one needs to pass through to reach a specific line from all the axial lines/segments in the system. These values suggest the extent to which a selected space in the system is more integrated (can be easily reached from other spaces), or more segregated (one has to travel through many spaces in order to reach that selected space)* (Nubani & Wineman 2005). Similarly, when utilising VGA and axial mapping a correlation is drawn between the visual sight connectivity and the movement lines/segments in the spatial system. This represents the measure of sight lines with the potential flow patterns or movement segments making the space spatially intelligible or unintelligible. The base plan spatial coefficient of $R^2$ 0.58 indicated that KDH (like MPH) has been designed spatially intelligible (noting that the planning layouts do vary but the observed use does not). The base plan non-observation analysis indicates that the planning had high potential for core integration - acceptably close to 0.65.

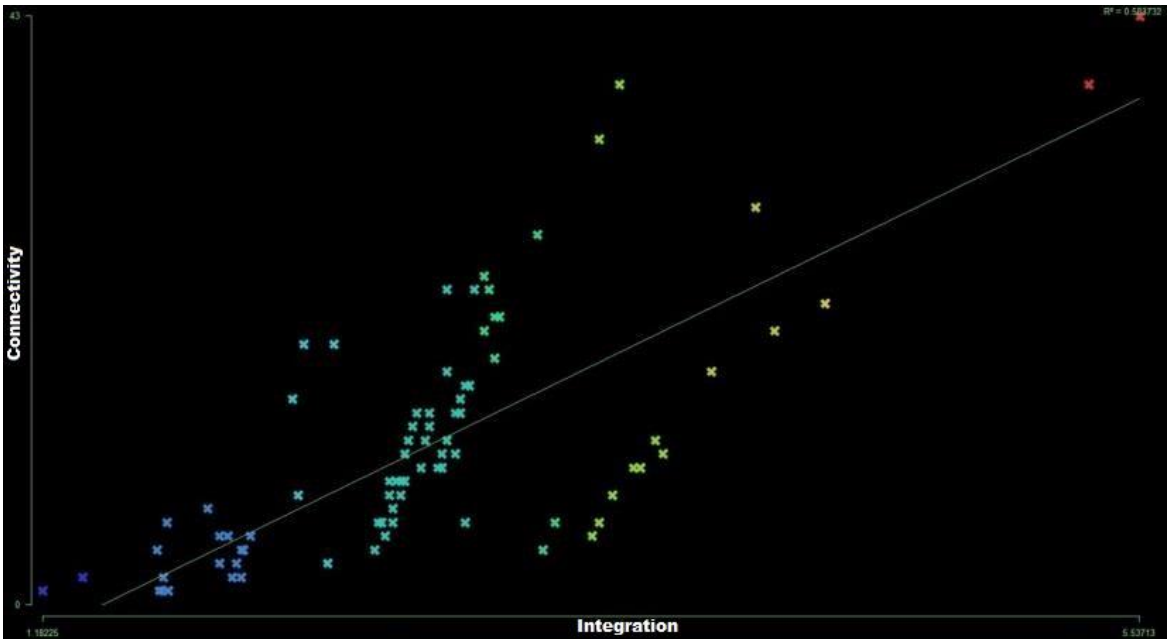



Figure 41: MPH graph – VGA of axial overlay: integration over connectivity

#### 7.3.2.3 KDH AND MPH VGA, AXIAL MAPPING AND BASE PLANS OVERLAY SUMMARY FINDINGS

These summary findings are based on visual simulations findings (VGA and axial mapping, and combined) and statistical analysis findings for each hospital unit. This summary makes reference to graphs and plots: Figure 24 to Figure 41. The simulations in DepthMap™ software provide insight into the spatial relationships within each A&E unit. The following findings are presented in this section: an interpretation of the base plan simulation, and the current design and on-site room planning as in use. Simulation offers spatial outcomes with maximum design potential. The DepthMap™ simulation outcomes have been tested, correlated and corroborated through past research (refer to Chapter 5), and is an accepted methodology for architectural spatial analysis as endorsed by UCL Bartlett school of architecture, United Kingdom. For this thesis, however, the information is utilised in a novel way, addressing IPC, infection transmission and microbial distribution. The combination of analyses provides insight into the spatial network dynamics of KDH and MPH.

Table 7.7: KDH and MPH comparative analysis data table

The data are taken from the preceding analysis assessments.

| | | |
|---|---|---|
| 1 | KDH | MPH |
| Mutual and centrally visual spaces are: Nurse Station, Trolley and Main Passage. Secondary: Resus, Nebulisation. The least: Triage Consult and Triage Waiting rooms/zones | | Mutual and visually central spaces are: Nurses' Station, Trolley and Main Passage. Secondary: Resus and Nebulisation. The least: Triage Consult and Triage Waiting. |
| 2 | KDH | MPH |

| | |
|---|---|
| The zones with the shortest direct connection within the network routes are: Nurses' Station, Trolley and Main Passage. Secondly: Resus and sub wait at Procedure share the same connection. Clusters of network connectedness are found in the Secondary Passage. The angular inclusion of the Triage Waiting room/zone proposes a stronger network link than the visual connectivity analysis suggests and will be confirmed by the gate count analysis and observation simulation. | The zones with the shortest direct connection within the network routes are: Nurses' Station, Main Passage and Triage Waiting rooms/zones. Secondly: Trolley and Resus. No evident clusters of network connectedness are found. The angular inclusion of the Triage Waiting and the Triage Consult rooms proposes a stronger network link than the visual connectivity analysis and will be confirmed by the gate count analysis and observation simulation. |
| 3 KDH | MPH |
| The most integrated spaces globally in the KDH network are: Nurses' Station and Trolley room/zone, followed by Resus and Nebulisation. Triage Consult and Procedure are the least integrated. The low through-movement correlation confirms this statement, but the linear spatial planning shows a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90. | The most integrated spaces globally in the MPH network are: Trolley, Nurses' Station, Main Passage and Triage Waiting, followed by Resus. Triage Consult, Nebulisation and Procedure are the least integrated. The low through-movement correlation confirms this statement, but the linear spatial planning shows a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90. |
| 4 KDH | MPH |
| Considering spatial depth and integration (potential human flow and movement), the KDH network can be graded from most to least as follows: Nurses' Station, Main Passage and portions of Trolley extending into the Triage Passage at the Triage Consult rooms/zones, followed by Trolley, Resus and Nebulisation. The Procedure room is not integrated. A micro integration occurs between the two Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.90. | Considering spatial depth and integration (potential human flow and movement), the MPH network can be graded from most to least as follows: Nurses' Station, Trolley, Main Passage and Triage Waiting. Second are the Resus and Nebulisation rooms/zones. The Procedure room is not integrated. A micro integration occurs at the Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.83. |
| 5 KDH | MPH |
| Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness as was found at KDH. | Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness, as was mostly found at MPH. (The VGA indicated lower connectedness than the axial mapping suggests, i.e. the Trolley and Triage Waiting rooms/zones were indicated as less visually connected, but the axial mapping showed higher integration.) |
| 6 KDH | MPH |
| KDH presents a statistically significant visual and flow correlation, with an integration and connectivity correlation value of $R^2$ 0.58. The KDH simulation shows a smaller central core through movement compared to MPH, and was even less connected to the entire network of the A&E with an $R^2$ value of 0.26. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.90. | MPH presents a statistically significant visual and flow correlation with an integration and connectivity correlation value of $R^2$ 0.58. MPH simulation shows a central core through movement; however, it is not well connected to the entire network of the A&E, as is evident from the $R^2$ value of 0.43. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.83. |

From the analysis the follow findings are reported: The spatial planning of MPH is more linearly connected than KDH, as is evident with the inclusion of the Triage Waiting area as the most

connected space. The Procedure and Triage Consult rooms/zones are spatially by extension physically isolated from the rest of the unit at KDH. This implies that potential IPC containment could prove higher at KDH than MPH in terms of total unit connectedness. MPH would require focused intervention in the Triage Waiting room. These data are further considered with environmental data under section 9.3 and Chapter 10. Again, it is apparent from the analysis that the spatial planning of MPH is more linearly connected than at KDH, as is evident from the additional inclusion of the Triage Waiting area and exclusion of the Trolley zone as shortest direct route. It is clear that both hospitals share strong correlation in the spatial configuration of room types. In both KDH and MPH we find that the Triage Consult and Triage Waiting rooms/zones are more integrated into the greater network. Greater metric inclusion between the Triage Consult and Triage Waiting rooms/zones at MPH and Triage Waiting at KDH is evident. The angular increased inclusion of both facilities - confirmed by gate count analysis and observation simulation under both the VGA and axial overlay - indicates similar values compared to the actual gate and flow values from Figure 52 to Figure 57 in section 7.3.4.2.

The linear design of both units provides a good global integration of all nodes and subsequent spaces. The spatial coefficient indicates that both KDH and MPH are spatially intelligible, which implies that they have defined central cores that are deeply integrated, as is evident from the linear design and Nurses' Station as core central hub. MPH is spatially more integrated than KDH, as reported previously. The linear design of both units provides good global integration of all nodes and subsequent spaces. MPH is globally less spatially integrated than KDH, but both are significantly integration correlated. The integration variation between MPH and KDH cannot be accounted for at this time; however, a micro integration network is seen at the Triage Consult rooms of both MPH and KDH. Lastly, the correlation values confirm the visual and axial simulation. Both MPH and KDH present equitable correlation $R^2$ values of 0.58 for sight and flow potential, therefore indicating spatial intelligibility. The correlation values confirm the reduced through movement of all nodes in the network and, as per the visual and axial simulation, a lower value at KDH than MPH, pointing to a strong central core. The mean depth and integration correlation of $R^2$ 0.80-0.90 for both MPH and KDH confirm the strong linear spatial network planning. In both hospitals, it is evident that some rooms are isolated from the main network, but the majority of the spaces are totally integrated. This situation implies a very high potential for transmission and shared microbiome and species distribution which will be analysed and discussed in Chapter 10

This various spatial findings have been correlated where applicable with the environmental data and visually compared with the microbial data; they are discussed in 8.3.2.3, 9.3.2.2 and Chapter 10,. The section reports on spatial findings and notes potential relationships to be confirmed by further analysis.

### 7.3.3 Observation analysis

This section consists of three parts. 1) Graphical analysis of the observation flow data modelled on the base plan drawings reported with findings. 2) Regression analysis of the observation flow data compared with the base plan regression analysis reported with findings. 3) Summary of correlations with occupancy and microbial data. Further deductions are presented in the concluding chapter 10, section 10.1 - 10.4

#### 7.3.3.1 GRAPHICAL ANALYSIS OF OBSERVATION PLAN MODELLING OF KDH AND MPH

Figure 42 and Figure 43 depict the level of spatial integration based on actual observation data imported into DepthMap™ from GIS. The following findings are presented for KDH:


Figure 42: KDH axial observation analysis - integration, summer

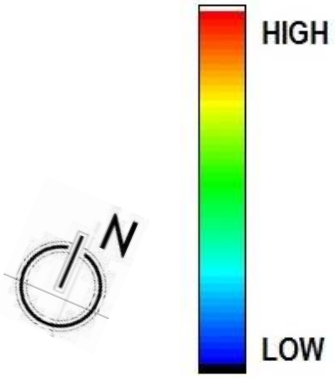




Figure 43: KDH axial observation analysis - integration, winter

An integration analysis was run on the observed data as per axial mapping methodology. When considering the seasonal variations at KDH, the summer observations reflect a high level of integration in the central zone, i.e. the Nurses' Station, and the Main Passage zone leading out onto the main external public waiting area and edging into the Trolley room/zone. (This is noted by the red, orange and yellow colours). Secondary integrated spaces were found to be the Trolley, Resus and Nebulisation rooms/zones, as well as the Triage Consult 1 room/zone and the Main Passage leading to the Procedure room. The winter spatial integration is similar to that of summer for all spaces mentioned, but lower in total value. The Procedure room/zone indicated more integration in winter than in summer, but it is the least integrated space based

on actual observed use. It is also noteworthy that the Triage Consult 2 was observed to be far more integrated in winter (possibly due to function) than in summer, and with Triage Consult 1 the inverse was observed. When compared to the base plan, the observed correlation values show a deeper integration in the Main Passage and in the passage at the Procedure room than was expected (see Figure 34 , Figure 42 and Figure 43). The variation between the base plan and the observation plan for KDH could be due to the function value associated with the spaces that indicate more integration; thus, function within the A&E has an influence on spatial configuration and use patterns. Figure 44 and Figure 45 depict the level of spatial integration based on actual observation data imported into DepthMap™ from GIS. The following findings are presented for Mitchells Plain District Hospital (MPH):

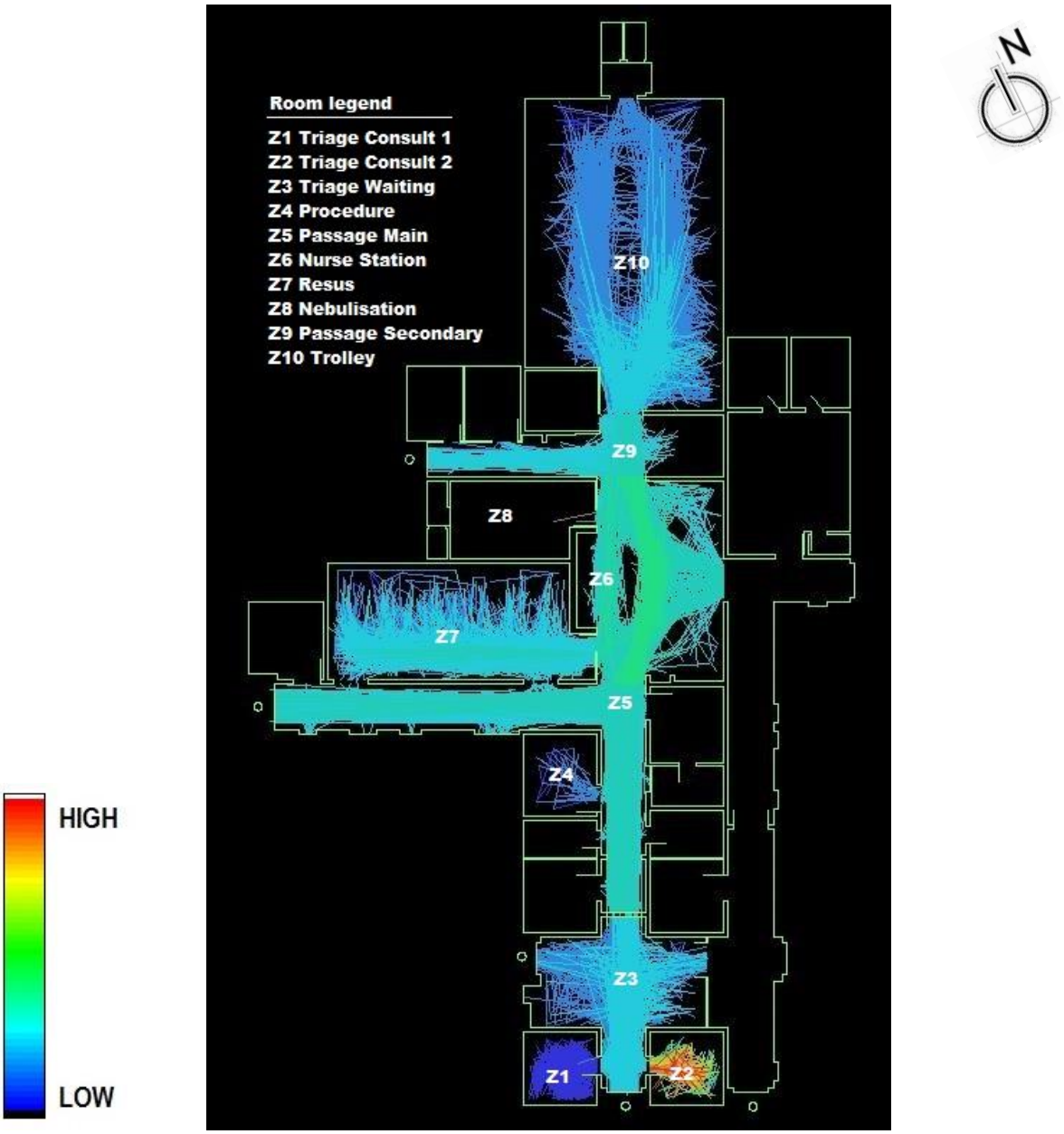



Figure 44: MPH axial observation analysis – integration, summer


Figure 45: MPH axial observation analysis – integration, winter

An integration analysis was run on the observed data, as per axial mapping methodology. Considering the seasonal variation at MPH, the summer observation reflects integration in the central zone, i.e. the Nurses' Station, Main Passage and Triage Waiting rooms/zones. Secondary connectivity was found in the Trolley, Nebulisation and Triage Consult 2 rooms/zones, and the passage leading to the ambulant entry and exit. The winter spatial integration is similar to that of summer for all spaces mentioned, but reflects greater integration in total value. The Procedure room displayed less integration in winter than in summer, but is the least integrated space based on observation of its actual use. It is also noteworthy that Triage Consult 2 was observed to be highly integrated (potentially due to function) in both seasons and more so than Triage Consult 1 (this was also evident for KDH). When compared to the base plan, the potential integration matches the observed values. The observed analysis

shows a deeper integration in the Trolley and Triage Waiting areas (refer to Figure 29), which is less than the observed data indicate. The variation in the base plan and the observation plan for MPH could be due to the function value associated with the spaces that indicate more integration; it could be attributed to barriers put in place between Triage Waiting and the Main Passage. The high number of emergency cases indicates higher than expected travel in the ambulant passage; thus, function within the A&E plays an important part in the spatial configuration and use patterns.

#### 7.3.3.2 REGRESSION ANALYSIS ON OBSERVATION PLAN MODELLING KDH AND MPH

An analysis of base plan (non-observation versus observation) - Figure 42, Figure 43, Figure 44 and Figure 45 - and graphs - Figure 46, Figure 47, Figure 48 and Figure 49 - considers the planned space use versus the actual space use in factors of integration over connectivity/choice and mean depth. An acceptable $R^2$ coefficient correlation value for spatial analytics is 0.65: *Numerous SS studies indicated poor correlations at below 50%; personal communication with SS UCL lecturers indicate 65% as acceptable $R^2$ correlation; and as for "soft" social science in general (including architecture) with regards to regression analysis, two or more variables matching by more than 60% is considered an acceptable confidence level for correlations, where 100% represents the observed dependant variable perfectly matching (for "hard" science this value must be in excess of 95% – 99%.*)

##### KHAYELITSHA DISTRICT HOSPITAL (KDH)

Regression analysis KDH set one: Applying regression analysis for the variables integration versus connectivity in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer observations (Figure 46) an **$R^2$** value of **0.40** compared to the base non-observation analysis that measured an **$R^2$** value of **0.58.** For MPH winter observations (Figure 47) an **$R^2$** value of **0.42**, again compared to the base non-observation analysis that measured an **$R^2$** value of **0.58**. Correlations are drawn with the base plan and the observed plan by importing observed flow lines. The number of points in space that can be connected to a single point in the VGA graph is compared to the level of axial integration in the axial graph (*number of times a node connects to other lines that it intersects). The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, thus potential destinations or cores* are a measure of visual sight versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.58 indicated that KDH (as with MPH) had been designed spatially intelligible (noting that the planning layouts do vary but the observed use does not). The base plan non-observation analysis indicates that the planning had high potential for core integration acceptably close to 0.65, but the factual observed measure of integration and connectivity only achieved $R^2$ 0.40 & 0.42. This indicates that observed use of space reflects a lower intelligibility, implying that the core is more under connected than designed and planned for, consistently for both for summer and winter but marginally more than in the case of MPH, as seen in the graphics (Figure 42, Figure 43, Figure 44 and Figure 45). The similarity in findings for summer and winter confirms closely related space use patterns, which implies that the reported space use is in fact the standard patterns for KDH A&E. This finding is marginally more than that of MPH. From the findings we can infer the following. Firstly, the A&E department planning is not optimally utilised. Secondly, more central cores and operations would improve zones of similar functions with reference to the three functional categorisations suggested in this thesis: Administration, Assessment and Treatment - that would provide three potential

distinct cores. The data (analysis graph) did, however, show reduced integration of the Triage Waiting and ancillary space which could indicate a separate core development.

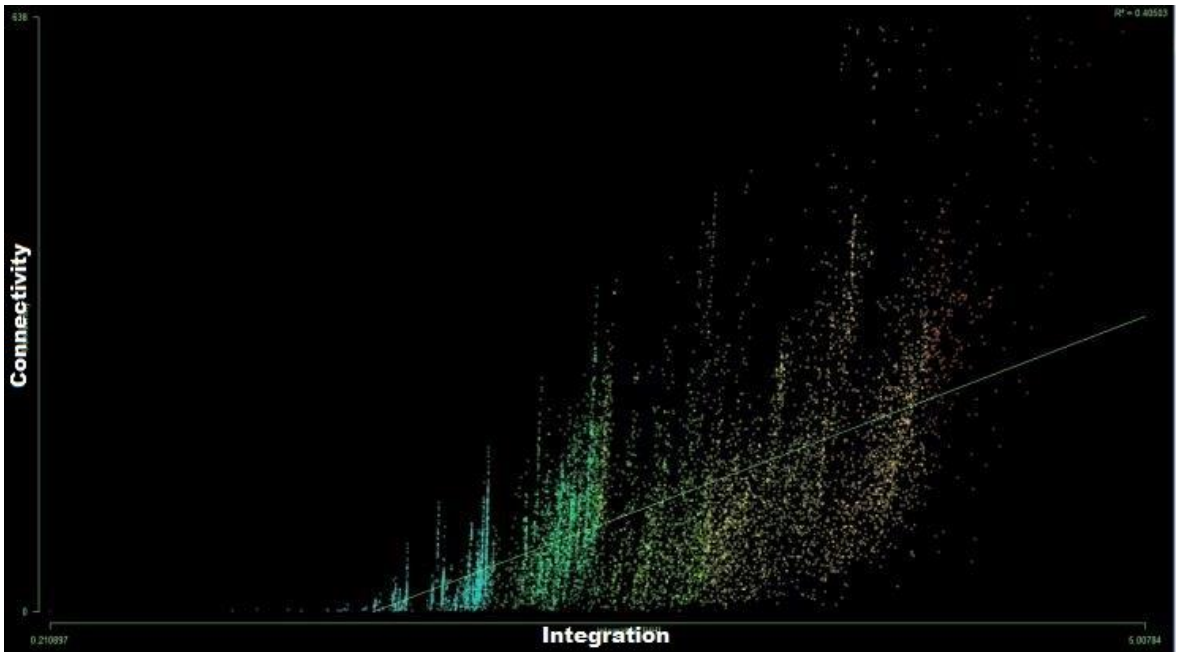



Figure 46: KDH axial observation analysis - integration vs connectivity, summer

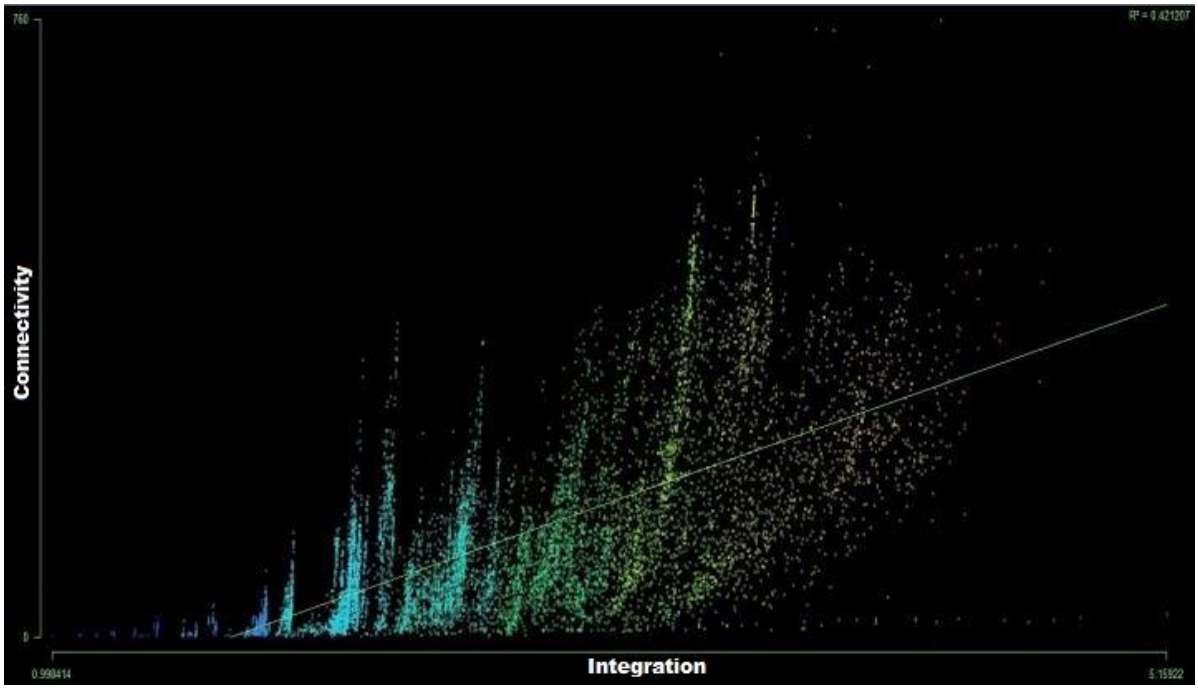



Figure 47: KDH axial observation analysis - integration vs connectivity, winter

Regression analysis KDH set two: Applying regression analysis for the variables integration versus choice in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer observations (no graphic provided) an **$R^2$** value of **0.03** compared to the base non-observation analysis that measured an **$R^2$** value of **0.43.** For MPH winter observations (no graphic provided) an **$R^2$** value of **0.03**, again compared to the base non-observation analysis that measured an **$R^2$** value of **0.43**. Correlations are

drawn with the base plan and the observed plan by importing observed flow lines. Applying the variable choice refers to through movement in a spatial network and is comparable to the level of axial integration. Choice over integration refers to the measure of freedom of access versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.43 indicated a marginally acceptable correlation. However, the observation spatial coefficient of $R^2$ 0.03 for summer and winter is even lower; thus, no correlation exists between choice and integration.

Regression analysis MPH set three: Applying regression analysis for the variables integration versus mean depth in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer and winter observations (no graphic provided) an **$R^2$** value of **0.92** compared to the base non-observation analysis that measured an **$R^2$** value of **0.90**. Correlations are drawn with the base plan and the observed plan by importing observed flow lines. Applying the variable mean depth refers to the shortest path through the VGA graph compared to all other nodes (SS lines) within the graph, summed and divided by all nodes in the graph, and compared to the level of axial integration (*mean depth over integration refers to the measure of sight lines versus a measure of potential flow patterns*). The base plan spatial coefficient of $R^2$ 0.90 indicated a high confidence correlation. The observation spatial coefficient of $R^2$ 0.92 for summer and winter showed high confidence correlations. Again, as per analysis one and two, the similarity in correlations for summer and winter confirms the reported space use is in fact the standard patterns for KDH A&E and the flow patterns closely follow the sight lines, even more so than in the case of MPH. This is again evident when reviewing the graphics (Figure 42, Figure 43, Figure 44 and Figure 45), which suggest a highly visually (open plan) connected network planning with clear sightlines and functions.

### MITCHELLS PLAIN DISTRICT HOSPITAL (MPH)

Regression analysis MPH set one: Applying regression analysis for the variables integration versus connectivity in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer observations (Figure 48) an **$R^2$** value of **0.30** compared to the base non-observation analysis that measured an **$R^2$** value of **0.58.** For MPH winter observations (Figure 49) an **$R^2$** value of **0.38**, again compared to the base non-observation analysis that measured an **$R^2$** value of **0.58**. Correlations are drawn with the base plan and the observed plan by importing observed flow lines. The number of points in space that can be connected to a single point in the VGA graph are compared to the level of axial integration in the axial graph (*number of times a node connects to other lines that it intersects). The extent to which a line is connected to all other lines in a graph reflects how well they are integrated, thus potential destinations or cores* are a measure of visual sight versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.58 indicated that MPH was designed spatially intelligible; however, the observed use does not. The base plan non-observation analysis indicates that the planning had high potential for core integration - acceptably close to 0.65. However, the factual observed measure of integration and connectivity only achieved $R^2$ 0.30 & 0.38; this indicates that observed use of space reflects a lower intelligibility, implying that the core is more under connected than designed and planned for, consistently for both for summer and winter. The similarity in findings for summer and winter confirms closely related space use patterns, which denotes that the reported space use is in fact the standard patterns for MPH A&E. This finding is marginally less than that of KDH. From the findings we can infer the following: firstly, the A&E department planning is not optimally utilised; secondly, more central cores and operations would improve zones of similar

functions with reference to the three functional categorisations suggested in this thesis: Administration, Assessment and Treatment - that would provide three potential distinct cores. The data (analysis graph) did, however, show reduced integration of the Triage Waiting and ancillary space which could indicate a separate core development.

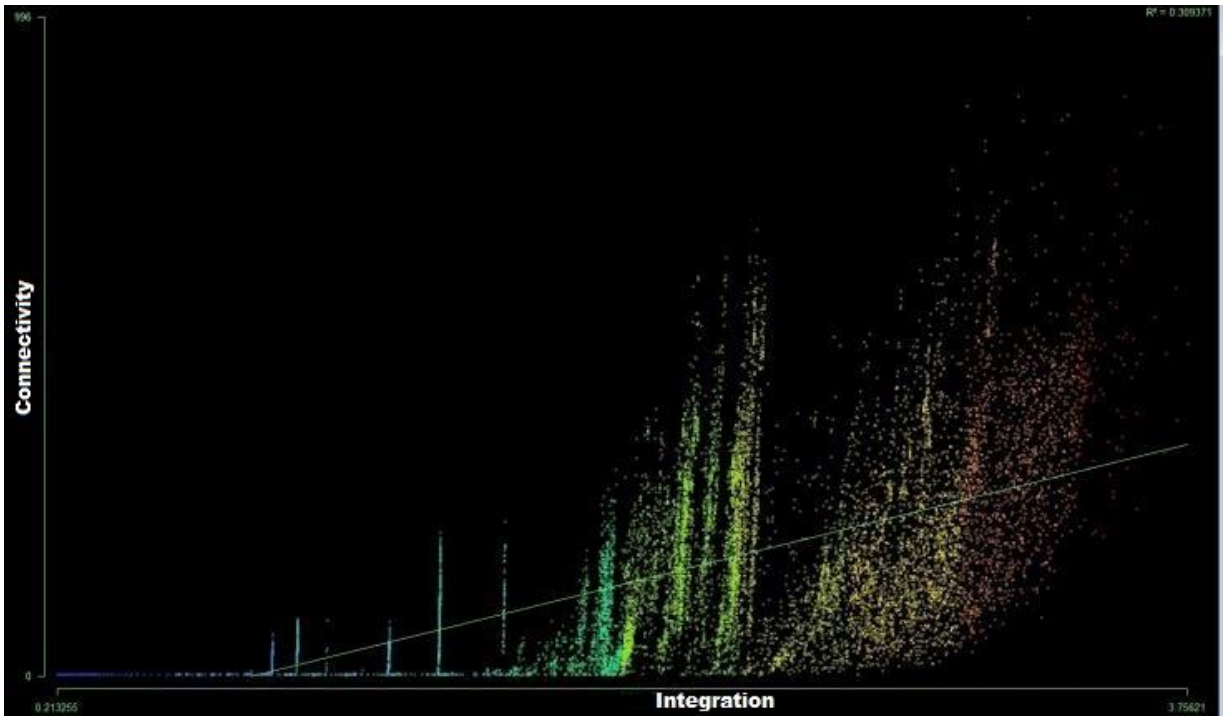



Figure 48: MPH axial observation analysis - integration vs connectivity, summer

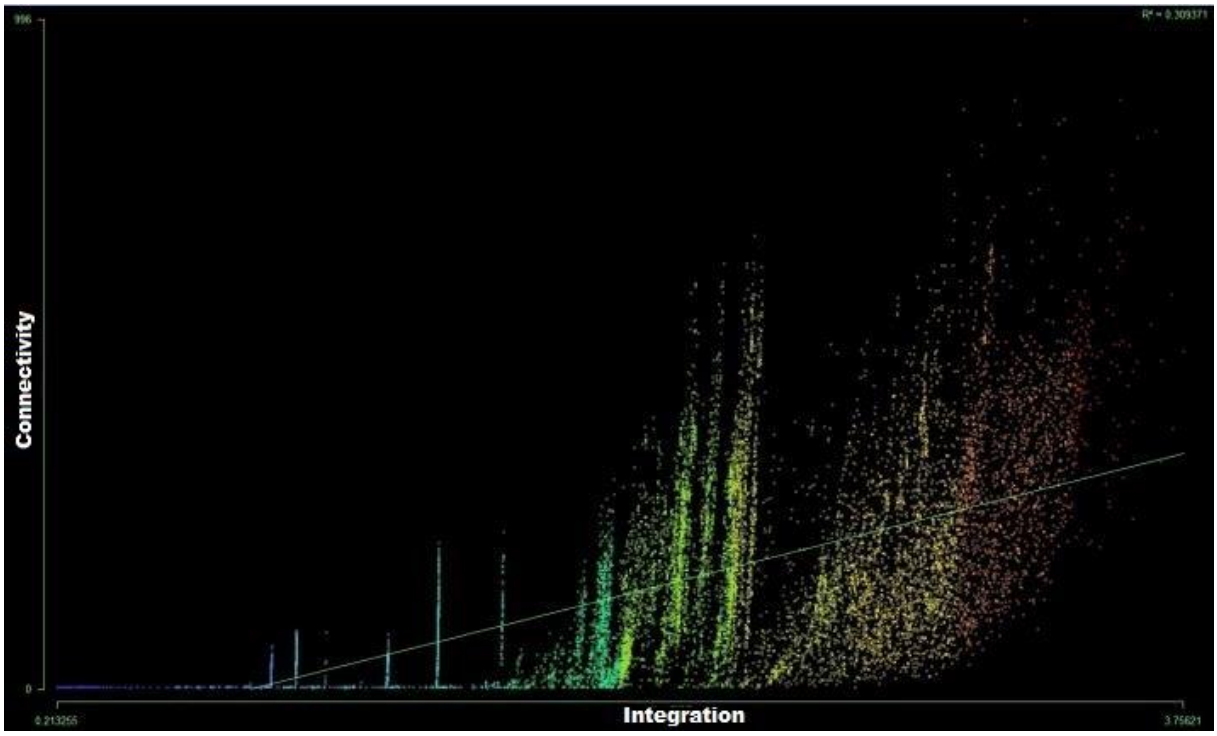



Figure 49: MPH axial observation analysis - integration vs connectivity, winter

Regression analysis MPH set two: Applying regression analysis for the variables integration versus choice in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer observations (no graphic provided) an **$R^2$** value of **0.01** compared to the base non-observation analysis that measured an **$R^2$** value of **0.43.** For MPH winter observations (no graphic provided) an **$R^2$** value of **0.02**, again compared to the base non-observation analysis that measured an **$R^2$** value of **0.43**. Correlations are drawn with the base plan and the observed plan by importing observed flow lines. Applying the variable choice refers to through movement in a spatial network and is comparable to the level of axial integration. Choice over integration refers to the measure of freedom of access versus a measure of potential flow patterns. The base plan spatial coefficient of $R^2$ 0.43 indicated a marginally acceptable correlation. However, the observation spatial coefficient of $R^2$ 0.01, 0.02 for summer and winter is even lower; thus, there is no correlation between choice and integration. Again, as per analysis one, the similarity in findings for summer and winter confirms the reported space use is in fact the standard patterns for MPH A&E.

Regression analysis MPH set three: Applying regression analysis for the variables integration versus mean depth in the axial & VGA graphs for both KDH and MPH observation methods, the following correlations are reported. For MPH summer observations (no graphic provided) an **$R^2$** value of **0.85** compared to the base non-observation analysis that measured an **$R^2$** value of **0.83.** For MPH winter observations (no graphic provided) an **$R^2$** value of **0.82**, again compared to the base non-observation analysis that measured an **$R^2$** value of **0.83**. Correlations are drawn with the base plan and the observed plan by importing observed flow lines. Applying the variable mean depth refers to the shortest path through the VGA graph compared to all other nodes (SS lines) within the graph, summed and divided by all nodes in the graph, and compared to the level of axial integration (*mean depth over integration refers to the measure of sight lines versus a measure of potential flow patterns*). The base plan spatial coefficient of $R^2$ 0.83 indicated a high confidence correlation. The observation spatial coefficient of $R^2$ 0.85, 0.82 for summer and winter showed high confidence correlations. Again, as per analysis one and two, the similarity in findings for summer and winter confirms the reported space use is in fact the standard patterns for MPH A&E and the flow patterns closely follow the sight lines, which indicate a visually connected network planning with clear sightlines and functions.

#### 7.3.3.3 KDH AND MPH BASE PLANS AND OBSERVATION PLANS SUMMARY FINDINGS

This summary findings are based on visual simulations findings, statistical analysis findings and cross data set observation findings (Occupancy and Microbial) for each hospital unit. This summary makes reference to graphs and plots (Figure 42, Figure 43, Figure 44 and Figure 45) and graphs (Figure 46, Figure 47, Figure 48 and Figure 49).

Table 7.8: KDH and MPH comparative analysis data table: base plan versus observation plan

| | | |
|---|---|---|
| 1 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *Mutual and centrally visual spaces are: Nurse Station, Trolley and Main Passage. Secondary: Resus, Nebulisation. The least: Triage Consult and Triage waiting rooms/zones.* | *The mutual and visually central spaces are: Nurses' Station, Trolley and Main Passage. Secondary: Resus and Nebulisation. The least: Triage Consult and Triage Waiting.* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |

| | | |
|---|---|---|
| | When compared to the gate crossing analysis (7.3.4.2), the most travelled spaces, and those most connected by functional use, matched the VGA spaces. The secondary spaces indicated an exception of the Triage Consult 1 room/zone; the VGAs indicated that all the Triage rooms/zones are the least connected. | When compared to the gate crossing analysis (7.3.4.2), the most travelled spaces, and those most connected by functional use, matched the VGA spaces, except for the Triage Waiting room/zone that is included. The secondary spaces matched, and the Triage rooms/zones (excluding Triage Waiting) were the least connected. |
| 2 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *The zones with the shortest direct connection within the network routes are: Nurses' Station, Trolley and Main Passage. Secondly: Resus and sub wait at Procedure share the same connection. Clusters of network connectedness are found in the Secondary Passage. The angular inclusion of the Triage Waiting room/zone proposes a stronger network link than the visual connectivity analysis suggests and will be confirmed by the gate count analysis and observation simulation.* | *The zones with the shortest direct connection within the network routes are: Nurses' Station, Main Passage and Triage Waiting rooms/zones. Secondly: Trolley and Resus. No evident clusters of network connectedness are found. The angular inclusion of the Triage Waiting and the Triage Consult rooms propose a stronger network link than the visual connectivity analysis confirmed by the gate count analysis and observation simulation.* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |
| | From the observations as per Figure 42: For summer, the Nurses' Station and Main Passage zone were the most integrated, followed by Trolley, Resus and Nebulisation, as well as Triage Consult 1 and the Procedure room. For winter, the same was experienced, except that Triage Consult 2 replaces Triage Consult 1, and the Procedure room was more integrated (Figure 43). | From the observations as per Figure 44: For summer, the Nurses' Station, Main Passage and Triage Waiting rooms/zones were the most integrated, followed by Trolley, Nebulisation and Triage Consult 2. For winter (Figure 45) the same was experienced, except that the Procedure room was more integrated in winter, and the total average level of integration was greater in winter than in summer. |
| 3 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *The most integrated spaces globally in the KDH network were: The Nurses' Station and Trolley room/zone, followed by Resus and Nebulisation. Triage Consult and Procedure are the least integrated. The low through-movement correlation confirms this statement, but the linear spatial planning shows a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90.* | *The most integrated spaces globally in the MPH network were: Trolley, Nurses' Station, Main Passage and Triage Waiting, followed by Resus. Triage Consult, Nebulisation and Procedure are the least integrated. The low through-movement correlation confirms this statement, but the linear spatial planning shows a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90.* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |
| | The central zone: The Nurses' Station and Main Passage zone leading out onto the main external public waiting area and edging into the Trolley room/zone were observed as the most integrated. Secondary integrated spaces were found to be Trolley, Resus and Nebulisation, as well as Triage Consult 1 and the passage leading to the Procedure room. The base data are comparable to the observation | The central zone: The Nurses' Station, Main Passage and Triage Waiting rooms/zones compare to the base plan.<br>Secondary connectivity is found in Trolley, Nebulisation and Triage Consult 2, and the passage leading to the ambulant entry and exit is comparable to the base plan.<br>The winter spatial integration is similar to summer for all spaces mentioned, but reflects a higher total integration correlation coefficient (Figure 42 - Figure 45). |

| | | |
|---|---|---|
| | plan, except for the Triage Consult 1 room/zone (Figure 42 - Figure 45). | |
| 4 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *Considering spatial depth and integration (potential human flow and movement), the KDH network can be graded from most to least as follows: Nurses' Station, Main Passage and portions of Trolley extending into the Triage Passage at the Triage Consult rooms/zones, followed by Trolley, Resus and Nebulisation. The Procedure room is not integrated. A micro integration occurs between the two Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.90.* | *Considering spatial depth and integration (potential human flow and movement), the MPH network can be graded from most to least as follows: Nurses' Station, Trolley, Main Passage and Triage Waiting. Second are the Resus and Nebulisation rooms/zones. The procedure room is not integrated. A micro integration occurs at the Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.83.* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |
| | The observation plan correlation coefficient for integration versus mean depth gave an $R^2$ value of 0.92, comparable to that of the base plan of $R^2$ 0.90 | The observation plan correlation coefficient for integration versus mean depth gave an $R^2$ value of 0.82, 0.85, comparable to that of the base plan of $R^2$ 0.83. |
| 5 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness as were found at KDH.* | *Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness, as were mostly found at MPH. (The VGA indicated lower connectedness than the axial mapping suggests, i.e. the Trolley and Triage Waiting rooms/zones were indicated as less visually connected, but the axial mapping showed higher integration.)* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |
| | Observation: Nurses' Station, Main Passage and Trolley. Secondary: Trolley, Resus, Nebulisation and Triage Consult 1, indicate the following room order grading (Table 7.17 and Table 7.18), with a 100% match between summer and winter (69-73% match between KDH and MPH). Primary: Main Passage, Nurses' Station and Trolley. Secondary: Resus, Triage Consult 1, Nebulisation, Triage Waiting, etc. | Observation: Nurses' Station, Main Passage, Triage Waiting and Trolley. Secondary: Trolley, Resus, Nebulisation and Triage Consult 1 & 2, indicate the following room order grading (Table 7.17 and Table 7.18) with an 80% match between summer and winter (69-73% match between KDH and MPH). Primary: Nurses' Station, Main Passage, and Triage Waiting. Secondary: Trolley, Resus, Triage Consult 1, Nebulisation, Triage Consult 2, etc. |
| 6 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *KDH presents a statistically significant visual and flow correlation, with an integration and connectivity correlation value of $R^2$ 0.58. The KDH simulation shows a smaller central core through movement compared to MPH and was even less connected to the entire network of the A&E with an $R^2$ value of 0.26. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.90.* | *MPH presents a statistically significant visual and flow correlation with an integration and connectivity correlation value of $R^2$ 0.58. MPH simulation shows a central core through movement; however, it is not well connected to the entire network of the A&E, as is evident from the $R^2$ value of 0.43. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.83.* |
| | **KDH Observation plan overlay** | **MPH Observation plan overlay** |
| | No correlation on through movement exists. | No correlation on through movement exists. |

From the analysis the follow findings are reported: The observation plan data and the gate crossing data (which refer to the most connected rooms/zones based on functional use through entry and exit) were in fact very similar for both KDH and MPH. The base plan data indicated a linear design planning for both KDH and MPH, which was observed; however, the data

indicated that MPH had a stronger linear planning over KDH (Figure 42 - Figure 45). The Procedure and Triage Consult rooms/zones were found to be isolated from the rest of the global spaces in the A&E unit (Figure 42 - Figure 45) (for both hospitals). Observation data at KDH compared to the base plan for integration revealed the top three integrated rooms to be similar, with the Main Passage being more integrated than the Trolley room in the observation plan for summer. Secondly, Trolley and Resus match the base plan, but the observation data revealed higher integration at the Nebulisation room/zone, as well as Triage Consult 1 or Triage Consult 2 (winter) and the Procedure room than the base plan. The base plan indicated Triage Consult 1 and 2 as well as Triage Waiting to be a micro network cluster. The observations at MPH compared to the base plan integration revealed the exact same top three integrated rooms for summer and winter. Secondly, Trolley and Resus match the base plan, including the Triage Waiting and Triage Consult 1 and 2 rooms/zones. A total higher integration correlation was experienced for winter than summer. When comparing the observations at MPH and KDH, the top three integrated rooms match, the secondary rooms match, but the Triage spaces are more integrated at MPH than the micro network cluster found in KDH.

The observation plan analysis shows a stronger integration in the Main Passage and Procedure passage (Figure 42 - Figure 45). The observation plan for both KDH and MPH indicated a linear design; however, KDH presented a higher and more stable integration over both seasons with a correlation coefficient $R^2$ value of 0.40 and 0.42, versus an $R^2$ value of 0.30 and 0.38 for MPH. Both the observation plan and the base plan of KDH and MPH were very well correlated for global integration. The spatial integration correlation coefficient on average for both KDH and MPH was lower than that of the base plan, with an average of $R^2$ of 0.40 and an $R^2$ of 0.34 respectively. The observation plan data did not indicate a micro integration network for the triage rooms/zones for both hospitals, hence the isolation comment previously. This was especially evident for KDH due to the layout, which presented a fully integrated Triage Waiting room/zone. Comparing observation at KDH to the gate count (section 7.3.4.2) indicated the same top three zones, but with an order grading variation. Secondary spaces varied by more than 50% in grading variation. Observation at KDH compared to the internal flow indicated a match for both top three and secondary spaces, with a grading variation of no more than 10%. Observation at MPH compared to the gate count indicated a match for the top three in grading. Secondary spaces varied by no more than 10% in grading. Observation at MPH compared to the internal flow indicated a match for the top three, due to the fact that internal flow for winter and summer had only a 40% match. The comparison with the observation is similar at 40%, with rooms mostly changing a single position on the grading scale. Integration vs mean depth analysis for the observation plan data for both MPH and KDH is comparable to the integration correlation values found in the base plan. The observation plan data for both MPH and KDH are lower on all correlations than the base plan correlation coefficient, but the linear design is again still evident. Zonal isolation was evident in the overlay of the observation plan and the base plan. The correlation coefficients for both KDH and MPH concerning integration versus choice on the observation plan were comparable. However, when compared to the base plan, higher correlation coefficients were achieved ($R^2$ of 0.26 and $R^2$ of 0.43.); still, these are poor correlation levels in spatial analytics.

Final remarks: When the global flow patterns of the observed MPH use for both summer and winter were compared to the base plan, the correlation factor varied between the two seasons. Higher correlations were found in winter than in summer; with a correlation coefficient $R^2$ value of 0.38 vs an $R^2$ value of 0.30 vs a base plan $R^2$ value of 0.58. Greater core integration was

observed in winter. A change in flow patterns was observed at MPH, i.e. higher utilisation of the Trolley room/zone and the Main Passage zone. There was a marked variation in utilisation of the Procedure and Triage Consult 1 rooms/zones over the two seasons. The data indicated that at MPH the spatial distribution correlated better in winter. The occupancy data revealed an increase of +30% over winter and, based on the axial analysis, a total increased integrated use of space occurred (check OTUs). The observed flow at KDH generated a correlation coefficient value of $R^2$ 0.40 average across both seasons. The difference between KDH and MPH could be inferred from the variation in utilisation of function and layout between seasons, because of the increased occupancy rate found in winter of 30+% at MPH, and the increased occupancy rate at the central Nurses' Station of more than 120%. Whereas the same flow pattern analysis was done for KDH, no variation between the seasons was observed in the flow pattern; thus, the facility is used the same way in both seasons. The increased occupancy rate also showed an increase in the number of identified OTUs compared to other rooms; thus, a correlation does exist between increased occupancy and the abundance of organisms; micro analysis is required to confirm the magnitude of influence by building activity (flow patterns).

### 7.3.4 GIS GATE AND FLOW ANALYSIS

From the observation data collected, a GIS simulation was performed on the observed flow rate of people moving through each space, the number of people in each space, and the person type most active within each space. The results are represented seasonally for winter and summer. The investigator assumed that the dry (summer) and wet (winter) Cape seasons adequately represented the seasonal dynamics of the Cape Flats, with expected minor variations during the autumn and spring seasons. The following correlations and analyses were run:

1. Total gate count (gate count density ratio/GC) over the total season study period.
2. Total internal flow (internal flow ratio/IF) over the total season study period.
3. Total occupancy and users (occupancy and main users) over the total season study period.

These data will firstly be evaluated in isolation with deductions, and then against the base plan and observation plan analysis.

#### 7.3.4.1 GRAPHICAL ANALYSIS OF GIS GATE AND FLOW SIMULATION FOR KDH AND MPH

Refer to Table 7.9 for the selection of rooms/zones. Refer to Figure 70 and Figure 71 for the position of rooms/zones on plan, in space or, for ease of reference, to Figure 52 to Figure 69.

Table 7.9: Room zone classification

| | |
|---|---|
| Z1 | Triage Consult 1 |
| Z2 | Triage Consult 2 |
| Z3 | Triage Waiting |
| Z4 | Procedure 1 |
| Z5 | Passage Main |
| Z6 | Nurses' Station |
| Z7 | Resuscitation |
| Z8 | Nebulisation |
| Z9 | Passage Secondary |

| | |
|---|---|
| Z10 | Trolley |
| Z11 | (Not indicated) refer to external sampling area 1 |
| Z12 | (Not indicated) refer to external sampling area 1 |


Figure 50: KDH A&E study zone (Figure 16)

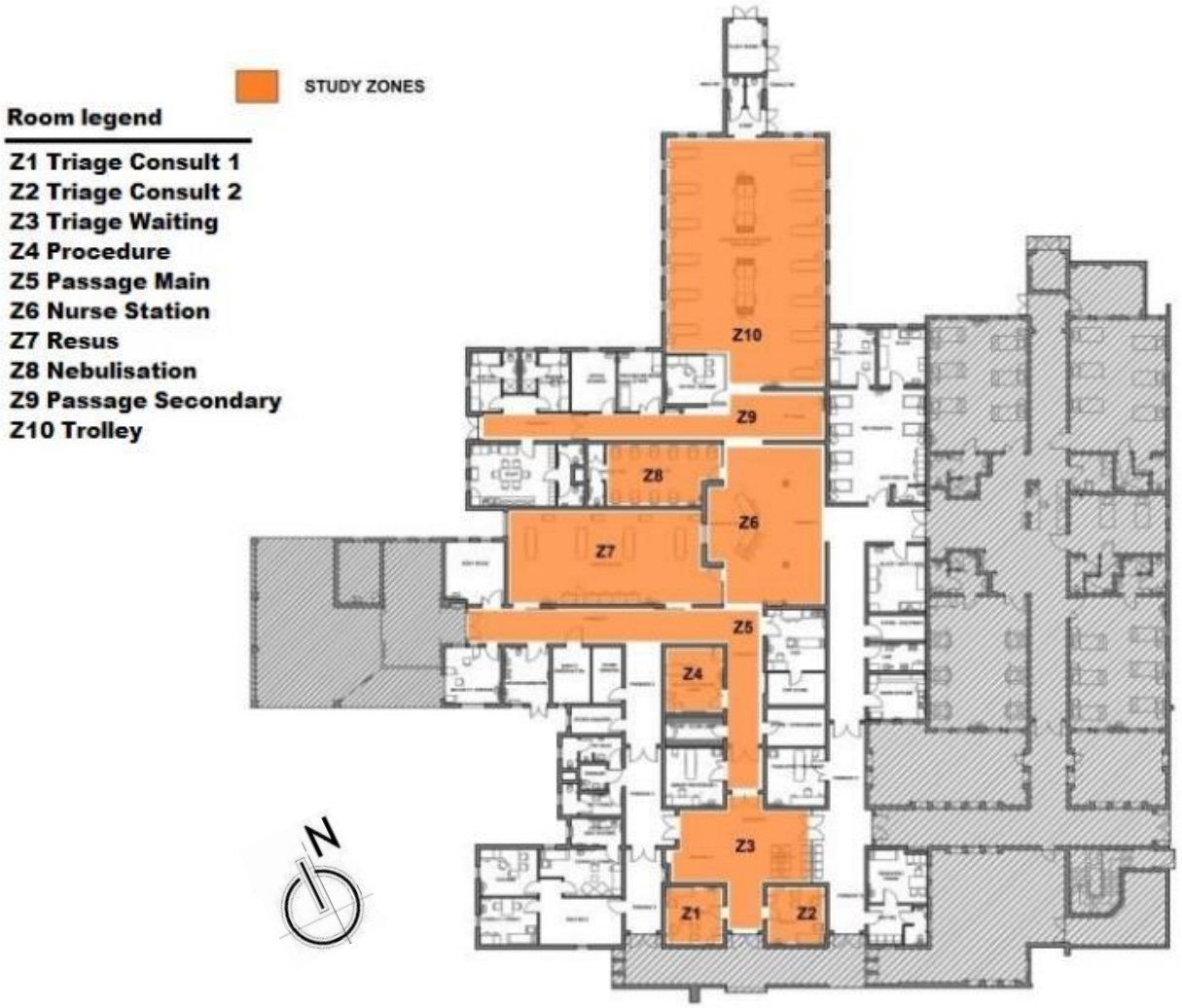



Figure 51**:** MPH A&E study zones (Figure 17)

## GATE COUNT DENSITY RATIO FOR MPH AND KDH

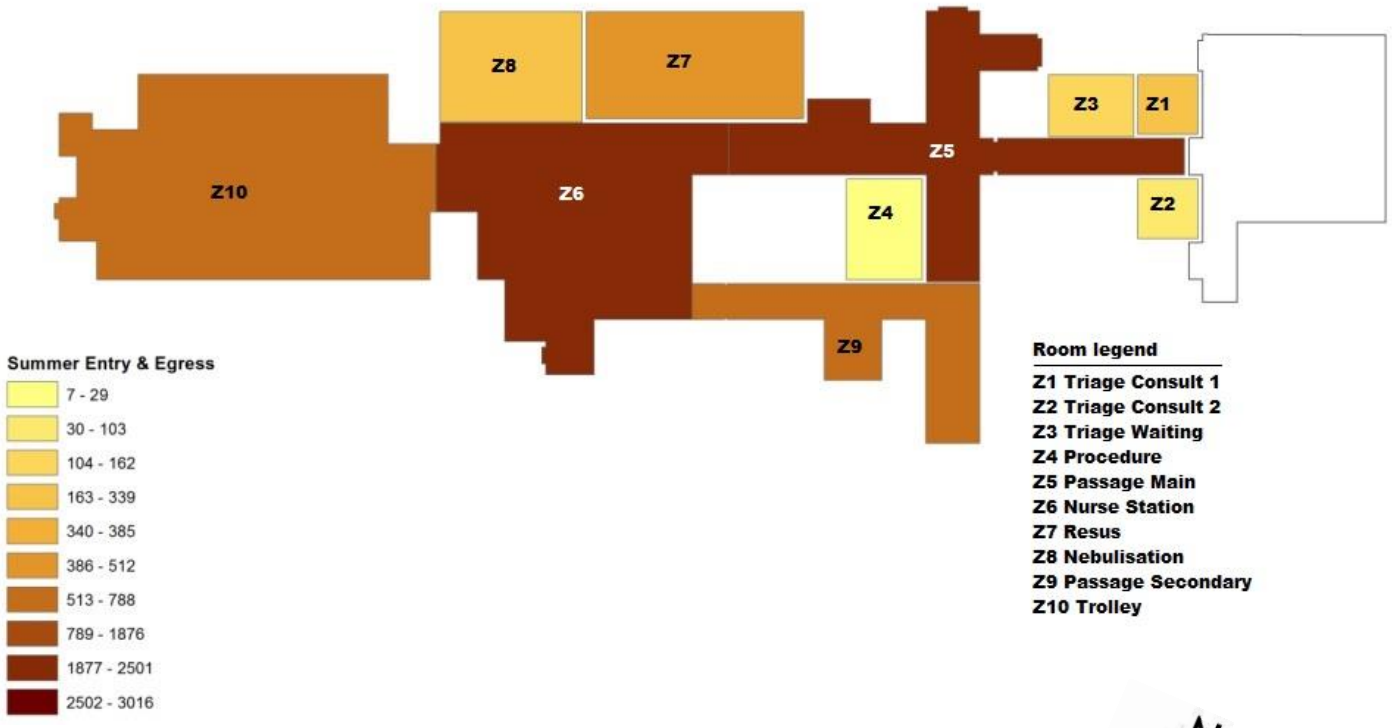



Figure 52: KDH gate count density, summer

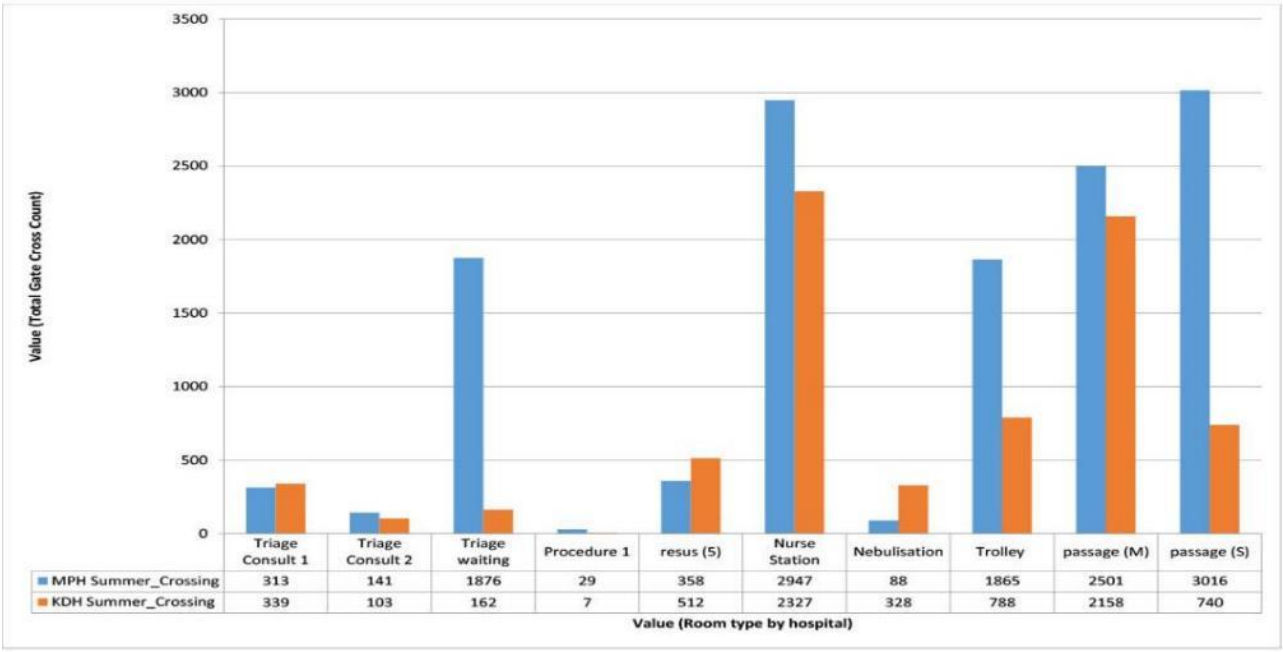



Figure 53: MPH and KDH gate cross chart, summer

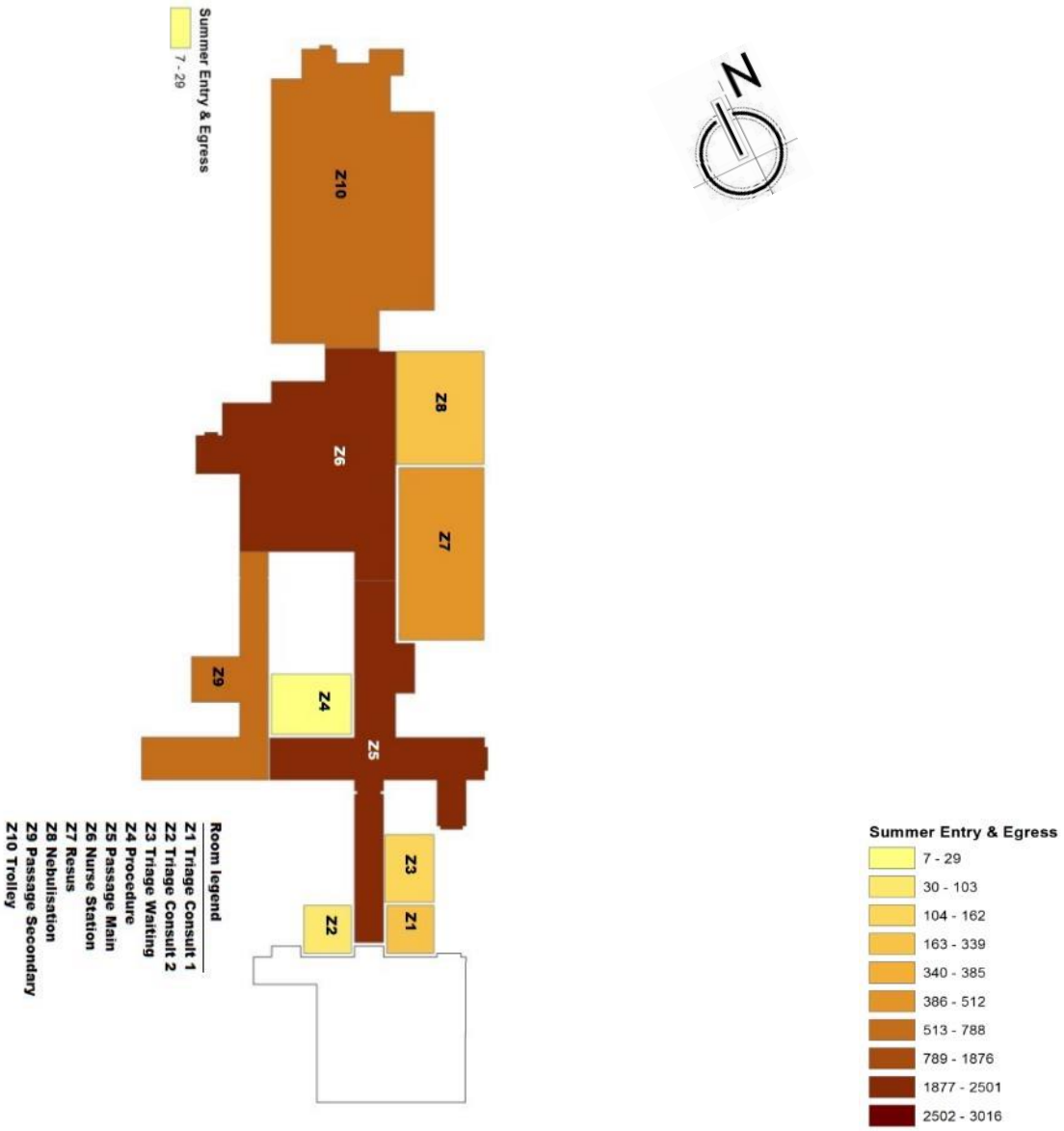



Figure 54: MPH gate count density, summer

**A 73% gate crossing and room type correlation exists between MPH and KDH**.

Table 7.10: MPH and KDH gate count chart, summer

| **KDH** | **MPH** | |
|---|---|---|
| Passage Main | Nurses' Station | |
| Nurses' Station | Passage Main | |
| Trolley | Triage Waiting | |
| Resus | Trolley | |
| Triage Consult 1 | Resus | |
| Nebulisation | Triage Consult 1 | |
| Triage Waiting | Triage Consult 2 | |
| Triage Consult 2 | Nebulisation | |
| Procedure 1 | Procedure 1 | |

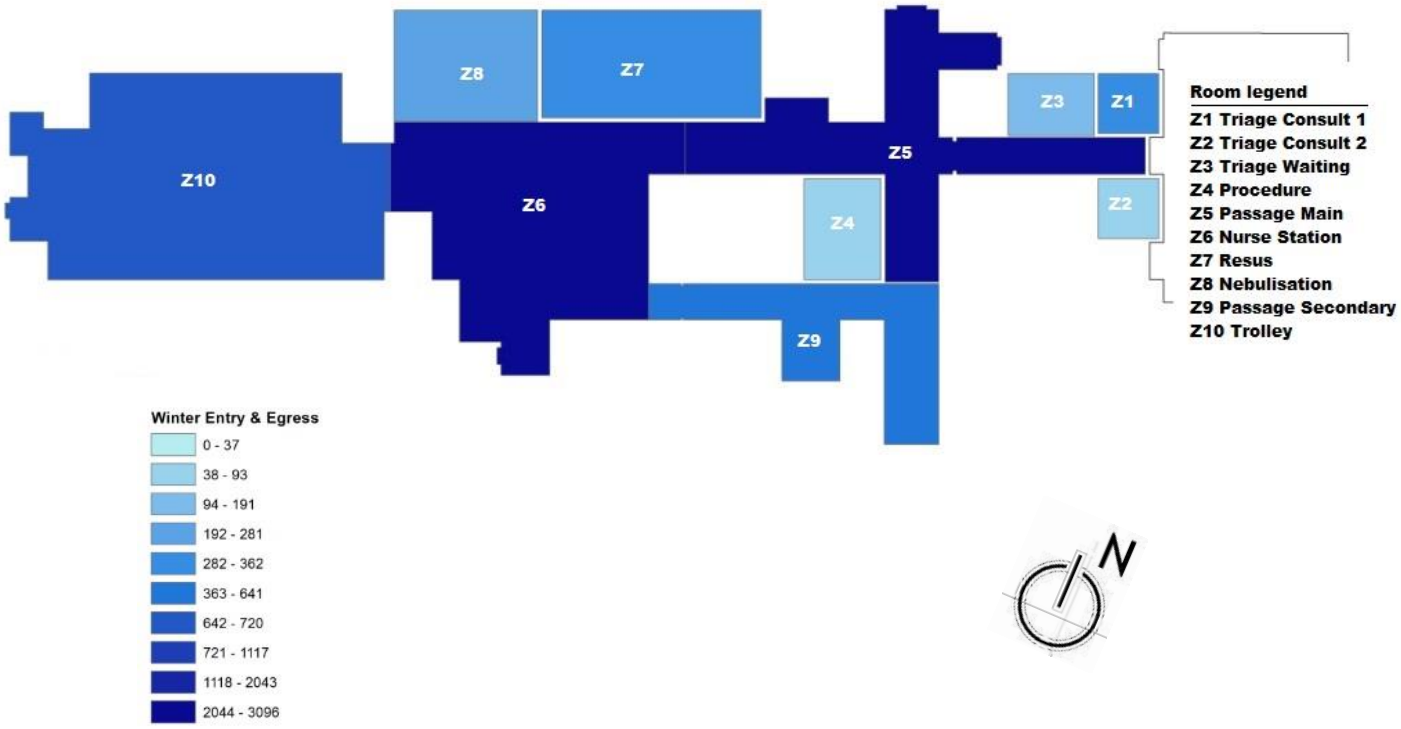



Figure 55: KDH gate count density, winter

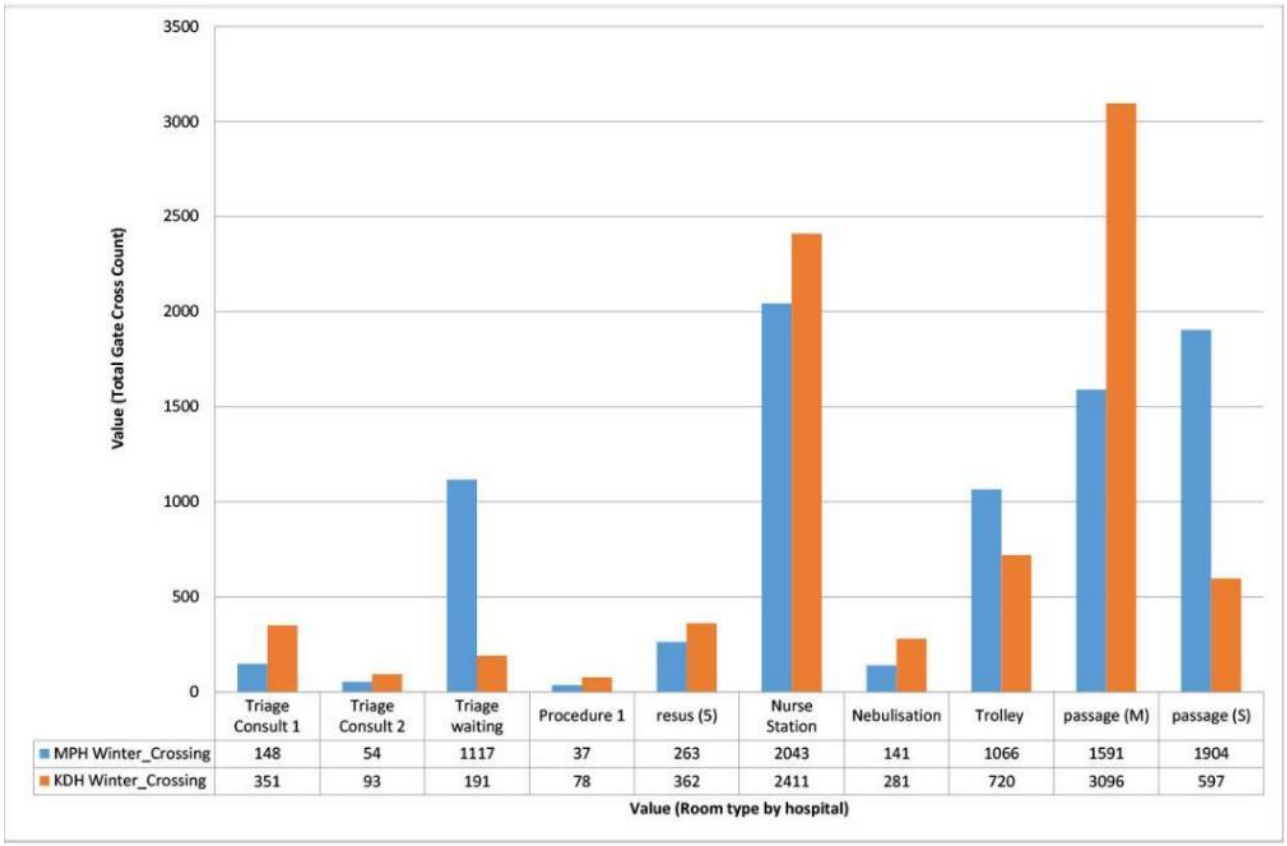



Figure 56: MPH and KDH gate cross chart, winter

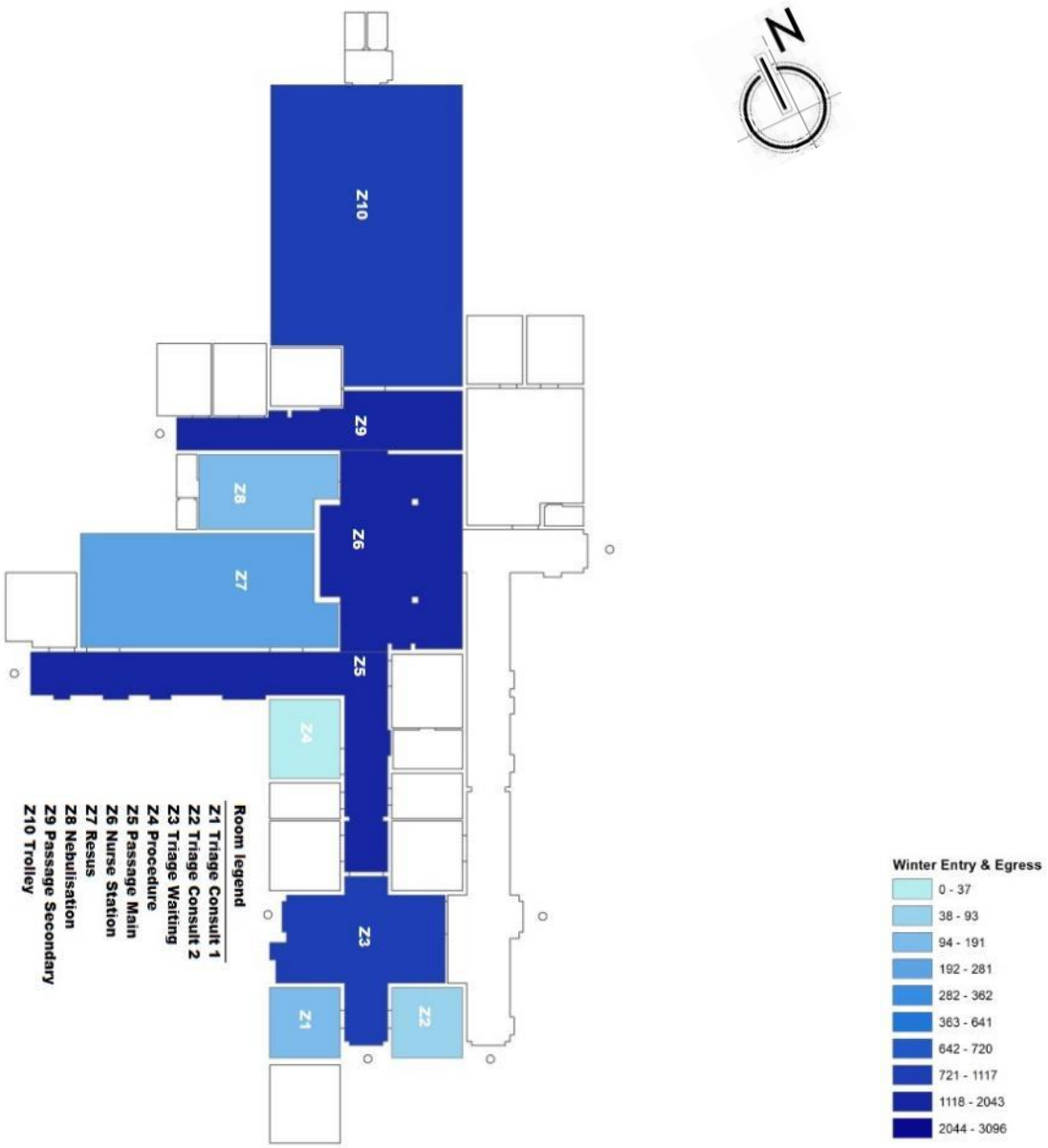



Figure 57: MPH gate count density, winter

**A 69% gate crossing and room type correlation exists between MPH and KDH.**

Table 7.11: MPH and KDH gate cross user grading, winter

| **KDH** | **MPH** | |
|---|---|---|
| Passage Main | Nurses' Station | |
| Nurses' Station | Passage Main | |
| Trolley | Triage Waiting | |
| Resus | Trolley | |
| Triage Consult 1 | Resus | |
| Nebulisation | Triage Consult 1 | |
| Triage Waiting | Nebulisation | |
| Triage Consult 2 | Triage Consult 2 | |
| Procedure 1 | Procedure 1 | |

## INTERNAL FLOW RATIO FOR MPH AND KDH

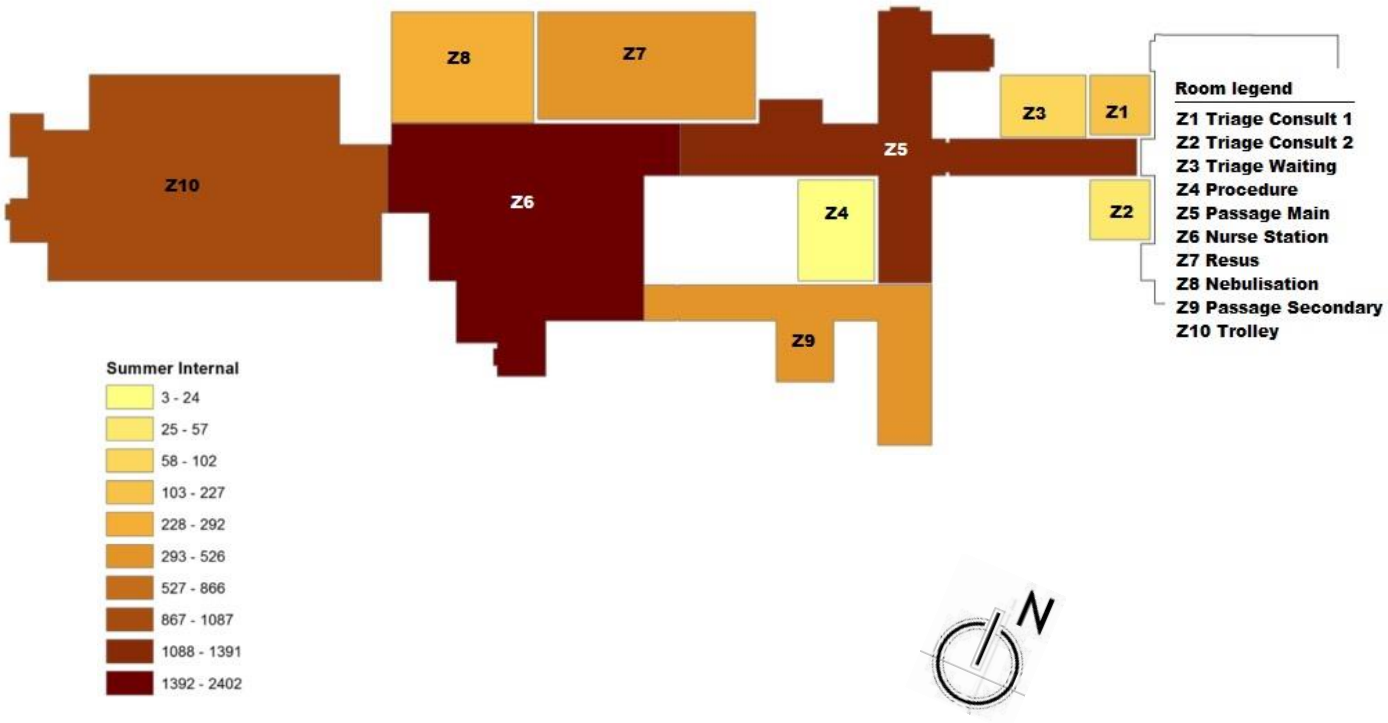



Figure 58: KDH Internal flow count, summer

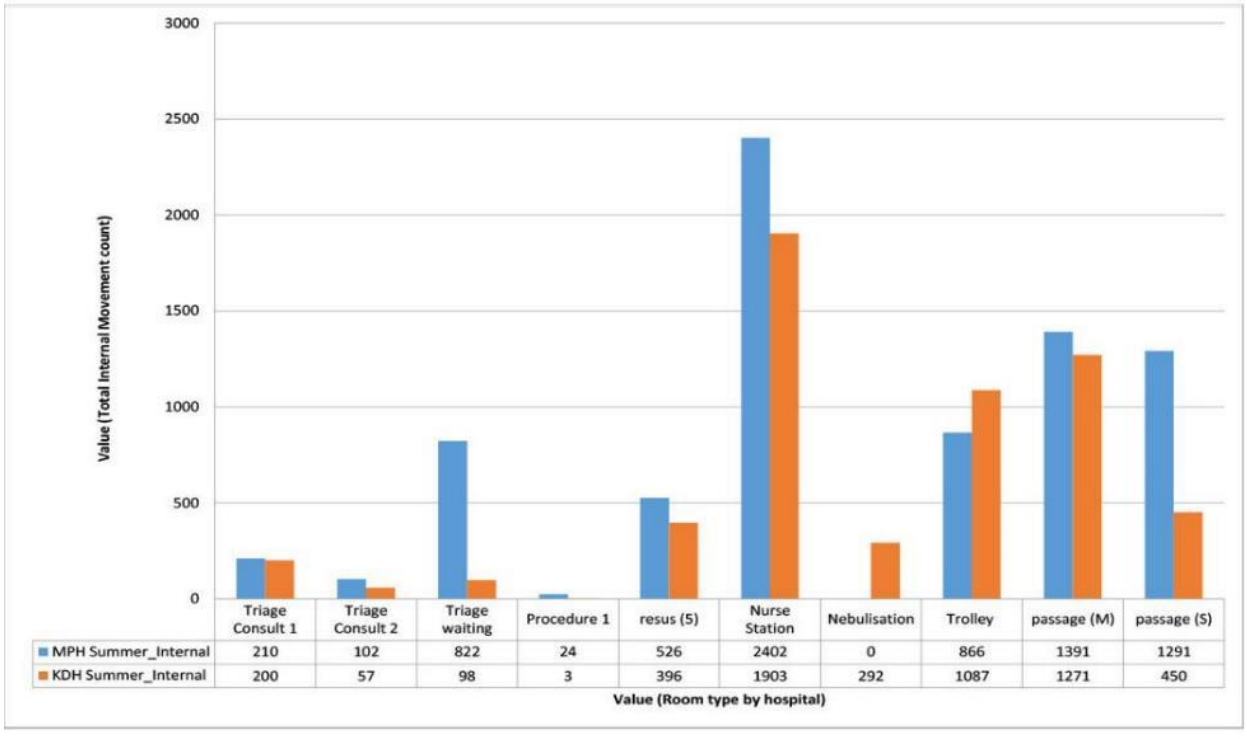



Figure 59: MPH and KDH internal flow chart, summer

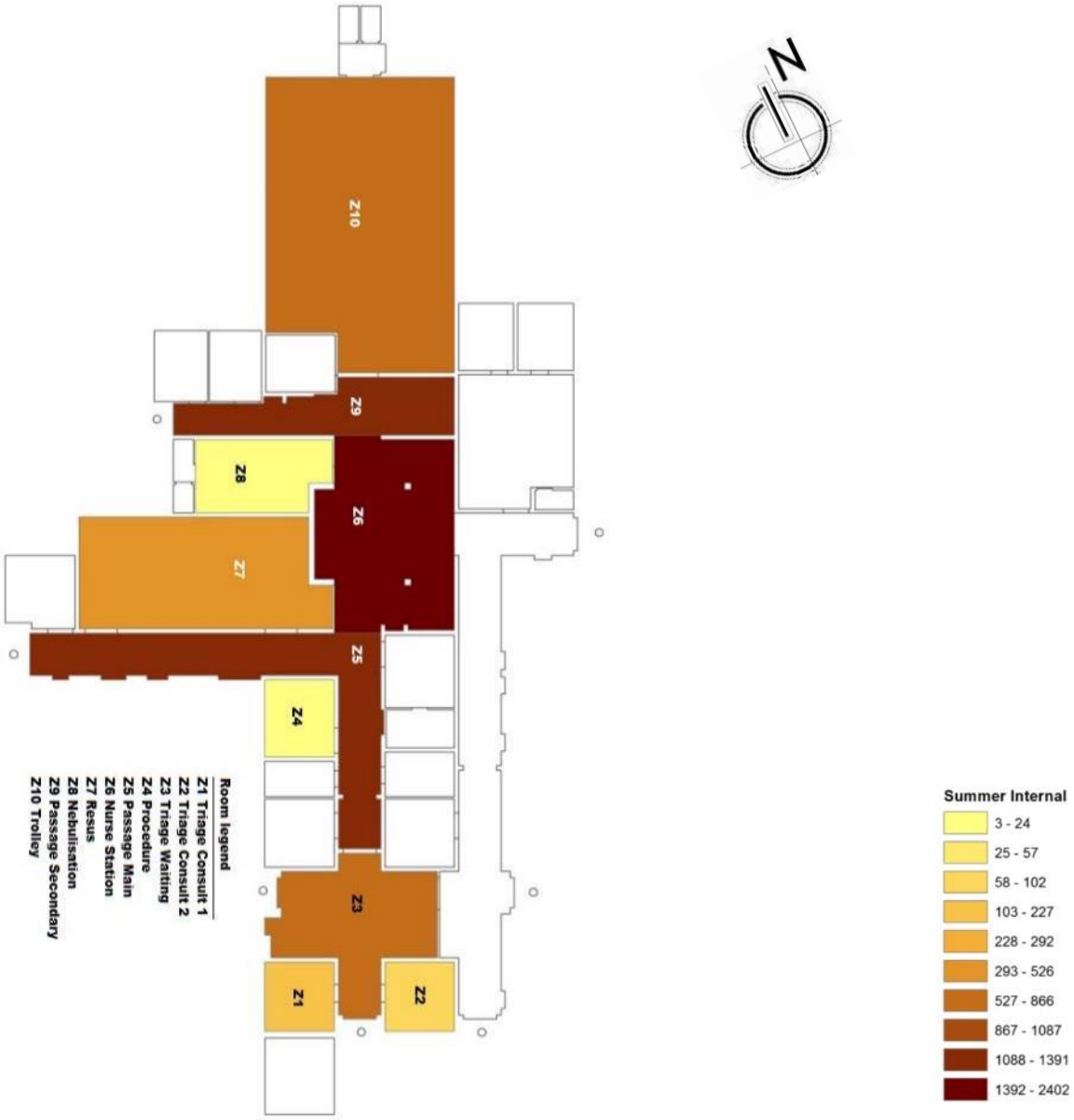



Figure 60: MPH Internal flow count, summer

**An 87% internal flow and room type correlation exists between MPH and KDH**.

Table 7.12: MPH and KDH internal flow chart, summer

| **KDH** | **MPH** | |
|---|---|---|
| Nurses' Station | Nurses' Station | |
| Passage Main | Passage Main | |
| Trolley | Trolley | |
| Resus | Triage Waiting | |
| Nebulisation | Resus | |
| Triage Consult 1 | Triage Consult 1 | |
| Triage Waiting | Triage Consult 2 | |
| Triage Consult 2 | Nebulisation | |
| Procedure 1 | Procedure 1 | |

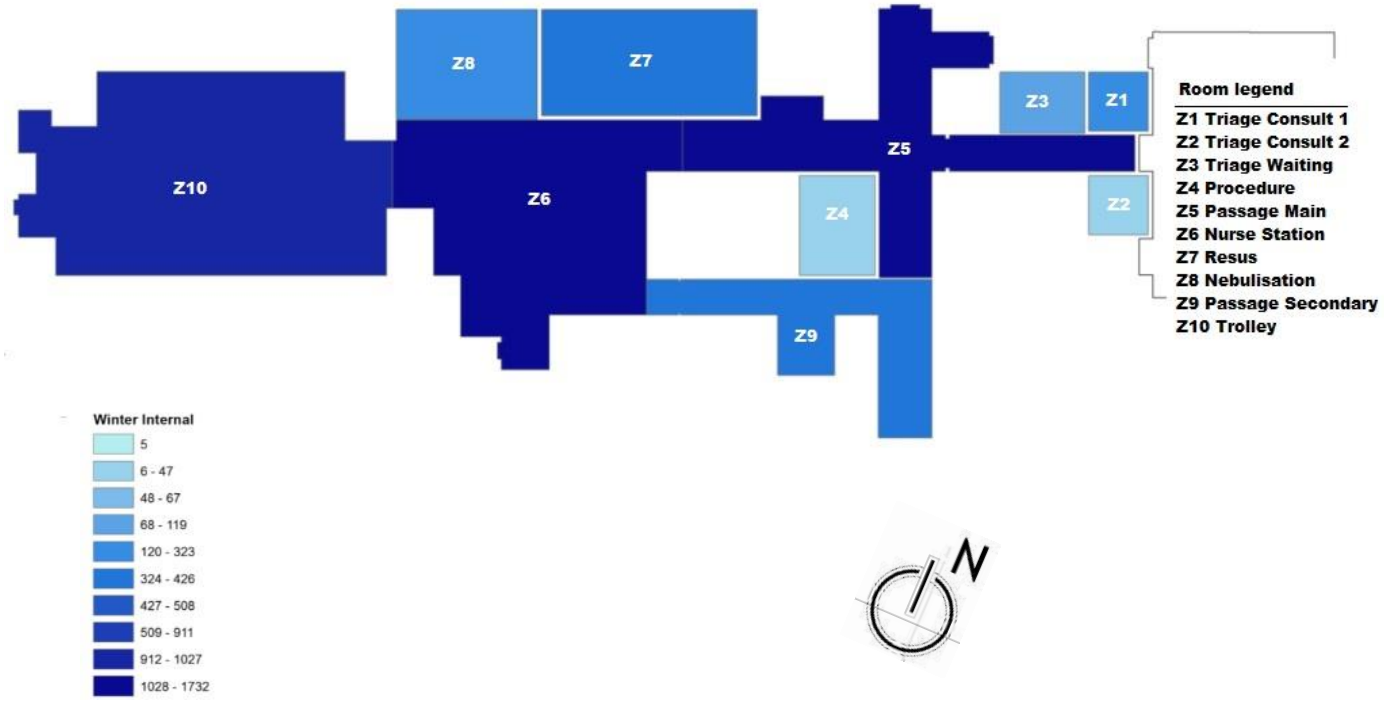
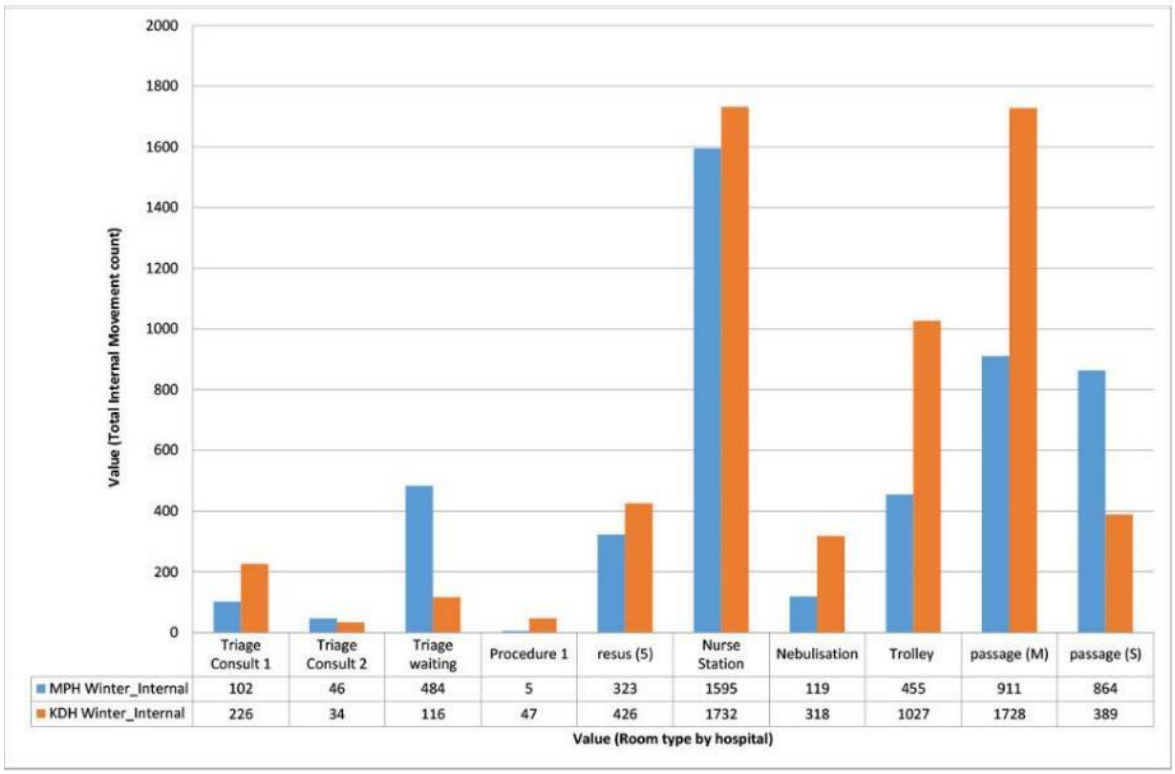



Figure 61: KDH internal flow count, winter




| | Triage Consult 1 | Triage Consult 2 | Triage waiting | Procedure 1 | resus (5) | Nurse Station | Nebulisation | Trolley | passage (M) | passage (S) |
|---|---|---|---|---|---|---|---|---|---|---|
| MPH Winter_Internal | 102 | 46 | 484 | 5 | 323 | 1595 | 119 | 455 | 911 | 864 |
| KDH Winter_Internal | 226 | 34 | 116 | 47 | 426 | 1732 | 318 | 1027 | 1728 | 389 |

Figure 62: MPH and KDH internal flow chart, winter

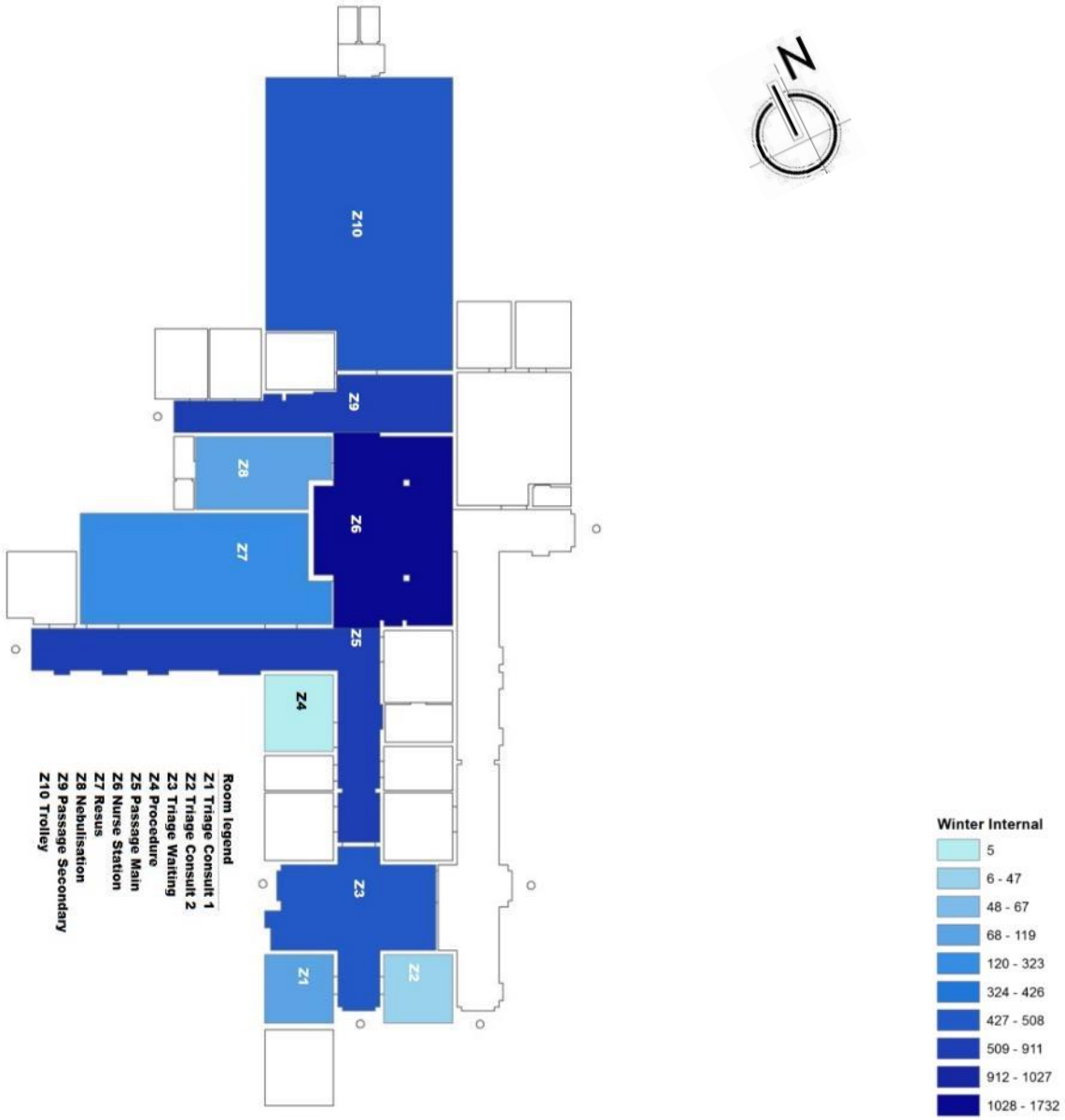



Figure 63: MPH internal flow chart, winter

**An 82% internal flow and room type correlation exists between MPH and KDH.**

Table 7.13: MPH and KDH internal flow chart, winter

| KDH | MPH | |
|---|---|---|
| Nurses' Station | Nurses' Station | |
| Passage Main | Passage Main | |
| Trolley | Triage Waiting | |
| Resus | Trolley | |
| Nebulisation | Resus | |
| Triage Consult 1 | Nebulisation | |
| Triage Waiting | Triage Consult 1 | |
| Procedure 1 | Triage Consult 2 | |
| Triage Consult 2 | Procedure 1 | |

## OCCUPANCY RATIO MPH AND KDH

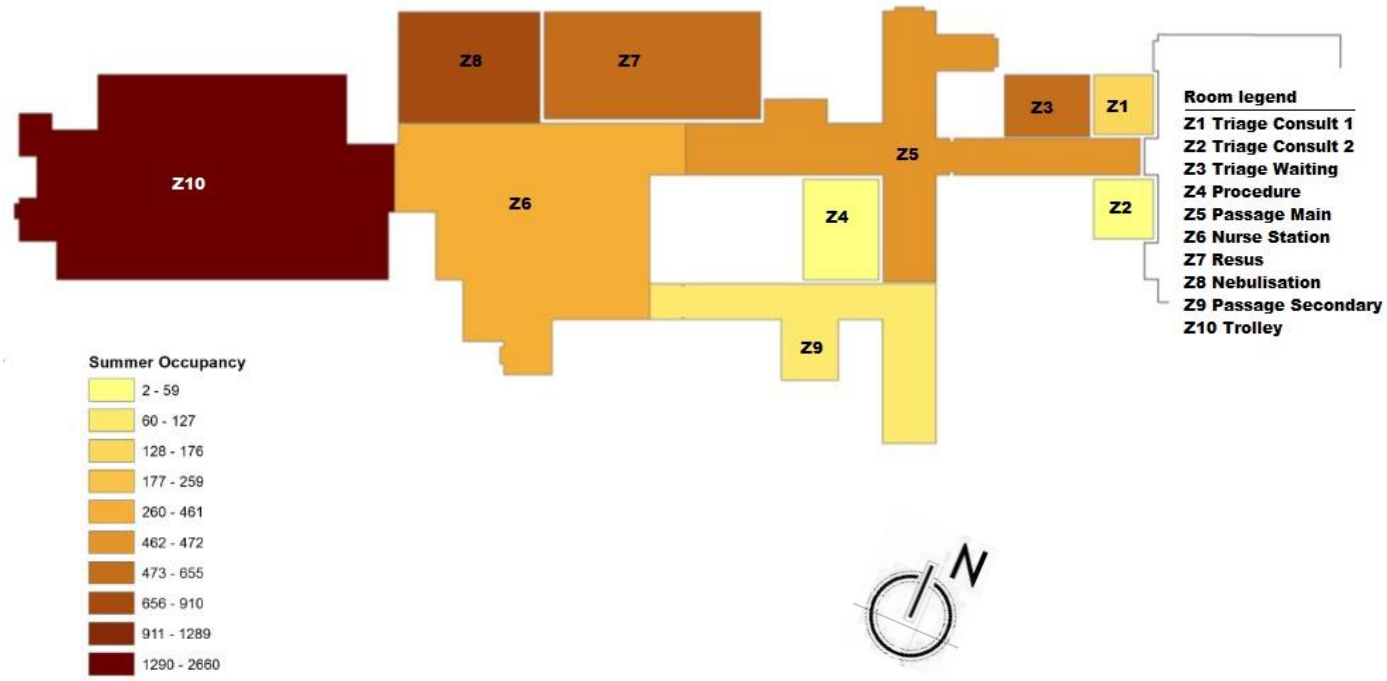



Figure 64: KDH occupancy count, summer

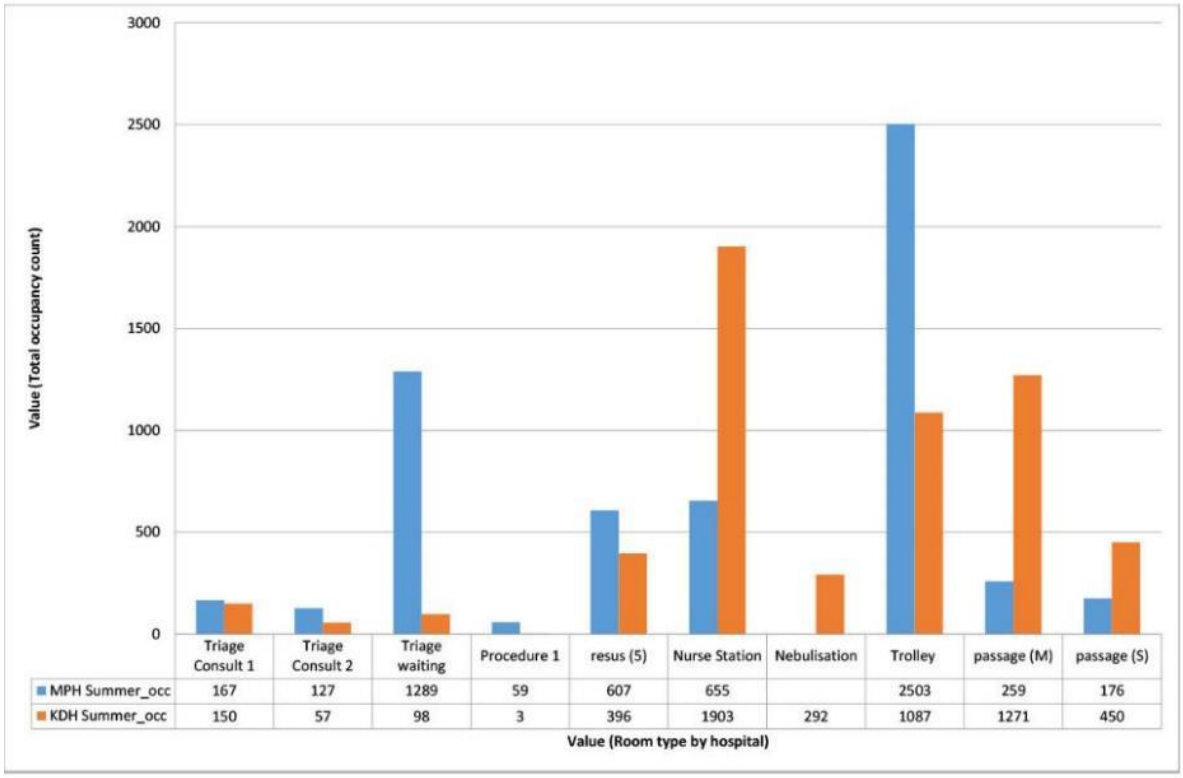



Figure 65: MPH and KDH occupancy count, summer


Figure 66: MPH occupancy count, summer

**A 59% occupancy and room type correlation exists between MPH and KDH.**

Table 7.14: MPH and KDH occupancy count, summer

| **KDH** | **MPH** | |
|---|---|---|
| Nurses' Station | Trolley | |
| Passage Main | Triage Waiting | |
| Trolley | Nurses' Station | |
| Resus | Resus | |
| Nebulisation | Passage Main | |
| Triage Consult 1 | Triage Consult 1 | |
| Triage Waiting | Triage Consult 2 | |
| Triage Consult 2 | Procedure 1 | |
| Procedure 1 | | |

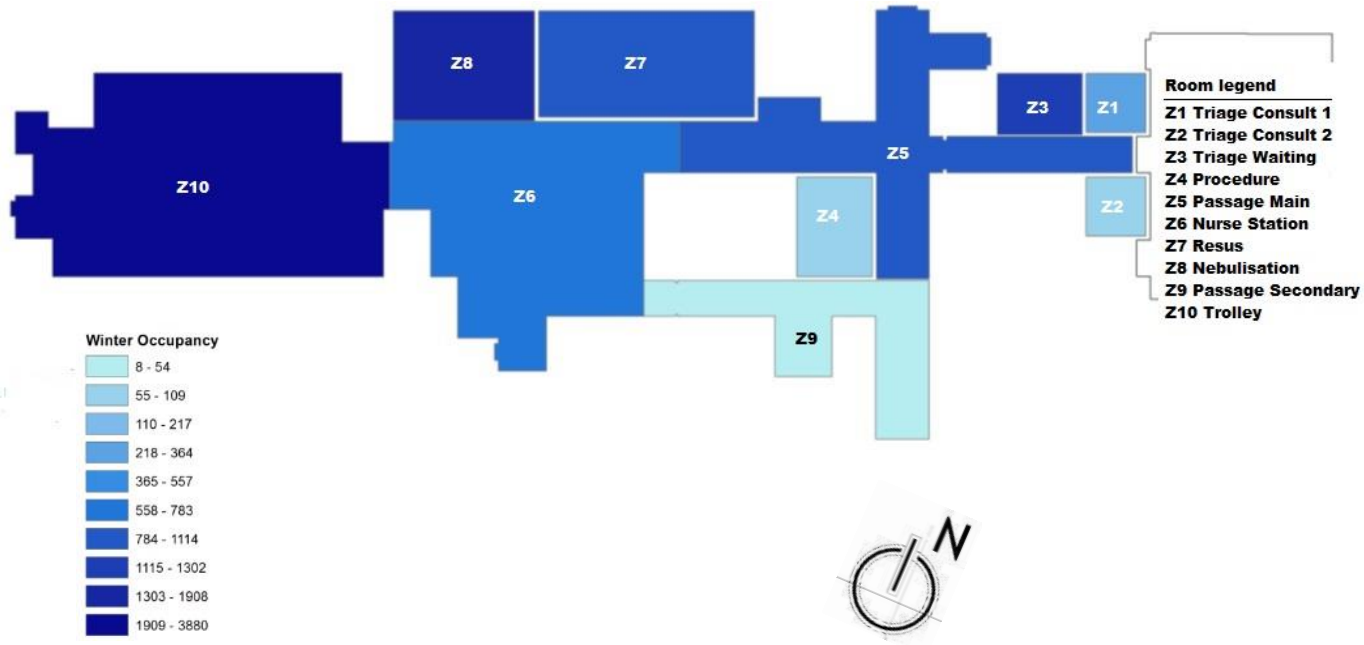
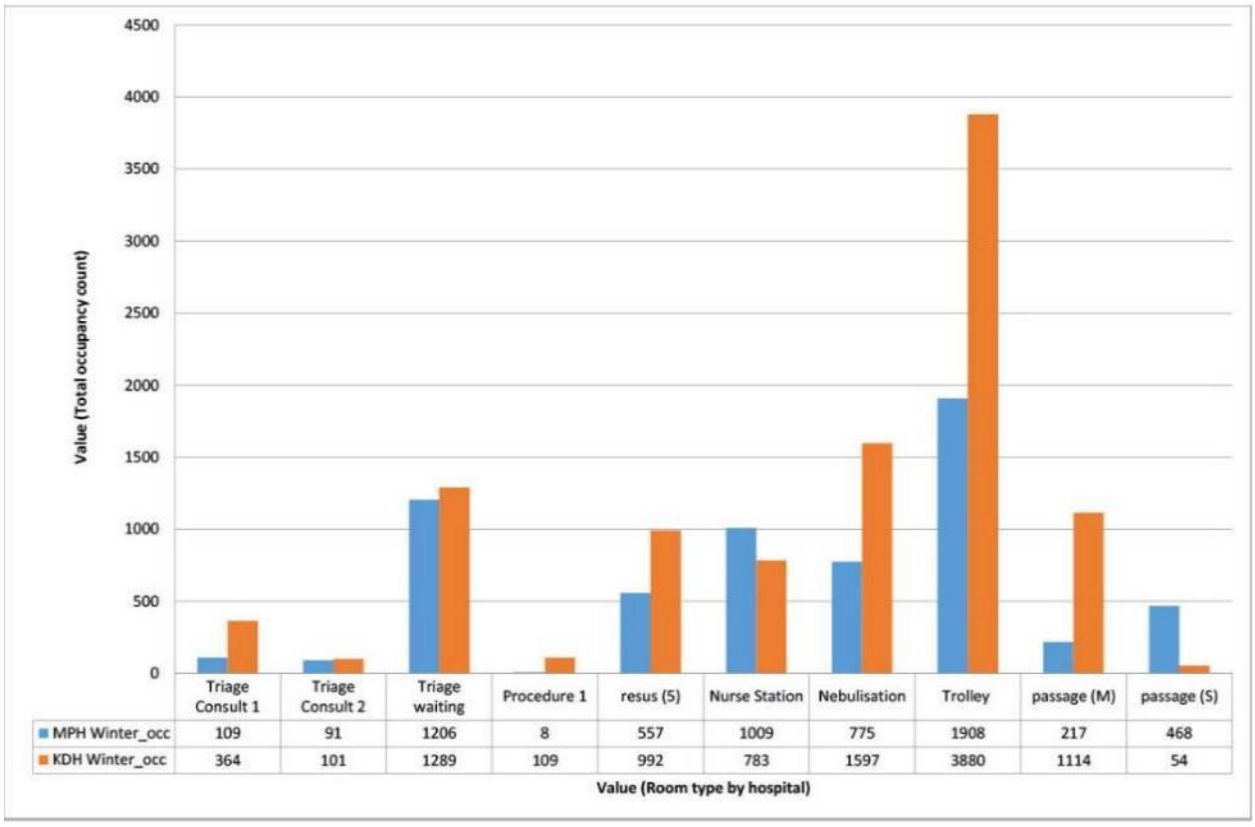



Figure 67: KDH Occupancy count, winter




| | Triage Consult 1 | Triage Consult 2 | Triage waiting | Procedure 1 | resus (S) | Nurse Station | Nebulisation | Trolley | passage (M) | passage (S) |
|---|---|---|---|---|---|---|---|---|---|---|
| MPH Winter_occ | 109 | 91 | 1206 | 8 | 557 | 1009 | 775 | 1908 | 217 | 468 |
| KDH Winter_occ | 364 | 101 | 1289 | 109 | 992 | 783 | 1597 | 3880 | 1114 | 54 |

Figure 68: MPH and KDH occupancy count, winter

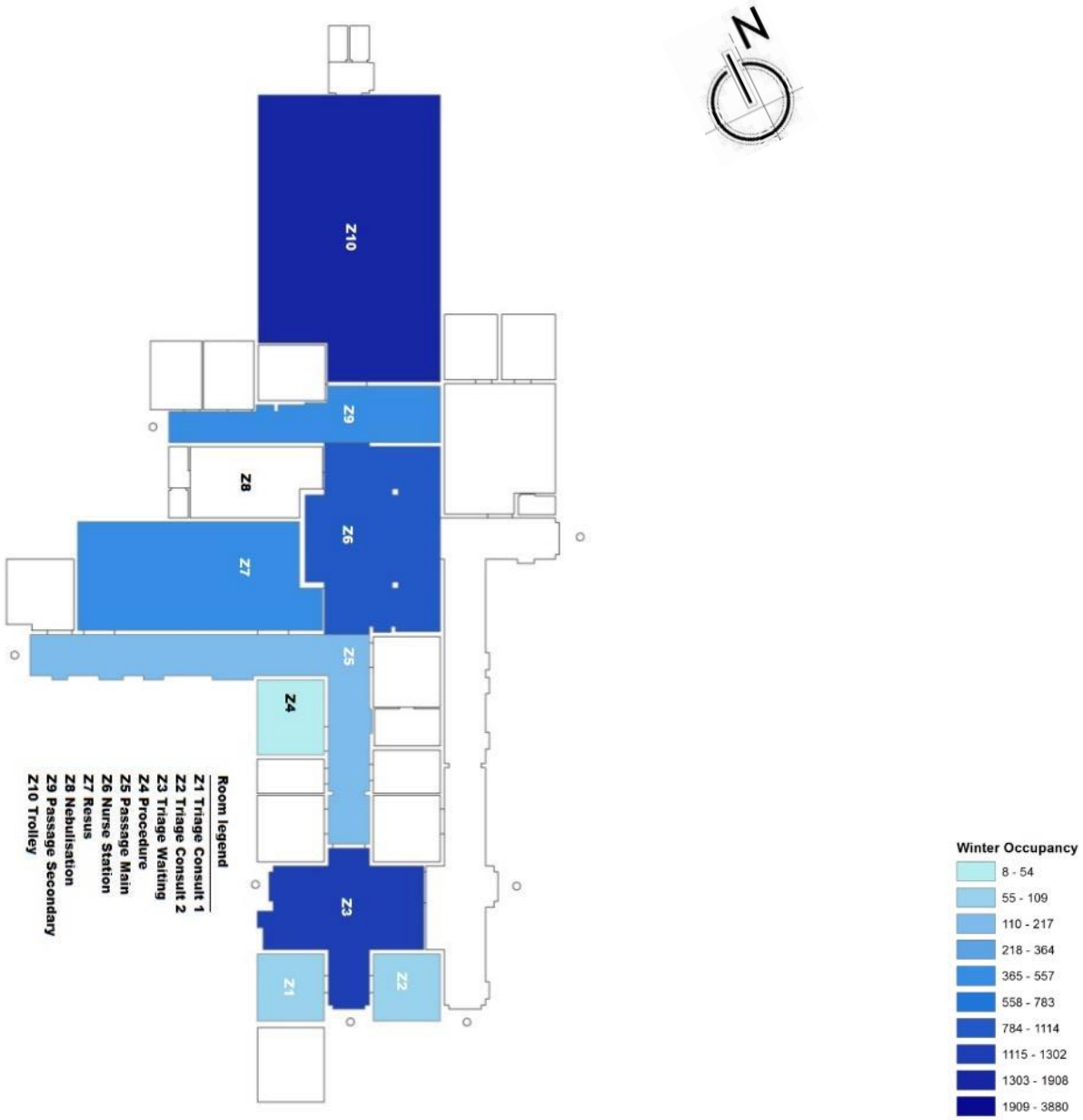



Figure 69: MPH occupancy ratio, winter

**An 86% occupancy and room type correlation exists between MPH and KDH**.

Table 7.15: MPH and KDH occupancy ratio, winter

| **KDH** | **MPH** | |
|---|---|---|
| Trolley | Trolley | |
| Nebulisation | Triage Waiting | |
| Triage Waiting | Nurses' Station | |
| Passage Main | Nebulisation | |
| Resus | Resus | |
| Nurses' Station | Passage Main | |
| Triage Consult 1 | Triage Consult 1 | |
| Procedure 1 | Triage Consult 2 | |
| Triage Consult 2 | Procedure 1 | |

In summary, the correlation between MPH and KDH for factors of gate crossing, internal flow and room occupancy are presented (discussed in further detail in section 7.3.4.2). The gate crossing (crossing the threshold of spaces - entering and exiting a room) indicates potential activity; that which did occur in the space was measured at matching 73% for summer and 69% for winter. When reviewing the internal flow (actual in room activity) and the room types that have most and least activity, a striking similarity of 87% for summer and 82% for winter was found. For factors of occupancy and occupancy and room type in the rooms for summer a correlation of 59% was found as opposed to 86% for winter. The findings reveal that by gate crossing the rooms utilised by both facilities seasonally are similar, and they are used in a highly similar fashion (thus the functional use of spaces for both MPH and KHD match); however, a clear occupancy variation exists between the sites and for specific room types, i.e. the Nurses' Station with 120%.

#### 7.3.4.2 GIS GATE AND FLOW SIMULATION SUMMARY FINDINGS

Refer to Table 7.10 and Figure 52 to Figure 57: Considering the gate counts in the summer season for both hospitals, it was found that MPH and KDH shared almost the exact same gate flow through the internal spaces; however, MPH experienced a near 100% increase over KDH in winter. Refer to Figure 58 to Figure 63: Considering the internal flow count in the summer season for both hospitals, it was found that MPH had 20% less internal flow through the internal spaces when compared to KDH; however, in winter the exact opposite occurred, with KDH experiencing 20% less activity internally than MPH.

Refer to Figure 64 to Figure 69, and Table 7.14 to Table 7.15: Considering the occupancy counts in the summer season for both hospitals, it was found that both MPH and KDH shared almost the exact same occupancy ratio over the study period; however, MPH hADDED0% more occupants in winter than KDH. These figures correlate well with gate counts in Table 7.10 and Figure 52 to Figure 57, and the increased internal flow as shown in Figure 58 to Figure 63. It can be deduced that MPH experienced an increase in patient service needs over winter and that both hospitals share a similar catchment population, as seen in the summer results. The 2011 census statistics for the Mitchells Plain (MP) and Khayelitsha (K) areas indicate that MP serves 31 000 people, and K serves 39 000 people (Frith 2011). It must also be noted that the catchment population is larger than the census indicates, and as per the Department of Health Western Cape (DoHWC) strategic framework plan (STP) the two hospitals serve the greater Cape Flats and regional area (being district hospitals), as is evident in the bed occupancy counts as per the DoHWC strategic plan (SP) (Househam 2015). When considering the relationship between the gate crossing count and internal flow rates, the following correlations were made in Table 7.16.

Table 7.16: Gate crossing over internal flow rate correlations at MPH and KDH

| Gate and flow count correlations | KDH | MPH |
|---|---|---|
| MPH winter gate count over MPH flow rate | | 92.9% correlation |
| MPH summer gate count over MPH flow rate | | 91.9% correlation |
| The total gate count over flow rate correlation | | 91.9% |
| KDH winter gate count over MPH flow rate | 94.8% correlation | |
| KDH summer gate count over MPH flow rate | 94.2% correlation | |
| The total gate count over flow rate correlation | 94.1% | |

When considering the internal flow rate is considered by quantifying the number of movements (movement in the space/room) and the gate counts by quantifying the number of crossings (the number of times the threshold of a room is crossed by entering or exiting), the data show similar outcomes and hence strong correlations. However, when compared with the occupancy rate (the number of people present in the space - Table 7.14 and Table 7.15, Figure 65 and Figure 68) the following was found: taking into account the variation between summer and winter in the microbial sampling, and an increase in indicator species related to air source, an increased "illness" rate could be attributed to winter. What is of value is the microbiome variation between MPH and KDH in winter versus summer (refer to section 8.3). No variation was found in the room type at KDH graded on highest number of gate crossings into and out of a zone for both seasons (Table 7.10 and Table 7.11); thus, the season played no role in function. Table 7.10 and Table 7.11 indicate that MPH had an 80% similarity in room/zone and gate crossing between the two seasons, except for the two lowest gate-crossing zones. The values are negligible for the two lowest zones and thus one can conclude that the seasons also did not play a role in function. With reference to Table 7.17, the Main Passage was the highest use zone, which can be attributed to its transitory nature, and the second was the Nurses' Station at KDH. The Nurses' Station was the highest use zone in MPH, followed by the Main Passage. In all seasons for both KDH and MPH the Procedure room/zone represented the least used space. A 69% correlation was found between rooms and gate crossings (MPH vs KDH) for winter, and 73% for summer.

Table 7.17: Gate cross room grade summary KDH and MPH

| KDH gate cross, summer | KDH gate cross, winter | MPH gate cross, summer | MPH gate cross, winter |
|---|---|---|---|
| Passage Main | Passage Main | Nurses' Station | Nurses' Station |
| Nurses' Station | Nurses' Station | Passage Main | Passage Main |
| Trolley | Trolley | Triage Wait | Triage Wait |
| Resus | Resus | Trolley | Trolley |
| Triage Consult 1 | Triage Consult 1 | Resus | Resus |
| Nebulisation | Nebulisation | Triage Consult 1 | Triage Consult 1 |
| Triage Wait | Triage Wait | Triage Consult 2 | Nebulisation |
| Triage Consult 2 | Triage Consult 2 | Nebulisation | Triage Consult 2 |
| Procedure 1 | Procedure 1 | Procedure 1 | Procedure 1 |

KDH shows an 80% similarity except for the two lowest internal flow zones between the two seasons. The values are negligible for the lowest two zones and thus one can conclude that the seasons did not play a role in activity. MPH shows a 40% similarity with most zones, swopping in activity level between the two seasons. One can conclude that the seasons did play a role in activity levels within zones. The Nurses' Station was the highest use zone in both hospitals in all seasons, and the Procedure room was the lowest activity space for 75% of the time.

Table 7.18: Internal flow rate room grade summary for KDH and MPH

| KDH flow rate, summer | KDH flow rate, winter | MPH flow rate, summer | MPH flow rate, winter |
|---|---|---|---|
| Nurses' Station | Nurses' Station | Nurses' Station | Nurses' Station |
| Passage Main | Passage Main | Passage Main | Passage Main |
| Trolley | Trolley | Trolley | Triage Waiting |
| Resus | Resus | Triage Waiting | Trolley |

| | | | |
|---|---|---|---|
| Nebulisation | Nebulisation | Resus | Resus |
| Triage Consult 1 | Triage Consult 1 | Triage Consult 1 | Nebulisation |
| Triage Waiting | Triage Waiting | Triage Consult 2 | Triage Consult 1 |
| Triage Consult 2 | Procedure 1 | Nebulisation | Triage Consult 2 |
| Procedure 1 | Triage Consult 2 | Procedure 1 | Procedure 1 |

Table 7.19 shows that the highest occupancy by room type for KDH varied completely between seasons, as did the user type, whereas MPH had matching occupancy by room type for both seasons, while user type varied (except for the omission of Nebulisation in summer due to a procedural change by management at MPH).

Table 7.19: Occupancy type room grade summary for KDH and MPH

| KDH winter | | KDH summer | | MPH winter | | MPH summer | |
|---|---|---|---|---|---|---|---|
| **Room** | **Type** | **Room** | **Type** | **Room** | **Type** | **Room** | **Type** |
| Trolley | Patient | Nurses' Station | Patient | Trolley | Patient | Nurses' Station | Patient |
| Nebulisation | Patient | Passage Main | Patient | Nebulisation | Patient | Passage Main | Patient |
| Triage Waiting | Patient | Trolley | Patient | Triage Waiting | Patient | Trolley | Patient |
| Passage Main | Other | Resus | Patient | Passage Main | Other | Resus | Patient |
| Resus | Patient | Nebulisation | Patient | Resus | Patient | Nebulisation | Patient |
| Nurses' Station | Doctor | Triage Consult 1 | Other | Nurses' Station | Doctor | Triage Consult 1 | Other |
| Triage Consult 1 | Nurse | Triage Waiting | Nurse | Triage Consult 1 | Nurse | Triage Waiting | Nurse |
| Procedure 1 | Doctor | Triage Consult 2 | Doctor | Procedure 1 | Doctor | Triage Consult 2 | Doctor |
| Triage Consult 2 | Patient | Procedure 1 | Patient | Triage Consult 2 | Patient | Procedure 1 | Patient |

For KDH and MPH, when comparing the occupancy to both gate crossing and internal flow levels based on room type, in all comparisons, except for KDH summer gate cross and internal flow, a very low 35% correlation was found; thus, we can establish that occupancy does not correlate either to the internal activity or to the function of the rooms. MPH showed a 30% increase in average occupancy from summer to winter, whereas KDH had a 2% increase in occupancy from summer to winter. Table 7.20 shows a comparative analysis of the findings from the base plan (non-observational) analysis, performed in DepthMap™. These are compared to the findings of the GIS simulation on the observed data for gate crossing (GC), internal flow (IF) and occupancy at both KDH and MPH.

Table 7.20: KDH and MPH: comparative analysis of base plan vs GIS simulation (refer to *Table 7.7*)

| | | |
|---|---|---|
| 1 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *The zones with the shortest direct connection within the network routes are: Nurses' Station, Trolley and Main Passage. Secondly: Resus and sub wait at Procedure share the same connection. Clusters of network connectedness are found in the Secondary Passage. The angular inclusion of the Triage Waiting room/zone proposes a stronger network link than the visual connectivity analysis suggests and will be confirmed by the gate count analysis and observation simulation.* | *The zones with the shortest direct connection within the network routes are: Nurses' Station, Main Passage and Triage Waiting rooms/zones. Secondly: Trolley and Resus. No evident clusters of network connectedness are found. The angular inclusion of the Triage Waiting and the Triage Consult rooms propose a stronger network link than the visual connectivity analysis confirmed by the gate count analysis and observation simulation.* |
| | **GIS simulation findings (Gate Cross, Internal Flow and Occupancy)** | |
| | (KDH Gate Cross: Passage Main, Nurses' Station, Trolley, Resus, Triage Consult 1, Nebulisation, Triage Waiting, Triage Consult 2, Procedure)<br><br>The base plan and GIS GC identified the same three rooms with the highest grade, followed by the Resus room/zone. The angular inclusion potential indicated a stronger network link in the base plan, but the observed GC presented a weaker, less active network link and association. | (MPH Gate Cross: Nurses' Station, Passage Main, Triage Wait, Trolley, Resus, Triage Consult 1, Triage Consult 2, Nebulisation, Procedure).<br><br>The base plan and GIS GC identified the same three rooms with the highest grade, followed by the same secondary rooms. From the GC it was found that the Triage Consult rooms/zones were still graded the lowest but were connected to the network of spaces. |
| 2 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *The most integrated spaces globally in the KDH network are: The Nurses' Station and Trolley room/zone, followed by Resus and Nebulisation. Triage Consult and Procedure are the least integrated. The low through- movement correlation confirms this statement, but the linear spatial planning confirms a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90.* | *The most integrated spaces globally in the MPH network are: Trolley, Nurses' Station, Main Passage and Triage Waiting, followed by Resus. Triage Consult, Nebulisation and Procedure are the least integrated. The low through-movement correlation confirms this statement, but the linear spatial planning confirms a visual and flow integration correlation with an $R^2$ value of 0.58; however, the global network is well integrated at an $R^2$ value of 0.80-0.90.* |
| | **GIS simulation findings (Gate Cross, Internal Flow and Occupancy)** | |
| | (KDH GC: Passage Main, Nurses' Station, Trolley, Resus, Triage Consult 1, Nebulisation, Triage Wait, Triage Consult 2, Procedure), (KDH IF: Nurses' Station, Passage Main, Trolley, Resus, Nebulisation, Triage Consult 1, Triage Waiting, Triage Consult 2, Procedure).<br><br>In both KDH and MPH a high correlation of 90% was found between the IF and GC per season. | (MPH GC: Nurses' Station, Passage Main, Triage Wait, Trolley, Resus, Triage Consult 1, Triage Consult 2, Nebulisation, Procedure), (KDH IF: Nurses' Station, Passage Main, Triage Wait, Trolley, Resus, Nebulisation, Triage Consult 1, Triage Consult 2, Procedure).<br><br>In both KDH and MPH a high correlation of 90% was found between the IF and GC per season. |
| 3 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *Considering spatial depth and integration (potential human flow and movement), the KDH network can be graded from most to least as follows: Nurses' Station, Main Passage and portions of Trolley extending into the Triage Passage at the Triage* | *Considering spatial depth and integration (potential human flow and movement), the MPH network can be graded from most to least as follows: Nurses' Station, Trolley, Main Passage and Triage Waiting. Second are the Resus and Nebulisation rooms/zones. The* |

| | | |
|---|---|---|
| | *Consult rooms/zones, followed by Trolley, Resus and Nebulisation. The Procedure room is not integrated. A micro integration occurs between the two Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.90.* | *procedure room is not integrated. A micro integration occurs at the Triage Consult rooms. The global network is well integrated at a correlation $R^2$ value of 0.83.* |
| | **GIS simulation findings (Gate Cross, Internal Flow and Occupancy)** | |
| | No discussion | |
| 4 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness, as was found at KDH.* | *Comparing potential flow and potential gate cross (entry and exit values) should indicate similar values of connectedness, as was mostly found at MPH. (The VGA indicated lower connectedness than the axial mapping suggests, i.e. the Trolley and Triage Waiting rooms/zones were indicated as less visually connected, but the axial mapping showed higher integration.)* |
| | **GIS simulation findings (Gate Cross, Internal Flow and Occupancy)** | |
| | (KDH GC: Passage Main, Nurses' Station, Trolley, Resus, Triage Consult 1, Nebulisation, Triage Waiting, Triage Consult 2, Procedure)<br><br>(KDH IF: Nurses' Station, Passage Main, Trolley, Resus, Nebulisation, Triage Consult 1, Triage Waiting, Triage Consult 2, Procedure) | (MPH GC: Nurses' Station, Passage Main, Triage Waiting, Trolley, Resus, Triage Consult 1, Triage Consult 2, Nebulisation, Procedure)<br><br>(MPH IF: Nurses' Station, Passage Main, Triage Waiting, Trolley, Resus, Nebulisation, Triage Consult 1, Triage Consult 2, Procedure) |
| 5 | *KDH (Base plan Table 7.7)* | *MPH (Base plan Table 7.7)* |
| | *KDH presents a statistically significant visual and flow correlation, with an integration and connectivity correlation value of $R^2$ 0.58. The KDH simulation shows a smaller central core through movement compared to MPH and was even less connected to the entire network of the A&E with an $R^2$ value of 0.26. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.90.* | *MPH presents a statistically significant visual and flow correlation with an integration and connectivity correlation value of $R^2$ 0.58. MPH simulation shows a central core through movement; however, it is not well connected to the entire network of the A&E, as is evident from the $R^2$ value of 0.43. Due to the linear spatial network design, the mean depth and integration value will be highly correlated, as is evident from the $R^2$ value of 0.83.* |

From the analysis the following findings are reported: For MPH, the base plan analysis indicated that a stronger network link would be found between the rooms, Triage Waiting and Triage Consult; however, this was not evident in the GIS GC analysis, implying a potential micro network between the Triage Consult rooms. Similarly, for KDH, the base plan presented a stronger network link than the observed GC (refer to item 1). For both MPH and KDH the internal flow observation and the base plan analysis found similar room types for primary, secondary and least activity spaces. Thus, the correlation of base plan versus observation is equitable. At both KDH and MPH a high correlation of 90% was found between the internal flow and the gate count per season, as well as room grading. Therefore, when comparing the observations to the base plan (overlaying VGA and axial map) as seen in Figure 34, which reflects a high correlation coefficient of integration into the global network, an $R^2$ value of 0.90 was found, similar to the GIS correlation. Thus, the base plan can be correlated with the GC and internal flow, as stated in Table 7.7. MPH indicated equitable levels of flow for both the Triage Waiting and Trolley, thus confirming the variation between the VGA overlay and the axial mapping. The axial map levels of integration are thus acceptable, and the base plan analysis is viable for future applications in planning projection.

# CHAPTER 8 MICROBIOLOGY

## 8.1 INTRODUCTION

Table 8.1 below is repeated; refer to section 7.1 for mutual shared information

Table 8.1 Room zone classification

| | |
|---|---|
| Z1 | Triage Consult 1 |
| Z2 | Triage Consult 2 |
| Z3 | Triage Waiting |
| Z4 | Procedure 1 |
| Z5 | Passage Main |
| Z6 | Nurses' station |
| Z7 | Resus [Resuscitation] |
| Z8 | Nebulisation |
| Z9 | Passage Secondary |
| Z10 | Trolley |
| Z11 | (Not indicated) refer to external sampling area 1 |
| Z12 | (Not indicated) refer to external sampling area 1 |

## 8.2 METHODOLOGY

The integrated literature review in section 8.2: methodology was developed from the literature analysis found in chapter 3, section 3.4. *Additional raw sequencing, analysis and datasets can be found in addenda AD 1, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 3, AD*). More consideration is given to papers that have conducted MoBE research. The main literature chapter 3 provides the selection criteria and methodology. Adams *et al. (*2015) report on the microbial sampling within the built environment. A comparison is made between 16 data sets on current BE microbial studies, published prior to May 2014, that employed High Through-put Screening (HTS) amplicon sequencing to target 16S rRNA genes in bacteria/archea or ITS/rRNA in fungi. The thesis author compiled a comparative matrix from 71+ papers, representing 16 surface sampling studies related to the built environment and 20 air (indoor and outdoor) sample studies related to the built environment. On sequencing techniques for the built environment, the author refers to the above noted matrix as well as a comparative study on sequencing techniques and technology for the indoor environment, compiled by Kelley and Gilbert (2013). Indicator species sampled in this study were compared to USA, European and published South African known literature data on most common HAI agents in hospital environments, noted in Table 8.2 below.

Table 8.2: HAI, Infection source and citation (Nice & Stone 2014)

| | Most common HAI | Related illness | Citation for reference |
|---|---|---|---|
| 1 | *Pseudomonas aeruginosa* | Wound infections, infected burn lesions, urinary tract infections | (Nseir, Di Pompeo, Pronnier, Beague, Onimus, Saulnier, Grandbastien, Mathieu, Delvallez-Roussel & Durocher 2002; Drugs.com 2017) |
| 2 | *Staphylococcus aureus* | Causes a wide variety of lung, bone, heart and bloodstream infections and is frequently resistant to antibiotics | (Claesson 2010; Nseir *et al.* 2002; Ducel *et al.* 2002; Drugs.com 2017) |

| | | | |
|---|---|---|---|
| 3 | *Acinetobacter baumannii* | Can cause serious infections in the lungs, blood and brain. It may also cause urinary tract and wound infections | (Nseir *et al.* 2002; Drugs.com 2017) |
| 4 | Legionella | Causes pneumonia | (Taylor, Ross & Bentham 2009; Ducel *et al.* 2002; Drugs.com 2017)http://www.drugs.com/cg/acinetobacter-baumannii-infection.html |
| 5 | *Pneumocystis carinii pneumonia* (PCP) | Causes inflammation and fluid build-up in the lungs | (Stringer, Beard, Miller & Wakefield 2002; Drugs.com 2017) |
| 6 | *Streptococcus pneumoniae* | Causes pneumonia | (Murray 2005; Drugs.com 2017) |
| 7 | *Pneumocystis jirovecii pneumonia* | Causes pneumonia | (Murray. 2005; Drugs.com 2017) |
| 8 | *Enterococcus faecalis* | Urinary tract infections and blood in heart lesions | (Claesson 2010; Drugs.com 2017) |
| 10 | *Cocci* | | (Claesson 2010) |
| 11 | *Coagulase negative staphylococci (CoNS)* | | (Claesson 2010) |

| **Most common HAI – USA specific** | | | |
|---|---|---|---|
| 1 | *Escherichia coli* | Causes infections of the urogenital tract and of neonatal meningitis | (Jarvis & Martone 1992; Ducel *et al.* 2002; Drugs.com 2017) |
| 2 | *Staphylococcus aureus* | Causes a variety of lung, bone, heart and bloodstream infections and is frequently resistant to antibiotics | |
| 3 | *Enterococci* | | |
| 4 | *Pseudomonas aeruginosa* | Wound infections, infected burn lesions, urinary tract infections | |
| 5 | *Coagulase-negative staphylococci* | | |
| **Most common HAI sources – USA specific** | | | **Citation** |
| 1 | Gram-positive organisms cause 65% | | (Wisplinghof, Bischoff, Tallent, Seifert, Wenzel & Edmond 2004) |
| 2 | Gram-negative organisms cause 25% | | |
| 3 | Fungi cause 9.5%. | | |

### 8.2.1 Guidance for developing a sampling strategy and sampling plan

*A sampling strategy includes the approach or combination of approaches used to select locations at which to collect samples and provides any relevant guidance to inform decision support and data interpretation processes. The sampling strategy is a high level or general document that guides the collection of samples for characterization (extent of contamination, differentiated zones or sectors based on use or airflow)* (Bryson *et al.* 2011:8)*. A sampling plan is an executable plan of action that addresses the sampling and analytical requirements of a specific situation and adheres to the specific sampling strategy. The sampling plan must specify the sampling approaches, methods, and analyses, as well as the number, types, and*

*locations of samples to be collected in a given physical space. The sampling plan should account for the area under consideration, the number of samples, and the collection locations needed for statistical confidence as determined by directed and/or statistical sampling designs…Directed sample collection utilizes an expert in the field (indoor environment engineer or microbial Ecologist) to determine the suitability of the plan to meet the experimental objectives. Statistical sampling utilizes a mathematical framework to determine if the number and location of sample collection sites meet specific characterization objectives* (Bryson *et al.* 2011:8).

### 8.2.2 Study zones and room types

For reference, the study zone drawings in section 7.1.2 are repeated here. See Table 7.1 and Figure 70 and Figure 71 below for study zones.

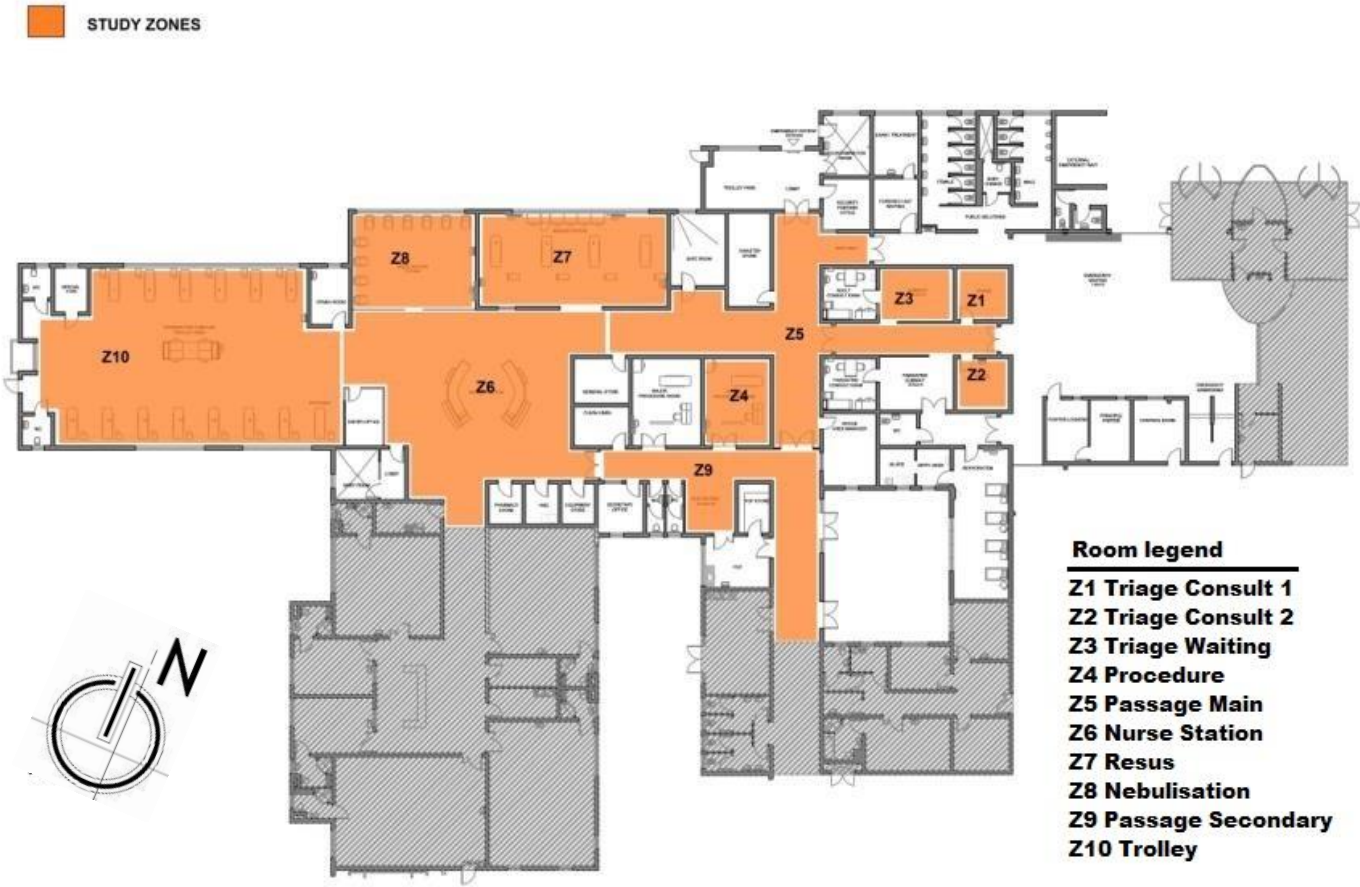



Figure 70: KDH A&E study zones (Figure 16)


Figure 71: MPH A&E study zones (Figure 17)

### 8.2.3 Microbiology methodology introduction

This microbiology methodology has been developed from a broad literature review that includes sampling, equipment, analysis, sequencing techniques, database selection and the selection of bioinformatics platforms. Furthermore, it refers to MoBE research and other comparable studies. A similar investigation was conducted by Meadow *et al.* (2014) and Kembel *et al.* (2014) in classrooms at Oregon University and Ramos *et al*. (2015) and Lax *et al.* (2017) into a hospital microbiome, USA. Adams *et al. (*2015) recommend in their metadata analysis on sampling for the indoor microbiome that standard methodologies for sampling and sequencing are imperative to facilitate the comparison of similar studies in future research. For this thesis, portions of the sampling and analysis methodologies applied by Hewitt *et al.* (2013) were adopted, and other studies and guidance from an extensive literature analysis were considered. Refer to Addenda 1 & 2.

### 8.2.4 Site sampling sterilisation protocol

Between each two samples, full on-site sterilisation to prevent sample contamination was conducted on the Bio-sampler inlet, outlet, tangential nozzles and collection vessel. Equipment was sprayed with a 70% ethanol solution and sterilised over a mini burner flame. Gloves were used at all times. Samples were poured (20ml) into sterile vials and stored on ice for the short term at between 0°C and 4°C. Samples were transported on ice in cooler boxes and stored overnight in a freezer at sub 0 degrees Celsius, and transported by flight in the cooler boxes on ice at between 0°C and 4°C. For final storage these were placed in a -20°C laboratory freezer at the University of Pretoria Genomic Laboratory. Care was taken to reduce the number

of times the samples were removed, as repeated thawing and refreezing of samples (bacteria) have been reported to reduce cell viability (Germann *et al.* 2013).

### 8.2.5 Pre-sampling tests

In the laboratory testing was performed prior to the sampling experiment, to test the equipment and to test the DNA extraction methodology. Pre-sterilisation mock runs were conducted before the study commenced. Pilot study samples were taken to test the selection of media. Results from the pilot study indicated that a longer sample period was required for sufficient biomass in buildings indoors (based on the results from electrophoresis and nanodrop on the DNA extracted test samples) when a low biomass was detected. The sample collection period was increased from 40 min to 60 min per zone. Similarly, the pilot samples used distilled water for sampling and “blank” samples were taken to site and returned and tested with the pilot samples. High levels of biomass were present IN the blank samples, indicating contamination. This finding was similar to the 2012 study by Kembel *et al.* in which liquid impinger samplers were used. Due to this finding the sample media were changed to molecular-grade UV filtered water sample types.

From the available literature on sampling study design the following sampling types were selected: Adams *et al.* (2015) recommend firstly that a common repeatable MoBE sampling strategy should be employed that would enable comparison with other studies and, secondly, that the number of samples should be increased. The sampling must consider airborne, dust, and surface microbes. Hospodsky *et al.* (2012) found a strong correlation between the surface sampled dust and the airborne microbiota, implying that the surface samples strongly represent the air microbiota. In addition to sampling indoors, outdoor samples are required for source tracking and to accurately define the source of indoor microbes. This has been done in a number of studies, i.e. Kembel *et al.* (2014) and Meadow *et al.* (2014). Adams *et al.* (2015) recognise that the choice of sampling must be determined by the particular research question. A time-resolve study would be more representative if vacuum filtration sampling were used than if sampling dust were collected. For this study a combination of sampling types was utilised to define a typical community and the active community. Adams *et al.* (2015) emphasise the importance of using kit control to check potential contamination of taxa when sampling, as is evident in many BE studies. They also recommend concurrently sequencing blank DNA extraction alongside all samples.

#### Surface sampling

According to the literature the majority of studies employed cotton surface swabs for surface sampling, while vacuum filtration was utilised less often, although also common. The swab method of collection was employed for surface sampling in this study. The thesis field work employed the sampling methodology from Hewitt *et al.* (2013), using dual-tip cotton swabs - supplier specification: Dual tip sterile cotton swabs (BBL CultureSwab™, catalog # 220135, Becton Dickinson, Sparks, MD). On flat surfaces approximately 120 $cm^2$ of surface area was swabbed. After sampling, the swab was placed in an ice box at between 0°C and 4°C and transported to the freezer for overnight storage at between 0°C and -10°C.

#### Indoor air sampling

For indoor air sampling the standard microbiology methodology and equipment were used. The literature indicates a large variation in air sampling types, the most common being the

Anderson impinger and other liquid impingers. Factors that influenced the selection of the air sampler include the flow/volume, the filter aerosol diameter and sampling media; these can, however, vary. The relationship between flow rate and time is of importance, especially in sensitive areas such as hospitals. High flow rates will better represent the resident microbial community. A high flow rate could potentially imply less time for sampling and vice versa. The literature indicates varying study methodologies, i.e. 2,0 L/m (eight hrs = 1000L), 4 L/m (eight hrs = 1920L), 28.3 L/m (0.05 hr), 12.5 L/m (five hrs), 3.5 L/m (six hrs), and 12.5 L/m (one hr = 1500L). In accordance with the recommendations for microbial study proposed by Adams *et al.* (2015), the study methodology of Meadow *et al. (*2013) and the study by Kembel *et al. (*2014) were applied for the surface sampling, as mentioned above. The only variation in the thesis study is the equipment used. The total volume of air sampled by Meadow *et al. (*2013) was 192 $m^3$, collected at four L/m for eight hrs.

For the thesis study, SKC™ liquid bio-samplers (resembling impingers) with sonic flow BioLite pumps were used (Manufacturer: SKC Ltd, Blandford Forum Dorset, UK). The flow rate was set at 12.5 L/m, maintained for one hour. Results from the pilot study indicated that a longer sample period was required for sufficient biomass in these environments (based on the results from electrophoresis and nanodrop on the DNA extracted which indicated a low yield). The sample collection period was increased from 40 min to 60 min per zone. Similarly, the pilot samples used distilled water for sampling. “Blank” samples were taken to site and returned and tested; high levels of biomass were present without sampling. This finding was similar to the 2012 study by Kembel *et al.* in which liquid impinger samplers were used. As a result, molecular-grade water which was UV filtered was used as sample medium.

### OUTDOOR AIR SAMPLING

Numerous MoBE research papers propose the need to sample the outdoor environment (Adams *et al.* 2015; Kembel *et al.* 2013; Meadow *et al.* 2014). Sampling the outdoor environment enables source tracking and defines whether the indoor sampling is from humans indoors or the outdoor environment. It allows the level of outdoor organisms infiltrating indoors to be determined. In fact, studies indicate a mean proportion of 59% outdoor compared to14% indoor air samples. Horner *et al.* (2004) collected outdoor samples 16 meters away from the entrance door of the study building and followed the same procedure as the indoor sampling conducted for this study, i.e. high-flow model sampling by impingers. Meadow *et al.* (2013) collected outdoor samples from four corners on the roof top of their research building, approximately 3m above ground.

For the thesis study, a SKC™ liquid bio-sampler (resembling an impinger) (Manufacturer: SKC Ltd, Blandford Forum Dorset, UK) with a sonic flow BioLite pump (Manufacturer: SKC Ltd, Blandford Forum Dorset, UK) was used. The flow rate of 12.5 L/m was maintained for 30 minutes. The pilot study indicated that a longer sampling time would be required to gain sufficient biomass. A sample collection period of 30 min for external sampling was then implemented. Two external samples were collected per day from each site. Both samples were collected on ground level, 15 meters away from the buildings, at two positions at opposite corners of the buildings, as the sites do not allow for access to the roofs of the A&E departments. This was done at both hospital sites.

### 8.2.6 SAMPLE ENVIRONMENTS

#### SURFACE SAMPLES

Surface samples were taken by swabs. A total of 120 $cm^2$ per swab was sampled. Each swab was swiped in the sample zone on various materials (high-touch and low-touch areas) and at various sites in the room (refer to Table 8.3 and Table 8.4). This was done consistently for each swab in that specific room zone environment for each of the four days of sampling per season. Refer to Table 7.2, Table 7.3, Table 8.3 and Table 8.4.

Table 8.3: Surface sample environments in KDH

| Zone room type | Area | Surface |
|---|---|---|
| KDH Z1 Triage Consult 1 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin |
| KDH Z2 Triage Consult 2 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, treatment couch | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| KDH Z3 Triage Waiting | Patient seating, wall | Various seat bases and backing plastic, bumper-rail wood, plastic frame |
| KDH Z4 Procedure 1 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, treatment couch | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| KDH Z6 Nurses' Station | HCW seat, HCW work table, top of cupboard, walls | Seat handle and backing plastic, bumper-rail wood, melamine table top, computer keyboard, plastic frame |
| KDH Z7 Resus | HCW work table, basin area, loose equipment, top of cupboard, treatment couch, window sill | Bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| KDH Z8 Nebulisation | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, treatment couch, window sill | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| KDH Z10 Trolley | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, patient bed, window sill | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |

Table 8.4: Surface sample environments in MPH

| Zone room type | Area | Surface |
|---|---|---|
| MPH Z1 Triage Consult 1 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin |
| MPH Z2 Triage Consult 2 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, treatment couch | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| MPH Z3 Triage Waiting | Patient seating, wall | Various seat bases and backing plastic, bumper-rail wood, plastic frame |
| MPH Z4 Procedure 1 | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, treatment couch | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| MPH Z6 Nurses' Station | HCW seat, HCW work table, top of cupboard, walls | Seat handle and backing plastic, bumper-rail wood, melamine table top, computer keyboard, plastic frame |
| MPH Z7 Resus | HCW work table, basin area, loose equipment, top of cupboard, treatment couch, window sill | Bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |
| MPH Z8 Nebulisation | Patient seat, basin area, loose equipment | Seat handle and backing of synthetic leather, bumper-rail wood, stainless steel equipment, plastic frame, ceramic basin |
| MPH Z10 Trolley | Patient seat, HCW work table, basin area, loose equipment, top of cupboard, patient bed, window sill | Seat handle and backing plastic, bumper-rail wood, melamine table top, pressed-wood cupboard, stainless steel equipment, plastic frame, ceramic basin, bed steel and material mattress |

### AIR SAMPLES

Air samples were taken from the centre of each room as far as possible, with consideration for the operational conditions of the hospital. Each sample was taken in the same location consistently, with consideration for the operational condition of the hospital. Refer to Figure 72 and Figure 73.

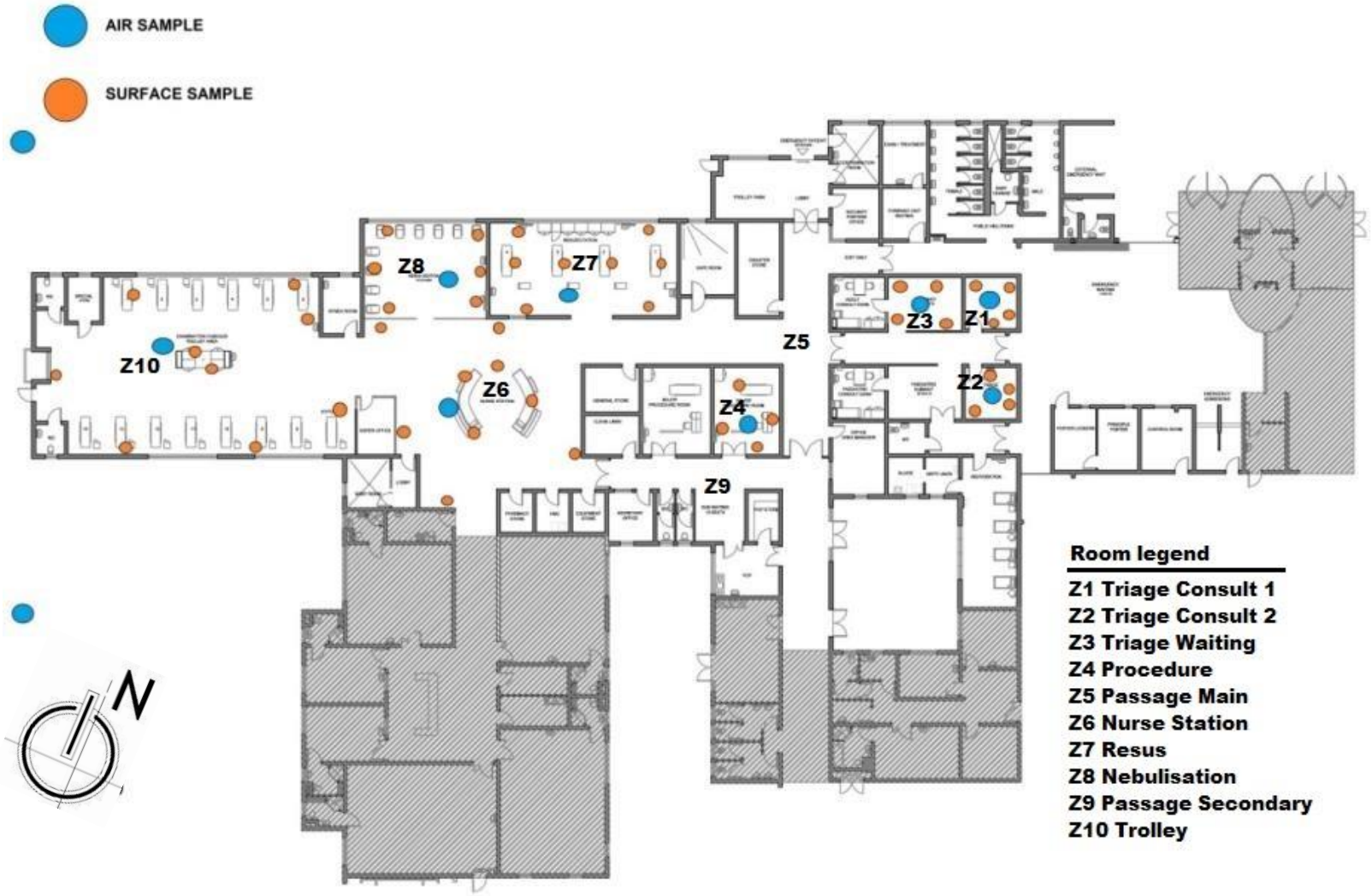



Figure 72: KDH microbial sampling zones, surface and air

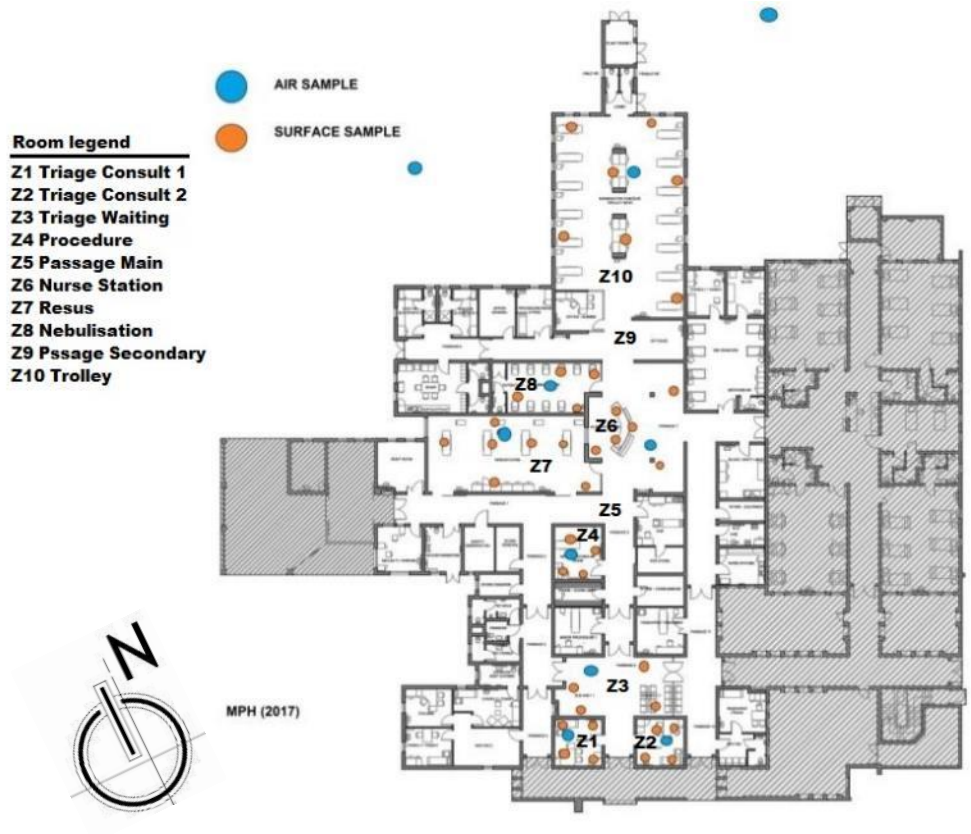



Figure 73: MPH microbial sampling zones, surface and air

### 8.2.7 Sampling duration and media

The sampling was conducted over two seasons, i.e. winter and summer, for four days per season. Two surface samples were taken once daily per zone, one for culture and the other for DNA; and for air once daily per zone. One additional air sample per hospital was collected daily for culture analysis. Only two air samplers were utilised, one at each site, which required consistent sequential sampling, unless unforeseen circumstances required a change as both sites were working hospitals (for more detail refer to 7.1.3).

#### Surface sampling media

The surface sampling area and media can vary from one study to the next. However, the most common surface sampling techniques, according to literature for the MoBE studies, were swabs and vacuum collection. Hewitt *et al.* (2012) used dual-tip culture swabs, sampling 120cm$^2$ of flat surface area per swab for a neonatal ICU which included keyboard, door handle, sink counter, etc. Rintala *et al.* (2008); Frankell *et al.* (2012); Horner *et al.* (2004); Kembel *et al.* (2014) and Hospodsky *et al.* (2012) all utilised the vacuum sampling method for surface dust sampling.

**Swab sample duration**: For this study, the swab sample duration is represented in surface area. This investigation followed the methodology of Hewitt *et al.* (2013) of 120 cm$^2$ per swab.

**Swab media selection**: For this study, the SKC™ Sterile Surface Swab Kit was used. The swabs are manufactured with rayon tips for good sample retrieval and absorption, and included are sterile swab transport tubes to contain the sample under transport (SKC™, Cat no: 225-2402).

### INDOOR AIR SAMPLING DURATION

The MoBE literature indicates a duration variation between sample studies. The duration is a factor of flow rate and time for collecting a sufficient number of airborne organisms. Many studies found that long sampling durations or high-volume sampling with high flow rates were required to collect sufficient biomass. High flow rate pumps are much louder and are a concern in sensitive environments such as hospitals. Considering the literature: 2,0 L/m (8hr = 1000L), 4,0 L/m (8hr = 1920L), 28.3 L/m (0.05hr), 12.5 L/m (5hr), and 3.5 L/m (6hr). For the thesis study 12.5 L/m (1hr = 1500L) was used. Meadow *et al.* (2013) used an 8 hr sampling period with a flow rate of 4,0 L/m, which allowed for a total volume of air collection of 1.92$m^3$ per classroom for 8 classrooms.

**The thesis indoor air sample duration:** With the proposed SKC™ bio-sampler and sonic flow BioLite pump 12.5 L/m flow was achieved, with a reasonably quiet air pump. Samples were collected in both hospitals simultaneously, using two samplers. To equate the Kembel *et al.* (2014) study of three consecutive days, as well as the Meadow *et al.* (2014) study, the thesis study sampled 750L per zone, which required 60 minutes of sampling time per zone/sample for four days, over two seasons. The total daily volume of air sampled was 15000L for the total of 160 project samples.

**The thesis indoor air sampling height:** The sampling height, as recommended by Kembel *et al.* (2012), was taken at 830mm above the level of the patient bed (equating to 1600mm above ground level), and in accordance with Meadow *et al.* (2014), was taken 900mm above ground. For this thesis a table height of 900mm above ground level was used.

### INDOOR AIR MEDIA SELECTION

The selection of a sample medium is dependent on the organism to be cultivated, type, size and the viability for PCR and other sequencing to be performed, as well as usability for the DNA extraction kit. The Meadow *et al.* (2014) study used 1.4µm pore diameter ester filters and Kembel *et al.* (2012) used molecular water for the impinger. Other studies used similar size pumps and liquid impinges such as Meadow *et al.* (2013), using 1.4µm diameter cellulose ester membrane filters sampling for any organism in the indoor environment at 4L/m (8hr). UC Oregon (2012) typically used both the 1.2µm diameter SKC mixed cellulose-ester membrane filters and sampled for any organism in the indoor environment at 4.0 L/m (5hr) and 0.4µm to 10µm diameter liquid impinge sterile water filtered with 0.22µm cellulose filter and sampled for any organism in the indoor environment at 12.5 L/m. UC Berkley (2012) used 1.2µm diameter pore size, SKC mixed cellulose-ester membrane filters and sampled for any organism in the indoor environment at 4.0 L/m (24hr). Kembel *et al.* (2012) used molecular grade water for impinges and sampled for any organism in the indoor environment at 12.5 L/m (1hr). Frankell *et al.* (2012) used 1µm diameter polycarbonate filters, and sampled for any organism in the indoor environment at 12.5 L/m (5hr). De Boer *et al.* (2006) used glass fibre filters, and sampled Pneumocystis organisms at 2.0 L/m (8hr).

**The thesis media selection**: As in the study by Kembel *et al. (*2012), the medium selected for the thesis study was molecular-grade water that had been UV treated. It is viable for PCR, culture, etc. For this study an SKC liquid (resembling an impinger) bio-sampler was used, with a sonic flow BioLite pump. The flow rate of 12.5 L/m was maintained for a sample collection period of 60 min per zone.

OUTDOOR AIR SAMPLE DURATION AND MEDIA

**The thesis outdoor air sample duration:** For this study the same procedure as for indoor sampling was followed for outdoor air sampling, using the SKC™ liquid bio-sampler. The recommended sampling period of 20 minutes for 250 L of air (Horner, Worthan & Morey 2004) was increased to 30 min due to the low biomass found in the pilot samples during DNA extraction. This was done for two zones per site per day, for four days and for two seasons, sampling a total of 4000 L of outdoor air for the total study.

### 8.2.8 SAMPLE SIZE

The literature as presented by Adams *et al. (*2015) indicates an average sampling quantity per collection type of 130 samples, ranging from three to 680 total samples collected. The number of zones collected from varied for each study. Below is a brief summary of the study variations. Air sampling days varied from 24hr, to three-day and nine-day studies. In all the studies the sampling time of 1hr, 5hrs, 6hrs and 8hrs implies a single sample per day for airborne microorganisms. Swab surface samples collected by Hewitt *et al.* (2012) occurred once for a total of 30 samples. Buttner *et al.* (2004) collected a single sample per different material for each of their study sampling methods. Rintala *et al.* (2008) collected four vacuum samples from each building, one per season. Frankel *et al.* (2012) sampled air once a week. They suggest that a day-long sampling measure is representative of a microorganism prevalence period of two months. Hospodsky *et al.* (2012) collected a single floor sample daily.

**The thesis sample size:** For this thesis investigation, and based on the literature consulted, a surface sample was collected with each air sample, excluding the outdoor air samples. The daily duration of sampling was an estimated 10 hours per site, and one hour per indoor sample and 30 minutes per outdoor air sample. The samples were collected by starting and ending at the same time at both facilities. Refer to Figure 72 and Figure 73 for sampling zones. In summary: Eight surface samples were taken per day (for four days) per hospital, one per zone for eight zones, i.e. a total of 64 samples per season for both hospitals, plus an additional surface sample per room for culture purposes. Refer to Table 8.3 and Table 8.4 for zone and area of surface sample. Indoor air samples were taken daily over four days: One air sample per zone for each of the eight zones at each hospital in both sample seasons (i.e. a total of 64 samples per season) plus one additional indoor air sample per day per hospital for culture purposes (total of only 4 samples per hospital per season). Two outdoor air samples were taken per day at both hospitals for four days per season, i.e. a total of 16 outdoor air samples over two seasons. It is noted that in this study both the number of samples and the sampling duration differ between outdoor and indoor sampling sites, and as such a direct comparison of microbial biomass between the two areas is not strictly valid. Identification and quantification of shared biota was the motivation.

Table 8.5: Total microbial samples per season - both hospitals combined

| | **Summer samples** | **Winter Samples** | **Total samples** |
|---|---|---|---|
| Indoor air samples: DNA | 64 | 64 | 128 |
| Surface swab samples: DNA | 64 | 64 | 128 |
| Indoor air samples: culture | 8 | 8 | 16 |

| | | | |
|---|---|---|---|
| Surface swab samples: culture | 64 | 64 | 128 |
| Outdoor air samples | 16 | 16 | 32 |
| **Total** | **216** | **216** | **432** |

### 8.2.9 SAMPLE STORAGE

At the site, samples were packed in cooler boxes filled with ice, and kept at between 0°C and 4°C. In the short term, samples were stored in the hotel fridge in cooler boxes at between -10°C and 0°C. During transport, for a period of five hours, the samples were packed in cooler boxes filled with ice, kept at between 0°C and 4°C, sealed, and checked into the cargo hold. In the long term, samples were stored at -20°C in the laboratory freezer. Long-term DNA samples were stored at between -20°C and -80°C in the laboratory freezer.

### 8.2.10 DNA EXTRACTION

There are various methods of DNA extraction; however, to maintain comparable results a single type of extraction for all samples needs to be considered, which would include both liquid-based sample collection and swab-based material kits. In addition, due to the variance in DNA extraction kits on sequencing results, it is recommended that the same kit is used for both applications.

In Kembel *et al.* (2014), whole genomic DNA was isolated from the samples using MoBio PowerLyzer™ PowerSoilH DNA Isolation Kit (MoBio, Carlsbad, CA), in accordance with the manufacturer's instructions but with the following modifications: bead tubes were vortexed for 10 min and solutions C4 and C5 were substituted for PW3 and PW4/PW5 solutions from the same manufacturer's PowerWaterH™ DNA isolation kit. In Meadow *et al.* (2013), whole genomic DNA was extracted using the MoBio PowerWater DNA™ Isolation Kit (MoBio Laboratories, Carlsbad, CA, USA) in accordance with the manufacturer's instructions but with the following modifications: air filters were incubated with Solution PW1 in a 65°C water bath for 15 min prior to bead beating. Bead beating length was extended to 10 min and samples were eluted in 50 ll Solution PW6. Paired filters underwent DNA extraction simultaneously.

**The thesis DNA extraction:** The PowerSoilH DNA™ Isolation Kit (MoBio, Carlsbad, CA) was used in accordance with the manufacturer's instructions and as follows. For liquid media samples: initial centrifuge of liquid impinge samples was done at 4000 G for 10 minutes at room temperature. It was, however, found by Nano Drop™ and electrophoresis that the levels of biomass and richness were too low. Subsequently all air samples in liquid media were filtered through 0.2 µm carbon filters/cellulose acetate/sotorius AG using a BioLite™ pump to extract liquid media and deposit residue organisms for DNA extraction. Dissected filter pieces were transferred back into the vial for DNA extraction. Between extractions, equipment was sterilised with a 70% ethanol solution and precipitated by burner flame. Samples were stored at -20°C. Prior to DNA extraction, carbon filters with sample media were cut into smaller pieces and placed into power bead tubes. This process was conducted in a ventilated cabinet, new sterile blades were used for each sample, and equipment was sterilised between each two samples using a 70% ethanol mix and precipitated by burner flame before DNA extraction by PowerSoilH™ kit.

For swab samples: The swabs were removed from the sterile housing, the housing discarded, and the swab cotton tip aseptically removed and placed into the power bead tubes. DNA

extraction by PowerSoilH™ kit was performed in accordance with the manufacturer's instructions. Post extraction, each DNA sample was checked for DNA, RNA and protein quantification with 1 µL of DNA using the Thermo Scientific NanoDrop™ spectrophotometers. Thereafter horizontal electrophoresis (Gel) was run for 35 minutes at 100 Volts. 4 µL of DNA was used per sample, with 2 µL of Gel red. The nucleic acid stain was visualised through the Gel imager to indicate DNA resolution. Low biomass was still shown in all cases. PCR amplification was performed on the samples to ensure biomass and quality; 100 samples were PCR amplified. Acceptable levels of DNA were found, after which the samples were sent for microbial metagenomics DNA sequencing by 16SrRNA. This was performed on the Illumina MiSeq 2x300 bp™ PE diversity assays for full community identification.

### 8.2.11 Sequencing and bio-informatics

Benjamin *et al.* (2013) recommend the use of metagenomics sequencing to define entire microbial communities in each sample, while Kelley and Gilbert (2013) further established the value of this sequence methodology for the built environment by finding that … *this technique enables broad observation of the taxonomic and functional genes from an entire community, without the bias associated with amplicon sequencing. With sufficiently deep sequencing, it is also possible to reassemble microbial genomes and other genetic elements* (2013:8). Yale University, Oregon University and UC Berkeley used PCR (amplicon sequencing) for their respective built environment studies. UC Berkeley further prescribes PCR for 16SPCR sequencing. In each of the mentioned studies, the objective was total community identification and characterisation. Smith *et al.* (2013) applied metagenomics with further culture identification, as suggested by other laboratories. Tringe *et al. (*2008) used 16s rDNA PCR analysis for 16s primers. Meadow *et al.* (2013) used Illumina amplicon sequencing of 16S rRNA genes for total community identification and the MoBio™ power water DNA isolation kit for whole genome DNA extraction. The V4 region of the 16S rRNA gene was amplified, the PCR 1 and PCR 2 processes were followed, and the raw sequences were processed using the FastX™ Toolkit and the QIIME™ pipeline.

The Hewitt *et al.* (2013) ICU indoor study also utilised 16S rRNA sequencing and amplification. This was performed for all swab samples collected by pyrosequencing, conducted on a 454 Life Science FLX™ Genome Sequencer. Hewitt *et al.* (2013) also used the QIIME™ database for analysis. They note that a substantially larger diverse community was found using 16S rRNA methods rather than typical culture-based methods. Kelley and Gilbert (2013) discuss the various sample processing and analysis methods applicable to the BE. The majority of the BE studies investigated bacterial diversity by sequencing 16S rRNA gene amplicons with much success. The limitation, however, is not being able to identify viability, as this would require culturing via PCR. Hewitt *et al.* (2013) mention the limits of using amplicon sequencing. For this thesis it is noted under section 8.2.14: Experiment delineations. Hewitt *et al.* (2013) suggest using Shotgun™ metagenomics and whole-genome sequencing; these are both costly and unaffordable for this study, and potentially many others. Lastly, Adams *et al. (*2015) compiled a literature review of 23 studies that utilised 16S rRNA sequencing (by 454 Illumina platforms) data. The majority of studies used the Illumina Miseq™ platform and targeted the V4 515f_806r primer region, while some targeted the V1-V2 27f_338r region. Most of the studies used the Qiime™ database.

**This study's sequencing and bio-informatics:** Based on the literature, and constrained by cost considerations, this study performed culture analysis with selected media to detect growth

of identified HAI indicator organisms – refer to section 8.2.13, Table 8.6 and Table 8.7 for figures for culture and sequencing. This was followed by colony identification via the MS VITEK™ mass spectrometer and protocol for sequencing. DNA-extracted and PCR-checked samples were sent for microbial metagenomics DNA sequencing by 16S rRNA, performed on the Illumina MiSeq™ 2x300 bp PE diversity assays for full community identification. As noted, Pyrosequencing and Shotgun metagenomics were not financially viable for this study. The V4 515f_806r primer region (illCUs515F GTGYCAGCMGCCGCGGTAA; new806RB GGACTACNVGGGTWTCTAAT) was targeted due to the broad range of the illcus515-new806R assay (Note: It has a few biases but achieves more than 95% coverage overall). The QIIME™ database was used on the Illumina Miseq™ platform. Final analysis was done on QIIME™ 1.9.1 64-bit (MD5: 0c30d069dadaa4e8f3acda11d7df54eb).

Table 8.6: Total planned samples for sequencing

| | **Summer samples** | **Winter samples** | **Total sequences** |
|---|---|---|---|
| 16S rRNA planned | 144 | 144 | 288 |
| Culture Vtec planned | 72 | 72 | 144 |

Table 8.6 shows the number of samples taken; however, the final number of colonies identified from samples increased the number of cultured samples. Similarly, the final number of samples sequenced for DNA decreased due to sample loss (from storage) and low biomass. Table 8.7 indicates this variation. Table 8.8 specifies the organisms that were intentionally cultured for viable identification.

Table 8.7: Total actual samples sequenced

| | **Summer samples** | **Winter Samples** | **Total sequences** |
|---|---|---|---|
| 16S Runs actual | 143 (-1) | 140 (-4) | 283 (-5) |
| Culture Vtec™ actual | 146 (+74) | 116 (+44) | 262 (+118) |
| Culture Vtec™ negative samples | 16 | 36 | 52 |

Table 8.8: HAI identified indicator organisms for culture identification

| |
|---|
| *Staphylococcus aureus* (surfaces) |
| *Pseudomonas aeruginosa* (surfaces) |
| *Pneumocystis carinii* pneumonia (PCP) (air) |
| *Mycobacteria tuberculosis* (air) |

### 8.2.12 Analysis and Sequence processing

#### Sequence processing

Raw Illumina sequence data were processed using QIIME™ v1.8.0 (Caporaso, Kuczynski, Stombaugh, Bittinger, Bushman, Costello, Fierer, Pena, Goodrich, Gordon, Huttley, Kelley, Knights, Koenig, Ley, Lozupone, McDonald, Muegge, Pirrung, Reeder, Sevinsky, Turnbaugh, Walters, Widmann, Yatsunenko, Zaneveld & Knight 2010). Briefly, sequences that were <200 bp, contained more than 2 ambiguous characters, and had quality scores <20, were excluded

from further downstream analyses. Chimeric sequence detection and OTU selection at 97% sequence similarity were conducted using USEARCH v6.1. Taxonomies were assigned to each OTU using the RDP Naïve Bayesian Classifier with the SILVA-ARB (release 123) SSU databases for 16S rRNA. OTUs of which the classifications did not match their expected taxonomic kingdoms (bacteria) were removed. Singletons were excluded and each sample was randomly subsampled (rarefied) to the same number of sequences per sample.

#### ANALYSIS

OTU richness and diversity indices (richness, Shannon, inverse Simpson and Chao1 evenness), together with rarefaction curves were calculated using the vegan package by Oksanen, Guillaume, Friendly, Kindt, Legendre, McGlinn, Minchin, O'Hara, Simpson, Solymos, Stevens and Szoecs (2007) referenced from Kamutando, Vikram, Kamgan-Nkuekam, Makhalanyane, Greve, Le Roux, Richardson, Cowan and Valverde (2017) and phyloseq package (McMurdie & Holmes 2013) for R, developed by the R development core team (2013). Futhermore a mixed model ANOVA was applied to determine significant differences in microbial diversity. In these analyses, hospital was specified as a random factor. Abiotic data were standardised and pair-wise distances computed based on Euclidean distances. Community data matrices were Hellinger-transformed and the Bray-Curtis distance measure was used to generate a dissimilarity matrix (Kamutando, Vikram, Kamgan-Nkuekam, Makhalanyane, Greve, Le Roux, Richardson, Cowan & Valverde 2017). The effect of abiotic data in explaining variation in microbial community structures was assessed by PERMANOVA (Anderson 2001), implemented in the adonis function of the vegan package. The reason the "adonis" method was used is that adonis can accommodate both continuous and categorical predictors and their interactions.

### 8.2.13 CULTURE SAMPLE ANALYSIS

**This study's culture sample analysis:** the MS VITEK™ protocol and identification methodology was used, performed by Aspirata (Pty) Ltd. Laboratories. The following section is an excerpt from the report by Aspirata Laboratories on the process that was followed to perform the identification, as requested by the author for culture sequencing. *VITEK MS™ – This is a mass spectrometer that is used to obtain data about microbial samples. It operates in conjunction with the acquisition station software on the acquisition station. The VITEK MS™ is a MALDI TOF™ mass spectrometer that uses MALDI (Matrix-assisted laser desorption ionization), which is the process used to ionize a sample into the gas phase. When identifying the plates, the slide is prepared using a freshly prepared (24 hour) plate with Ecoli ATCC 8739 used as the QC organism in determining the working condition of the MS VITEK™. The matrix CHCA is used to smear the spot on the slide, thus making a suspension to be identified. If the plates fail, they can be re-streaked and repeated on the MS VITEK™ to determine the organism, giving a 99.9% accuracy. If the QC culture (Ecoli) fails (Red spot) the MS will not identify any spot on the test spots.*

*During the identification process, the following steps take place: A pulsed laser beam is directed on to the sample. Energy from the laser beam desorbs and ionizes the sample. Extraction plates provide high-voltage electrical fields to accelerate the ionized particles upwards through the flight tube. An ion lens focuses the ions. Deflector plates steer the ions on a path towards the linear detector at the top of the flight-tube. An ion gate blanks out low mass ions (for example, derived from matrix). The detector detects the ions directly from the sample (lower-molecular weight ions followed by higher-molecular weight ions). Ions hitting*

*the detector cause the electrical signal which is recorded. The recorded signal is processed by the software and presented as a spectrum of intensity versus mass, in Daltons (Da). The organism is thus identified giving a percentage it matches to. Highly comparable organisms give a 99.9% confidence* (Aspirarta 2017).

The preparation of culture samples for colony extraction for identification was performed in the CSIR Natural Resources and the Environment Laboratory by Wouter Le Roux. This section is an excerpt from personal communication from Le Roux (2017) on the process followed to perform sample preparation and culture and colony extraction and submission, as requested by the author for culture sequencing: *Swab samples were stored at 4°C until being processed. During analysis the cotton tip was aseptically removed from the shaft and placed inside a sterile 1.5 ml microcentrifuge tube (Quality Scientific Plastics, USA). Phosphate buffered saline (PBS) was prepared from commercial PBS tablets (Sigma Life Science, USA) and heat sterilized by autoclaving, and 500 µL of PBS was added to each swab-containing microcentrifuge tube. The cotton tips were incubated in the PBS buffer for 30 minutes at room temperature (22°C +/- 2°C), and vortexing was used to dislodge and re-suspend bacteria. Subsequently 100 µL of the PBS buffer from each microcentrifuge tube was used to spread-plate onto sheep's blood agar plates (OXOID, England); the agar plates contained erythrocytes at a concentration of 5% and were prepared by Thermo-Fisher Scientific (Johannesburg, South Africa). The blood agar plates were incubated overnight at 35°C. The resultant bacterial growth was sub-cultured onto new blood agar plates by selecting morphologically distinct colonies. The colonies were selectively streaked out (only one type per agar plate) using a sterile inoculation loop. The agar plates containing the sub-cultured colonies were incubated at 35°C overnight. Selective sub-culturing from the original spread-plate was performed within seven days, with the cultured spread-plates stored at 8°C until utilized. Sub-cultured blood agar plates were stored at 8°C until Matrix-Assisted Laser Desorption/Ionization. Time-of-Flight Mass Spectrometry (MALDI-TOF MS™) was utilized to identify the bacterial pure cultures. MALDI-TOF MS™ identification was performed by Aspirata (Pty) Ltd (Centurion, South Africa) using a VITEK® MS instrument.*

*Liquid water based media samples: Initially water samples were processed in two ways. Firstly, by spread-plating 100 µL of the un-concentrated water sample onto sheep's blood agar plates (as done with the PBS buffer from the swab samples). Secondly, the micro-organisms were concentrated by subjecting 10 µL of the water sample to centrifugation at 8000 G for 3 minutes; the supernatant was discarded and bacterial cells were re-suspended in 200 µL sterile PBS buffer (Sigma Life Science, USA). Spread-plating (using 100 µL of the re-suspension) was once again used to culture onto sheep's blood agar plates. Sub-culturing, storage and identification were performed in a similar fashion as that described for the swab samples. Water samples received subsequently were only processed using the first approach (direct spread-plating) as the concentration step led to over-grown agar plates when the concentration approach was used. Special note: For the first batch of samples (both swabs and water) spread-plating was also done onto Middlebrook 7H10 agar (BD™ & Difco™, USA) enriched with BBL™ Middlebrook OADC (BD™, USA). The media [are] designed for the selective isolation of Mycobacterium spp. However, all the swab and water samples contained other bacteria that rapidly overgrew the Middlebrook plates. Mycobacterium typically requires a week or more to grow to visible colonies; whereas the other bacterial species that were present swamped the agar plates within 48 hours. Subsequently the use of Middlebrook agar was discontinued.* (Le Roux 2017).

### 8.2.14 DELINEATION OF THE EXPERIMENT

1. The A&E core area within each unit was delineated as the investigation study zone. These areas experience the highest traffic levels and contain the highest number of functional spaces in the hospital. Cost and time considerations informed the study boundaries.
2. The selection of organisms for culture analysis was based on literature studies and the most common HAI, including high-burden airborne disease bacteria as per USA statistics, and disease burden as per WHO report for South Africa. HAI statistics for South Africa are largely unknown (Dramowski & Whitelaw 2017).
3. For air sampling it is assumed that the room air represents a well-mixed environment; where mechanical ventilation was utilised, on-site testing was conducted to confirm the airflow speed, ACH, and the pressure differential in certain rooms.
4. This experiment sampled for a maximum of four days only per season over two seasons.
5. The author accepts the known limitations for sequencing and analysis of Kelley and Gilbert (2013) as per literature: 1) *PCR bias; 2) Variable copy numbers per genome; 3) Limited taxonomic resolution; and 4) Indirect functional knowledge (that is, inference of community function through phylogenetic relationships).*

## 8.3 FINDINGS

### 8.3.1 TESTING THE HYPOTHESES

For reference, the hypotheses from Chapter 6 are repeated prior to discussing the investigation findings.

Primary research hypotheses:
Hypothesis A: Building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health architectural design, based on the biome composition (abundance and richness) of indicator organisms.

Therefore…

Hypothesis B: Social behavioural science studies which consider factors of human movement patterns, occupancy and functional use of space influence the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus, the indoor environmental factors of hospitals MPH and KDH influence the composition of both the micro (room level) and macro biome (building level) environments.

Secondary research hypotheses:
Sub-hypothesis A: The source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room;

&

Sub-hypothesis B: The levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.

### 8.3.2 THE FINDINGS

This section is the second of three sections dealing with the findings of the investigation. The findings presented in this section refer to the microbiology investigation. Lastly, the conclusions are measured against the research questions and presented in Chapter 10. Of the 288 samples collected, 175 randomly selected samples were analysed. The randomisation was done to reduce the number of samples to achieve an equitable number of samples (5 per room, season and hospital). The minimum read threshold per operational taxonomic unit (OTU) was 6493, with 4397 OTUs from 175 samples (where a single OTU represents a cluster of reads at 97% similarity). A p-value of 0.05 and lower was accepted. 113 6275 sequences were received, with 6493 sequences per sample (175). The 175 samples included 90 for KDH (45 summer, 45 winter) and 85 for MPH (40 summer, 45 winter). No Resus samples were assigned for summer for MPH due to technical challenges. The analysis of the sampling data will be presented as data from both hospitals combined into a single data set. The results are described from a macro site to a micro room level (Alpha, Beta and Gamma diversity) and, lastly, the conclusions are measured against the research questions and presented in 8.3.2 and Chapter 10

#### 8.3.2.1 ANALYSIS OF SEQUENCING

Alpha diversity refers to the diversity of each sample. Beta diversity represents the differences in the species composition among samples. Gamma diversity refers to the diversity of the entire landscape of all sample types combined (regional species pool). Based on an Alpha diversity analysis, a variation was noted in the number of taxa found in surface and air samples. This indicates that the surface samples alone do not reflect the air samples or the total Alpha community (see Figure 74). Considering the full samples set, it is evident that there is interaction between the season and the type of sample (air, surface). A tendency of increased OTUs in the air and surface samples was observed in winter ($P < 0.05$). Figure 75 classifies the major phyla and their relative abundance present in the community, both in the air and on the surfaces over the two seasons of study. An interaction between the season and the type of sample was found. Specific phyla were associated with air and surfaces, with a diverse (almost inverse) variation of each in winter and summer. The main phyla identified included Proteobacteria, *Firmicutes* and Actinobacteria. This finding, except for *Firmicutes,* aligns with other MoBE studies (Kembel *et al.* 2013). The relative abundance of *Firmicutes* increased in the air during summer and on the surface during winter. Actinobacteria also increased in the surface in winter, whereas the relative abundance of Proteobacteria increased in the air in winter and on the surface in summer. Refer to Table 8.17 for culture findings, organism by phylum association for comparison. From the data we can confirm a seasonal variation in the microbial community for both hospitals. It is also evident that the surface and air communities are sufficiently different and therefore require focused study for each in future studies. Not only is there variation, but the type of sample (air or surface) show seasonal relationships. The phyla identified indoors are similar to those of other MoBE studies; this contributes to the current theories and datasets for MoBE research.

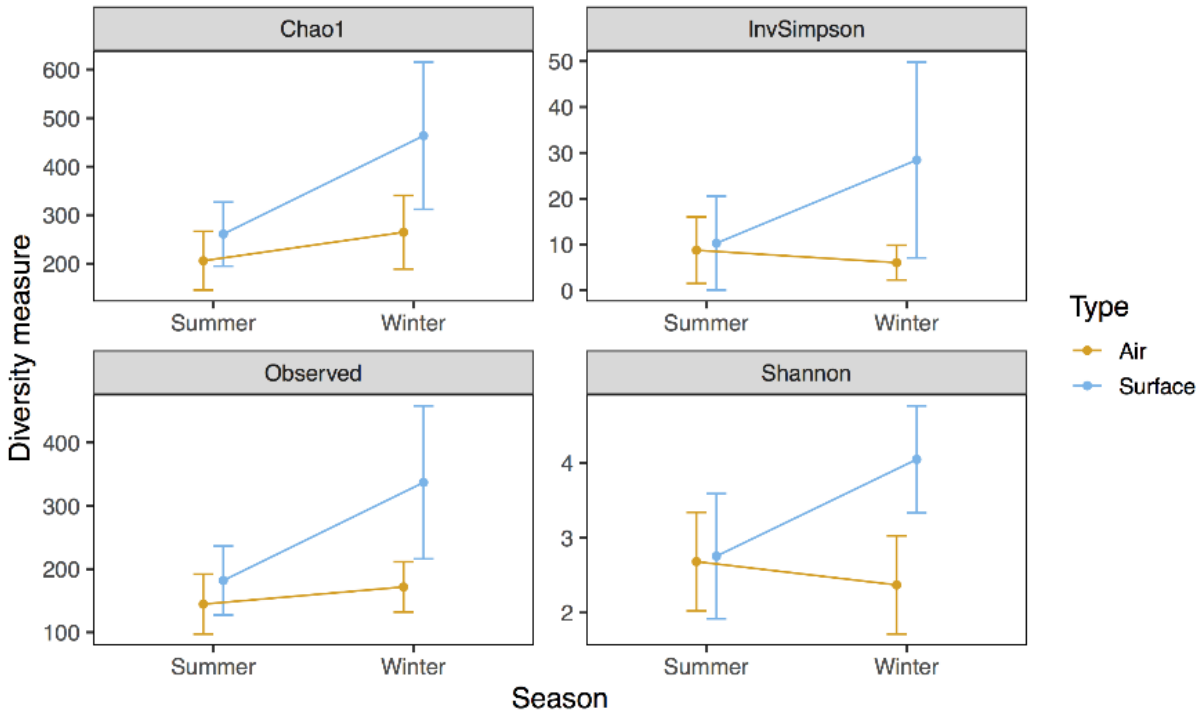



Figure 74: Alpha diversity for air and surface by season for KDH and MPH

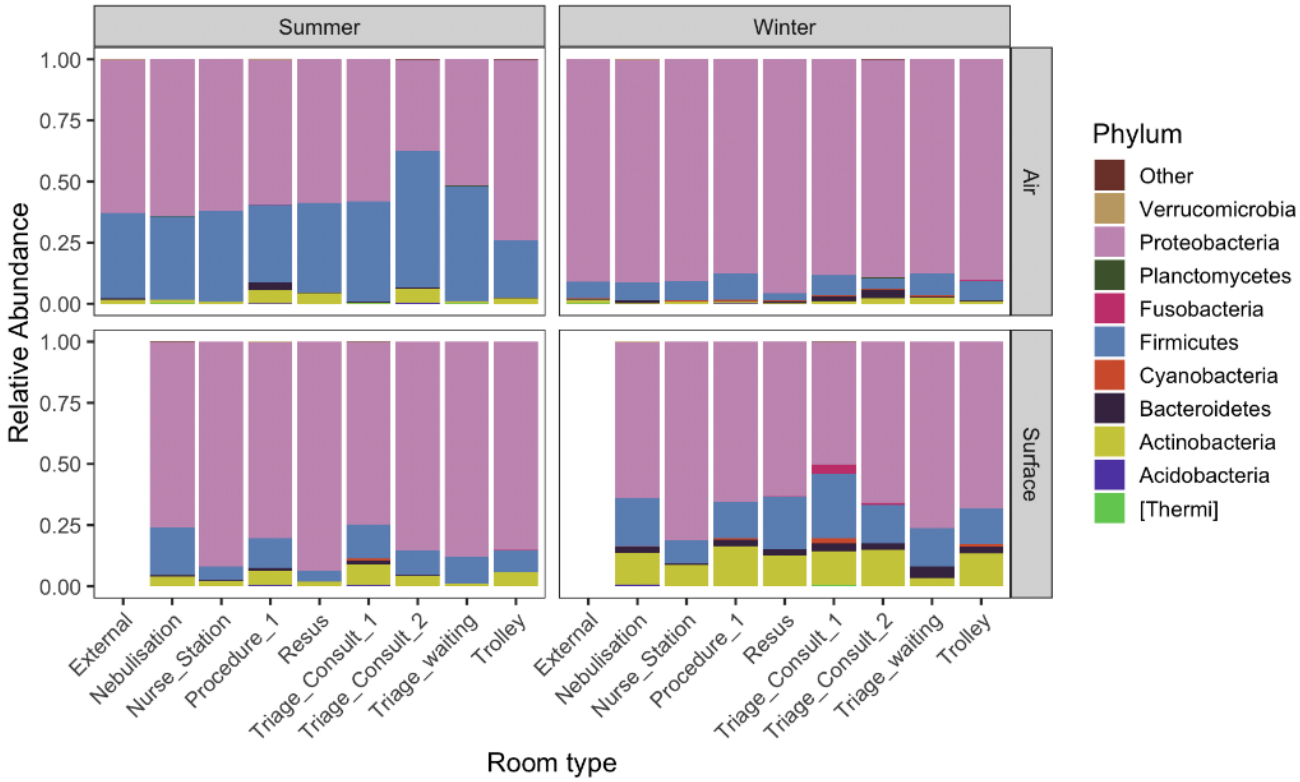



Figure 75: KDH & MPH classification of relative phylum abundance (air and surface, winter and summer)

Figure 76 depicts a principal coordinate analysis (PCoA) commonly used to reduce and represent patterns present in distance matrices displaying dissimilarities among objects or factors (Ramette 2007) in this sample type (air, surface) and season (summer and winter). The Beta diversity patterns in

Figure 76 indicate a notable dissimilarity in the air samples in summer and winter, thus a clear seasonal variation. The surface samples show strong similarity in both winter and summer. The variation explained by the Axis1 accounts for 5.8% of the total variation.

Figure 76 was generated from Bray-Curtis distances, using 175 randomised samples. A similar graphic (Figure 77) to that of

Figure 76 was generated, but with factor “hospitals” replacing factor “season”. This indicates that the two hospital communities had no effect, as corroborated by the Permanova results in Table 8.9.

Table 8.9: Non-parametric analysis dissimilarities

| Factor | Sums of Sqs | $R^2$ | Pr > F |
|---|---|---|---|
| Season | 2.093 | 0.03072 | 0.001 |
| Type (air & surface) | 2.776 | 0.04074 | 0.001 |
| Hospital | 0.451 | 0.00662 | 0.157 |
| Season: Type | 1.691 | 0.02483 | 0.001 |
| Season: Hospital | 0.445 | 0.00653 | 0.174 |
| Type: Hospital | 0.414 | 0.00608 | 0.344 |
| Season: Type: Hospital | 0.458 | 0.00673 | 0.122 |
| Note: Permanova test: p-values are from permutation tests involving 999 permutations, and are only reported down to 0.001 (Adonis Bray-Curtis distances) | | | |

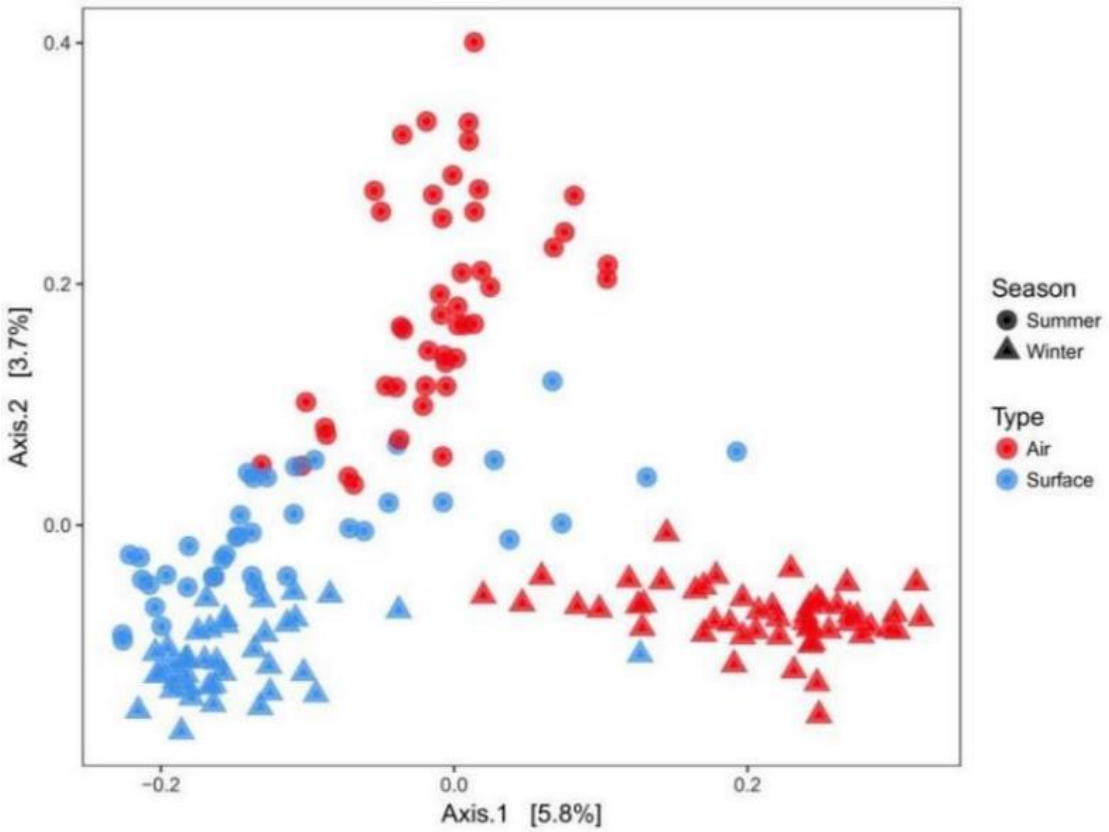
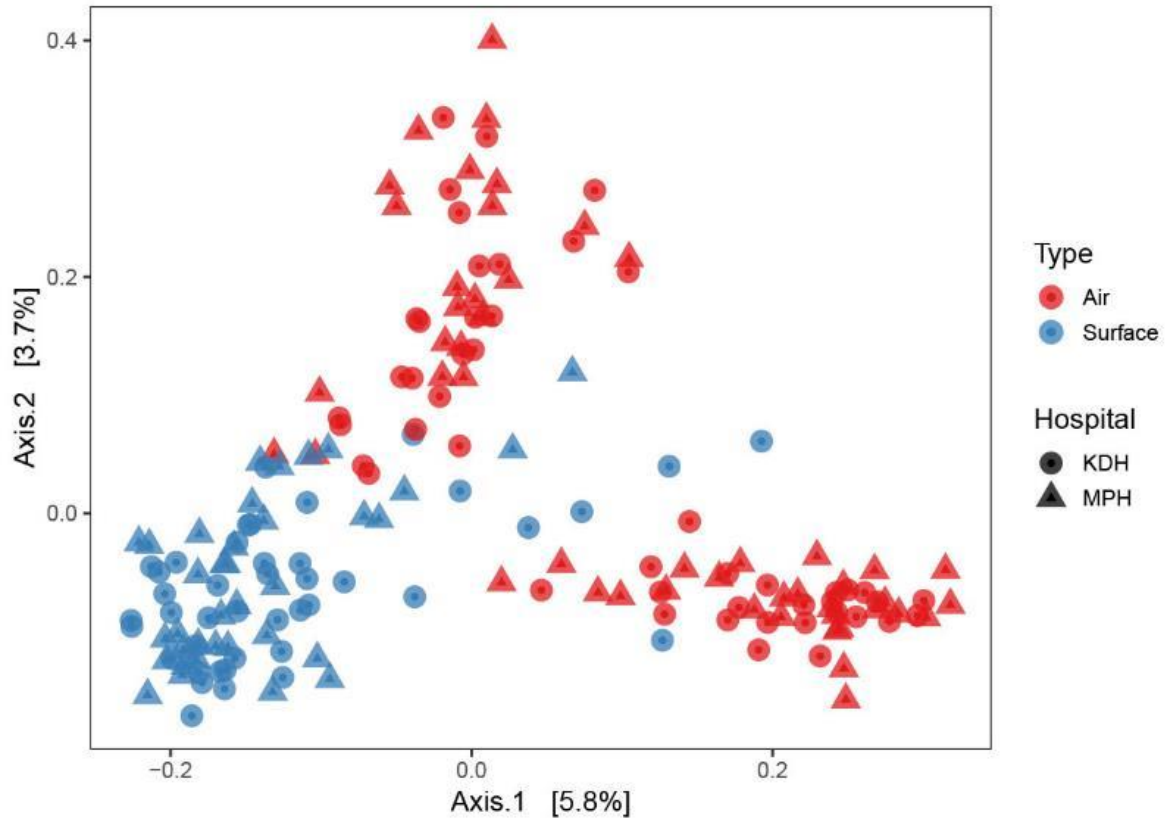



Figure 76: PCoA BETA Diversity for air, surface, summer and winter - factors for MPH and KDH




.

Figure 77**:** PCOA BETA DIVERSITY for air, surface and hospitals - factors for MPH and KDH

Figure 78 shows the distribution of the different classes within the Proteobacteria by season for each room type. It represents the full Gamma diversity of the hospital landscapes (biomes) for both KDH and MPH. All the rooms reflect high abundance of the class Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose of outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria (Kembel *et al.* 2013). This investigation showed little or no Alpha-Proteobacteria, but rather Beta-*Proteobacteria,* with Beta dominating in summer. Refer to Table 8.17 for Culture findings. The summer season indoor environment reflected outdoor sources, but the majority were Gamma-*Proteobacteria* attributed to indoor environments. It is therefore likely that the majority of indoor taxa are human source (further discussion on pp. 210-211). The Beta diversity findings indicate that MPH and KDH are not dissimilar and share a similar indoor microbiome.

Figure 79 below shows the composition of bacteria by sample type (air and surface) for each room type (for both hospitals). It represents the full Gamma diversity of the hospital landscapes (biomes) for both KDH and MPH. The most dominant class is evidently Gamma-*Proteobacteria*, with substantially lower abundance based on reads per OTU of Beta *Proteobacteria* and some rooms presenting Alpha-*Proteobacteria*. This was evident for both surface and air samples. The outdoor air taxa displayed a notably high abundance of Gamma-*Proteobacteria* and Beta *Proteobacteria,* with the Beta abundance far in excess of any in the internal rooms. Other MoBE studies found that the dominant taxa for airborne communities are Beta *Proteobacteria* (Kembel *et al.* 2013, 2014) whereas this thesis presents Gamma-*Proteobacteria* followed by a far lower relative abundance of Beta *Proteobacteria.* For surfaces, Gamma-*Proteobacteria* were found to be the most abundant. Alpha-*Proteobacteria* taxa were mostly found on the surfaces as compared to the air community. Delta–*Proteobacteria* and Epsilon-*Proteobacteria* taxa were not found on the surface or air communities.

Figure 80 indicates the relative abundance of the class *Firmicutes* seasonally. Figure 81 indicates the relative abundance by type of sample (air and surface). Seasonally, the class *Bacilli* predominate in both winter and summer in all room types including outdoors, followed by *Clostridia*. The summer season presents a higher relative abundance of *Bacilli* than winter. *Clostridia* has a higher relative abundance in winter than summer. There is an increase in the abundance of *Clostridia* for all spaces excluding the nurse station over the winter season. In Figure 81 the air samples (air community) reflect a higher abundance of *Bacilli* than the surface sample (surface community); in addition the surface samples present notionally higher *Clostridia* than the air samples on average per room. The outdoor samples present significantly more *Bacilli* than any indoor room. This study confirms the findings from other MoBE studies, indicating a high relative abundance of *Firmicutes* in surface and air samples (Kembel *et al.* 2013, 2014). The class *Bacilli* contains several well-known pathogens commonly found in indoor environments - refer to Table 8.17 for the culture findings and Figure 82 for the genus indicators.

The following taxa that relate to human skin have been derived from the literature, including MoBE associated studies (Lax *et al.* 2017; Grice *et al.* 2011; Cogen *et al*. 2008; Watanabe *et al.* 2018, Hospodsky *et al*. 2012; Van Rensburg *et al.* 2015). The literature reports four main phyla that strongly associate with human skin, namely: *Actinobacteria, Firmicutes, Proteobacteria,* and *Bacteroidetes*, all of which were found in this thesis study. It important to note that many members of these phyla are environmental, such as soil, and for this reason further identified present and abundant genera reported for skin were defined. The genera reported by these studies were *Propionibacterium, Corynebacterium, Staphylococcus, Micrococcus, Prevotella, Streptococcus, Acinetobacter, Brevibacterium, epidermidis, P. acnes,* and *Peptoniphilus*. Of these genera, the most commonly reported genera were *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus* and *Acinetobacter.* A common feature of gut and skin microbial communities is the low diversity at the phylum level, but high diversity at the species level. From the thesis study data, data set for indicator organism by room, the corresponding genera were identified. They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter*. They were globally reported and not by type (air or surface) or by season (winter and summer) but by room. Refer to Table 8.10 below. Due to the number and complexity of spaces sampled, source tracking was not technically feasible for this investigation. In a meta table produced by Adams *et al*. (2016:227) from reviewing multiple study data and findings, human-sourced bacteria indoor were reported to be up to 40% of the bacteria sampled indoors. In this study 65% of the organisms sampled did not match the outdoor biota and thus were present indoors and not outdoors. However, the quanta associated directly with human source will be fewer; most likely a generous estimation would be 25%. The human associated indicator species below were done using the indicator value (IndVal) index, which combines relative abundance and relative frequency of occurrence (Dufrene & Legendre 1997). In the table species that are in the 30 most common genera identified for air both KDH and MPH have been marked (a large percentage of the genera have been commonly identified), sourced from Table 8.13.

Table 8.10: Indicator genera by room type (for all hospitals), filtered by human skin associated only

| **Room/site** | **Phylum** | **Family** | **Genus** |
|---|---|---|---|
| External | *Firmicutes* | *Streptococcaceae* | **Streptococcus* |
| | *Actinobacteria* | **Corynebacteriacea* | **Corynebacterium* |
| Procedure 1 | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| Resus | *Firmicutes* | **Staphylococcaceae* | **Staphylococcus* |
| | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| | *Firmicutes* | *Peptostreptococcaceae* | **Corynebacterium* |
| | *Firmicutes* | *Streptococcaceae* | **Streptococcus* |
| Triage consult 1 | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| Triage consult 2 | *Proteobacteria* | *Moraxellaceae* | *Acinetobacter* |
| | *Firmicutes* | *Staphylococcaceae* | *Jeotgalicoccus* |
| | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| | *Actinobacteria* | *Micrococcaceae* | *Microbispora* |
| Triage waiting | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacteriaceae* |
| | *Actinobacteria* | *Micrococcaceae* | *n/a* |
| | *Firmicutes* | **Staphylococcaceae* | **Staphylococcus* |
| Nebulisation | - | - | - |
| Nurse Station | - | - | - |
| Trolley | - | - | - |
| ** indicates a top 30 most common genera identified in surface and air for KDH and MPH* | | | |

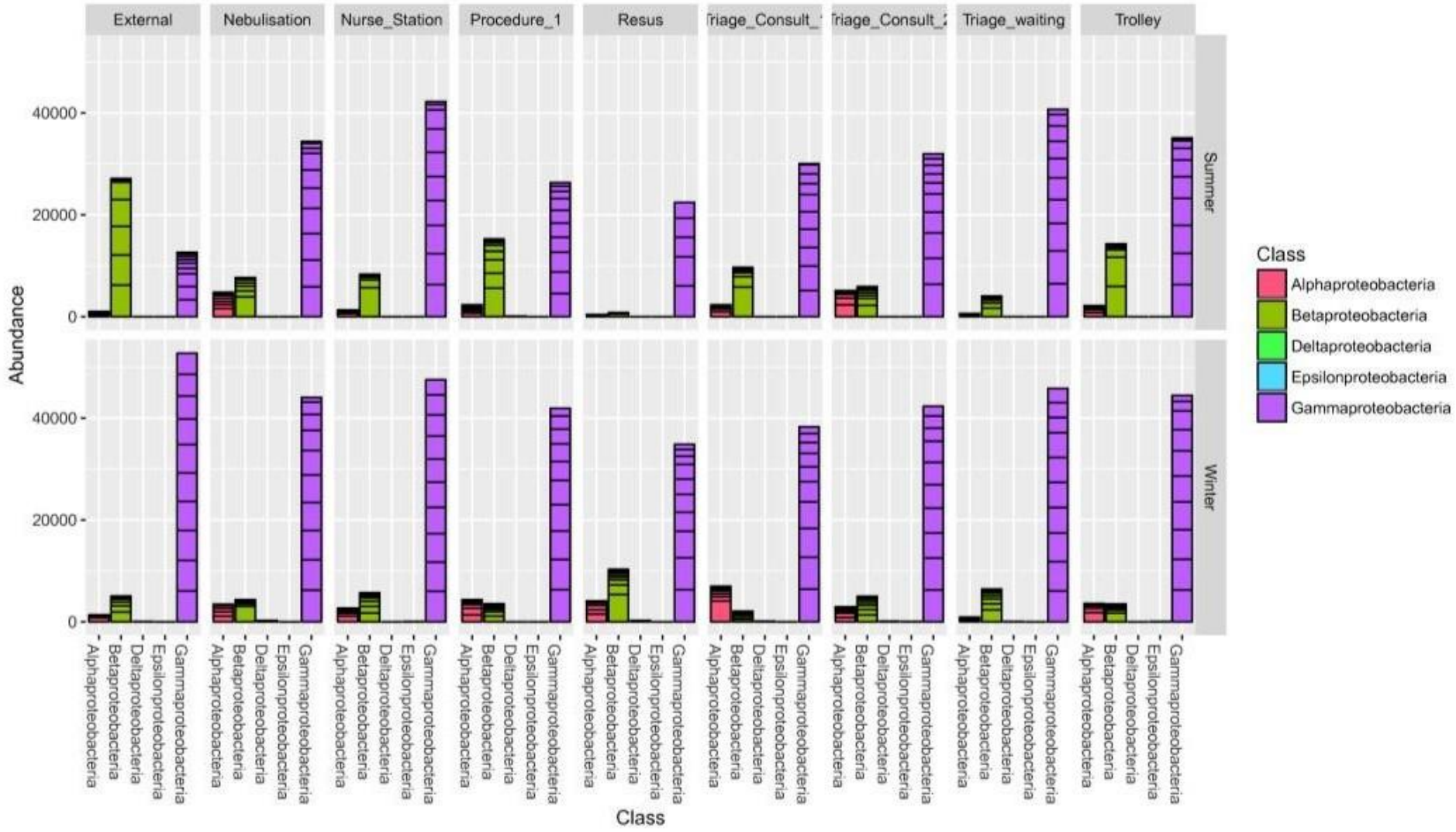



Figure 78: Relative abundance of Gamma diversity *Proteobacteria* per class, by room and season

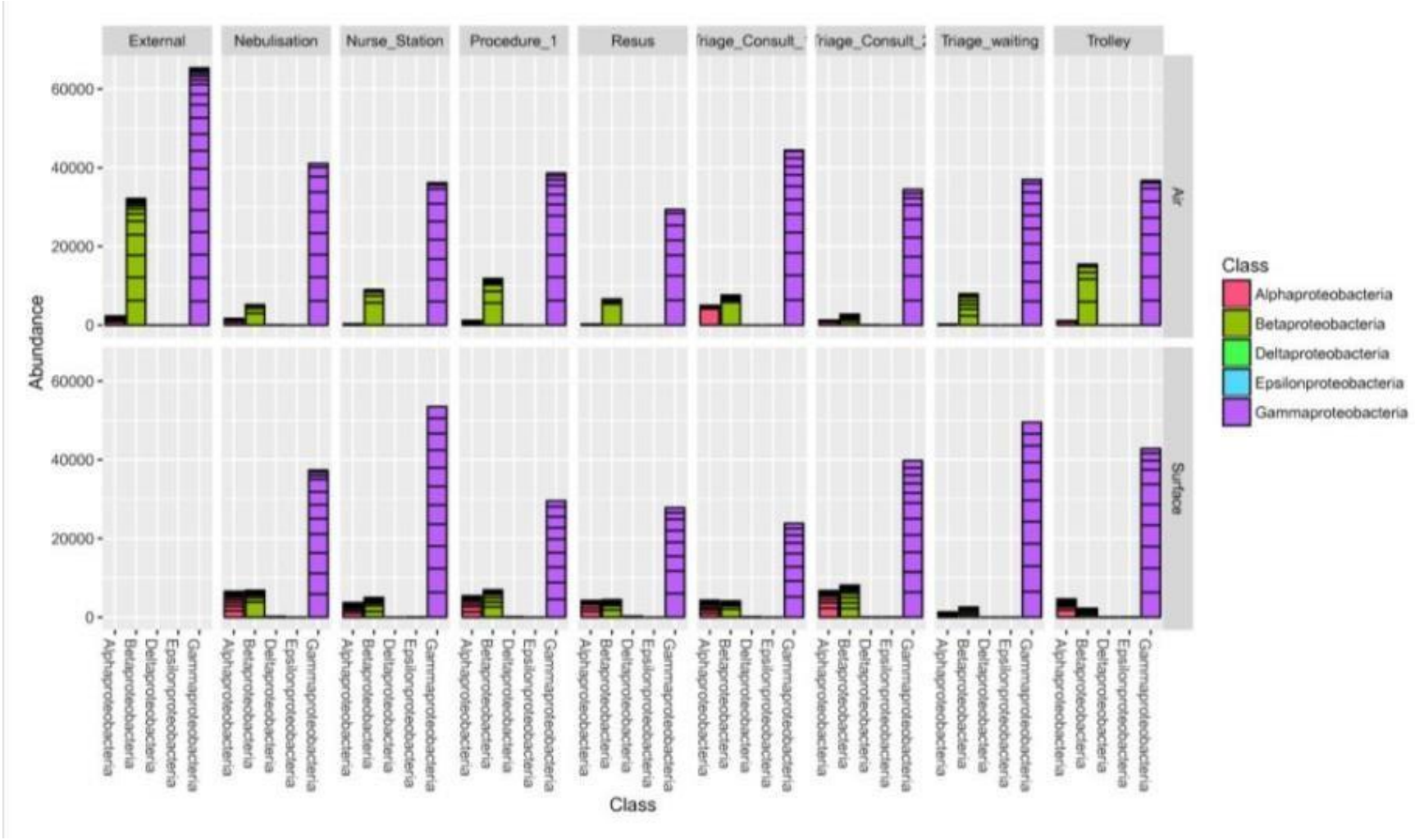



Figure 79: Relative abundance of Gamma diversity *Proteobacteria* per class, by room, air and surface

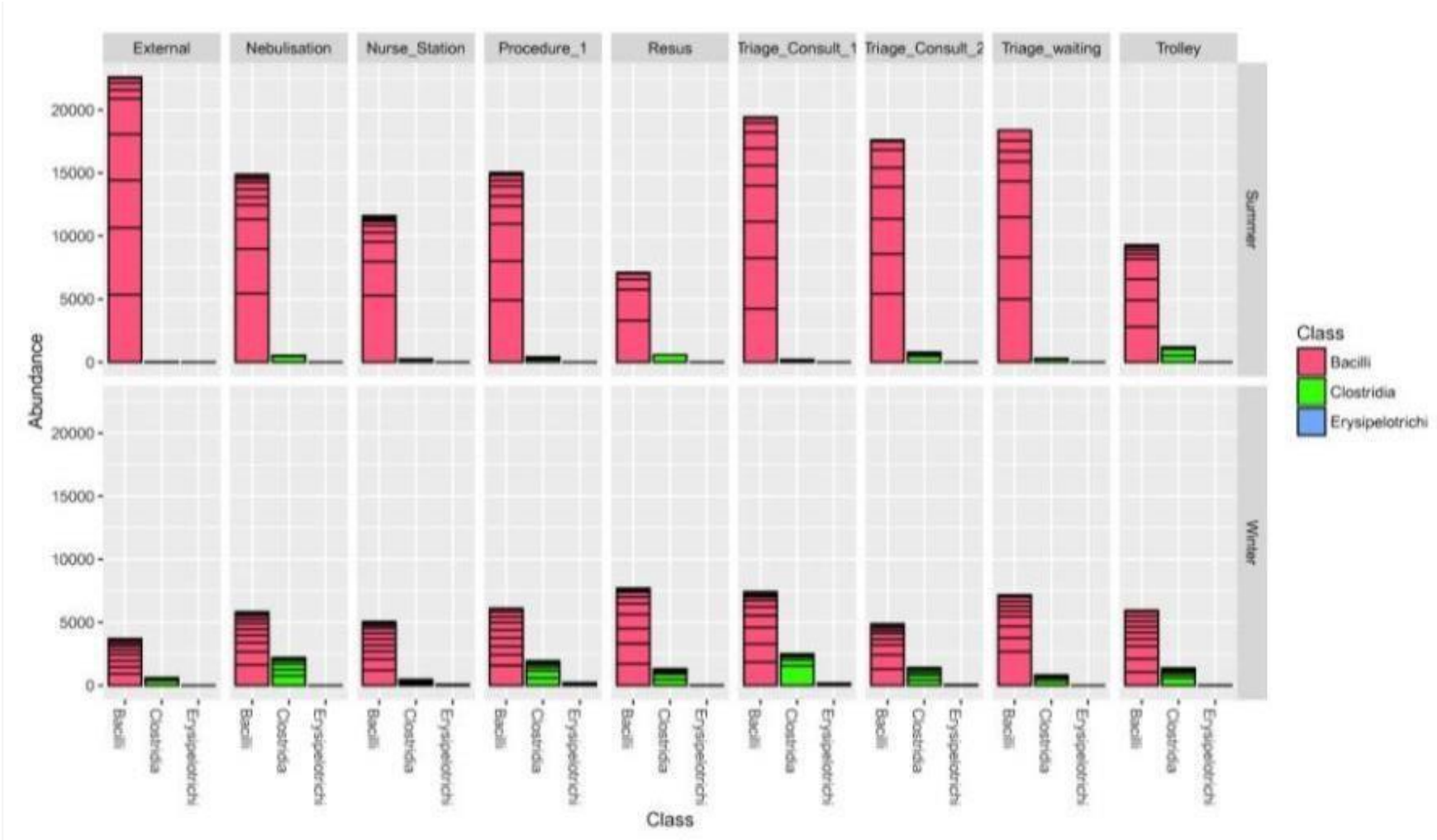



Figure 80: Relative abundance of *Firmicutes* phyla per class and room, summer and winter: KDH and MPH

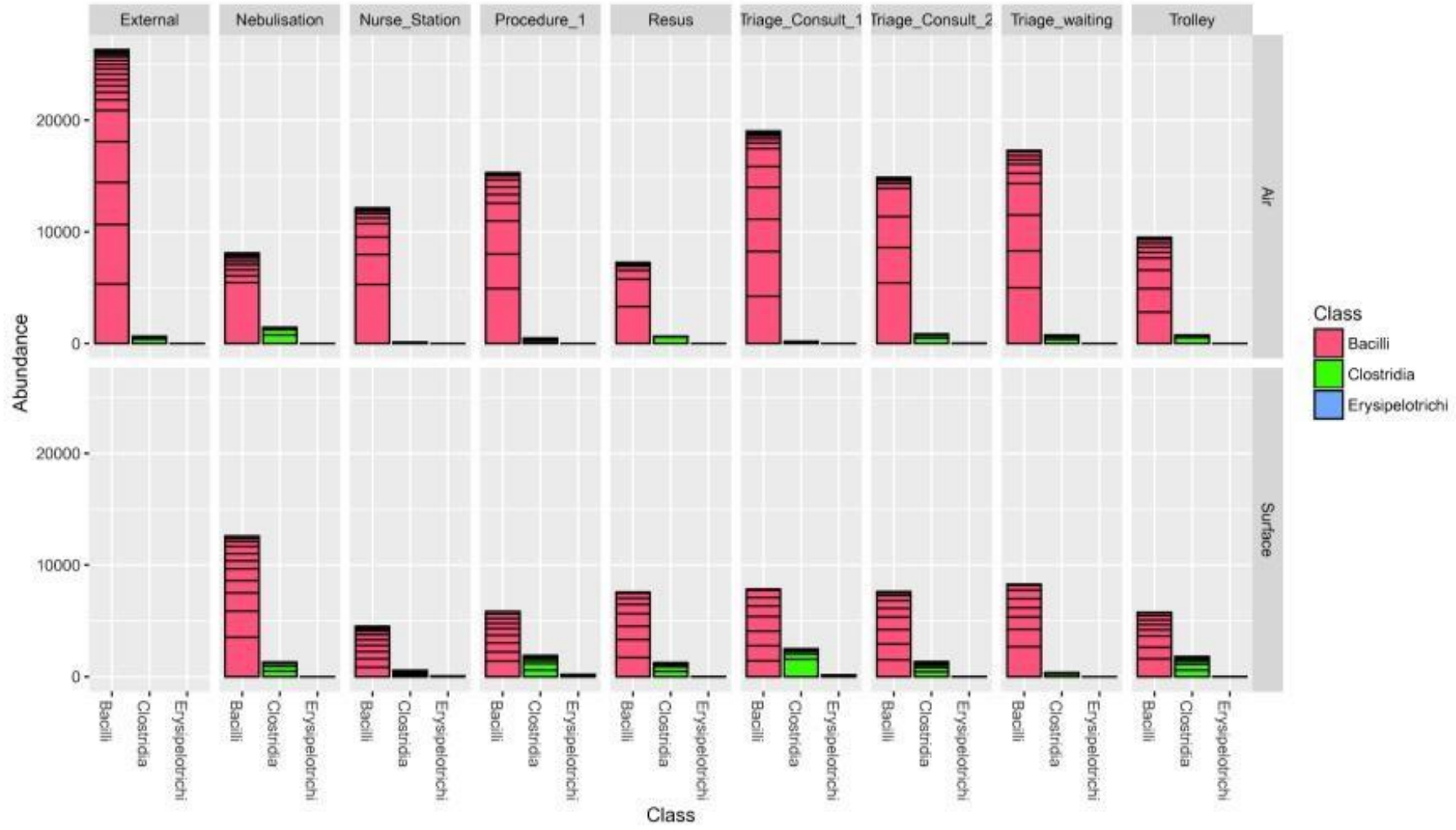



Figure 81: Relative abundance of *Firmicutes* phyla per class and room, air and surface: KDH and MPH

The indicator genera for each room type are shown in Figure 82. An evident variation exists between the abundance of the indicator genera for air and surface samples. It is clear that the majority of airborne species identified belong to the genus *Burkholderia*. This is more commonly found in offices and hospitals (Kelley *et al.* 2013:3). The viability of the identified indicator taxa is confirmed with the culture samples identification. 40-50% of the genus indicator species were identified in the culture samples, thus implying the viability of potential pathogens found in KDH and MPH. Refer to Table 8.17 for culture findings.

Table 8.11 provides a summary of the HAI list found and verifies the indicator genera identified in this study. Three prevalent HAI species have been identified; all three have been positively cultured. In addition, this thesis presents the unlisted pathogenic viable microorganisms found in KDH and MPH.

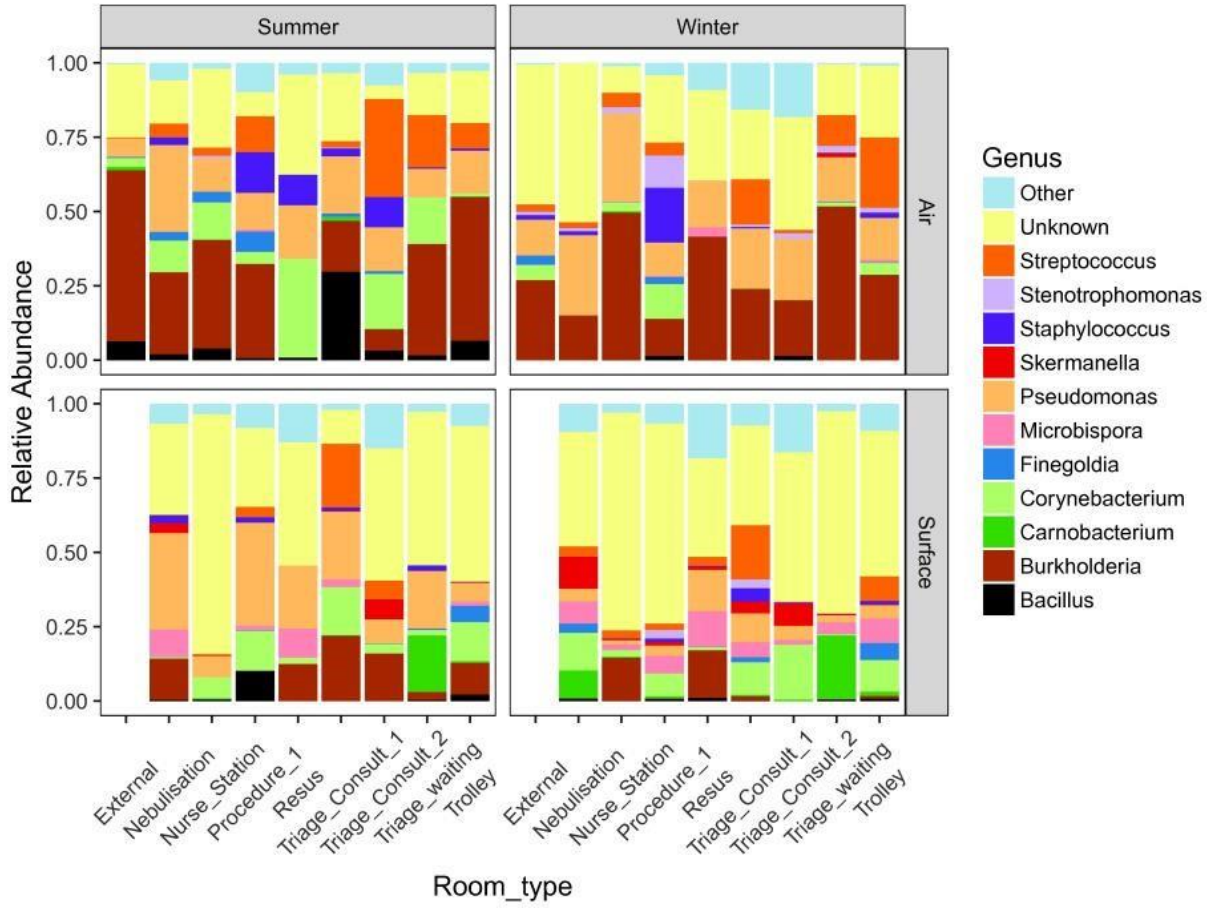



Figure 82: Relative abundance of genera taxa indicators by room for air and surface for KDH and MPH

Table 8.11: HAI USA pathogen list compared to thesis genus and culture identification findings

| | **USA HAI** | **Genus and identified cultures at MPH & KDH** |
|---|---|---|
| 1 | *Escherichia coli* | - |
| 2 | *Staphylococcus aureus* | *Staphylococcus* (by genus sequencing) |
| 3 | *Enterococci* | - |
| 4 | *Pseudomonas aeruginosa* | *Pseudomonas* (by genus sequencing) |
| 5 | *Coagulase*-negative *Staphylococci* | *Staphylococcus* (by genus sequencing) |

| | | |
|---|---|---|
| | (Jarvis & Martone 1992, Ducel *et al.* 2002; Wisplinghof *et al.* 2004) | |
| **Unlisted viable pathogens found in MPH and KDH** | | |
| * | *Bacillus cerues* | |
| * | *Acinetobacter lwoffii* | |
| | *Cellulosimicrobium cellulans* | |
| | *Proteus penneri* | |
| | *Proteus vulgaris* | |
| * | *Achromobacter denitricans* | |
| * | *Nocardia cyriacigeorgica* | |
| * | *Streptococcus pneumoniae* | |
| * | *Ralstonia insidiosa* | |
| * | *Nocardia cyriacigeorgica* | |
| * | *Streptococcus agalactiae* | |
| *Emerging pathogen, pathogen, HAI known, fatal | | |

Of the USA HAI list of pathogens, *Staphylococcus* (by genus sequencing, *Pseudomonas* (by genus sequencing) and *Staphylococcus* (by genus sequencing) were found as viable pathogens cultured from the samples taken; they were also identified in the sequencing. This is of particular concern to the KDH and MPH - refer to Table 8.2 for detail on the pathogens noted.

Table 8.12: Identified genera indicator species list with noted pathogenicity

| SPECIE | DEFINITION |
|---|---|
| ***Stenotrophomonas*** | *Although an uncommon pathogen in humans,* S maltophilia *infection in humans, especially nosocomial, has been increasingly recognized* (Cunha 2017). |
| ***Staphylococcus*** | *Most are harmless and reside normally on the skin and mucous membranes of humans and other organisms.* Staphylococcus *frequently colonize the skin and upper respiratory tracts of mammals and birds* (Al-Zharani 2012). |
| ***Psychrobacter*** | *Some of those bacteria were isolated from humans and can cause humans infections such as endocarditis and peritonitis.[6][7] This genus of bacteria is able to grow at temperatures between −10 and 42°C.* |
| ***Pseudomonas*** | *The bacteria are found widely in the environment, such as in soil, water, and plants. Pseudomonades are fairly common pathogens involved in infections acquired in a hospital setting. A pathogen is a microorganism that causes disease* (Caffaso & Rogers 2016). |
| ***Enterococcus*** | *Enterococci are part of the normal intestinal flora of humans and animals. They have been long recognized as important human pathogens and are becoming increasingly so (IE) (Fraser 2017).* |
| ***Delftia*** | *It is usually a nonpathogenic environmental organism and is rarely clinically significant. Although D.acidovorans infection most commonly occurs in hospitalized or immunocompromised patients, there are also several reports documenting the infection in immunocompetent patients. (Huseyin, Sarmis, Tigen, Soyletir & Mulazimoglu 2015).* |
| ***Corynebacterium*** | *They are widely distributed in nature in the microbiota of animals (including the human microbiota) and are mostly innocuous. Can cause human disease, including most notably diphtheria, which is caused by C. diphtheria; they usually are not pathogenic but can occasionally opportunistically become pathogenic (Russel 2017:112).* |
| ***Burkholderia*** | *Burkholderia is a genus of Proteobacteria whose pathogenic members include Burkholderia mallei, responsible for glanders, Burkholderia pseudomallei, causative agent of melioidosis; and Burkholderia cepacia, an important pathogen of pulmonary infections in people with cystic fibrosis both animal and plant pathogens, as well as some environmentally important species. Pseudomallei are considered to be potential biological warfare agents, targeting livestock and humans (Microbe Wiki 2010).* |

| | |
|---|---|
| ***Bacillus*** | *Bacillus includes both free-living (nonparasitic) and parasitic pathogenic species. Under stressful environmental conditions, the bacteria can produce oval endospores that are not true "spores", but to which the bacteria can reduce themselves and remain in a dormant state for very long periods. Other species of Bacillus are important pathogens, causing anthrax and food poisoning (Russel 2017:107).* |
| ***Acinetobacter*** | *They are important soil organisms, where they contribute to the mineralization of, for example, aromatic compounds. Acinetobacter species are a key source of infection in debilitated patients in the hospital, in particular the species Acinetobacter baumannii (Brisou & Prevot 1954).* |

The top 30 most frequently identified genera from 374 identified by sequencing are listed in Table 8.12. The table includes viable organisms identified by culture (the culture identification was exclusively performed for the identification of *Staphylococcus aureus, Pseudomonas aeruginosa, Pneumocystis carinii pneumonia* and *Mycobacteria tuberculosis*.) This list gives an indication of the variation in, and abundance of, organisms in South African hospitals. It directly reflects the typical Cape Flats, Western Cape hospital environment (which as per the findings that both hospital biomes are significantly similar).

Table 8.13: Top 30 genera identified in KDH & MPH from surface and air samples by culture viability

| No | TYPE | Frequency - Reads p/S | Culture viable |
|---|---|---|---|
| 1 | *Pseudomonas* | 186 | Yes |
| 2 | *Bacillus* | 184 | Yes |
| 3 | *Corynebacterium* | 128 | |
| 4 | *Acinetobacter* | 112 | Yes |
| 5 | *Staphylococcus* | 78 | Yes |
| 6 | *Prevotella* | 75 | |
| 7 | *Streptococcus* | 63 | |
| 8 | *Burkholderia* | 61 | |
| 9 | *Paracoccus* | 52 | |
| 10 | *Sphingomonas* | 51 | |
| 11 | *Enterococcus* | 46 | Yes |
| 12 | *Lactobacillus* | 38 | |
| 13 | *Anaerococcus* | 36 | |
| 14 | *Blautia* | 34 | |
| 15 | *Rhodoplanes* | 34 | |
| 16 | *Psychrobacter* | 30 | Yes |
| 17 | *Delftia* | 29 | Yes |
| 18 | *Kaistobacter* | 29 | |
| 19 | *Coprococcus* | 27 | |
| 20 | *Faecalibacterium* | 25 | |
| 21 | *Geobacillus* | 25 | |
| 22 | *Hymenobacter* | 23 | |
| 23 | *Stenotrophomonas* | 23 | |
| 24 | *Haemophilus* | 21 | |
| 25 | *Ruminococcus* | 21 | |
| 26 | *Clostridium* | 19 | |
| 27 | *Flavisolibacter* | 19 | |
| 28 | *Mycobacterium* | 19 | |
| 29 | *Methylobacterium* | 18 | |
| 30 | *Actinomyces* | 17 | |

From Table 8.14 and Table 8.15, on average ±35% of the OTUs, including surface and air samples, were shared between outdoor and indoor environments. See the previous section on human associated biota indoors. It is also evident that both KDH and MPH presented a higher number of OTUs in winter than in summer and a larger number of shared OTUs in winter than in summer. The seasonal variation and increase in OTUs could be attributed to both higher occupancies measured, and the higher humidity and driving wind conditions experienced. For KDH the variance is minor; for MPH it is much greater.

Table 8.14: OTU per room type, for room, external and shared spaces for KDH

| **KDH Summer** | **OTU** | | | **KDH Winter** | **OTU** | | |
|---|---|---|---|---|---|---|---|
| **Room type** | **Room** | **External** | **Shared** | **Room type** | **Room** | **External** | **Shared** |
| Nebulisation | 529 | 182 | 191 | Nebulisation | 435 | 228 | 287 |
| Nurses' Station | 323 | 187 | 186 | Nurses' Station | 481 | 237 | 278 |
| Procedure 1 | 405 | 151 | 222 | Procedure 1 | 466 | 224 | 291 |
| Resus | 341 | 194 | 179 | Resus | 435 | 225 | 290 |
| Triage Consult 1 | 392 | 165 | 208 | Triage Consult 1 | 735 | 194 | 321 |
| Triage Consult 2 | 323 | 194 | 179 | Triage Consult 2 | 467 | 230 | 285 |
| Triage Waiting | 313 | 204 | 169 | Triage Waiting | 485 | 243 | 272 |
| Trolley | 407 | 169 | 205 | Trolley | 749 | 207 | 308 |

Table 8.15: OTU per room type, for in room, external and shared for MPH

| **MPH Summer** | **OTU** | | | **MPH Winter** | **OTU** | | |
|---|---|---|---|---|---|---|---|
| **Room type** | **Room** | **External** | **Shared** | **Room type** | **Room** | **External** | **Shared** |
| Nebulisation | 358 | 196 | 186 | Nebulisation | 775 | 216 | 321 |
| Nurses' Station | 306 | 193 | 189 | Nurses' Station | 519 | 205 | 332 |
| Procedure 1 | 470 | 173 | 209 | Procedure 1 | 617 | 246 | 291 |
| Resus | NA | NA | NA | Resus | 576 | 216 | 321 |
| Triage Consult 1 | 304 | 183 | 199 | Triage Consult 1 | 453 | 236 | 301 |
| Triage Consult 2 | 541 | 192 | 190 | Triage Consult 2 | 937 | 231 | 306 |
| Triage Waiting | 299 | 168 | 214 | Triage Waiting | 462 | 214 | 323 |
| Trolley | 452 | 166 | 216 | Trolley | 460 | 218 | 319 |

The indicator OTUs belonged to the phyla *Proteobacteria, Firmicutes*, *Bacteroidetes* and *Actinobacteria*. It is again evident that season and sample type play a significant role in the composition of the biome and/or community. Figure 83 indicates the observation of a clear

variation between the seasonal relative abundance within the phyla genera. Winter presented a reduced relative abundance in the air community compared to summer. The surface community in winter showed increased relative abundance compared to summer with the greatest source of phyla *Proteobacteria,* many of which are known to be human-associated (Grice *et al*. 2011; Van Rensburg *et al*. 2015). A deduced possible conclusion may be that the majority of phyla species that compose this indoor environment are in fact human-sourced. Some caution is, however, required, as representatives of the phylum *Proteobacteria* are also common soil taxa. No conclusive relationship could be found to exist in the room types and associated phyla per season, except for the total increase and/or reduction that was found. Room specific analyses will be discussed later on.

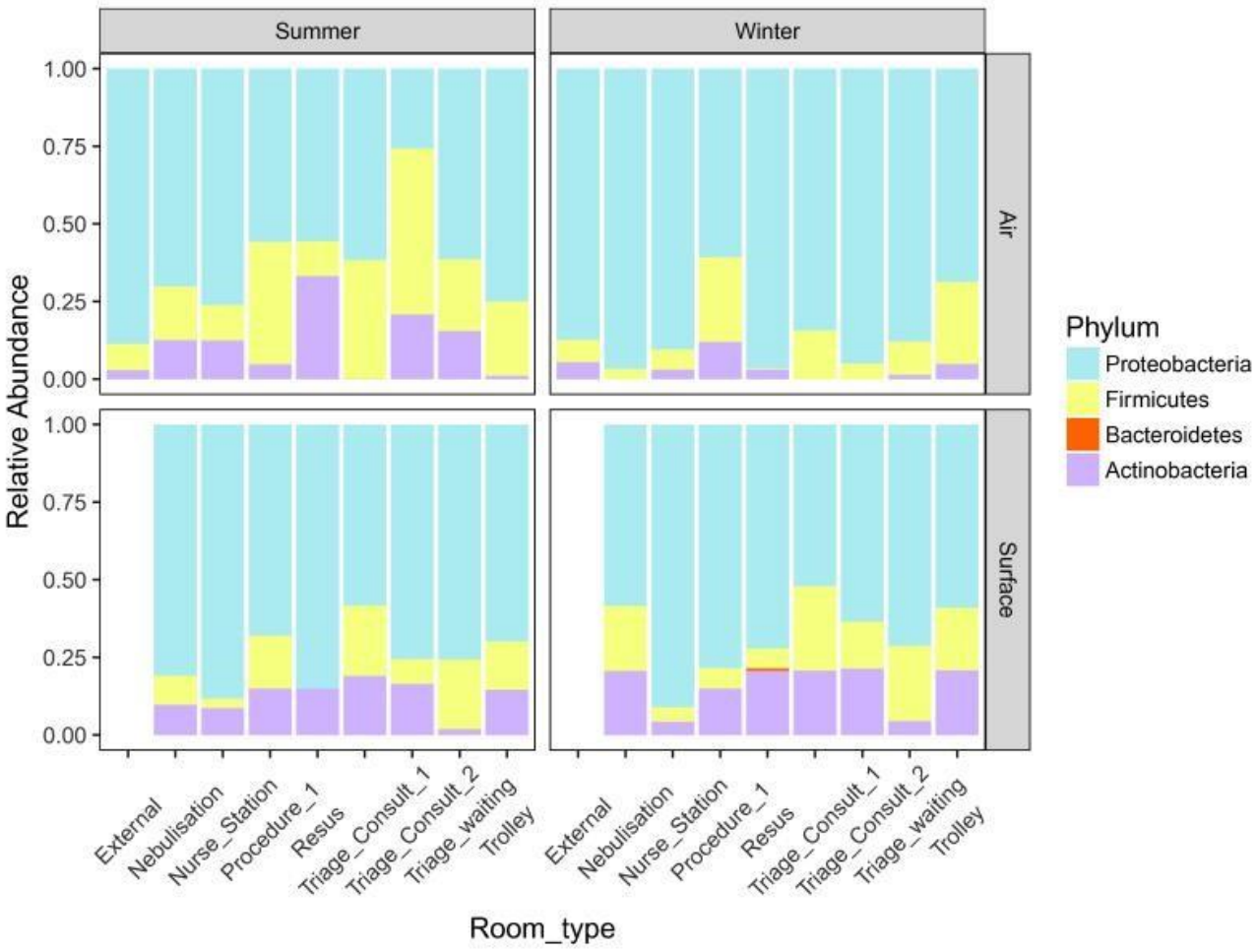



Figure 83: Relative abundance of phylum by room type, season, air and surface for KDH and MPH

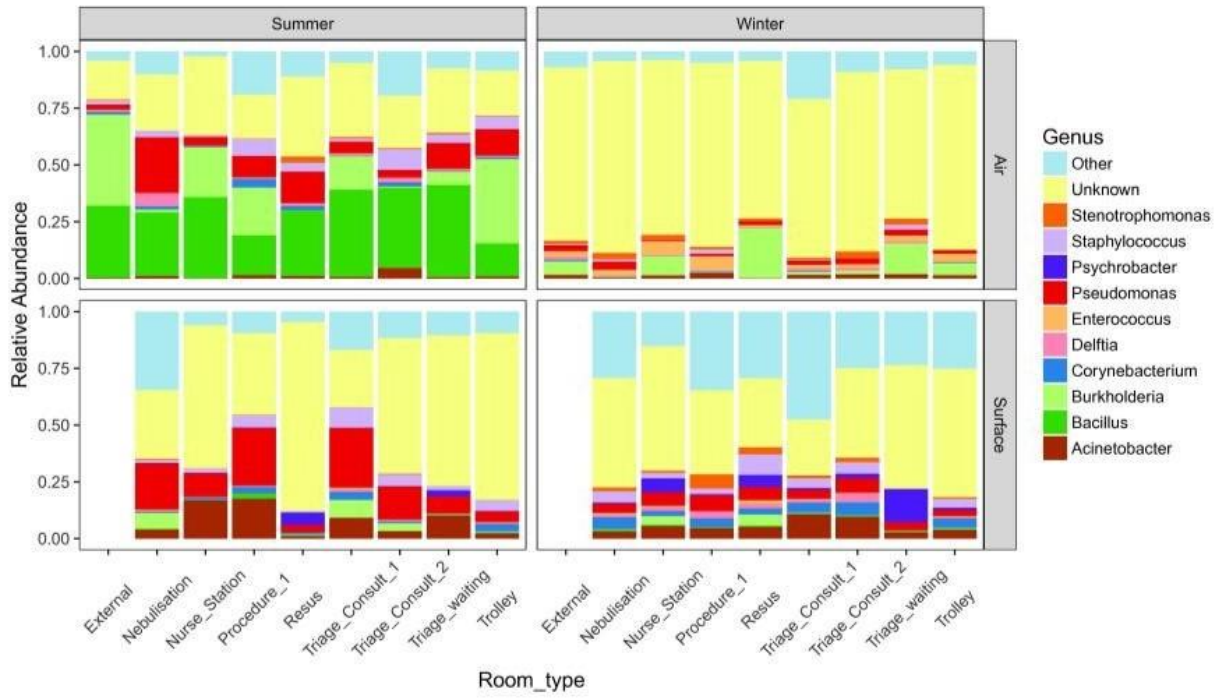



Figure 84: Relative abundance of genera taxa by room type, season, air and surface for KDH and MPH

The indicator OTUs serve to classify the most abundant indicator species that define the microbiome of the Western Cape public hospitals in the Cape Flats region. From Figure 84 one can establish that firstly, the indicators vary between seasons, secondly, the relative abundance of indicators is notably reduced by season and, lastly, a vast number of unknown genera exist. From the genera that are identifiable at this time, *Bacillus*, *Burkholderia* and *Pseudomonas* dominate summer for air; and *Burkholderia, Pseudomonas, Enterococcus* and *Actinobacteria* dominate in winter. The surface community is constituted mostly of *Pseudomonas*, *Actinobacteria* and *Delftia* in summer, and *Staphylococcus, Pseudomonas,* and *Acinetobacter* in winter. Greater species diversity was found in the surface community in winter. For reference, Table 8.12 has been included for organism definitions.

Secondly, a richer diversity was found in winter than in summer as per Figure 84. The Nat-V-M (the presence or absence of natural ventilation) factor, which represented data, was sourced on rooms that had openable windows and rooms that did not have. When applying adonis using Bray-Curtis distances, comparing the Nat-V-M and four other factors to the sample set, a P value of 0.277 for Nat-V-M was found, which implied no correlation with ventilation source; the only factors that did show correlation were season and type - air and surface (refer to Figure 84). The above is at odds with the shared source data, which indicate a 35% shared indoor and outdoor taxa. This implies that ventilation strategy does influence the microbiome composition, as found in the study by Kembel *et al.* (2013, 2014) and others. The data in Table 8.14 and Table 8.15, as noted previously, show that the indoor spaces contained on average 35% shared organisms from the outdoors; therefore, 65% of the organisms found were sourced from within the building, of which an estimated 25% were potentially human-sourced biota based on the organism identified and abundance count; however, it is noted that physical transport of soil and other environmental organisms into the sampled rooms, followed by resuspension of dust particles, also represents a potential route for “human-sourced”

microorganisms. Nevertheless, in this discussion the principal focus is on organisms which are human-associated (skin, hair, etc.) rather than vicariously associated (with shoes, clothing, etc).The ventilation systems in both KDH and MPH, as per the MC data in Table 9.2 and Table 9.3, showed that 66% of the rooms that were reliant on mechanical ventilation had no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66% not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome which is corroborated by other studies (Adams *et al.* 2015; Adams *et al.* 2016; Ramos & Stephans 2014; Kembel *et al.* 2013, 2014; and others). Refer to the literature review in chapter 3.

The data in Table 8.16 were developed using Permanova (calculated with the function adonis in the vegan package) which allows one to investigate the factors that are important to explain beta-diversity (community composition) patterns. From Table 8.16 one can see that only season (summer vs winter) and type (air, surface) have an effect on community composition. Season explains 3% ($R^2$=0.03072) and Type (air & surface) 4% of the variation ($R^2$=0.04074) in the community composition. The other factors that were compared were the type of ventilation present at that sample (Nat-V-M), the number of crossings into that space where samples were taken referring to access and flow (gateway cross) and the occupancy and internal movement of the space where samples associated with that space were taken (internal movement). The BE factors (the three noted) showed no correlation.

Table 8.16: Non-parametric analysis of pairwise dissimilarities

| Factor | Sums of Sqs | $R^2$ | Pr > F |
|---|---|---|---|
| Season | 2.093 | 0.03072 | 0.001 |
| Type (air & surface) | 2.776 | 0.04074 | 0.001 |
| Nat-V-M | 0.427 | 0.00626 | 0.277 |
| Gateway cross | 0.449 | 0.00659 | 0.155 |
| Internal movement | 0.375 | 0.00551 | 0.788 |
| Only season and type showed a significant association correlation | | | |
| Note: Permanova test: p-values are from permutation tests involving 999 permutations, and are only reported down to 0.001 | | | |

The room type OTU and shared external OTU data indicate that rooms that had open windows and rooms that relied only on mechanical ventilation had similar shared OTUs from the outside; the same applied to the relative abundance classification of genera by room type. The data suggest that the ventilation system did play a significant role in both facilities. What is more important is that KDH had more rooms that shared natural ventilation than MPH, and therefore more natural ventilation, but this made no notable difference in the organism distribution. It is significant when considering infection prevention and control (IPC) for surface and air that all the rooms were/still were at equal risk of cross infection. The open windows did not improve the indoor air quality, as ± 65% of the air still represented human-sourced OTUs and thus potential pathogenic bacteria (refer to

Table 8.11, etc.). In the mechanical characterisation study discussed in chapter 7, the HVAC air source was found to be 80-100% fresh air (outdoor air as per WCDoH policy). A cautionary note: both the number of samples and the sampling duration differ between outdoor and indoor

sampling sites, and as such a direct comparison of microbial biomass between the two areas is not strictly valid. Identification and quantification of shared biota was the motivation.

From the PERMANOVA results, we can deduce that there is no statistically significant difference between the two hospitals' biomes. Both Cape Town hospitals with a similar burden of disease, in the same climate zone and within 10km of each other, had the same indoor biome in their A&E departments. When comparing the core diversity of the 16S rRNA, DNA samples for each room type (samples of both KDH and MPH), nine core indicator organisms were identified and can be classified as the biome, or indicators of the WC, Cape Flats hospital biome. These include *Pseudomonas, Enterococcus, Delftia, Corynebacterium, Burkholderia, Bacillus, Acinetobacter, Stenotrophomonas,* and *Staphylococcus*. A large number of unidentified and uncharacterised organisms were found. Combined with the indicators identified from sequencing, culture samples were taken. When compared with the core indicators organisms, 45% were cultured and thus viable indicator species taxa. This shows that the hospital biomes did in fact host a large number of viable organisms (refer to

Table 8.11) that have the potential to cause HAI amongst staff, patients and visitors. As per item 16 and Table 8.16, correlations are given on occupancy as factor. The result indicated that in no event did the occupancy by room type have any significant correlation. This was similar to internal movement and gateway crossing (the interrelationships between these three factors have been established and supported in chapter 7).

In item 16 and Table 8.16, correlations are given on various BE factors. The result indicated no effective significant correlation, implying that the hospital type, season and sample type were the most influential factors. The number of samples enabled a global broad study of the indoor environment. These findings oppose those of other MoBE studies that did in fact find a correlation between BE factors and microbial samples. A more focused room study with additional samples could provide more BE-related correlations. Nonetheless, the full BE data factors were collected for this study and future analysis of the meta data could provide more information. The BE factors by total number will always be in excess of the sample size of a microbial study (Kembel *et al.* 2013, 2014). The sample size threshold that will provide both global and local relevance is yet to be determined and further studies, particularly more focused studies, should be undertaken.

#### 8.3.2.2 ANALYSIS OF SEQUENCING AND CULTURE SAMPLES

Table 8.17 below presents the indicator organisms identified per room type, with organisms identified by culture sequencing indicating viability. The indicator species analysis was done using the indicator value (IndVal) index, which combines relative abundance and relative frequency of occurrence (Dufrene & Legendre 1997).

Table 8.17: Indicator organisms by room type for viable culture identification for KDH and MPH

| *Items in bold type are viable species identified in culture sequencing<br>*Items in standard italics are from 16S rRNA | | | | |
|---|---|---|---|---|
| | **Nebulisation** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Pseudomonas* | *Delftia* | *Stenotrophomonas* | *Delftia* |
| | *Enterococcus* | *Corynebacterium* | ***Staphylococcus*** | *Corynebacterium* |
| | *Delftia* | *Burkholderia* | *Psychrobacter* | *Burkholderia* |
| | *Corynebacterium* | *Bacillus* | ***Pseudomonas*** | ***Bacillus*** |

| | | | | |
|---|---|---|---|---|
| | *Burkholderia* | *Acinetobacter* | ***Enterococcus*** | ***Acinetobacter*** |
| | *Bacillus* | ***Pseudomonas*** | *Delftia* | ***Pseudomonas*** |
| | *Acinetobacter* | *Staphylococcus* | *Corynebacterium* | *Staphylococcus* |
| | *Stenotrophomonas* | | *Burkholderia* | |
| | *Staphylococcus* | | ***Bacillus*** | |
| | | | *Acinetobacter* | |
| **Culture associated with genera sequenced** | **0%** | **14%** | **40%** | **42%** |
| | **Nurse Station** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Acinetobacter* | *Pseudomonas* | *Stenotrophomonas* | *Stenotrophomonas* |
| | *Pseudomonas* | *Enterococcus* | ***Staphylococcus*** | *Staphylococcus* |
| | *Enterococcus* | *Delftia* | *Psychrobacter* | *Psychrobacter* |
| | *Delftia* | *Corynebacterium* | ***Pseudomonas*** | ***Pseudomonas*** |
| | *Corynebacterium* | *Burkholderia* | *Enterococcus* | *Delftia* |
| | *Burkholderia* | *Bacillus* | *Delftia* | *Corynebacterium* |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Corynebacterium* | *Burkholderia* |
| | *Staphylococcus* | *Staphylococcus* | *Burkholderia* | ***Bacillus*** |
| | | | ***Bacillus*** | ***Acinetobacter*** |
| | | | ***Acinetobacter*** | |
| **Culture associated with genera sequenced** | **0%** | **0%** | **40%** | **33%** |
| | **Procedure** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | *Staphylococcus* |
| | *Pseudomonas* | *Pseudomonas* | *Psychrobacter* | *Psychrobacter* |
| | *Enterococcus* | *Enterococcus* | ***Pseudomonas*** | ***Pseudomonas*** |
| | *Delftia* | *Delftia* | *Delftia* | *Delftia* |
| | *Corynebacterium* | *Corynebacterium* | *Corynebacterium* | *Corynebacterium* |
| | *Burkholderia* | *Burkholderia* | *Burkholderia* | ***Bacillus*** |
| | *Acinetobacter* | *Bacillus* | ***Bacillus*** | ***Acinetobacter*** |
| | | *Acinetobacter* | ***Acinetobacter*** | |
| **Culture associated with genera sequenced** | **0%** | **0%** | **44%** | **38%** |
| | **Resus** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Staphylococcus* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | ***Psychrobacter*** |
| | *Psychrobacter* | | *Psychrobacter* | ***Pseudomonas*** |
| | *Pseudomonas* | *Pseudomonas* | ***Pseudomonas*** | *Corynebacterium* |
| | *Enterococcus* | *Enterococcus* | *Enterococcus* | *Burkholderia* |
| | *Delftia* | *Delftia* | *Delftia* | *Bacillus* |
| | *Corynebacterium* | *Corynebacterium* | *Corynebacterium* | *Acinetobacter* |
| | *Burkholderia* | *Burkholderia* | *Burkholderia* | |
| | *Acinetobacter* | *Bacillus* | ***Bacillus*** | |
| | | *Acinetobacter* | ***Acinetobacter*** | |
| **Culture associated with genera sequenced** | **0%** | **0%** | **40%** | **42%** |
| | **Triage 1** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | ***Staphylococcus*** |
| | *Psychrobacter* | ***Pseudomonas*** | *Psychrobacter* | *Psychrobacter* |
| | *Pseudomonas* | *Enterococcus* | ***Pseudomonas*** | ***Pseudomonas*** |
| | *Enterococcus* | *Delftia* | ***Enterococcus*** | *Enterococcus* |

| | | | | |
|---|---|---|---|---|
| | *Delftia* | *Corynebacterium* | ***Delftia*** | *Delftia* |
| | *Corynebacterium* | *Burkholderia* | *Corynebacterium* | *Corynebacterium* |
| | *Burkholderia* | *Bacillus* | *Burkholderia* | *Burkholderia* |
| | *Bacillus* | *Acinetobacter* | ***Bacillus*** | ***Bacillus*** |
| | *Acinetobacter* | | *Acinetobacter* | ***Acinetobacter*** |
| **Culture associated with genera sequenced** | **0%** | **22%** | **50%** | **40%** |
| | **Triage 2** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | ***Staphylococcus*** |
| | *Pseudomonas* | *Pseudomonas* | *Psychrobacter* | ***Psychrobacter*** |
| | *Enterococcus* | *Enterococcus* | ***Pseudomonas*** | ***Pseudomonas*** |
| | *Delftia* | *Delftia* | ***Enterococcus*** | *Delftia* |
| | *Burkholderia* | *Corynebacterium* | *Delftia* | *Corynebacterium* |
| | *Bacillus* | *Burkholderia* | *Corynebacterium* | *Burkholderia* |
| | *Acinetobacter* | *Bacillus* | *Burkholderia* | ***Bacillus*** |
| | | *Acinetobacter* | ***Bacillus*** | ***Acinetobacter*** |
| | | | ***Acinetobacter*** | |
| **Culture associated with genera sequenced** | **0%** | **0%** | **50%** | **55%** |
| | **Triage Waiting** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Staphylococcus* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | *Psychrobacter* |
| | *Pseudomonas* | ***Pseudomonas*** | *Psychrobacter* | ***Pseudomonas*** |
| | *Enterococcus* | *Enterococcus* | ***Pseudomonas*** | *Enterococcus* |
| | *Delftia* | *Delftia* | *Enterococcus* | *Delftia* |
| | *Corynebacterium* | *Corynebacterium* | *Corynebacterium* | *Corynebacterium* |
| | *Burkholderia* | *Burkholderia* | *Burkholderia* | *Burkholderia* |
| | *Bacillus* | *Bacillus* | ***Bacillus*** | ***Bacillus*** |
| | *Acinetobacter* | *Acinetobacter* | ***Acinetobacter*** | ***Acinetobacter*** |
| **Culture associated with genera sequenced** | **0%** | **11%** | **44%** | **33%** |
| | **Trolley** | | | |
| | **WINTER AIR** | **SUMMER AIR** | **WINTER SURFACE** | **SUMMER SURFACE** |
| | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* | *Stenotrophomonas* |
| | *Staphylococcus* | *Staphylococcus* | ***Staphylococcus*** | *Staphylococcus* |
| | *Pseudomonas* | ***Pseudomonas*** | *Psychrobacter* | ***Psychrobacter*** |
| | *Enterococcus* | *Delftia* | ***Pseudomonas*** | ***Pseudomonas*** |
| | *Delftia* | *Corynebacterium* | *Enterococcus* | *Enterococcus* |
| | *Corynebacterium* | *Burkholderia* | *Delftia* | *Delftia* |
| | *Burkholderia* | *Bacillus* | *Corynebacterium* | *Corynebacterium* |
| | *Acinetobacter* | *Acinetobacter* | *Burkholderia* | *Burkholderia* |
| | | | ***Bacillus*** | ***Bacillus*** |
| | | | *Acinetobacter* | ***Acinetobacter*** |
| **Culture associated with genera sequenced** | **0%** | **13%** | **30%** | **40%** |

As noted, a number of the pathogens and non-pathogenic microorganism were identified. The culture analysis was performed to determine viability of the community identified by sequencing. A shortcoming of current sequencing technology is the inability to detect viability. As such culture techniques are still relevant, even though the culturing process does not reflect

the true wild type environment experienced. It does, however, give evidence of viability and raise pathogen presence and potential virulence of a given environment.

#### 8.3.2.3 ANALYSIS OF SEQUENCING AND ROOM TYPES

Table 8.18 to Table 8.22 represent the core zones ranked highest to lowest per category assigned to the table; included are the unique - and shared with external - OTUs sequenced per room type classification per hospital. The data presented in these tables associate spatial dynamics with community abundances in comparing the hospital sites. The total OTUs (unique and shared with external) are assigned to the room types per season and total to compare spatial dynamic grading changes as noted in each table. Only Table 8.18 averages both seasons' OTUs. The following spatial findings are tested with the community abundance by OTU count to compare hospital site.

- Core spaces by base plan analysis grading – high to low
- Core spaces by observation (integration) analysis grading – high to low
- Core spaces by gate crossing analysis grading – high to low
- Core spaces compared for type a season – no grading

The OTUs shown in this table were made up of totalling per room type the unique OTUs plus the shared OTUs, with the external source sampling, which constituted the total OTUs for that room type in that hospital for that season. The total OTUs for summer and for winter were then averaged for each of the rooms which represented the average OTU count for that room type. For example, consider the Nurse Station value in Table 8.18.

| | |
|---|---|
| KDH summer: | Unique room OTUs: 323 |
| KDH summer: | Shared with external OTUs:186 |
| KDH winter: | Unique room OTUs:481 |
| KDH winter: | Shared with external OTUs: 278 |

Total summer:509
Total winter: 759
Average: 634 OTUs as assigned in Table 8.18 below

Table 8.18: Core spaces total average OTU assignment, graded by base plan KDH and MPH

| | KDH | Avg season OTU | MPH | Avg season OTU |
|---|---|---|---|---|
| 1 | Nurses' Station | 634 | Nurses' Station | 673 |
| 2 | Passage Main | - | Trolley | 723 |
| 3 | Trolley | 834 | Passage Main | - |
| 4 | Resus | 622 | Triage Waiting | 649 |
| 5 | Nebulisation | 721 | Resus | 448 |
| 6 | Triage Consult 1 | 828 | Nebulisation | 820 |
| 7 | Triage Waiting | 619 | Triage Consult 1 | 628 |
| 8 | Triage Consult 2 | 627 | Triage Consult 2 | 987 |
| 9 | Procedure | 692 | Procedure | 793 |

Refer to Table 8.18 for the core hospital areas by base plan analysis overlay by integration from highly integrated to low integration. Considering that integration is a global measure of the network of space where it takes into account the relationship of all elements to a certain element, highly integrated space should have high movement or activity associated with it. Based on the data table with averaged OTUs, one could expect high counts for highly

integrated spaces. However, it must be noted that a number of factors would influence the microbial load, e.g. the type of activity and the rate of activity. Secondly, this analysis is based on the base plan, not the observed space use, and it was evident from the analysis that the observed use correlation was 40% whereas the base plan was 58%. Also: the seasons are average and from the data it was observed that seasonal dynamics influenced the microbial community and the hospital occupancy as well as core R. The data, however, were inconsistent, and no clear correlation can be determined from the table. Let's consider actual observation values:

Table 8.19: Core spaces average OTU assignment, graded by observation KDH and MPH

| | Winter | | | | Summer | | | |
|---|---|---|---|---|---|---|---|---|
| | **KDH** | **OTU** | **MPH** | **OTU** | **KDH** | **OTU** | **MPH** | **OTU** |
| 1 | Nurses' Station | 759 | Nurses' Station | 851 | Nurses' Station | 509 | Nurses' Station | 495 |
| 2 | Passage Main | - | Passage Main | - | Passage Main | - | Passage Main | - |
| 3 | Trolley | 1057 | Triage Waiting | 785 | Trolley | 612 | Triage Waiting | 513 |
| 4 | Nebulisation | 722 | Trolley | 779 | Resus | 520 | Trolley | 668 |
| 5 | Resus | 725 | Resus | 897 | Nebulisation | 720 | Resus | - |
| 6 | Triage Consult 1 | 1056 | Nebulisation | 1096 | Triage Consult 1 | 600 | Triage Consult 2 | 731 |
| 7 | Triage waiting | 757 | Triage Consult 2 | 1243 | Triage Waiting | 482 | Triage Consult 1 | 503 |
| 8 | Triage Consult 2 | 752 | Triage Consult 1 | 754 | Triage Consult 2 | 502 | Procedure | 679 |
| 9 | Procedure | 757 | Procedure | 908 | Procedure | 627 | - | - |

Refer to Table 8.19 for the core hospital areas by base plan observation overlay by integration from highly integrated to low integration and note the previous variable factors. However, this analysis is based on the observed space use, which was less correlated than the base plan at 40%. The data are still inconsistent, though central integrated spaces (semi-integrated) tended to have higher counts.

Table 8.20 Core spaces average OTU assignment, graded by gate crossing KDH and MPH

| | Winter | | | | Summer | | | |
|---|---|---|---|---|---|---|---|---|
| | **KDH** | **OTU** | **MPH** | **OTU** | **KDH** | **OTU** | **MPH** | **OTU** |
| 1 | Passage Main | - | Nurses' Station | 851 | Passage Main | - | Nurses' Station | 495 |
| 2 | Nurses' Station | 759 | Passage Main | - | Nurses' Station | 509 | Passage Main | - |
| 3 | Trolley | 1057 | Triage Wait | 785 | Trolley | 612 | Triage Wait | 513 |
| 4 | Resus | 725 | Trolley | 779 | Resus | 520 | Trolley | 668 |
| 5 | Triage Consult 1 | 1056 | Resus | 897 | Triage Consult 1 | 600 | Resus | - |
| 6 | Nebulisation | 722 | Triage Consult 1 | 754 | Nebulisation | 720 | Triage Consult 1 | 503 |
| 7 | Triage Wait | 757 | Nebulisation | 1096 | Triage Wait | 482 | Triage Consult 2 | 731 |
| 8 | Triage Consult 2 | 752 | Triage Consult 2 | 1243 | Triage Consult 2 | 502 | Nebulisation | 544 |
| 9 | Procedure 1 | 757 | Procedure 1 | 908 | Procedure 1 | 627 | Procedure 1 | 679 |

Refer to Table 8.20 for the core hospital areas graded by gate crossing, from high crossing/ inferred activity down to low activity/ gate crossing. The gate crossing count is considered an

activity metric measure and has been utilised by other studies for activity indication. This study found a strong correlation between gate counts and flow measures. It is evident that the OTU count is higher in winter than summer. Again no clear correlation can be drawn from the table. What is interesting is that for most cases as seen in the previous analysis, centrally integrated rooms tended to have higher OTU count.

Table 8.21: Core spaces average OTU assignment, graded by flow count KDH and MPH

| | Winter | | | | Summer | | | |
|---|---|---|---|---|---|---|---|---|
| | **KDH** | **OTU** | **MPH** | **OTU** | **KDH** | **OTU** | **MPH** | **OTU** |
| 1 | Nurses' Station | 759 | Nurses' Station | 851 | Nurses' Station | 509 | Nurses' Station | 495 |
| 2 | Passage Main | - | Passage Main | - | Passage Main | - | Passage Main | - |
| 3 | Trolley | 1057 | Triage waiting | 785 | Trolley | 612 | Trolley | 668 |
| 4 | Resus | 725 | Trolley | 779 | Resus | 520 | Triage waiting | 513 |
| 5 | Nebulisation | 722 | Resus | 897 | Nebulisation | 720 | Resus | - |
| 6 | Triage Consult 1 | 1056 | Nebulisation | 1096 | Triage Consult 1 | 600 | Triage Consult 1 | 503 |
| 7 | Triage Waiting | 757 | Triage Consult 1 | 754 | Triage Waiting | 482 | Triage Waiting | 731 |
| 8 | Procedure 1 | 757 | Triage Waiting | 1243 | Triage Consult 2 | 502 | Nebulisation | 544 |
| 9 | Triage Consult 2 | 752 | Procedure 1 | 908 | Procedure 1 | 627 | Procedure 1 | 679 |

Refer to Table 8.21 for the core hospital areas by flow count which is the actual activity count in space, from high activity to low activity measured. This study found a strong correlation between gate counts and flow measures. Therefore, a similar, or no, correlation should be evident. Again no clear correlation can be drawn from the table. What is interesting is that in all seasons the data seem to converge from low to the median and high to the median very strongly as opposed to the previous three analyses, with the mid value rooms consistently the highest. This could indicate that those space are less active in movement and allow the settlement and deposition of biota, noting that the mid-range activity space shows the highest microbial count.

Table 8.22: Comparing core spaces with seasonal average OTU assignment, KDH and MPH

| Winter | | | | Summer | | | |
|---|---|---|---|---|---|---|---|
| **KDH** | **OTU** | **MPH** | **OTU** | **KDH** | **OTU** | **MPH** | **OTU** |
| Nebulisation | 722 | Nebulisation | 1096 | Nebulisation | 720 | Nebulisation | 544 |
| Nurses' Station | 759 | Nurses' Station | 851 | Nurses' Station | 509 | Nurses' Station | 495 |
| Procedure_1 | 757 | Procedure 1 | 908 | Procedure 1 | 627 | Procedure 1 | 679 |
| Resus | 725 | Resus | 897 | Resus | 520 | Resus | - |
| Triage Consult 1 | 1056 | Triage Consult 1 | 754 | Triage Consult 1 | 600 | Triage Consult 1 | 503 |
| Triage Consult 2 | 752 | Triage Consult 2 | 1243 | Triage Consult 2 | 502 | Triage Consult 2 | 731 |
| Triage Waiting | 757 | Triage Waiting | 785 | Triage Waiting | 482 | Triage Waiting | 513 |
| Trolley | 1057 | Trolley | 779 | Trolley | 612 | Trolley | 668 |

Lastly, refer to Table 8.22 for the core hospital rooms by OTU assignment seasonally per hospital, taking into account only room type and therefore by extension function of space. Since room type and OTU count are relational, similar values seasonally should be found. This was evident for only some rooms (considering a 10% maximum variation). The values for summer are more related; less so for winter. For summer: Nurses' Station, Procedure, Triage Consult, Triage Waiting and Trolley area. For winter: Procedure, Resus and Triage Waiting. The only two rooms that were similar for both winter and summer were Procedure and Triage Waiting. Interestingly, these rooms were either the lowest (Procedure) or mid high (Triage Waiting).

# CHAPTER 9 ENVIRONMENTAL DATA COLLECTION

## 9.1 INTRODUCTION

Table 9.1 below is repeated; further refer to section 7.1 for mutual shared information.

Table 9.1: Room zone classification

| | |
|---|---|
| Z1 | Triage Consult 1 |
| Z2 | Triage Consult 2 |
| Z3 | Triage Waiting |
| Z4 | Procedure 1 |
| Z5 | Passage Main |
| Z6 | Nurses' station |
| Z7 | Resus [Resuscitation] |
| Z8 | Nebulisation |
| Z9 | Passage Secondary |
| Z10 | Trolley |
| Z11 | (Not indicated) refer to external sampling area 1 |
| Z12 | (Not indicated) refer to external sampling area 1 |

## 9.2 METHODOLOGY

Environmental data collection was done through fixed sensors, spot measures by hand-held equipment, and a ventilation system characterisation done prior to the study. The ventilation systems of both KDH and MPH were characterised, measuring airflow, air changes (ACH) and $CO_2$ for each study zone/room at each extract and supply duct, and window status – open or closed – was noted. Lux levels of room lighting and lighting sources were measured and noted. External $CO_2$ measures were taken prior to the study for reference purposes. Building data, including room size and volume, were calculated. Refer to section 9.2.1, Table 9.2, Table 9.3 and Table 9.4 for detailed information regarding the HVAC characterisation.

The data loggers were placed in each study zone, excluding zones five and nine. Refer to Figure 86 and Figure 85, and see Table 9.1 for room zone classifications. Data collection was set at one minute, 30 second intervals for continuous measurement of temperature, relative humidity and $CO_2$. The loggers were fixed on counter tops and wall surfaces. The loggers were removed after the last observation round on day four. Data were downloaded using proprietary software Gaslab® and analysed in MS Excel and R® statistics.

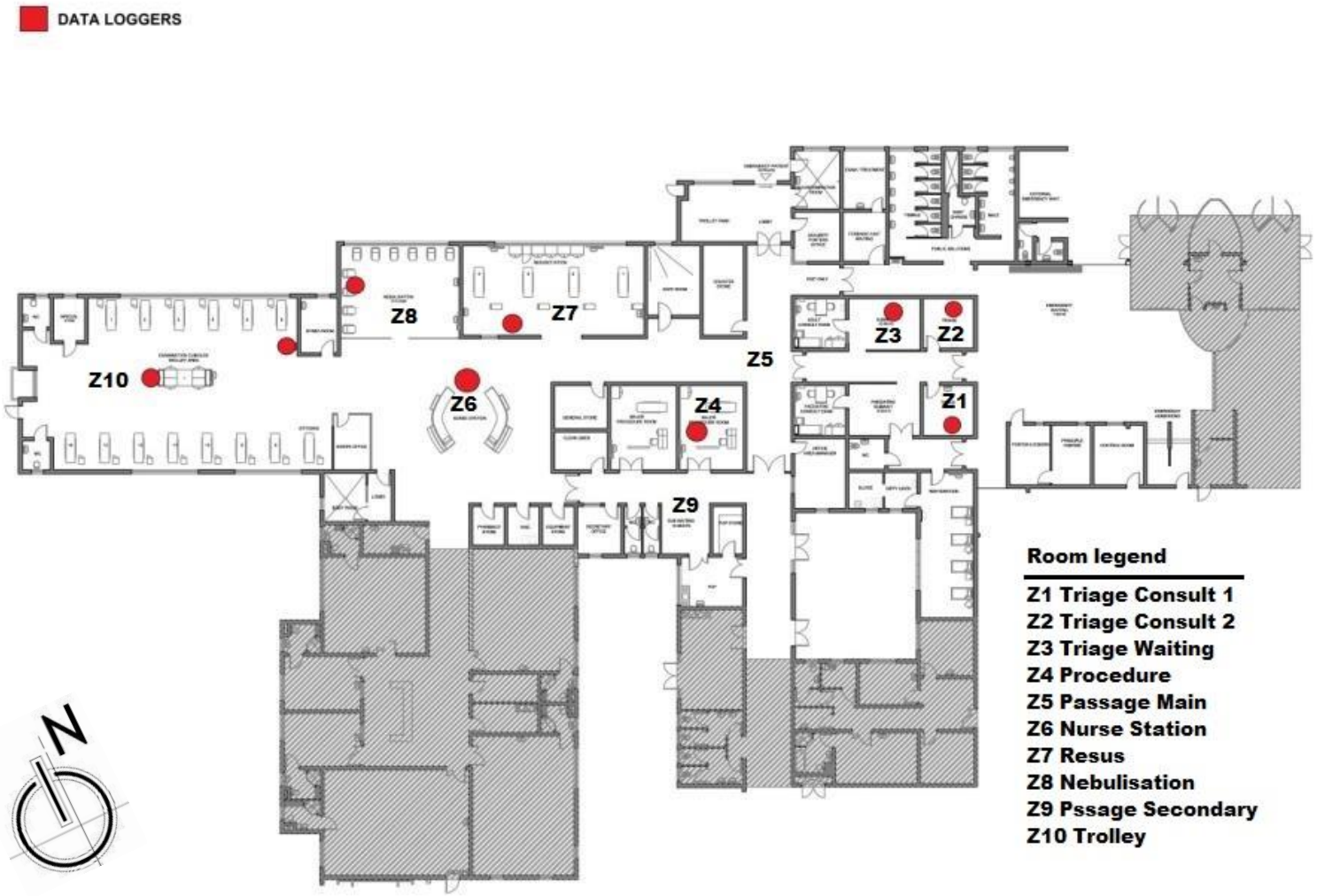



Figure 85: Locations of data loggers at MPH

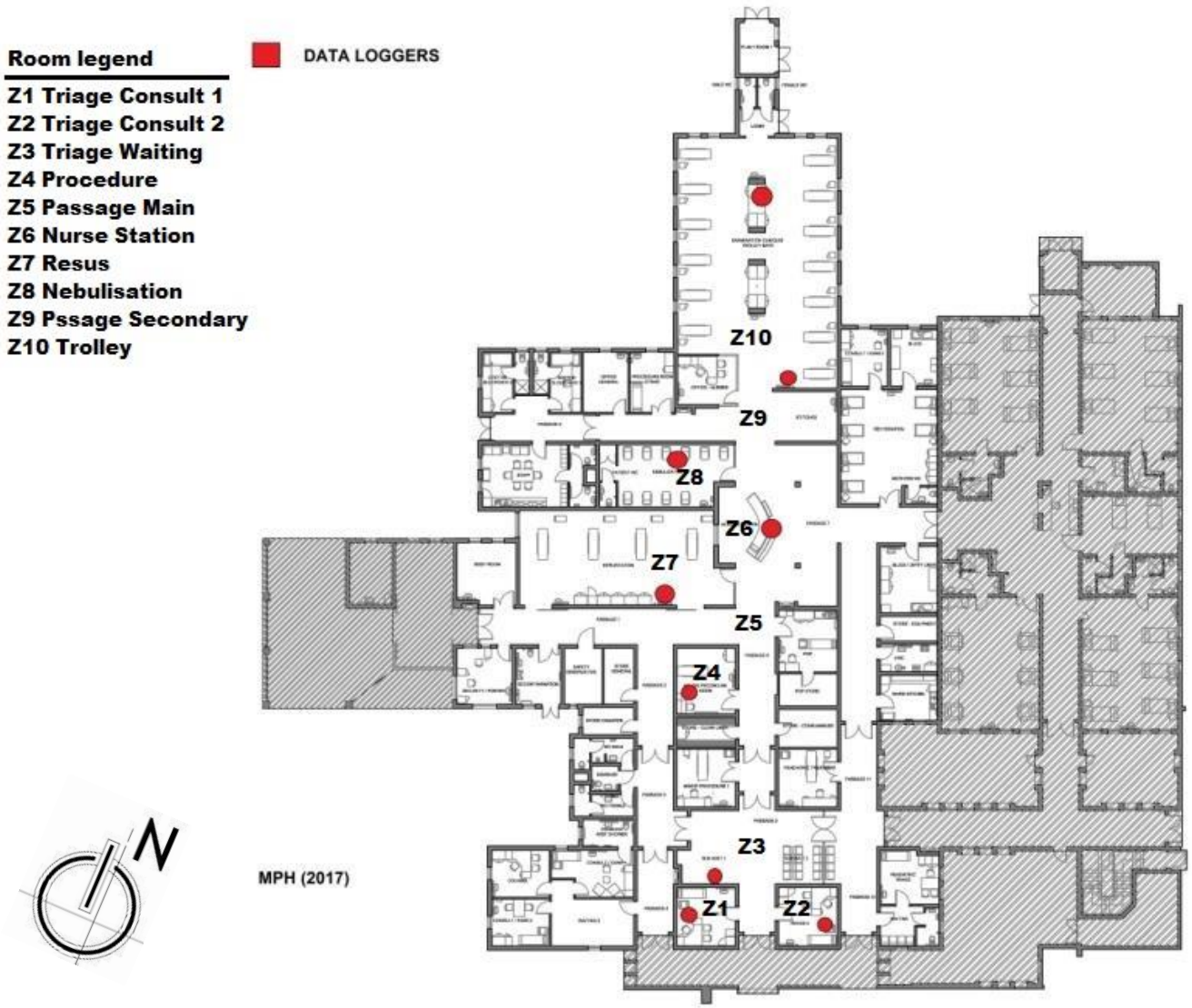



Figure 86: Location of data loggers at KDH

### 9.2.1 MECHANICAL CHARACTERISATION (MC)

Refer to addenda 6 for the full 2016 mechanical characterisation Excel data set. See Table 9.2 and Table 9.3 below for the data on the ventilation characterisation of KDH and MPH. From the data it is evident that both hospitals employ predominantly mechanical ventilation strategies. KDH supports openable windows in the Trolley, Resus and Nebulisation rooms; MPH supports openable windows in the Trolley and Resus rooms, which can provide a mixed-mode ventilation condition, but with limited effect, as these windows are restricted to open and very few windows have been provided.

#### 9.2.1.1 MECHANICAL CHARACTERISATION METHODOLOGY

The author requested drawings of both MPH and KDH, which included architectural and mechanical drawings, and received architectural drawings from the Department of Health Western Cape (DoHWC) for MPH and KDH. The author received the mechanical engineering drawings from DoHWC consultants for MPH, as well as the most current scoping report compiled in 2015 (Tricon Consulting Engineers 2015) for the upgrade of the A&E of MPH. The author did not receive the mechanical engineering drawings for KDH or any status quo report despite numerous requests. Findings in the report were compared to the study data referenced in Table 9.2 and Table 9.3. Each A&E was manually characterised by the author, supported by Tobias van Reenen, resident mechanical engineer and senior researcher at the CSIR. A mobile air capture hood - “Steve” - was constructed of Corex® board. The dimensions: under-side measure 0.136msq, top side 750mmx750mm, length 1200mm. Steve was used to calculate airflow at the exhaust and supply vents. The number of ventilation exhaust and supply vents was counted per room type. The outdoor $CO_2$ measure was taken as baseline before starting the flow measures, and these were 340ppm for MPH and 377ppm for KDH. The temperature, humidity and $C0_2$ values were captured using a TSI IAQ-Calc® indoor air quality meter, Model 7525. ($C0_2$: 0-5000 ppm, 3% accuracy or ± 50ppm, resolution 1ppm, NDiR sensor); (Temperature: range 0-60°C, 1°C accuracy, 30 second response time; type: thermistor); (Humidity: 5%-95% RH, 3% accuracy, 0.1% resolution, 20 second response time. Sensor: thin-filmed capacitive). Logging intervals: 1 second - 1 hour, range: 30 300 data points; TSI VelociCal® air velocity meter, model 5725; velocity range: 0.25 to 30m/s, 1% accuracy of +-0.02 m/s. Duct size: 0-16msq; temperature: 0°C - 60°C; accuracy 0.5°C; resolution: 0.1°C; intervals: 1second – 1 hour. Range: 12 700 data points. Room area and volumes were measured using a Bosch GKM50® professional laser distance meter (GLM 50 3601 k72 200). The openable windows were counted for each room type. All the data were captured onto an Excel spreadsheet using the accepted calculations as outlined below. Refer to addenda 6.

The maximum instantaneous ventilation rate, in ACH or L/s per person, is calculated using the following methodology. Each sedentary person in the space is a predictable and consistent source of $CO_2$ with $CO_2$ generation rates of 0.30 l/min at exhalation rates of 8.0 l/min (Rudnick & Milton 2003). At steady state, this causes a differential in equilibrium between the outdoors (typically 350-400 PPM) and the indoor space, which has a greater volumetric concentration. Solving the mass exchange rate calculation (equation 2) determines the corresponding ventilation rate for the measured $CO_2$ concentration. The calculated ventilation rate represents the maximum theoretical ventilation rate. The volume fraction of $CO_2$ added by exhaled breath was assumed to be 38 000 PPM (0.038 %). The equation used to calculate the probability for airborne contamination is the rebreathe fraction described below which is derived from the Wells Reilly equation:

**Equation 1**

$$1) \quad f = \frac{Ve}{V} = \frac{C-Co}{Ca}$$

| | |
|---|---|
| F | is equivalent to the fraction of indoor air that is exhaled breath, which is also the rebreathed fraction |
| Ca | Is the volume fraction of $CO_2$ added by exhaled breath during breathing |
| V | is the volume of the shared air space, |
| Ve | is the equivalent volume of exhaled breath contained in indoor air ($m^3$) |
| C | is the volume fraction of $CO_2$ in indoor air, and |
| Co | is the volume fraction of $CO_2$ in outdoor air |

(Rudnick & Milton 2003)

From the parameters in the above calculation, the following ventilation calculation is used to calculate the ACH and L/S per person. This is an accepted methodology as prescribed in the ASTM standard D6245 -18, recently updated in 2018 – E741 – 11 (ASTM 2018).

**Equation 2**

$$2) \quad Q_P = 10^6 \times G_p l \, (C_{in,eq} - C_{out})$$

| | |
|---|---|
| $Q_P$ | outdoor airflow rate per person into the zone, L/s per person, and |
| $G_p l$ | $CO_2$ generation rate in the zone per person, L/s per person. |
| $C_{in,eq}$ | equilibrium $CO_2$ concentration in the zone, ppm(v), and |
| $C_{out}$ | outdoor $CO_2$ concentration, ppm(v). |

(ASTM 2018)

To determine the ACH and L/s per person, the result of the calculate above is used in the calculation below.

**Equation 3**

$$3) \quad n_{eq} = \frac{G}{V} \times 3.6$$

| | |
|---|---|
| $n_{eq}$ | equivalent ventilation rate in the zone, indicated in ACH |
| Q | zone ventilation rate, L/s, and |
| V | volume of the zone, L. |

(ASTM 2018)

These formulas were used to calculate the ACH and L/s per person in the study data. Table 9.2 and Table 9.3 are the data tables sourced from addenda 6 for the MC data set. The measurements for the data were taken by the TSI IAQ-Calc® indoor air quality meter, Model 7525. The manufacturer indicates a sensor accuracy range of ± 50ppm. The low $CO_2$ values measured and the resultant differentials between sources point to a large potential deviation in the results. An accepted calculation and manufacturer recommendation for using $CO_2$ to calculate the quanta of fresh air/ outside air in room is noted below. (TSI 2013) and ANSI

**Equation 4**

$$\%\ outside\ air = \frac{return\ airmovent\ t* - supply\ air\ movement\ t*}{return\ airmovent\ t* - outside\ air\ movement\ t*}$$

#### 9.2.1.2 MECHANICAL CHARACTERISATION FINDINGS

The source data for Table 9.2 and Table 9.3 can be found in addenda 6.

Table 9.2: Mechanical system characterisation data KDH

| | Room | Zone | Volume $m^3$ | Ventilation type | | Total Flow (L/s) | Average $CO_2$ supply | °C | Average $CO_2$ return | Correct Average ACH | Correct Average L/s pp | Average RH | Windows |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KDH | Triage Consult 1 | Z1 | 30.05 | 1 | Supply | 90 | 361 | - | 517 | 11.67 | 32.48 | 55 | None |
| KDH | Triage Consult 2 | Z2 | 30.05 | 1 | Supply | 79.64 | 356 | 25.5 | 453 | 12.52 | 52.23 | 57 | None |
| KDH | Triage Waiting | Z3 | 53.16 | 2 | Supply | 187.77 | 378 | 25.2 | 519 | 15.15 | 42.07 | 55 | Top light, closed |
| KDH | Nurses' Station | Z6 | 448.38 | 4 | Supply | 619.96 | 367 | 25.5 | 391 | 11.86 | 211.11 | 53.5 | Top light, closed |
| KDH | Resus | Z4 | 200.52 | 3 | Supply | 440.33 | 341 | 26 | 356 | 62.49 | 348.06 | 52.5 | Top hung, open 20% |
| KDH | Nebulisation | Z7 | 134.88 | 7 | Exhaust | 316.52 | 360 | 26.3 | 384 | 50.71 | 211.11 | 51.7 | Top hung, open 20% |
| KDH | Procedure 1 | Z8 | 68.31 | 4 | Supply | 291.80 | 346 | 22 | 399 | 12.64 | 119.92 | 64 | None |
| KDH | Trolley (1) Main | Z9 | 576.8 | 13 | Exhaust | 2392.74 | 466 | 25.4 | 535 | 25.15 | 95.45 | 54.1 | Open windows 70% Top hung, open 25% Top light, closed |
| | | | 576.8 | 4 | Supply 0.49m/sec | 1050 | 360 | | | 18.21 | 89.79 | | |

Table 9.3: Mechanical system characterisation data MPH

| | Room | Zone | Vol $m^3$ | Ventilation type | | Total Flow (L/s) | Avg CO2 supply | °C | Avg CO2 return | Correct Average ACH | Correct Average L/s pp | Average RH | Windows |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MPH | Triage Consult 1 | Z1 | 38.53 | 1 | Supply | 54.9 | 430 | 24.3 | 540 | 17.21 | 46.06 | 57 | None |
| MPH | Triage Consult 2 | Z2 | 38.53 | 1 | Supply | 55 | 360 | 23.2 | 432 | 19.72 | 70.37 | 58.7 | None |
| MPH | Triage Waiting | Z3 | 110.8 | 2 | Exhaust | 233.04 | 360 | 23.2 | 454 | 18.13 | 62.01 | 56 | None |
| MPH | Nurses' Station | Z6 | 239.68 | 3 | Supply | 418.51 | 367 | 22 | 437.33 | 9.53 | 70.48 | 56 | Top light, closed |
| MPH | Resus | Z7 | 212.61 | 3 | Supply | 313.52 | 360 | 23.3 | 556.66 | 4.64 | 34.20 | 61.2 | Top hung, open 25% |
| | | | | 4 | Exhaust | 815.87 | 360 | | 391.75 | 22.26 | 192.67 | | |
| MPH | Nebulisation/ Psychiatric | Z8 | 67.73 | 1 | Exhaust | 636 | 360 | 24.3 | 400 | 33.66 | 126.67 | 63.8 | None |
| | | | | 1 | supply | 13.4 | 357 | | 395 | 35.43 | 133.33 | | |
| MPH | Procedure 1 | Z4 | 38.74 | 1 | Supply | 75.93 | 362 | 24.3 | 394 | 29.43 | 158.33 | 57 | None |
| MPH | Trolley (1) Main | Z9 | 424.42 | 13 | Exhaust | 846.89 | 360 | 22.5 | 414 | 25.47 | 93.83 | 58.2 | Open windows 60% Top hung, open 25%. |
| | | | | 5 | Supply | 684.32 | 360 | | 450.8 | 15.70 | 57.84 | | |

Table 9.2 and Table 9.3 are the data tables sourced from addenda 6 for the MC data set. When equation 4 is applied to the data, for example the Triage Consult rooms as sample for the system, the following findings are evident.

KDH Triage Consult 1 = $^{156}/_{140}$ = 100+% outside air
KDH Triage Consult 2 = $^{76}/_{97}$ = 78% outside air
MPH Triage Consult 1 = $^{200}/_{110}$ = 100+% outside air
MPH Triage Consult 1 = $^{92}/_{72}$ = 100+% outside air

It can be deduced that the HVAC system supplies almost 100% fresh air/outdoor air to the building; this aligns with the NDoH and WCDoh accepted position on air recirculation in HVAC systems in clinical environments in healthcare buildings. Furthermore, the data show that KDH provides higher levels than MPH of air change (ACH), with lower relative humidity (RH) and temperature values. This could indicate that the HVAC system for MPH is not working optimally. In both hospitals the ACH fall under the required 12 ACH minimum for airborne precaution rooms in healthcare settings, as per the IUSS guidelines for good IAQ practice. Relatively high flow rates are achieved at both hospitals – refer to Chapter 9 for conclusions on microbial community distribution due to this factor. The accepted standard for assessing and quantifying the risk for airborne transmission utilises $CO_2$ and the re-breathed air fraction as it represents potential cross contamination. This requires considering occupancy rates, without which the acceptable ACH cannot be determined. Therefore, the accepted ventilation rate is based on L/s per person and not ACH. The A&E is largely a transitional environment with multiple patients regarded as TB presumptive. This implies that all spaces in this unit are "risk" spaces. However, special consideration must be given to the Nebulisation room which will host known TB and presumptive TB patients and can be considered to be a high risk environment. The following risk categories with reference to airborne contamination and TB were developed by WHO (WHO 2009):

1. Low Risk: (7.5 L/s per person). This represents areas where one does not expect cases of TB infection or presumptive TB infected patients/clients such as large volume admission space or service areas (7.5 L/s per person – reference to SANS 10400-O:2010); from Table 2).
2. Medium Risk: (60-80 L/s per person). This represents areas where undiagnosed cases of TB infection are expected, in accordance with the national TB infection rate (+- 600 per 100 000) of the population, such as OPD waiting areas, Rehabilitation and Accident and Emergency units.
3. High Risk: (80-160 L/s/per person). This represents areas where there is a high risk and known and presumptive TB infection, such as TB consulting rooms and TB units.

From the data, it can be accepted that the room sizes for matching clinical services at both the hospitals are similar in volume. Table 9.4, the summary of pertinent information from the Tricon report, includes background information for the Cape Flats region and will be accepted as applicable to both hospital sites. Detailed information on the performance of the MPH mechanical system will only be associated and compared with the author's data on MPH. It is important to note that more than a year has passed between the report and the Mechanical characterisation. It is therefore highly likely that the data would indicate variations, and in light of this (as communicated by the facility manager) the HVAC system would be upgraded. This work was due to start in 2018.

#### 9.2.1.3 TRICON REPORT

The Tricon report refers to MPH only. (No report was found and/or issued to the author for KDH.) The report was due to imminent upgrades of the ventilation system in MPH. Table 9.4 includes the 2016 MC assessment data for direct comparison with the report's findings.

Table 9.4: Tricon report information (Tricon 2015)

| **MPH data and report** | | | | |
|---|---|---|---|---|
| **Room type** | **2015 Tricon report: ACH** | **2015 Tricon report: L/s pp** | **2016 MC assessment: ACH** avg e+s | **2016 MC assessment: L/s pp** avg e+s |
| Triage Consult 1 | 6.2 | 77 L/s pp | 17.21 | 46.06 L/s pp |
| Triage Consult 2 | 6.2 | 77 L/s pp | 19.72 | 70.37 L/s pp |
| Triage waiting | 8 | 300 L/s pp | 18.13 | 62.01 L/s pp |
| Nurses' Station | 5.6 | 346 L/s pp | 9.53 | 70.48 L/s pp |
| Resus | 6.4 | 346 L/s pp | 13.44 | 113.43 L/s pp |
| Nebulisation/ Psychiatric | 4.8 | 120 L/s pp | 34.55 | 130 L/s pp |
| Procedure 1 | 6.8 | 84 L/s pp | 29.43 | 158.33 L/s pp |
| Trolley (1) Main | 6.4 | 875 L/s pp | 20.58 | 75.83 L/s pp |
| **General data**<br>Ambient condition for Cape Flats region outdoors:<br>Summer: 32˚C DB; 22˚C WB<br>Winter: 4˚C DB; | | | | |
| Ambient condition for MPH indoors:<br>Summer 23˚C ± 1.5˚C<br>Winter: 21˚C ± 1.5˚C<br>No humidity control exists | | | | |

The 2015 report ACH and L/s are disparate. The indicated ACH would be too low for the indicated L/s. The L/s values are more comparable to the 2016 MC data. The Triage consult spaces and Nebulsation/Psychiatric are comparable. The 2015 report L/s for Triage waiting, Resus, Nurses' Station and Trolley are extremely high and questionable. Hospital staff informed the author that changes were being made to the air supply during that time, which could account for this variation. Lastly, the report indicates that the system's performance is below the required and designed rates for extraction in all areas when considering ACH; however, as noted the L/s rates are disparate and would indicate much higher ACH rates.

### 9.2.2 PRE-SAMPLING TESTS

Prior to sampling (logging), a test run of the equipment was performed which took measurements consecutively for four days, testing the battery life and data quality. In addition, a weather station was used, but due to theft of the weather station no data were collected. It was decided not to replace the station and to rely on commercial weather data, if required. The Gaslab® proprietary software was tested with the data collected. This test was done in June 2015 (winter) as part of a risk analysis study, and mechanical characterisation was done in November 2016 (summer). A loss of two of the 18 loggers was experienced and attributed to logger errors and faulty sensors. During the total period of collection for the experiment (summer and winter), similar losses were experienced from three of the 18 data loggers at KDH Z1 & Z3 and at MPH Z1.

### 9.2.3 SAMPLE TYPES

Data were collected using data loggers, mobile measuring equipment, and commercially available weather data, if required. Refer to Table 9.5 for data type collected per sampler type.

Table 9.5: Environmental samplers and data types

| **Sampler type** | **Data type** |
|---|---|
| DL | $CO_2$ |
| DL | Temperature |
| DL | Relative humidity |
| MME | Volume |
| MME | Area |
| MME | Lux |
| MME | Ventilation type |
| MME | Mechanical ventilation: air changes |
| MME | Mechanical ventilation: air volume |
| MME | Mechanical ventilation: air humidity, $CO_2$ and temperature |
| WD | Outdoor weather data: wind, temperature and humidity |
| **(DL) data Logger, (MME) mobile measuring equipment, (WD) weather data* | |

#### 9.2.3.1 DATA LOGGERS (DL)

Loggers were strategically placed in the selected rooms. The data loggers used were single manufactured units by $CO_2$Meter® Inc., Ormond Beach, Florida, United States, unit type CM-0018AA. The unit included built-in sensors collecting $CO_2$, temperature and relative humidity data, adding a date and time stamp. The loggers were placed either on a surface at counter-top height, i.e. at 900mm, or wall mounted at 1500mm. The data were recorded via a built-in SD Card that was disseminated on completion of the investigation using GasLab® software, as provided by the manufacturer of the data loggers. The expected battery life of the unit was four to five days, and batteries were checked daily by the researchers to prevent data loss due to unforeseen power down time. Data logger characteristics: Temperature ±2°C, over full temperature range; sampling rate: > 1 Hz logging set at one minute 30 second intervals. Relative Humidity ±5% RH over full temperature range; sampling rate: > one Hz logging at one minute 30 second intervals. $CO_2$ sampling method by diffusion; non-dispersive infrared (NDIR); measurement range: 0 to 2,000 ppm (0 to 0.2%); accuracy: ±50ppm ± 2.5% of measured value; sampling rate: > one Hz logging at one minute 30 second intervals. A one minute 30 second logging interval was selected to ensure that full four-day data readings could be collected.

#### 9.2.3.2 MOBILE MEASURING EQUIPMENT (MME)

Characteristics of mobile measuring equipment:

1. Meter Bosch, GKM50® Professional laser distance meter (GLM 50 3601 k72 200), for taking distance, area and volume measurements.
2. Tenmars® Lux/FC light (TM-202), measure range: 200, 2000, 20 0000, 200 000 Lux, accuracy 3% (incandescent), 8% (other visible sources).
3. TSI IAQ-Calc® Indoor Air Quality Meter, Model 7525, $C0_2$, humidity and temperature meter ($C0_2$: 0-5000 ppm, 3% accuracy or ±50ppm, resolution 1ppm, NDiR sensor); (temperature: range 0-60°C, 1°C accuracy, 30 second response time, type: thermistor); (humidity: 5%-

95% RH, 3% accuracy, 0.1% resolution, 20 second response time, sensor: thin-filmed capacitive); logging intervals: 1 second – 1 hour, range: 30300 data points.
4. TSI VelociCal® Air Velocity Meter, Model 5725, velocity range: 0.25 to 30m/s, 1% accuracy of ±0.02 m/s, duct size: 0-16msq, temperature: 0°C - 60°C, accuracy 0.5°C, resolution: 0.1°C.; intervals: 1second – 1 hour, range: 12700 data points.
5. Mobile air capture hood "Steve" constructed of Corex® board. Under size measure: 0.136msq, top side 750mmx750mm, length 1200mm.

#### 9.2.3.3 WEATHER DATA (WD)

Outdoor temperature, outdoor wind direction and wind speed were drawn from commercially available weather data, when required (this was not used, only qualitatively noted).

### 9.2.4 SAMPLING DURATION

The RH, temperature and ambient $CO_2$ sampling were logged by the data loggers (DLs) continuously at one minute 30 second intervals, for four days in two seasons, in winter and summer. The mobile measuring equipment (MME) data were logged on spot checks as required.

### 9.2.5 SAMPLE SIZE

The characterisation of the indoor environment of the core rooms at the KDH and MPH A&E units were represented by 10 zones, of which eight zones had data loggers installed. Refer to Table 9.1 for room zone classification, and Figure 86 and Figure 85 for zones and logger location. Logging extended over 96 hours, with an estimated 3200 data points collected per logger.

### 9.2.6 ANALYSIS

The data were analysed using GasLab™ software – as recommended and provided by the manufacturer of the data loggers – followed by MS Excel and R® statistics. Data included the $CO_2$ levels, temperature and RH of each zone as measured by the loggers. Correlation analysis was done with occupancy, microbial samples and spatial flow statistics – see Chapter 10 for results.

### 9.2.7 EXPERIMENTAL DELINEATION

The research limits to the experimental investigation are listed below.

1. The hourly observation period over 12 hours per day was assumed to represent the daily average usage pattern of the studied environment, in alignment with the Space Syntax methodology and published study correlations.
2. The study observations were limited to the two selected hospitals, KDH and MPH, and represent the average space use of the A&E units at high-burden healthcare facilities in South Africa. Refer to section 7.2.6.
3. The A&E core areas within each unit were delineated as the investigation study zones. These areas experience the highest traffic levels and contain the highest number of functional spaces. Cost and time considerations informed the study boundaries. The findings are limited to the described environments; they may not represent the rest of the hospital.

4. The selected rooms represented the high traffic zones in the selected departments and thus the utility and low occupancy spaces were not considered.
5. This experiment provided sampling for a maximum of four days only per season due to cost limitations, and the distribution of days represented peak high and peak low times as found in the questionnaire. Refer to Table 7.4.
6. This experiment considered only two seasons as representative of the full variation of climatic conditions over a year.
7. Meters used for this experiment provided $CO_2$, RH and temperature as provided by CO2meters.com. See below for the sensor limitations:
   Measuring principle: $CO_2$, non-dispersive infrared (NDIR) sensor; measuring range: 1%; $CO_2$ models 0-10,000 ppm; 30% $CO_2$ models 0-300,000 ppm (0-30% vol.). Repeatability: 1%; $CO_2$ models ±20 ppm, ±1% measured value; 30% $CO_2$ models ±0.1%, ±2% of measured value. Accuracy: 1%; $CO_2$ models ±30ppm, ±3% measured value; 30% $CO_2$ models ±0.2%, ±3% of measured value. $CO_2$ Sensor ratings: life expectancy >15 years; warm-up time <1 min (instant measurements). Temperature sensor: range -40°C to 120°C; repeatability ±0.1°C; accuracy ±0.5°C. Relative humidity sensor: range 0-100%; repeatability ±0.1%; accuracy ±3%. Dimensions: L x W x D; (mm). Data logging: data points 15,000 (CM-0016, -0017); 5,400 (CM-0018, -0018AA, -0019, -0209, -0210); Programmable interval data: date, time, $CO_2$, %RH, temp. Power: input voltage 5VDC (use only supplied adapter); power consumption: 500 mA (while charging); charging time 5-8 hrs (approximately); battery type/capacity 4xAA (CM-0016, -0017, -0018AA); Li-Ion battery lifetime: 2-3 years, depending on cycles. ($CO_2$ meters.com 2017)

## 9.3 FINDINGS

### 9.3.1 TESTING THE HYPOTHESES

For reference, the thesis hypotheses (Chapter 6) are repeated for context to the findings.

Primary research hypotheses:
Hypothesis A: Building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health architectural design, based on the biome composition (abundance and richness) of indicator organisms.

Therefore…

Hypothesis B: Social behavioural science studies which consider factors of human movement patterns, occupancy and functional use of space influence the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus, the indoor environmental factors of hospitals MPH and KDH influence the composition of both the micro (room level) and macro biome (building level) environments.

Secondary research hypotheses:
Sub-hypothesis A: The source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room;

&

Sub-hypothesis B: The levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.

### 9.3.2 THE FINDINGS

This section is the third of three sections dealing with the findings of the investigation. The findings presented in this section refer to the environmental data collected which are important factors in understanding the ecology of the built environment. Lastly, the conclusions are measured against the research questions and presented in Chapter 10. Eighteen data loggers were utilised, collecting ±115 000 data points for temperature, RH and $CO_2$. Three hundred and sixty observation sheets were recorded and 25 580 flow lines were observed and drawn. A total of 31 690 occupants were observed and tabled. KDH and MPH hospital staff completed ten questionnaires. A master data matrix of 40 BE data factors and 22 070 data points was created. The data factors for the BE data that were collected include: sequence type, sample ID, session ID, sample classification, natural ventilation, sample type, DNA or culture, culture identification, indoor or outdoor, hospital type, zone, room type, season, start date and time, end date and time, gate crossing, internal movement, room volume, room area, HVAC, flow (L/s), ACH, daylight-artificial light-mixed type light, sample average $CO_2$, sample average temperature, sample average humidity, session average $CO_2$, session average temperature, session average humidity, session average doctor, session average nurse, session average other, session average patient, session average total, and session main user. See addenda 2: Master microbiology database (Excel) for reference. Table 8.16 reflects all BE factors measured, with the data collection tools and programs in support of the data table found in Addenda 1: Master data base.

Table 9.6: BE data factors collected and sampled for KDH and MPH

| No | Factor | Method |
|---|---|---|
| 1 | Temperature:<br>Sample average & session average | Loggers, observation association |
| 2 | Relative humidity:<br>Sample average & session average | Loggers, observation association |
| 3 | $CO_2$:<br>Sample average & session average | Loggers, observation association |
| 4 | Lux levels | Lux hand-held meter |
| 5 | Light source | Observation |
| 6 | Ventilation source | Observation |
| 7 | ACH | Equipment (see Ch 3) |
| 8 | Flow L/s | Equipment (see Ch 3) |
| 9 | Room volume | CAD |
| 10 | Room area | CAD |
| 11 | Hospital | Identification |
| 12 | Gate crossing | Observation, CAD, GIS, DepthMap™ |
| 13 | Internal flow movement | Observation, CAD, GIS, DepthMap™ |
| 14 | Session main user | Observation, CAD, GIS |
| 15 | Occupancy | Observation, CAD, GIS |

The analysis of the BE environmental data will be presented in the following sequence: firstly, the hospital data are provided for each hospital, but in a combined format for simple comparative purposes. Secondly, the hospitals are compared individually and then correlated where applicable and, thirdly, the findings are measured against the research questions and presented in section Chapter 10.

#### 9.3.2.1 COMBINED HOSPITAL DATA

The following table contains data collected for all factors categorised per room for both hospitals. The figures are either summed, averaged or other, depending on the required application. The data include $CO_2$, temperature, humidity, occupancy rates, user types, gate crossing, internal flow, occupancy per room, air changes, airflow rate, area, volume, lux levels and ventilation source. The data account for each room type and for both KDH and MPH for summer and winter. Gate crossing is summed per room (total count) calculation for GC p/minute. This calculation considers the daily observations (18), time taken per observation (3 minutes) and the total study days (4) as representative of a per minute representation (The more the number of observations and the longer the study duration, the more accurate the representation - this study period was in excess of most space syntax studies). The calculation for GC p/min is as follows.

$GC\ p/min = \frac{Obs}{t}$ thus for this study the values apply: $GC\frac{p}{min} = \frac{Obs}{(3min \times 18\ observations\ \times 4days)}$

| | |
|---|---|
| $GC\ p/min$ | Gate crossing per minute. This value is the estimated number of gate crossings per minute daily. |
| $Obs$ | Observation. This is the total number of observations captured over the period of the study. |
| $t$ | Time. This is total observation time in minutes. |

This observation equation was used for observation flow measures to determine flow rates per minute in each observed space. By replacing the Obs value with Obs flow value this can be achieved.

Table 9.7: BE factors (13) data table for KDH and MPH

| | MPH | | | | KDH | | |
|---|---|---|---|---|---|---|---|
| **$CO_2$ avg (ppm)** | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | 0 | | 597.7 | | 467.2 | | 804 |
| Nurse Station | | 522.5 | | 586.4 | | 469.5 | | 480.9 |
| Procedure 1 | | 448 | | 542 | | 412 | | 465 |
| Resus | | 487.4 | | *Logger error* | | 424.1 | | 537.9 |
| Triage consult 1 | | 596.8 | | 554.4 | | 563.5 | | *Logger error* |
| Triage consult 2 | | 585.8 | | 649.5 | | 457.7 | | 760.8 |
| Triage waiting | | 498.9 | | *Logger error* | | 441.7 | | 700.7 |
| Trolley | | 512 | | 597.7 | | 445.5 | | 548.6 |
| | **MPH** | | | | **KDH** | | | |
| **Temperature avg (°C)** | | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | *Logger error* | | 22.8 | | 24.3 | | 20.1 |
| Nurses' Station | | 24.1 | | 22 | | 23.1 | | 22.1 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Procedure 1 | | 25.3 | | 22.5 | | 19.3 | | 25.5 |
| Resus | | 23.3 | | *Logger error* | | 22.8 | | 23.6 |
| Triage Consult 1 | | 24.9 | | 24.7 | | 23.5 | | *Logger error* |
| Triage Consult 2 | | 24.9 | | 22.5 | | 22.8 | | 21.5 |
| Triage Waiting | | 24.9 | | *Logger error* | | 18.3 | | 21.6 |
| Trolley | | 23.1 | | 22 | | 23.9 | | 22.3 |
| | **MPH** | | | | **KDH** | | | |
| **Humidity avg (%)** | | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | *Logger error* | | 51.3 | | 49.7 | | 56.8 |
| Nurses' Station | | 48.4 | | 51.7 | | 52.4 | | 47.1 |
| Procedure 1 | | 43.8 | | 44.4 | | 67.2 | | 37.7 |
| Resus | | 50.7 | | *Logger error* | | 52.7 | | 41.3 |
| Triage Consult 1 | | 48 | | 44.2 | | 53 | | *Logger error* |
| Triage Consult 2 | | 49.6 | | 45.2 | | 52.4 | | 50.8 |
| Triage Waiting | | 46.9 | | *Logger error* | | 39.4 | | 51.1 |
| Trolley | | 51.5 | | 50.6 | | 53.4 | | 47.8 |
| | **MPH** | | | | **KDH** | | | |
| **Occupancy rate avg per room (person ratio)** | | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | | | 17.3 | | 10.3 | | 14.4 |
| Nurses' Station | | 7.3 | | 17 | | 6.7 | | 4.9 |
| Procedure 1 | | 1.7 | | 0.9 | | 0.3 | | 1.9 |
| Resus | | 7.7 | | 8.8 | | 7.1 | | 7.2 |
| Triage Consult 1 | | 2.2 | | 2.2 | | 2.7 | | 3.4 |
| Triage Consult 2 | | 1.9 | | 2.0 | | 1.7 | | 1.6 |
| Triage Waiting | | 15.2 | | 18.5 | | 8.6 | | 9.7 |
| Trolley | | 28.8 | | 29.8 | | 39.8 | | 36.3 |
| | **MPH** | | | | **KDH** | | | |
| **Highest user (user type)** | | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | | | patient | | patient | | patient |
| Nurses' Station | | Nurse | | patient | | Nurse | | Nurse |
| Procedure 1 | | Patient | | Nurse/patient | | Nurse/Doctor | | Doctor |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Resus | | Patient | | Nurse/patient | | Nurse | | Nurse |
| Triage Consult 1 | | Nurse | | Nurse | | Nurse | | Nurse |
| Triage Consult 2 | | Patient | | Doctor | | Doctor | | Patient |
| Triage Waiting | | Patient | | Patient | | Patient | | Patient |
| Trolley | | Patient | | Patient | | Patient | | Patient |
| | **MPH** | | | | **KDH** | | | |
| **Gate crossing summed per room (count) & p/min rate** | | | | | | | | |
| **Room type** | **p/min** | **Summer** | **p/min** | **Winter** | **p/min** | **Summer** | **p/min** | **Winter** |
| Nebulisation | - | - | 0.65 | 141 | 1.52 | 328 | 1.30 | 281 |
| Nurses' Station | 13.64 | 2947 | 13.64 | 2043 | 10.77 | 2327 | 11.16 | 2411 |
| Procedure 1 | 0.13 | 29 | 0.17 | 37 | 0.03 | 7 | 0.36 | 78 |
| Resus | 1.66 | 358 | 1.21 | 263 | 2.37 | 512 | 1.68 | 362 |
| Triage Consult 1 | 14.50 | 3131 | 0.69 | 148 | 1.57 | 339 | 1.63 | 351 |
| Triage Consult 2 | 0.65 | 141 | 0.25 | 54 | 0.48 | 103 | 0.43 | 93 |
| Triage Waiting | 8.69 | 1876 | 5.17 | 1117 | 0.75 | 162 | 0.88 | 191 |
| Trolley | 8.63 | 1865 | 4.94 | 1066 | 3.65 | 788 | 3.33 | 720 |
| Passage Main | 11.58 | 2501 | 7.37 | 1591 | 9.99 | 2158 | 14.33 | 3096 |
| | **MPH** | | | | **KDH** | | | |
| **Internal flow movement summed per room (count) & p/min rate** | | | | | | | | |
| **Room type** | **p/min** | **Summer** | **p/min** | **Winter** | **p/min** | **Summer** | **p/min** | **Winter** |
| Nebulisation | - | - | 0.55 | 119 | 1.35 | 292 | 1.47 | 318 |
| Nurses' Station | 11.12 | 2402 | 7.38 | 1595 | 8.81 | 1903 | 8.01 | 1732 |
| Procedure 1 | 0.11 | 24 | 0.02 | 5 | 0.01 | 3 | 0.22 | 47 |
| Resus | 2.44 | 526 | 1.50 | 323 | 1.83 | 396 | 1.97 | 426 |
| Triage Consult 1 | 0.97 | 210 | 0.47 | 102 | 0.93 | 200 | 1.05 | 226 |
| Triage Consult 2 | 0.47 | 102 | 0.212 | 46 | 0.26 | 57 | 0.16 | 34 |
| Triage Waiting | 3.81 | 822 | 2.24 | 484 | 0.45 | 98 | 0.54 | 116 |
| Trolley | 4.01 | 866 | 2.11 | 455 | 5.03 | 1087 | 4.75 | 1027 |
| Passage Main | 6.44 | 1391 | 4.22 | 911 | 5.88 | 1271 | 8.00 | 1728 |
| | **MPH** | | | | **KDH** | | | |
| **Occupancy total summed per room (people count)** | | | | | | | | |
| **Room type** | | **Summer** | | **Winter** | | **Summer** | | **Winter** |
| Nebulisation | | - | | 775 | | 292 | | 1597 |
| Nurses' Station | | 655 | | 1009 | | 1903 | | 783 |
| Procedure 1 | | 59 | | 8 | | 3 | | 109 |
| Resus | | 607 | | 557 | | 396 | | 992 |
| Triage Consult 1 | | 167 | | 109 | | 150 | | 364 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Triage Consult 2 | | 127 | | 91 | | 57 | | 101 |
| Triage Waiting | | 1289 | | 1206 | | 98 | | 1289 |
| Trolley | | 2503 | | 1908 | | 1087 | | 3880 |
| Passage Main | | 259 | | 217 | | 1271 | | 1114 |
| | **MPH** | | | | **KDH** | | | |
| **ACH (air changes per hour ) & L/s per person** | | | | | | | | |
| **Room type** | **L/s pp** | **ACH** | **n/a** | **n/a** | **L/s pp** | **ACH** | **n/a** | **n/a** |
| Nebulisation | (S 133.33) (E126.67) **130** | (S 35.43) (E 33.66) **34.55** | | | **211.11** | **50.71** | | |
| Nurses' Station | **70.48** | **9.53** | | | **211.11** | **11.86** | | |
| Procedure 1 | **158.33** | **29.43** | | | **119.92** | **12.64** | | |
| Resus | (S 4.63) (E 22.26) **124.76** | (S 4.64) (E 22.26) **13.44** | | | **348.06** | **62.49** | | |
| Triage Consult 1 | **46.06** | **17.21** | | | **32.48** | **11.67** | | |
| Triage Consult 2 | **70.37** | **19.72** | | | **52.23** | **12.52** | | |
| Triage Waiting | **62.01** | **18.13** | | | **42.07** | **15.15** | | |
| Trolley | (S 57.7) (E 93.83) **79.99** | (S 15.70) (E 25.47) **24.02** | | | (S 89.21) (E 95.45) **89.79** | (S 18.21) (E 25.15) **18.21** | | |
| | **MPH** | | | | **KDH** | | | |
| **Air Flow (L/s)** | | | | | | | | |
| **Room type** | | **Rate** | | | | **Rate** | | |
| Nebulisation | | 325 | | | | 53 | | |
| Nurses' Station | | 147 | | | | 207 | | |
| Procedure 1 | | 76 | | | | 73 | | |
| Resus | | 161 | | | | 127 | | |
| Triage Consult 1 | | 60 | | | | 90 | | |
| Triage Consult 2 | | 61 | | | | 80 | | |
| Triage Waiting | | 115 | | | | 102 | | |
| Trolley | | 118 | | | | 201 | | |
| | **MPH** | | | | **KDH** | | | |
| **Area / Volume ($m^2$, $m^3$)** | | | | | | | | |
| **Room type** | | **Area** | | **Volume** | | **Area** | | **Volume** |
| Nebulisation | | 26 | | 68 | | 102 | | 135 |
| Nurses' Station | | 75 | | 240 | | 140 | | 448 |
| Procedure 1 | | 15 | | 39 | | 26 | | 68 |
| Resus | | 82 | | 213 | | 77 | | 221 |
| Triage Consult 1 | | 15 | | 38 | | 12 | | 30 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Triage Consult 2 | | 14 | | 37 | | 12 | | 30 |
| Triage Waiting | | 42 | | 108 | | 23 | | 70 |
| Trolley | | 127 | | 372 | | 205 | | 577 |
| | **MPH** | | | | **KDH** | | | |
| **Lux levels** | | | | | | | | |
| **Room type** | | **Lux level** | | **Source** | | | **Lux level** | **Source** |
| Nebulisation | | - | | Artificial | | | 731 | Artificial |
| Nurses' Station | | 205.3 | | Artificial + Natural | | | 205.3 | Artificial + Natural |
| Procedure 1 | | 646 | | Artificial | | | 164 | Artificial |
| Resus | | 610 | | Artificial + Natural | | | 239 | Artificial + Natural |
| Triage Consult 1 | | 331.2 | | Artificial | | | 272 | Artificial |
| Triage Consult 2 | | 338.5 | | Artificial | | | 346 | Artificial |
| Triage Waiting | | 108.9 | | Artificial + Natural | | | 359.1 | Artificial |
| Trolley | | 392 | | Artificial + Natural | | | 516 | Artificial + Natural |
| | **MPH** | | | | **KDH** | | | |
| **Ventilation source** | | | | | | | | |
| **Room type** | | **Mechanical** | | **Natural** | | | **Mechanical** | **Natural** |
| Nebulisation | | Yes | | Yes | | | Yes | No |
| Nurses' Station | | Yes | | No | | | Yes | No |
| Procedure 1 | | Yes | | No | | | Yes | No |
| Resus | | Yes | | Yes | | | Yes | Yes |
| Triage Consult 1 | | Yes | | No | | | Yes | No |
| Triage Consult 2 | | Yes | | No | | | Yes | No |
| Triage Waiting | | Yes | | No | | | Yes | No |
| Trolley | | Yes | | Yes | | | Yes | Yes |

The BE data in Table 9.7 are discussed below, and will be referred to in later sections in Chapter 10 for further analysis. MPH experienced a 30% increase in occupancy in winter, whereas at KDH occupancy rates remained stable through both seasons. From the $CO_2$ measured at KDH and MPH, both hospitals accounted for higher $CO_2$ levels in winter. On average, MPH had higher $CO_2$ levels in summer and KDH in winter. $CO_2$ is regarded as a surrogate measure for re-breathed air and is factored for airborne risk assessment. The $CO_2$ levels must be considered with the occupancy numbers to ascertain true risk. From the data, rooms of concern in KDH are Triage Waiting and Triage Consult 1 and 2. In MPH, rooms of concern are Triage Consult 1 and marginally Triage Waiting, as reported in 9.2.1 (section on mechanical characterisation). The ACH presented by the Tricon report are greatly at odds with the measures taken for the study. For MPH the report indicates that 90% of the rooms are of

concern, whereas the findings in this study show elevated levels. This could be due to the open windows with mixed air sources elevating the values.

The temperature and humidity measured in MPH for both seasons were stable, indicating that the environment was in fact mechanically controlled and that the system was working. The elevated levels of $CO_2$ found in MPH in summer indicated that the functioning and stable HVAC system was not providing the required ACH and/or there was an increase in occupancy as found in Table 9.8 that impacted the acceptable IPC, as is evident from the MC and report found in section 9.2.1. They had similar levels of humidity with a marginal increase in winter, which could be due to the wet, rainy season at the Cape, as was experienced over the period of the study. The temperature and humidity at KDH varied far more, with a 20% variation in humidity and 12% in temperature, indicating that the HVAC system was not balanced or performing efficiently, even though an increase in humidity was expected in winter. Ramos and Stephens (2015) make reference to a number of studies that showed that environmental conditions such as temperature, relative humidity, and humidity ratio influence both surface-bound and airborne microbes in varying ways. The impact on microbial communities by minor variation in measures (T, Hr, $CO_2$) is still unknown and being studied.

Table 9.8: Data table of selected BE factors for KDH and MPH

| **BE Factor, averaged** | | **MPH** | | | **KDH** | |
|---|---|---|---|---|---|---|
| | **%** | **Summer** | **Winter** | **%** | **Summer** | **Winter** |
| Humidity | 5 | 45.86 | 48.22 | 20 | 49.85 | 40.49 |
| Temperature | 1 | 22.86 | 22.91 | 12 | 21.12 | 18.65 |
| Average occupancy rate | 50 | 64.8 | 92.9 | 1 | 77.3 | 79.6 |

From the summary in Table 9.8, taken from the data in Table 9.7, KDH experienced stable occupancy through both seasons; MPH experienced an increase in the winter season. The performance of the HVAC system was stable at MPH, as seen in the temperature and RH value, whereas KDH experienced large fluctuations in temperature and RH, implying an increased reliance on natural ventilation. The variation between summer and winter for MPH and KDH showed great variation. MPH RH varied by 5% and Temperature by 1% but occupancy by 50%, whereas KDH RH varied by 20%, Temperature by 12% and occupancy by only 1%. The environment in KDH was invariable, but the occupancy was stable; the opposite was true for MPH.

#### 9.3.2.2 COMBINED HOSPITAL DATA ANALYSIS

Figure 87 to Figure 92 compare BE data sets, categorised seasonally into room types per hospital. In this subsection, an overview is provided of the indoor environments through comparing hospitals and room types. It is a graphical representation of Table 9.6, and places the data in context. Commentary to follow for each figure.

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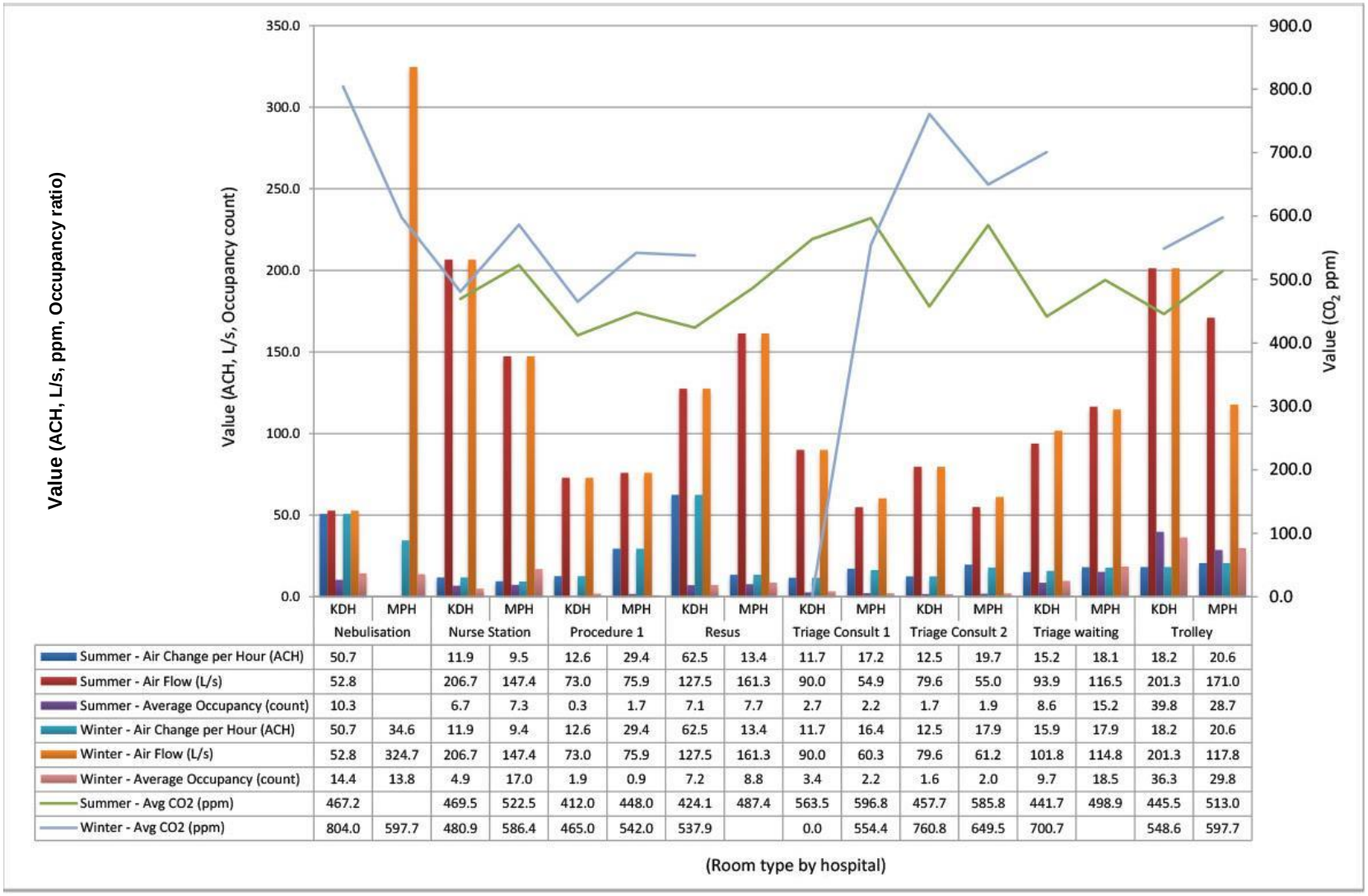
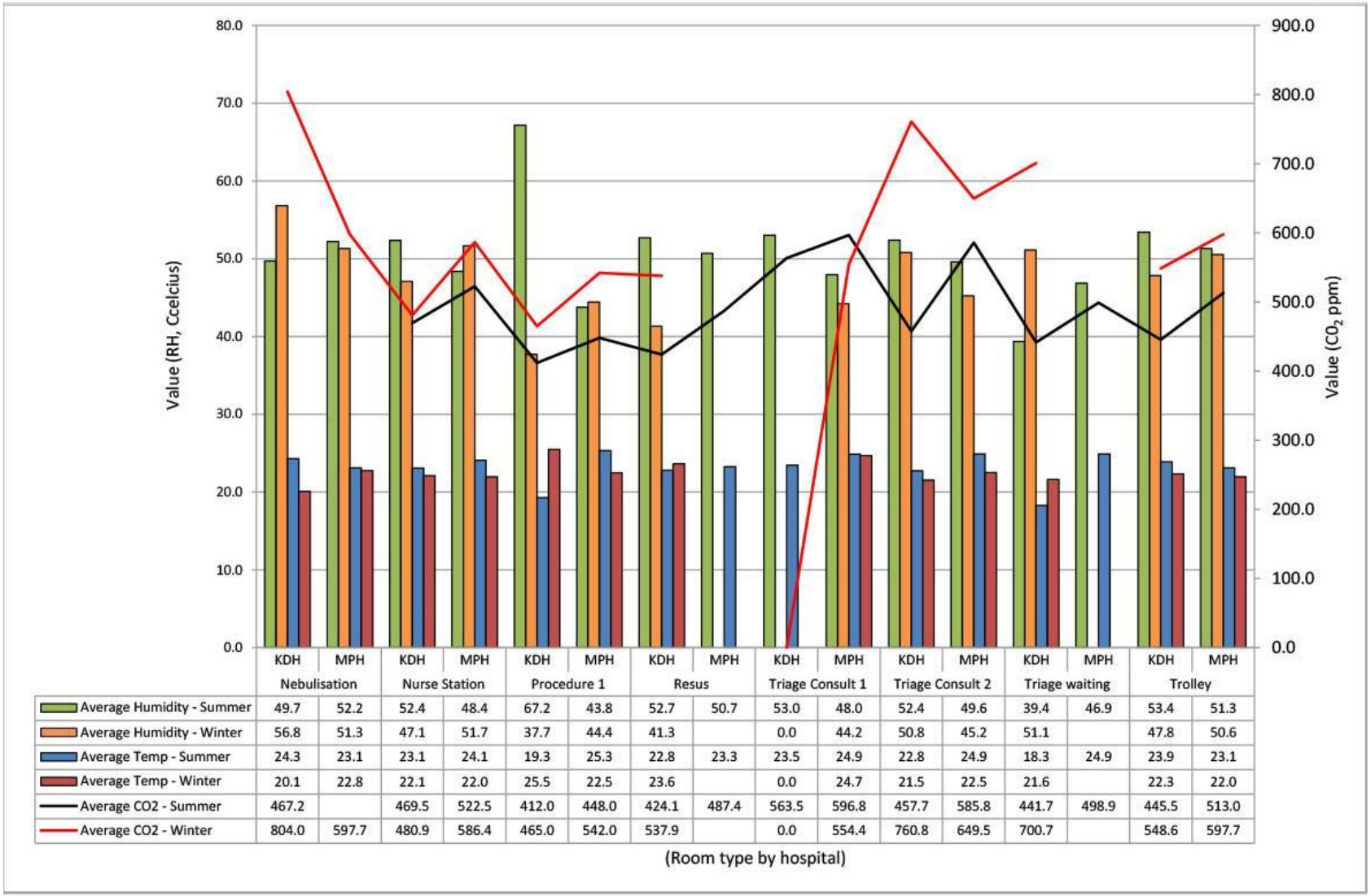



| | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Nebulisation | | Nurse Station | | Procedure 1 | | Resus | | Triage Consult 1 | | Triage Consult 2 | | Triage waiting | | Trolley | |
| Summer - Air Change per Hour (ACH) | 50.7 | | 11.9 | 9.5 | 12.6 | 29.4 | 62.5 | 13.4 | 11.7 | 17.2 | 12.5 | 19.7 | 15.2 | 18.1 | 18.2 | 20.6 |
| Summer - Air Flow (L/s) | 52.8 | | 206.7 | 147.4 | 73.0 | 75.9 | 127.5 | 161.3 | 90.0 | 54.9 | 79.6 | 55.0 | 93.9 | 116.5 | 201.3 | 171.0 |
| Summer - Average Occupancy (count) | 10.3 | | 6.7 | 7.3 | 0.3 | 1.7 | 7.1 | 7.7 | 2.7 | 2.2 | 1.7 | 1.9 | 8.6 | 15.2 | 39.8 | 28.7 |
| Winter - Air Change per Hour (ACH) | 50.7 | 34.6 | 11.9 | 9.4 | 12.6 | 29.4 | 62.5 | 13.4 | 11.7 | 16.4 | 12.5 | 17.9 | 15.9 | 17.9 | 18.2 | 20.6 |
| Winter - Air Flow (L/s) | 52.8 | 324.7 | 206.7 | 147.4 | 73.0 | 75.9 | 127.5 | 161.3 | 90.0 | 60.3 | 79.6 | 61.2 | 101.8 | 114.8 | 201.3 | 117.8 |
| Winter - Average Occupancy (count) | 14.4 | 13.8 | 4.9 | 17.0 | 1.9 | 0.9 | 7.2 | 8.8 | 3.4 | 2.2 | 1.6 | 2.0 | 9.7 | 18.5 | 36.3 | 29.8 |
| Summer - Avg CO2 (ppm) | 467.2 | | 469.5 | 522.5 | 412.0 | 448.0 | 424.1 | 487.4 | 563.5 | 596.8 | 457.7 | 585.8 | 441.7 | 498.9 | 445.5 | 513.0 |
| Winter - Avg CO2 (ppm) | 804.0 | 597.7 | 480.9 | 586.4 | 465.0 | 542.0 | 537.9 | | 0.0 | 554.4 | 760.8 | 649.5 | 700.7 | | 548.6 | 597.7 |

Figure 87: BE data (ACH, air flow, $CO_2$ and occupancy per room type) for KDH and MPH




| | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Nebulisation | | Nurse Station | | Procedure 1 | | Resus | | Triage Consult 1 | | Triage Consult 2 | | Triage waiting | | Trolley | |
| Average Humidity - Summer | 49.7 | 52.2 | 52.4 | 48.4 | 67.2 | 43.8 | 52.7 | 50.7 | 53.0 | 48.0 | 52.4 | 49.6 | 39.4 | 46.9 | 53.4 | 51.3 |
| Average Humidity - Winter | 56.8 | 51.3 | 47.1 | 51.7 | 37.7 | 44.4 | 41.3 | | 0.0 | 44.2 | 50.8 | 45.2 | 51.1 | | 47.8 | 50.6 |
| Average Temp - Summer | 24.3 | 23.1 | 23.1 | 24.1 | 19.3 | 25.3 | 22.8 | 23.3 | 23.5 | 24.9 | 22.8 | 24.9 | 18.3 | 24.9 | 23.9 | 23.1 |
| Average Temp - Winter | 20.1 | 22.8 | 22.1 | 22.0 | 25.5 | 22.5 | 23.6 | | 0.0 | 24.7 | 21.5 | 22.5 | 21.6 | | 22.3 | 22.0 |
| Average CO2 - Summer | 467.2 | | 469.5 | 522.5 | 412.0 | 448.0 | 424.1 | 487.4 | 563.5 | 596.8 | 457.7 | 585.8 | 441.7 | 498.9 | 445.5 | 513.0 |
| Average CO2 - Winter | 804.0 | 597.7 | 480.9 | 586.4 | 465.0 | 542.0 | 537.9 | | 0.0 | 554.4 | 760.8 | 649.5 | 700.7 | | 548.6 | 597.7 |

Figure 88: BE data ($CO_2$, RH and temperature) per room type for KDH and MPH

The data in Figure 87 and Figure 88 (factors of ACH, air flow, Occupancy, and $CO_2$) indicate that in 55% of the rooms the ACH at MPH are higher than KDH, whereas the air flow L/s for the rooms are similar for KDH and MPH, but vary considerably between room types. When considering the average $CO_2$ levels over the same periods, the $CO_2$ levels for summer were 400–600 ppm, and in winter 480-800ppm. For summer, the $CO_2$ levels at MPH were higher than at KDH for all rooms, which aligns with the ACH and L/s per person rates measured, also considering the average occupancy was higher at MPH than KDH for most rooms in both seasons. However, during winter KDH had significantly higher $CO_2$ values than MPH. A marked increase in the $CO_2$ values, of between 0ppm and 300ppm (room dependent), can be seen in winter for both hospitals. The $CO_2$ levels in winter were higher on all counts for both hospitals, except for the Triage Consult 1 room at MPH. When compared to the occupancy, as there is a known correlation between occupancy and $CO_2$ values, the study finds no significant occupancy increase on average in the winter season to account for the higher $CO_2$ values. However, the low L/s per person rates for MPH compared to the average room occupancy considering the WHO rates for airborne infections (as presented previously) indicates risks for TB infection for a number of rooms (Triage 1 and Triage Waiting are especially high incident spaces for presumptive TB patients; refer to the Wells Riley mass balance equation).

Furthermore, the data in Figure 87 indicate relatively constant temperature and humidity levels for MPH with more varied values for KDH. The $CO_2$ values for winter exceed those of summer. The trend shows an increase in $CO_2$ values in the winter season for both KDH and MPH. KDH had an estimated 200ppm increase considering total measured values, which equates to a +-50% increase in winter. MPH had an estimated increase of +- 60ppm considering total measured values, which equates to a +- 10% increase in winter. The trend shows that MPH had higher $CO_2$ values compared to KDH for all spaces, but KDH had higher CO2 values for summer and seasonal differential. The trend shows that both hospitals had a functioning HVAC system based on the relative stability of temperature and humidity values; however, KDH was far less stable, as seen in the value variation between rooms (Table 9.8; refer to MC in section 9.2.1 for detailed information). Of all the spaces, the Triage Consult 2 at both KDH (+40% increase: 457.7 – 760.8ppm) and MPH (+10% increase 585.8 – 649.5ppm) showed a significant increase in $CO_2$ values in the winter season. The Nebulisation room data for KDH (+40%, increase 467.2 – 804ppm, Triage Waiting +60% increase: 441.7 – 7007.7ppm) also showed a significant increase in $CO_2$ over the winter season, but due to logger failure, this cannot be compared to MPH. On average for Temperature KDH reports a 12% seasonal variation versus 1% at MPH, for RH a 20% seasonal variation versus 5% and for occupancy the inverse, a 1% seasonal variation versus 50% at MPH.

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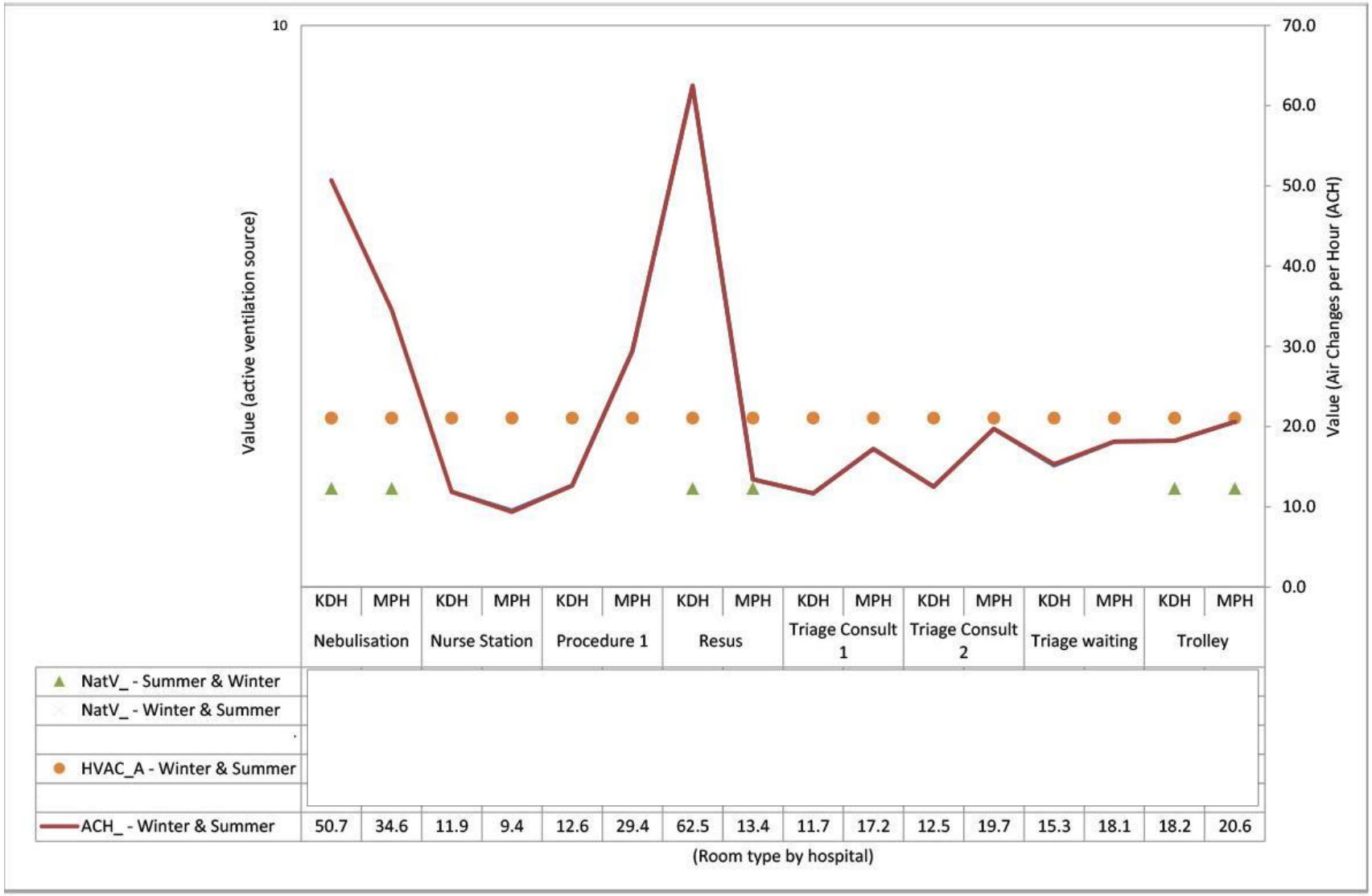



Figure 89: BE data (ACH, HVAC and natural ventilation) per room type for KDH and MPH

With reference to Figure 89, the Resus, Trolley and Nebulisation rooms in KDH had mixed mechanical and natural ventilation; the same rooms excluding Nebulisation in MPH had a form of mixed ventilation (additional open windows, which were constantly open). When considering the L/s per person ventilation rate values for KDH and MPH, a large number of the rooms do conform with the guidelines and minimum standards as prescribed by WHO and IUSS. However, when considering the marked increase in CO2 and occupancy as noted previously in the winter season, both facilities (based on standard averages) would in fact present much lower ventilation rates and higher risk environments. The A&E units in hospitals are considered to be one of the highest risk environments, with most (unpublished) incident areas by HCW contracting TB. The Triage Consult spaces (which are regarded as high risk spaces due to undiagnosed TB presumptive) are areas of concern with KDH between 32 and 52 L/s pp, and Triage Waiting 42L/s pp - not factoring winter (9.2.1.2). The results were similar but better for MPH Triage Consult 1 and 2 (between 46 and 70 L/s pp) and Triage Waiting (60 L/s pp). The Trolley areas at both facilities are high risk environments and should have indicated low ACH and L/s pp rates; however, as noted, both spaces have natural ventilation and mechanical ventilation; this has directly contributed to the improved rates at both facilities for these high occupancy and high risks environments.

TB patients present a risk, as the TB infection rate for the Cape Flats WC region is 1100+ per 100 000 people. This holds true for all areas with increased occupancy; for example, the occupancy variation in the Trolley area for KDH is 36 and 39 on average seasonally compared to the standard average of 29 (designed for occupancy) which the ventilation rate is based on; this will impact the ventilation rates required and imply high risk environments dropping, as is evident in KDH from 89 L/s pp to 26 – 32 L/s pp. MPH occupancy for the Trolley area is more stable and thus the average is still valid. Figure 91 indicates room area and volume per room type. On comparing KDH to MPH, the following was found: KDH boasts larger rooms and more volume per room type in a comparison of all instances, except for the Triage Waiting and Resus rooms/zones. KDH provides less ventilation ACH and consequentially L/s pp than MPH. In summary, MPH has smaller room areas and volume per room type, but higher ventilation rates than KDH. MPH has higher CO2 values, as can be expected (Figure 87 and Table 9.8), and a 30% increase in winter occupancy (Figure 90). From this data, KDH can be regarded as a higher-risk facility than MPH for airborne contagion such as TB. The Western Cape has a high number of HCWs contracting TB, based on published data (Grobler *et al.* 2016; Ayuk 2013). The epidemiology data on TB for the region, the building and spatial integration data, as well as the BE operational data presented in this thesis, validate this high infection rate.

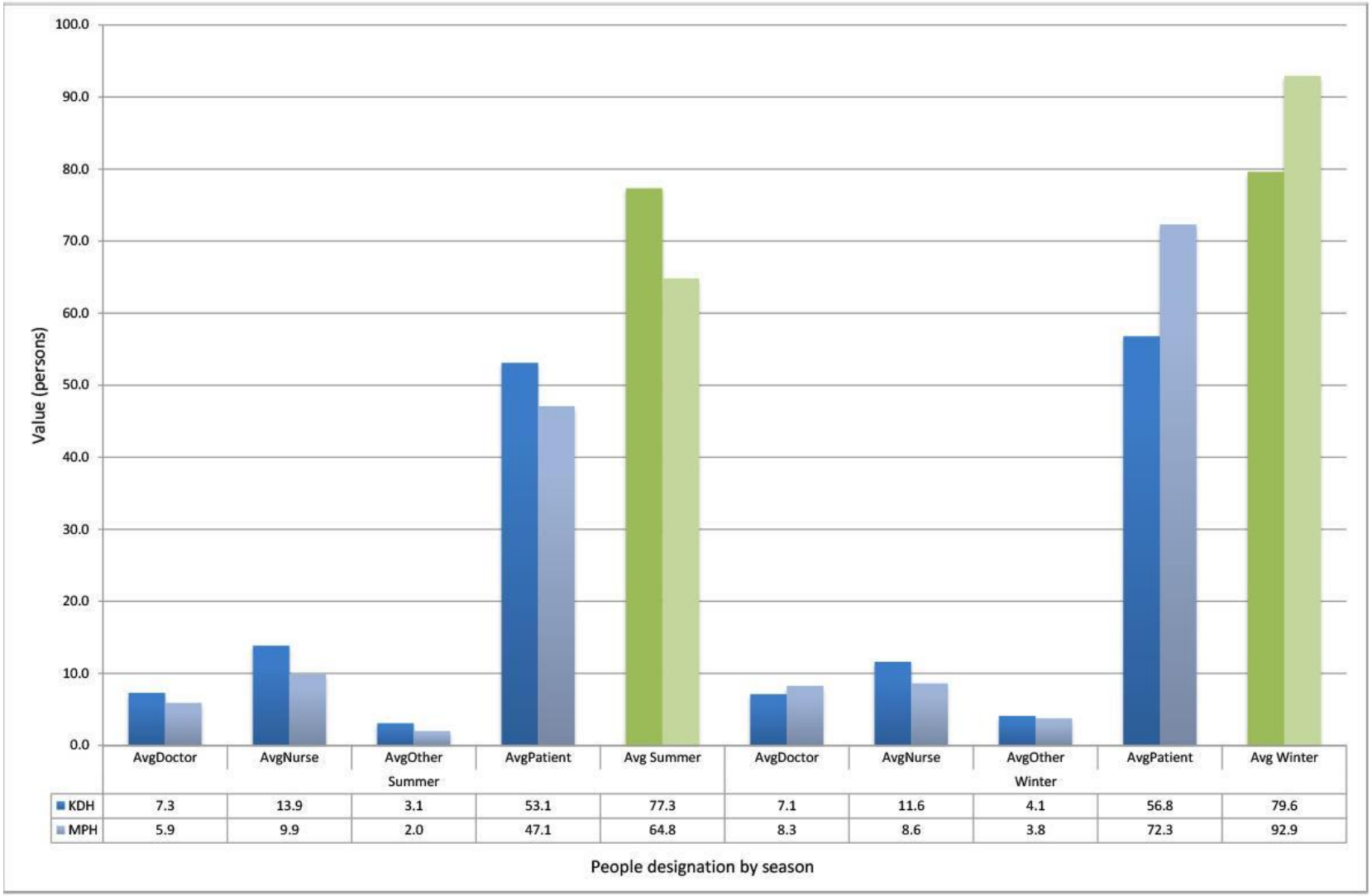



Figure 90: BE data for average room occupancy count, seasonally per occupant type for KDH and MPH

Figure 90 shows the user type distribution based on the seasonal occupancy averages. MPH has a lower occupancy count for summer and a 30% increase in winter, whereas KDH has a stable occupancy figure during both seasons. The occupancy user distribution is similar for winter and summer. The order from most to least is based on the observation data classification: 1) Patient, 2) Nurse, 3) Doctor, 4) Other. MPH has more patients in winter versus KDH, and fewer in summer. MPH has more doctors in winter versus KDH, and fewer in summer; the inverse is again evident. Furthermore, the values in Figure 91 are testament to variation in design planning and allocation of spaces of similar function between matching typologies. These data are important, indicating the large variation in health planning amidst the regulatory environment in healthcare planning in South Africa. Findings can be influenced if one only considers the room type and function without the metrics, and very often few standard metrics are used. This consideration needs to be incorporated into the variables in reporting MoBE findings (impact of occupancy over area, known CO2 influence with ventilation, and known MoBE influencing factors).

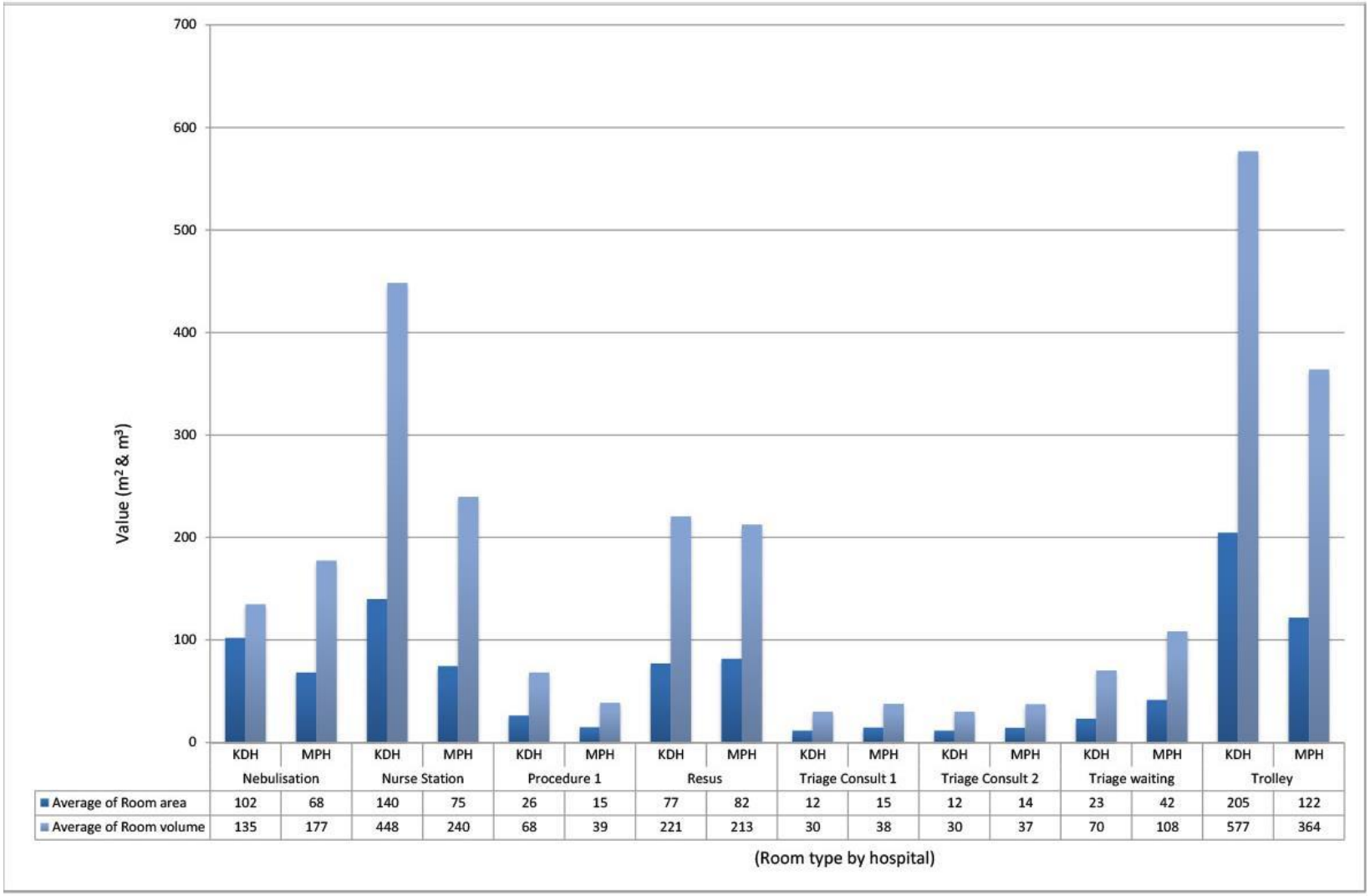
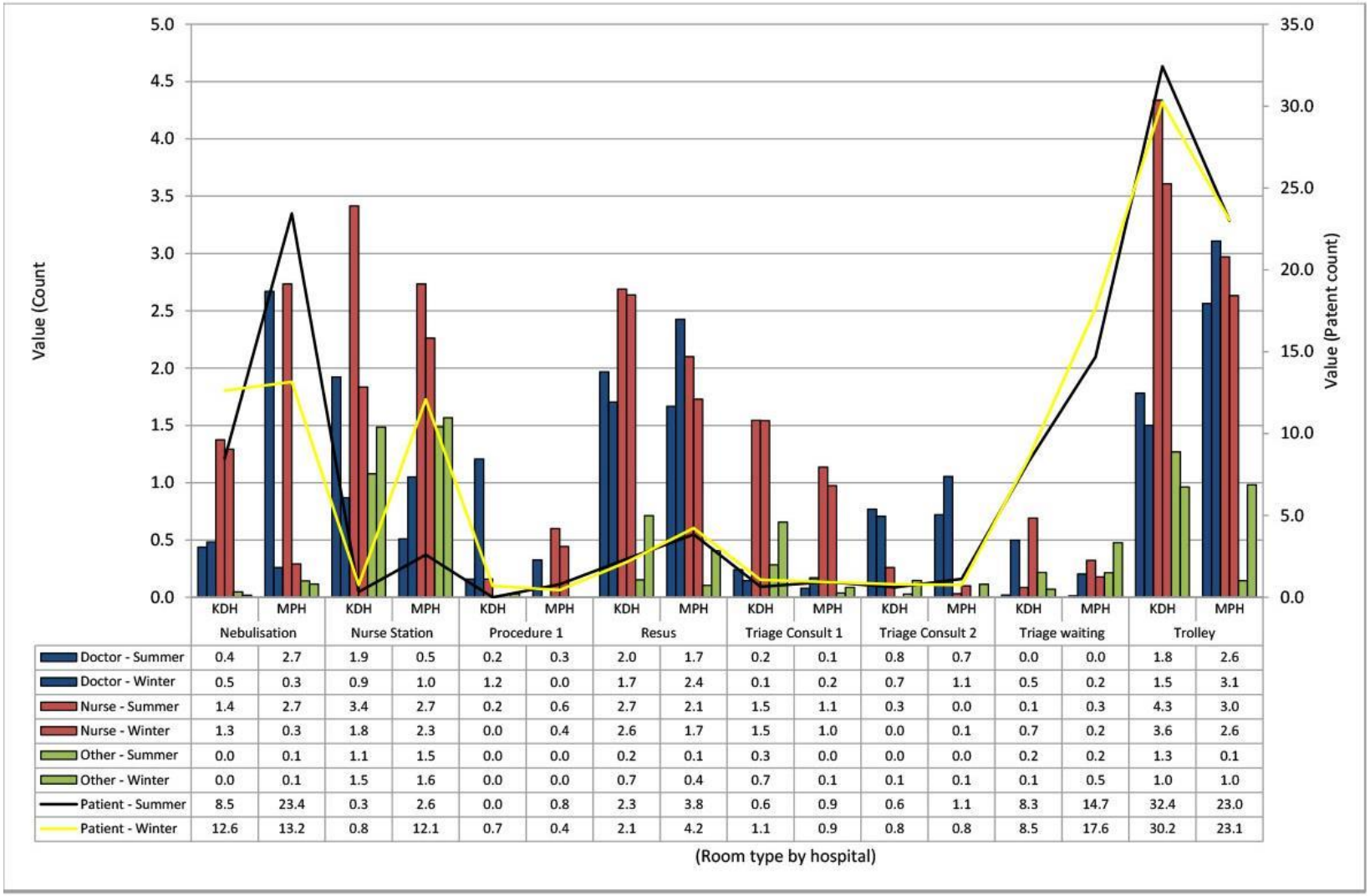



Figure 91: BE data for room area and volume per room type for KDH and MPH




| | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH | KDH | MPH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Nebulisation | | Nurse Station | | Procedure 1 | | Resus | | Triage Consult 1 | | Triage Consult 2 | | Triage waiting | | Trolley | |
| Doctor - Summer | 0.4 | 2.7 | 1.9 | 0.5 | 0.2 | 0.3 | 2.0 | 1.7 | 0.2 | 0.1 | 0.8 | 0.7 | 0.0 | 0.0 | 1.8 | 2.6 |
| Doctor - Winter | 0.5 | 0.3 | 0.9 | 1.0 | 1.2 | 0.0 | 1.7 | 2.4 | 0.1 | 0.2 | 0.7 | 1.1 | 0.5 | 0.2 | 1.5 | 3.1 |
| Nurse - Summer | 1.4 | 2.7 | 3.4 | 2.7 | 0.2 | 0.6 | 2.7 | 2.1 | 1.5 | 1.1 | 0.3 | 0.0 | 0.1 | 0.3 | 4.3 | 3.0 |
| Nurse - Winter | 1.3 | 0.3 | 1.8 | 2.3 | 0.0 | 0.4 | 2.6 | 1.7 | 1.5 | 1.0 | 0.0 | 0.1 | 0.7 | 0.2 | 3.6 | 2.6 |
| Other - Summer | 0.0 | 0.1 | 1.1 | 1.5 | 0.0 | 0.0 | 0.2 | 0.1 | 0.3 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 1.3 | 0.1 |
| Other - Winter | 0.0 | 0.1 | 1.5 | 1.6 | 0.0 | 0.0 | 0.7 | 0.4 | 0.7 | 0.1 | 0.1 | 0.1 | 0.1 | 0.5 | 1.0 | 1.0 |
| Patient - Summer | 8.5 | 23.4 | 0.3 | 2.6 | 0.0 | 0.8 | 2.3 | 3.8 | 0.6 | 0.9 | 0.6 | 1.1 | 8.3 | 14.7 | 32.4 | 23.0 |
| Patient - Winter | 12.6 | 13.2 | 0.8 | 12.1 | 0.7 | 0.4 | 2.1 | 4.2 | 1.1 | 0.9 | 0.8 | 0.8 | 8.5 | 17.6 | 30.2 | 23.1 |

Figure 92: BE Data for user type per room type seasonally for KDH and MPH

Figure 92 considers occupancy type and average count per room type. The following observations were made: The main users in the Nebulisation room for both hospitals are the patients. The main users at the Nurses' Station for KDH are nurses, and for MPH patients. There is a striking increase of over 400% (from two people to 12) in the number of patients at MPH in the Nurses' Station area in winter. The nurses are the main users of the KDH Resus room compared to patients in the MPH Resus room. The main users of the Triage Consult 1 rooms at both KDH and MPH are nurses, while those of the Triage Consult 2 rooms are doctors, implying a clear operational policy and process followed. When one considers the human as vector factor and known contaminator by handling especially HCW, one can infer that the potential for contamination by HCW on surfaces in this zone will be high. (A post study focusing on identified high occupancy and high turnover zones in the A&E correlated with the microbial sample will be very informative as guide to source contamination). Based on observations, the following flow and procedural path were observed at both hospitals:

> A patient is called to the Triage Waiting area from the main waiting room situated outside the unit adjacent to this section. The patient is first seen and assessed by a nurse in the Triage Consult 1 room for vitals and triage evaluation. The patient is then directed to the Triage Waiting area (for KDH two waiting areas are provided; the first waiting area referenced here was not sampled in this study, as it matched waiting area 2; in MPH this is a combined area). After having waited in the Triage waiting area, the patient is called to Triage Consult 2 to see the doctor, who performs a minor procedure and assessment or intervention, after which the patient again returns to Triage Waiting. The patient now waits to be either discharged (requiring a clearance document), admitted to an inpatient ward bed, or transferred to the Trolley or Nebulisation rooms. Refer to Figure 92.

Table 9.9: Triage Waiting room: BE risk factors for data collection

| **BE Factors** |
|---|
| $CO_2$ summer & winter |
| Room area |
| Room volume |
| ACH & L/s per person |
| Occupancy avg |
| Ventilation source |
| Openable windows |
| Potential risk |

The observed data confirm this process: the main users in Triage Waiting are patients. When one considers the patient occupancy number in this room, the room volume and area, the ACH & L/s pp and ventilation source combined with known TB incident rates, it is evident that this is a potential high-risk environment. Refer to Table 9.9 for typical risk factors to consider regarding indoor environments. Further user data and flow patterns combined with occupancy can provide guidance to functional use, as is evident in this finding.

# CHAPTER 10 CONCLUSION

From the findings presented in sections 7.3, 8.3 and 9.3 and other relevant sections of the thesis, core conclusions are drawn and presented below; these are structured in responses to the research questions posed in Chapter 1 and Chapter 6. The secondary questions are resolved in chaptered conclusion categories, namely: architectural space modelling by observation, the microbiology investigation, and the environmental investigation. The primary research questions are resolved through an interdisciplinary conclusion section drawing on each of the study fields, ending in testing the thesis hypotheses. For context reference is made to the thesis problem statements.

*The primary problem statement developed for this thesis is: A large number of people, in excess of 15% in developing world countries and 8-10% in developed world countries, contract some form of HAI in hospitals (Yates et al. 2016; Hamilton 2012). South Africa suffers the same burden. Numerous studies and investigations (of which only a few are referenced in chapters 1 and 3) point to the fact that indoor built environmenst affect the health and well-being of their users; however, little empirical evidence is available on the factors that contribute to this condition (Schweitzer et al. 2004; Yates et al. 2016; Lax et al. 2017). There is an apparent oversight or understudy of architectural factors, spatial networks in building design and planning being one such factor. Even with the research conducted to date on the microbiology of the built environment and building ecology, a lack of understanding and knowledge of the transmission and impacts of infectious microorganisms within the built environment still exist (Lax et al. 2017). The interdisciplinary nature of the research, in particular microbiology and architecture, requires focused statements for each field; collectively they share overlapping problems and approaches to solve them.*

Secondary problem one: Firstly, focused on microbiology*: Buildings and dwellings are colonised by pathogenic bacteria – microbes that have adapted to their extreme environmental conditions. Research has shown a decline in microbial biodiversity, and a rise in human pathogenic bacteria within engineered environments when compared to naturally ventilated biome spaces (Kembel et al. 2013). The relationship between spatial planning and the distribution and prevalence of microbes is largely unknown.*

Secondary problem two: Secondly, focused on architectural, engineering and spatial analytics: *The environmental conditions, including, but not limited to, ventilation and the understudied area of spatial networks in building design and planning of an environment, directly contribute to the spread of various surface-origin bacteria, NTMb and airborne bacteria such as Tuberculosis (Nardell et al. 1991); as a result they contribute to the high prevalence rates of nosocomial infections (the driver for NTMb, tuberculosis and other infections) in hospitals and other enclosed environments (Basu et al. 2007; Koenig 2008; Ducel et al. 2002). South African hospitals and the national health system suffer from a lack of HAI data sets even though this is mandated by the National Core Standards for Healthcare Establishments (Dramowski & Whitelaw 2017). As a result, hospital staff, recovering TB patients, HIV patients, unsuspecting patients and the public at large are at risk in nosocomial environments. Lastly, resources for implementing and maintaining costly mechanical systems are neither affordable nor sustainable in resource-limited settings (Block et al. 1999) such as South Africa. The field of architecture therefore requires a form of empirical risk validation for building designs for healthcare associated infection (HAI) in supporting sustainable approaches to infection control and healthcare design.*

## 10.1 ARCHITECTURAL SPACE MODELLING BY OBSERVATION: CONCLUSIONS

Refer to section 7.3 for findings and Chapter 5 for background context. This section presents the established core conclusions from the investigation. Due to the interdisciplinary nature of the questions, responses will fall in either one or two sections as noted where relevant. The secondary research questions are repeated, with their clause numbers, followed by the response.

**2.2** ***Do variations exist between indicator species based on room type?*** (Response in 10.2 and 10.3)

Yes, they vary between season and by hospital, as well as the compositional contribution of the air and surface communities. In an attempt to determine commonalities based on room type and abundance, the OTUs measured per room were graded by assigned spatial metrics. These metrics included (1) core spaces by base plan analysis, (2) spaces by observation (integration) analysis, (3) spaces by gate crossing analysis and (4) spaces compared for type and season. The common finding for all observed measures (except the base model) was a tendency of higher abundance in rooms that had mid activity i.e. for flow count the highest abundance rooms with the median activity were consistently Resus, Nebulisation and Triage Consult for both hospitals. This could be due to the reduced activity (movement)which allows for settlement and deposition of biota, thus a temporal factor of deposition and contact time. When considering only the room type and therefore by extension the function of space, it can be inferred that room type and OTU count are relational, therefore similar counts seasonally should be found (to allow for the large seasonal variation). This was evident for only some rooms (considering a 10% maximum variation). In general, the values for summer are more similar for types and less so for winter. Summer: Nurses' Station, Procedure, Triage Consult, Triage Waiting and Trolley area. For winter Procedure, Resus and Triage Waiting. The only two rooms that are similar for both winter and summer are Procedure and Triage Waiting. Interestingly, these rooms are either the lowest (Procedure) or mid high (Triage waiting); the dominant user for both hospitals for Triage Waiting was patients and for Resus was nursing staff. This implies a similar abundance of OTUs in those two rooms. Thus room type and the associated factors of activity do influence the microbial load. Further focused studies would be a contribution.

**3.1** ***What are the BE factors that can be attributed to influence the BE microbiome and test the factor of influence?*** (Response in 10.1 and 10.3)

From literature the following factors are attributed to influence the building microbiome: *Source of ventilation air, airflow rates, relative humidity and temperature were correlated with the diversity and composition of indoor bacterial communities. HR values on the same floors (spatial connect), HVAC system, hospital staff which implies occupancy, air and surface temperatures, HVAC particle filtration efficiency, human occupancy, human contact frequencies and surface characterizations: porosity, composition, and environmental conditions immediately adjacent to materials can all affect microbial community structure, growth, and survival; cleaning regimes for surfaces and human activities and patterns and building operation seem to have the greatest impact on indoor microbial ecology* Kembel *et al.* (2013). The various factors utilised in this study did not indicate significant correlation between the BE and the microbiome. The factors that did indicate correlation were hospital, season and sampling type. A possible reason for this might be sample size. The large number of BE factors

(40+) compared to the low number of microbial samples reduces the potential to find significant correlations. From the data, it was apparent that the ventilation strategy did affect the dispersal of microbes in that rooms that shared natural ventilation and rooms that only had mechanical ventilation had no notable difference in the organism distribution. The BE factors, including occupancy, gate crossing and internal flow count, did not correlate with the microbial sampling data. However, considering the spatial findings, the core areas (central space with highest occupancy and activity) at both MPH and KDH averaged 850 OTUs in winter, and 510 OTUs in summer. The core Triage areas of MPH and KDH averaged 890 OTUs in winter, and 550 OTUs in summer. The fact that MPH had a 50% increase in occupancy over the winter season combined with a higher abundance of air-associated organisms, indicates that occupancy and activity are indeed a factor. This is similar to the OTU abundance analysis showing diversity in room types; however, mid activity room types had the highest OTU abundance counts. This study must be viewed as a macrobiome study at building unit scale, and the data suggest that a focused selected room study measuring the same factors would be the next step in analysis, thus detailed studies focusing on temperature and sample types, HR and sample types, and $CO_2$ and sample types are recommended.

**3.2** ***What are the scientific environmental monitoring methodologies and technologies available for indoor built environment sampling?*** (Response in 10.1 and 10.3)

An extensive literature review was conducted to determine the various methods, tools and monitoring apparatus available. Furthermore, the 2017 MoBE report references the various applications. Refer to Chapter 3 sections 3.3 and 3.4.2 which review specific BE sampling requirements, opportunities and needs. A table was developed from over 90 reviewed literature articles that define a number of methodologies, techniques and models referenced in Table 3.21: Theoretical models and methodologies. This includes sampling tools for genomic sequencing and sampling for BE environmental factors. This study's master data set includes up to 40 data factors. For details on a large, but yet limited, number of parameter and collection methods refer to Table 3.20: Tools for improved collection of built environment data, taken from Ramos and Stephens (2014) For spatial analytics few tools have been utilised (there are only 4 studies that have conducted a high level spatial analysis, minus this study). The application of Space Syntax (SS) was not previously considered and applied in BE studies. A vast selection of technologies is available, each associated with a desired methodology. A detailed literature review is included which refers to a research methodology for environmental monitoring available and the elected methods applied for this thesis.

**4.1** ***Have spatial analytical tools been applied to MoBE investigations?***

Yes, but very limited and few. Most studies have not utilised spatial metrics. Refer to the detailed literature review on the application of spatial metrics in 3.3.1. Most existing methods are based on estimations of occupancy, whereas real-time rates would prove of greater value in dynamic microbial community characterisation; similarly, *much less attention has been given to detecting occupant activity* (their movement in space), *despite evidence indicating that such movements have a stronger effect than occupancy on certain aspects of IAQ* Desdeko *et al*. (2015). The limited measure of occupant activity (at most only by gate crossing/threshold crossing) presented in the various studies highlights an opportunity for new approaches in spatial analysis. The application of building design spatial factors is even rarer (Adams *et al.* 2015); the literature review only identified four studies that considered a form of occupant

activity and presence. This presents a far greater discrepancy, as by spatial factors we infer more than only occupancy per space, yet numerous studies have consistently confirmed the importance of human occupancy and user identification, human activity, space use and spatial relationships. DepthMap™ spatial analysis and GIS modelling are tools for assessing space use and flow, as the observed data correlated with the simulation. These would be appropriate tools to investigate distribution and potential interaction from an architectural perspective. More research will be needed, as well as an investigation into factorisation for correlation. This does allow for a form of real-time measure and in addition provides numerous factors previously not quantified but important: use type, flow activity, etc.

**4.2** ***Does a room type (and its associated function) host a unique biome? If so, are there overlaps in room type biomes within a hospital and between the two hospitals?*** (Response in 10.2 and 10.3)

With reference to 2.2: Yes, the room biomes vary between season and by hospital, as well as the compositional contribution of the air and surface communities. In an attempt to determine commonalities based on room type and abundance, the OTUs measured per room were graded by assigned spatial metrics. These metrics included (1) core spaces by base plan analysis, (2) spaces by observation (integration) analysis, (3) spaces by gate crossing analysis and (4) spaces compared for type and season. The common finding for all observed measures (except the base model) was a tendency of higher abundance in rooms that had mid activity i.e. for flow count the highest abundance rooms with the median activity were consistently Resus, Nebulisation and Triage Consult for both hospitals. This could be due to the reduced activity which allows for settlement and deposition of biota, thus a temporal factor of deposition and contact time. When considering only the room type and therefore by extension the function of space, it can be inferred that room type and OTU count are relational; similar counts seasonally should be found (to allow for the large seasonal variation). This was evident for only some rooms (considering a 10% maximum variation). In general, the values for summer are more similar for types and less so for winter. For summer: Nurses' Station, Procedure, Triage Consult, Triage Waiting and Trolley area. For winter: Procedure, Resus and Triage Waiting. The only two rooms that are similar for both winter and summer are Procedure and Triage Waiting. Interestingly, these rooms are either the lowest (Procedure) or mid high (Triage Waiting); the dominant user for both hospitals for Triage Waiting was patients and for Resus was nursing staff. This implies a similar abundance of OTUs in those two rooms. From the spatial analysis core clusters were identified, suggesting a high level of activity and flow. The rooms associated with these clusters were 1) Triage Wait and Consult 2) Nurses' Station (which could not be identified distinctly). Rooms were identified by prominent user, but further analyses would require source tracking of user type to determine the relationship between user type and biota similarities. All rooms had a unique microbiome and differed seasonally. No one room type had a matching community. Similarities are that all rooms had high abundance of *Gamma proteobacteria* and far less *Beta proteobacteria*; this was similar for *Bacilli* and far less for *Clostrida* and other. It was noted that various factors influence the microbial room structure, such as season and hospital. Refer to Figure 82 for variation between rooms and in seasons, with very evident non-correlations. With reference to figure 83, a number of rooms did indicate higher abundance of *Proteobacteria*, e.g. Nebulisation. We cannot confirm at this time that room types match in different healthcare buildings; however, the microbial composition of the two hospitals were not invariant.

**4.3** ***Correlate the spatial data of human movement patterns and space use with microorganism distribution and richness.***

Referring to 2.2: This was done but statistically no correlations were found. However, occupancy dynamics and space and time analysis are key due to the dynamic nature of microbial communities. The study did find increased abundance with relatively higher activity zones. Spatial network analysis could not determine the variant microbial communities between room types. This is most likely due to the global study level. A number of studies have noted niche focused research to elucidate microbial interaction with space and indoor environment.

**5.1** ***What are the known theoretical models and tools available for BE characterisation regarding risk, transmission and microbiome identification?*** (Response in 10.1 and 10.3)

Referring to Chapter 3: Please note that the application of SS was not previously considered. Refer to section 3.6, and Table 3.21 for a table of theoretical models and methodologies, as well Chapter 7 for the various research sampling methodologies. An extensive literature review was conducted to determine the methods, tools and monitoring apparatus available. Furthermore, the 2017 MoBE report references the various applications. Chapter 3 sections 3.3 and 3.4.2 review specific BE sampling requirements, opportunities and needs. A table was developed from over 90 reviewed literature articles that define a number of methodologies, techniques and models referenced in Table 3.21: Theoretical models and methodologies. These include sampling tools for genomic sequencing and sampling for BE environmental factors. This study's master data set includes up to 40 data factors. For details on a large, but yet limited, number of parameter and collection methods refer to Table 3.20: Tools for improved collection of built environment data, taken from Ramos and Stephens (2014)
For spatial analytics very few tools have been utilised; there are only 4 studies that have conducted a high level spatial analysis (minus this study). The application of Space Syntax (SS) was not previously considered and applied in BE studies. A vast selection of technologies is available, each associated with a desired methodology. A detailed literature review is included which refers to a research methodology for environmental monitoring available and the elected methods applied for this thesis.

**5.3** ***Can the building form and spatial planning unique to the hospital typology influence IPC outcomes?***

The spatial analysis indicates integrated and connected environments that are spatially intelligible. Similarly, it predicts spaces where clustering would occur, e.g. the Nurses' Station and triage areas. When occupancy data and user type data are combined with average $CO_2$ values for the activity period using known infection risk mass balance equations, IPC risk can easily be calculated. Risk planning based on predicted measures of spatial planning and user type could prove very valuable. When building form and spatial planning are compared with the observed flow data of people moving and people entering and exiting space, they provide insight and enable modelling verification. The gate counts and flow measures in many respects were strongly associated with the potential predicted simulations of where one would expect to find congregation and reduction of people. When considering IPC transmission models (ventilation, congregation settings, people distribution), the analytics provide insight for localised IPC approaches, and highlight potential rooms of higher risk. By combining spatial

data with environmental data (see appropriate approaches), IPC selections can be suggested. The overlay of microbial biome data per room type and the relationship between rooms could provide further insight into this probability. Yes, typology (linear in KDH and MPH) and spatial planning can influence IPC outcomes, guide IPC decision making, guide IPC selection, and recommend local focused intervention and global unit levels. It was evident that an increase in OTU counts was associated with mid-level activity spaces. Spatial data combined with environmental data are critical for risk evaluation. A focused study will lead to more robust conclusions with regards to microbial community identification. This study indicates that at macro level, with limited samples and less focused room areas, the results are not significant; however, the overlay of microbial biome data per room type and the relationship between rooms at a more focused level could provide further insight into this potential. Lastly, but certainly fundamental, the low correlation found between space use for integration of spaces, evidenced by the observed patterns, and the spatial potential at both facilities which was consistently $R^2$ of 0.4 and less opposed to $R^2$ 0.58, in fact supports the notion of a strong building program which is dominant in both of these facilities - where the building program (the manner in which it is used) often overrides the assigned space function (where function determines utilisation). This complicates space related IPC approaches and provides critical insight into approaches to BE design choices. The author postulates that a stronger program will present a more temporal and dynamic microbial community which is not only determined by spaces but also by the movement and activity between them.

## 10.2 MICROBIOLOGY INVESTIGATION: CONCLUSIONS

Refer to section 8.3 for the microbiology findings. This section presents the established core conclusions from the investigation. Due to the interdisciplinary nature of the questions, responses will fall in either one or two sections as noted where relevant. The secondary research questions are repeated followed by the response.

### 1.1 *Is there a link between the indoor and outdoor communities of both researched hospitals?*

Yes, they share an estimated 35% of the outdoor environment's organisms indoors, regardless of room type and ventilation supply source, as was observed at both MPH and KDH. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose of outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria. Similar to other studies reported, no indoor biota were found outdoors. Statistically no correlation with ventilation source was found; the only factors that did indicate correlation were season and type (air and surface). However, the ventilation systems in both KDH and MPH, as per the MC data, showed that 66% of the rooms were reliant on mechanical ventilation with no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66%

not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome - which is corroborated by other studies.

### 1.2 *Are the rooms in the hospital more representative of human-sourced bacteria or outdoor-sourced bacteria?*

Yes, the rooms are more representative of indoor human-sourced bacteria, as is shown by the Gamma diversity per room type and per season and sample type. However, from the thesis study data, data set for indicator organism by room, the corresponding genera were identified. They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus, Acinetobacter*. They were globally reported and not by type (air or surface) or by season (winter and summer), but by room. Due to the number and complexity of spaces sampled, source tracking was not technically feasible for this investigation. As depicted in Table 8.14 and Table 8.15, as noted previously, the indoor spaces contained on average 35% shared organisms from the outdoors; therefore, 65% of the organisms found are sourced from within the building, of which an estimated 25% are potentially human-sourced biota based on the organism identified and abundance count; however, it is noted that physical transport of soil and other environmental organisms into the sampled rooms, followed by resuspension of dust particles, also represents a potential route for "human-sourced" microorganisms. Nevertheless, in this discussion, the principal focus is on organisms which are human-associated (skin, hair, etc.) rather than vicariously associated (with shoes, clothing, etc).

Table 8.10: Indicator genera by room type (for all hospitals), filtered by human skin associated only referenced below, see page 210.

| Room/site | Phylum | Family | Genus |
|---|---|---|---|
| External | *Firmicutes* | *Streptococcaceae* | **Streptococcus* |
| | *Actinobacteria* | **Corynebacteriacea* | **Corynebacterium* |
| Procedure 1 | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| Resus | *Firmicutes* | **Staphylococcaceae* | **Staphylococcus* |
| | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| | *Firmicutes* | *Peptostreptococcaceae* | **Corynebacterium* |
| | *Firmicutes* | *Streptococcaceae* | **Streptococcus* |
| Triage Consult 1 | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| Triage Consult 2 | *Proteobacteria* | *Moraxellaceae* | *Acinetobacter* |
| | *Firmicutes* | *Staphylococcaceae* | *Jeotgalicoccus* |
| | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacterium* |
| | *Actinobacteria* | *Micrococcaceae* | *Microbispora* |
| Triage Waiting | *Actinobacteria* | **Corynebacteriaceae* | **Corynebacteriaceae* |
| | *Actinobacteria* | *Micrococcaceae* | *n/a* |
| | *Firmicutes* | **Staphylococcaceae* | **Staphylococcus* |
| Nebulisation | - | - | - |
| Nurses' Station | - | - | - |
| Trolley | - | - | - |
| ** indicates a top 30 most common genera identified in surface and air for KDH and MPH* | | | |

### 1.3 *Is there a seasonal variation in the built environment biomes of both hospitals?*

Yes, seasonal variation is very evident, specifically in the air samples for winter and summer. An interaction between the season and the type of sample was found. Specific phyla were associated with air and surfaces, with a diverse (almost inverse) variation of each in winter and

summer. From the data we can confirm a seasonal variation in the microbial community for both hospitals. It is also evident that the surface and air communities are sufficiently different to justify focused study for each in future. Not only is there variation, but the type of samples (air or surface) show seasonal relationships. The Beta diversity patterns in

Figure 76 indicate a notable dissimilarity in the air samples in summer and winter, thus a clear seasonal variation.

### 1.4 *Is there a correlation between the communities of the biomes of the two hospitals, indicating a similarity or variation between and within hospitals?*

The Beta diversity findings (Figure 78) indicate that MPH and KDH are not dissimilar and share a similar indoor microbiome. No, at the scale of the study the data reflected that the two hospitals tend to have similar biomes. The PCoA BETA Diversity for air, surface, summer and winter - factors for MPH and KDH with factor “hospitals” replacing factor “season” - indicates that the two hospital communities had no effect, as corroborated by the Permanova.

### 1.5 *Is there a link between the air samples and the surface samples at each hospital, inferring that the air-sample fall-out to the surface will represent the surface biome environment?*

The data indicate that there is a variation between the air samples and the surface samples. Not only is there variation, but the types of sample (air or surface) show seasonal relationships. The genera identification also confirms variations in identified indicator species. Based on an Alpha diversity analysis, a variation was noted in the number of taxa found in surface and air samples. This indicates that the surface samples alone do not reflect the air samples or the total Alpha community. Considering the full samples set, it is evident that there is interaction between the season and the type of sample (air, surface). A tendency of increased OTUs in the air and surface samples was observed in winter ($P < 0.05$). It can only be inferred that the fallout, if it occurred, would add to the diversity of the surface samples; however, sampling only surfaces will not prove effective in biome identification, as seen in the large variation and abundance of both genera and phyla. In accordance with other studies, it would be necessary to sample both communities to define the indoor biome. However, physical contact with surfaces (touching) by humans will certainly contribute to the sampled diversity.

### 2.1 *What are the indicator species prevalent in the hospital indoor environments in the Cape Flats region of the Western Cape?*

Core indictor organisms have been identified and can be classified at this point as the hospital biome of KDH and MPH. (A large number of unidentified OTUs were noted.) The indicators are: *Pseudomonas, Enterococcus, Delftia, Corynebacterium, Burkholderia, Bacillus, Acinetobacter, Stenotrophomonas, Staphylococcus* and *Stenotrophomonas.* The relative abundance and types of indicator species vary between room types. Refer to the tables on indicators, room types and viability (based on the identification and comparison of culture sample organisms). Furthermore: from the study data, data set for indicator organism by room, the corresponding genera were identified for human source (skin, etc.). They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter.* Refer to table 8.12 for genera identified at KDH and MPH.

**2.2** ***Do variations exist between indicator species based on room type?*** (Response in 10.1 and 10.2)

Yes, they vary between season and by hospital, as well as the compositional contribution of the air and surface communities. All the rooms reflect high abundance of the class Gamma-*Proteobacteria* followed by Beta-*Proteobacteria.* There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). Seasonally, the class *Bacilli* predominate in both winter and summer in all room types followed by *Clostridia*. There is an increase in the abundance of *Clostridia* for all spaces excluding the Nurses' Station over the winter season. Phyla that strongly associate with human skin: from the thesis study data, data set for indicator organism by room, the corresponding genera were identified. They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter*. They were globally reported and not by type (air or surface) or by season (winter and summer), but by room (table 8.9). In table 8.9: *Indicator genera by room type (for all hospitals), filtered by human skin associated only,* classification by room type and phylum, family and genus is listed. An evident variation exists between the abundance of the indicator genera for air and surface samples. From the data it is clear that the majority of airborne species identified in rooms belong to the genus *Burkholderia*. (This is more commonly found in offices and hospitals.) Considering the analysis on room type and relative abundance of phyla, no conclusive relationship could be found between the room types and associated phyla per season, except for the total increase and/or reduction that was established. Indicator genera for each room type were identified and presented in Figure 82. But no correlation can be attributed to specific room type. Seasonal variations in sample types (air and surface) also affect this finding. To further complicate this important question, the room type OTU and shared external OTU data indicate that rooms that had open windows and rooms that relied only on mechanical ventilation had similar shared OTUs and relative abundance classification of genera by room type from the outside, which implies the ventilation system played an influential role in dispersal. An analysis was performed on room types and OTU count identified by room. A relative abundance was assigned to a room type and to season for the room type. Variations exist seasonally, and variations exist between hospitals with the same room (same function). In closing, indicator species have been identified by room type for air and surface sample and by season. Certain rooms evidenced greater relative abundance and richness, but at the depth of analysis common room type indicators could not be identified and variation did show between matching room types in different hospitals. The dataset and spatial data gathered will enable further investigation. But it is critical to note the finding that various factors influence the microbial room structure. The rooms can be regarded as unique biomes.

**2.3** ***Correlate the prevalent microbes found with international HAI data lists.***

See previous reference: Table 8.2 HAI USA pathogen list compared to thesis genus and culture identification findings (Jarvis & Martone 1992, Ducel *et al.* 2002; Wisplinghof *et al.* 2004). This is a summary of the microbes found on the HAI list and verified against the indicator genera identified in this study. Three prevalent HAI species were identified; all three have been positively cultured: S*taphylococcus* (by genus sequencing, *Pseudomonas* (by genus sequencing) and *Staphylococcus* (by genus sequencing) were found as viable pathogens cultured from the samples taken, refer to Table 8.11. A number of the pathogens and non-

pathogenic microorganisms were identified. The culture analysis was performed to determine viability of the community identified by sequencing.

**3.3** ***Is there a statistically significant relationship between the organism present and the building ventilation system?*** (Response in 10.2 and 10.3)

No significant correlation was reported, but a relationship was found between the mechanical ventilation and outdoor air entering by natural means on the composition distribution. They share an estimated 35% of the outdoor environment's organisms indoors, regardless of room type and ventilation supply source, as was observed at both MPH and KDH. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose of outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria. Similar to other studies reported, no indoor biota were found outdoors. Statistically no correlation with ventilation source was found; the only factors that did indicate correlation were season and type (air and surface). However, the ventilation systems in both KDH and MPH, as per the MC data, showed that 66% of the rooms were reliant on mechanical ventilation and had no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66% not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome - which is corroborated by other studies.

**4.2** ***Does a room type (and its associated function) host a unique biome? If so, are there overlaps in room type biomes within a hospital and between the two hospitals?*** (Response in 10.1 and 10.2)

The room type correlation did not produce a significant correlation. When reviewing the data per indicators, a variation in genus and diversity is found between rooms, and also between seasons and between sample types in rooms. It is evident that the sample types have a relationship effect on each other; thus, each room has a unique surface and air biome that tends to be similar based on the ventilation distribution. These unique biomes differ in winter and summer. The spatial study overlays will provide a more informed outcome between room type and biome, which at this stage has not been established. This study indicated that a large sample set per room type (focused study temporal study) will be required, implying that more room samples need to be taken with real-time spatial data for fewer rooms with the same BE data factors.

## 10.3 ENVIRONMENTAL INVESTIGATION: CONCLUSIONS

Refer to section 9.3 for the findings of the environmental investigation. This section presents the established core conclusions from the investigation. Due to the interdisciplinary nature of the questions, responses will fall in either one or two sections as noted where relevant. The secondary research questions are repeated followed by the response.

**3.1** ***What BE factors can be attributed to influence the BE microbiome and test the factor of influence?*** (Response in 10.1 and 10.3)

From literature the following factors are attributed to influence the building microbiome: *Source of ventilation air, airflow rates, relative humidity and temperature, were correlated with the diversity and composition of indoor bacterial communities; HR values on the same floors (spatial connect), HVAC system, hospital staff which implies occupancy, air and surface temperatures, HVAC particle filtration efficiency, human occupancy, human contact frequencies, surface characterizations: porosity, composition, and environmental conditions immediately adjacent to materials can all affect microbial community structure, growth, and survival; and the cleaning regime for surfaces and human activities and patterns and building operation seem to have the greatest impact on indoor microbial ecology.* Kembel *et al.* (2013) The various factors utilised in this study did not indicate a significant correlation between the BE and the microbiome. The factors that did indicate correlation were hospital, season and sampling type. A possible reason for this might be sample size. The large number of BE factors (40+) compared to the low number of microbial samples reduces the potential to find significant correlations. From the data, it was apparent that the ventilation strategy did affect the dispersal of microbes in that rooms that shared natural ventilation and rooms that only had mechanical ventilation had no notable difference in the organism distribution. The BE factors, including occupancy, gate crossing and internal flow count, did not correlate with the microbial sampling data. However, considering the spatial findings, the core areas (central space with highest occupancy and activity) at both MPH and KDH averaged 850 OTUs in winter, and 510 OTUs in summer. The core triage areas of MPH and KDH averaged 890 OTUs in winter, and 550 OTUs in summer. The fact that MPH had a 50% increase in occupancy over the winter season, combined with a higher abundance of air-associated organisms, indicates occupancy and activity are indeed a factor. This is similar to the OTU abundance analysis showing diversity in room types; however, mid activity room types had the highest OTU abundance counts. This study must be viewed as a macrobiome study at building unit scale, and the data suggest that a focused selected room study measuring the same factors would be the next step in analysis, thus detailed studies focusing on temperature and sample types, HR and sample types, and $CO_2$ and sample types are recommended

**3.2** ***What are the scientific environmental monitoring methodologies and technologies available for indoor built environment sampling?*** (Response in 10.1 and 10.3)

An extensive literature review was conducted to determine the methods, tools and monitoring apparatus available. Furthermore, the 2017 MoBE report references the various applications. Chapter 3 sections 3.3 and 3.4.2 review specific BE sampling requirements, opportunities and needs. A table was developed from over 90 reviewed literature articles that define a number of methodologies, techniques and models referenced in Table 3.21: Theoretical models and methodologies. This includes sampling tools for genomic sequencing and sampling for BE environmental factors. This study's master data set includes up to 40 data factors. For details on a large, but yet limited, number of parameter and collection methods refer to Table 3.20: Tools for improved collection of built environment data, taken from Ramos and Stephens (2014) For spatial analytics few tools have been utilised; there are only 4 studies that have conducted a high level spatial analysis (minus this study). The application of Space Syntax

(SS) was not previously considered and applied in BE studies. A vast selection of technologies is available, each associated with a desired methodology. This study includes a detailed literature review, and refers to a research methodology for environmental monitoring available and the elected methods applied for this thesis.

**3.3 Is there a statistically significant relationship between the organism present and the building ventilation system?** (Response in 10.2 and 10.3)

No significant correlation was reported, but a relationship was found between the mechanical ventilation and outdoor air entering by natural means on the composition distribution. They share an estimated 35% of the outdoor environment's organisms indoors, regardless of room type and ventilation supply source, as was observed at both MPH and KDH. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose of outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria. Similar to other studies reported, no indoor biota were found outdoors. Statistically no correlation with ventilation source was found; the only factors that did indicate correlation were season and type (air and surface). However, the ventilation systems in both KDH and MPH, as per the MC data, showed that 66% of the rooms that were reliant on mechanical ventilation had no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66% not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome, which is corroborated by other studies.

**5.1 *What are the known theoretical models and tools available for BE characterisation regarding risk, transmission and microbiome identification?*** (Response in 10.1 and 10.3)

An extensive literature review was conducted to determine the methods, tools and monitoring apparatus available. Furthermore, the 2017 MoBE report references the various applications. Chapter 3 sections 3.3 and 3.4.2 review specific BE sampling requirements, opportunities and needs. A table was developed from over 90 reviewed literature articles that define a number of methodologies, techniques and models referenced in Table 3.21: Theoretical models and methodologies. This includes sampling tools for genomic sequencing and sampling for BE environmental factors. This study's master data set includes up to 40 data factors. For details on a large, but yet limited, number of parameter and collection methods refer to Table 3.20: Tools for improved collection of built environment data, taken from Ramos and Stephens (2014) For spatial analytics few tools have been utilised; there are only 4 studies that have conducted a high level spatial analysis (minus this study). The application of Space Syntax (SS) was not previously considered and applied in BE studies. A vast selection of technologies is available, each associated with a desired methodology. This study includes a detailed

literature review, and refers to a research methodology for environmental monitoring available and the elected methods applied for this thesis.

### 5.2 *Can BE factors be converted into indicators utilised for microbial risk in buildings?*

This question has not been answered in this thesis. The author, however, believes that spatial data will provide more insight into microbial distribution, as seen in the ventilation deduction (section 8.3.2.1) and the overlay of microbial biome data per room type. The relationship between rooms will provide further insight into this potential (refer to section 8.3.2.3). The current data for this thesis do not produce conclusive proof for this. The microbial sampling data do not show significant correlation with BE factors (environmental and spatial); however, ventilation was a BE factor finding, and this is due to the broad nature of the study design. A focused study with more localised samples from selected rooms will provide more insight. It was found that the number of BE factor samples by far outweighed the microbial samples. More microbiological samples are required to draw definitive conclusions at the micro room level. Further analysis of spatial data, observed data, BE factor data and room species indicators could provide some guidance towards this goal.

## 10.4 INTERDISCIPLINARY CONCLUSIONS

Correlations, comparisons and deductions comparing microbial, architectural spatial and environmental data and outcomes are discussed in this section. The investigation outcomes are built on the results and findings from Chapter 7, Chapter 8 and Chapter 9. This section responds to the primary research questions posed in the thesis.The prmary research questions are repeated followed by the response.

**Primary research question 1) What is the composition of the South African, Western Cape, Cape flats hospital microbiome?**

An estimated 35% of the outdoor environment's organisms were found indoors, regardless of room type and ventilation supply source, as was observed at both MPH and KDH. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose for outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria. Similar to other studies reported, no indoor biota were found outdoors. Statistically no correlation with ventilation source was found; the only factors that did indicate correlation were season and type (air and surface). However, the ventilation systems in both KDH and MPH, as per the MC data, showed that 66% of the rooms that were reliant on mechanical ventilation had no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66% not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome which is corroborated by other studies.

Of the organisms sampled, the indoors spaces are more representative of indoor human-sourced bacteria, as is shown by the Gamma diversity per room type and per season and sample type. However, from the thesis study data, data set for indicator organism by room, the corresponding genera were identified. They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter*. They were globally reported and not by type (air or surface) or by season (winter and summer), but by room. Due to the number and complexity of spaces sampled, source tracking was not technically feasible for this investigation. As depicted in Table 8.14 and Table 8.15, as noted previously, the indoor spaces contained on average 35% shared organisms from the outdoors; therefore, 65% of the organisms found are sourced from within the building, of which an estimated 25% are potentially human-sourced biota based on the organisms identified and abundance count. However, it is noted that physical transport of soil and other environmental organisms into the sampled rooms, followed by resuspension of dust particles, also represents a potential route for "human-sourced" microorganisms. Nevertheless, in this discussion, the principal focus is on organisms which are human-associated (skin, hair, etc.) rather than vicariously associated (with shoes, clothing, etc).

The Beta diversity findings (Figure 78) indicate that MPH and KDH are not dissimilar and share a similar indoor microbiome. At the scale of the study the data reflected that the two hospitals tend to have similar biomes. The PCoA BETA Diversity for air, surface, summer and winter - factors for MPH and KDH with factor "hospitals" replacing factor "season" - indicate that the two hospital communities had no effect, as corroborated by the Permanova. In addition, a seasonal variation is very evident, specifically in the air samples for winter and summer. An interaction between the season and the type of sample was found. Specific phyla were associated with air and surfaces, with a diverse (almost inverse) variation of each in winter and summer. The data confirm a seasonal variation in the microbial community for both hospitals. It is also evident that the surface and air communities are sufficiently different to justify a focused study for each in future. Not only is there variation, but the type of samples (air or surface) show seasonal relationships. The Beta diversity patterns in

Figure 76 indicate a notable dissimilarity in the air samples in summer and winter, thus a clear seasonal variation. The data show that there is a variation between the air samples and the surface samples. Not only is there variation, but the types of sample (air or surface) show seasonal relationships. The genera identification also confirms variations in identified indicator species. Based on an Alpha diversity analysis, a variation was noted in the number of taxa found in surface and air samples. This indicates that the surface samples alone do not reflect the air samples or the total Alpha community. Considering the full samples set, it is evident that there is interaction between the season and the type of sample (air, surface). A tendency of increased OTUs in the air and surface samples was observed in winter ($P < 0.05$). It can only be inferred that the fallout, if it occurred, would add to the diversity of the surface samples; however, sampling only surfaces will not prove effective in biome identification, as seen in the large variation and abundance of both genera and phyla. In accordance with other studies, it would be necessary to sample both communities to define the indoor biome. However, physical contact with surfaces (touching) by humans will certainly contribute to the sampled diversity.

**Primary research question 2) What pathogens are commonly found in South African hospitals, with specific reference to the Western Cape, Cape flats?**

Core indictor organisms have been identified and can be classified at this point as the hospital biome of KDH and MPH. (A large number of unidentified OTUs were noted). The indicators are: *Pseudomonas, Enterococcus, Delftia, Corynebacterium, Burkholderia, Bacillus, Acinetobacter, Stenotrophomonas, Staphylococcus* and *Stenotrophomonas.* The relative abundance and types of indicator species vary between room types. Refer to the tables on indicators, room types and viability (based on the identification and comparison of culture sample organisms). Furthermore: from the study data, data set for indicator organism by room, the corresponding genera were identified for human source (skin, etc.). They include *Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter* Refer to table 8.12 for genera identified at KDH and MPH.

**Primary research question 3) Which built environment factors contribute to and influence the composition of the built environment microbiome, and how?**

From literature the following factors are attributed to influence the building microbiome: *Source of ventilation air, airflow rates, relative humidity and temperature were correlated with the diversity and composition of indoor bacterial communitie;. HR values on same floors (spatial connect), HVAC system, hospital staff which this infers occupancy, air and surface temperatures, HVAC particle filtration efficiency, human occupancy, human contact frequencies, surface characterizations: porosity, composition, and environmental conditions immediately adjacent to materials can all affect microbial community structure, growth, and survival; the cleaning regime for surfaces and human activities and patterns and building operation seem to have the greatest impact on indoor microbial ecology.* Kembel *et al.* (2013)*.* The various factors utilised in this study did not indicate a significant correlation between the BE and the microbiome. The factors that did indicate correlation were hospital, season and sampling type. A possible reason for this might be sample size. The large number of BE factors (40+) compared to the low number of microbial samples reduce the potential to find significant correlations. From the data, it was apparent that the ventilation strategy did affect the dispersal of microbes in those rooms that shared natural ventilation and the rooms that only had mechanical ventilation - it made no notable difference in the organism distribution. The BE factors, including occupancy, gate crossing and internal flow count, did not correlate with the microbial sampling data.

However, considering the spatial findings, the core areas (central space with highest occupancy and activity) at both MPH and KDH averaged 850 OTUs in winter, and 510 OTUs in summer. The core triage areas of MPH and KDH averaged 890 OTUs in winter, and 550 OTUs in summer. The fact that MPH had a 50% increase in occupancy over the winter season, combined with a higher abundance of air-associated organisms, indicates occupancy and activity are indeed a factor. This is similar to the OTU abundance analysis showing diversity in room types; however, mid activity room types had the highest OTU abundance counts. This study must be viewed as a macrobiome study at building unit scale, and the data suggest that a focused selected room study measuring the same factors would be the next step in analysis, thus detailed studies focusing on temperature and sample types, HR and sample types, and $CO_2$ and sample types are recommended. No significant correlation was reported, but a relationship was found between the mechanical ventilation and outdoor air entering by natural

means on the composition distribution. They share an estimated 35% of the outdoor environment's organisms indoors, regardless of room type and ventilation supply source, as was observed at both MPH and KDH. There is a clear distinction between the outdoor (external) and indoor samples (it must be noted that the outdoor samples analysed were 10% of the total randomised samples analysed for the full sequenced set). The purpose of outdoor sampling was to ascertain outdoor prevalence indoors. The sequenced outdoor samples reflect only Beta-*Proteobacteria* and Alpha-*Proteobacteria*. The outdoor taxa varied between seasons, with summer presenting mainly Beta *Proteobacteria* followed by Gamma-*Proteobacteria*, and winter vastly more Gamma-*Proteobacteria* followed by Beta-*Proteobacteria*. This finding differs from that of other MoBE studies, where outdoor taxa are commonly dominated by Gamma-*Proteobacteria* and Alpha-Proteobacteria. Similar to other studies reported, no indoor biota were found outdoors. Statistically no correlation with ventilation source was found; the only factors that did indicate correlation were season and type (air and surface). However, the ventilation systems in both KDH and MPH, as per the MC data, showed that 66% of the rooms that were reliant on mechanical ventilation had no means of natural ventilation, whereas 33% of the rooms/spaces were mechanically ventilated and naturally ventilated through open windows. When considering that the microbial data identified 35% of the outdoor-sourced taxa in all rooms, including the 66% not accessible to natural ventilation, it can be inferred that the ventilation strategy contributed to this distribution outcome - which is corroborated by other studies,

**Primary research question 4) Is there any correlation between the distribution of the microbes in hospitals and the spatial design of the hospitals (considering user data and design data)? Does design and planning influence the composition of the microbiome?**

Most studies have not utilised spatial metrics. The majority of existing methods are based on estimations of occupancy, whereas real-time rates would prove of greater value in dynamic microbial community characterisation; similarly, *much less attention has been given to detecting occupant activity* (their movement in space), *despite evidence indicating that such movements have a stronger effect than occupancy on certain aspects of IAQ* Desdeko *et al*. (2015). The limited measure of occupant activity (at most only by gate crossing/threshold crossing) presented in the various studies indicates an opportunity for new approaches in spatial analysis. The application of building design spatial factors is even rarer (Adams *et al.* 2015). The literature review only identified four studies that considered a form of occupant activity and presence: this presents a far greater discrepancy, as by spatial factors we imply more than only occupancy per space, yet numerous studies have consistently confirmed the importance of human occupancy and user identification, human activity, space use and spatial relationships. DepthMap™ spatial analysis and GIS modelling are tools for assessing space use and flow, as the observed data correlated with the simulation. These would be appropriate tools to investigate distribution and potential interaction from an architectural perspective. More research will be needed, as well as an investigation into factorisation for correlation. This does allow for a form of real-time measure and in addition provides numerous factors previously not quantified but important: use type, flow activity, etc.

In an attempt to determine commonalities based on room type and abundance, the OTUs measured per room were graded by assigned spatial metrics. These metrics included (1) core spaces by base plan analysis, (2) spaces by observation (integration) analysis, (3) spaces by

gate crossing analysis and (4) spaces compared for type or season. The common finding for all observed measures (except the base model) was a tendency of higher abundance in rooms that had mid activity, i.e. for flow count the highest abundance rooms with the median activity were consistently Resus, Nebulisation and Triage Consult for both hospitals. This could be due to the reduced activity which allows for settlement and deposition of biota, thus a temporal factor of deposition and contact time. When considering only the room type and therefore by extension the function of space, assuming that room type and OTU count are relational, similar counts seasonally should be found (to allow for the large seasonal variation). This was evident for only some rooms (considering a 10% maximum variation). In general, the values for summer are more similar for types and less so for winter. For summer: Nurse Station, Procedure, Triage Consult, Triage Waiting and Trolley area. For winter: Procedure, Resus and Triage Waiting. The only two rooms that are similar for both winter and summer are Procedure and Triage Waiting. Interestingly, these room are either the lowest (Procedure) or mid high (Triage Waiting); the dominant user for both hospitals for Triage Waiting was patients and for Resus was nursing staff. This implies a similar abundance of OTUs in those two rooms. From the spatial analysis core clusters were identified, implying a high level of activity and flow. The rooms associated with these clusters were 1) Triage Wait and Consult 2) Nurses' Station (could not be identified distinctly). Rooms were identified by prominent user, but further analyses would require source tracking of user type to determine the relationship between user type and biota similarities. All rooms had a unique microbiome and differed seasonally. No one room type had a matching community. Similarities were that all rooms had high abundance of *Gamma proteobacteria* and far less *Beta proteobacteria*; it was similar for *Bacilli* and far less for *Clostrida* and others. It was noted that various factors influenced in the microbial room structure, such as season and hospital. Refer to Figure 82 for variation between rooms and in seasons, with very evident non-correlations. With reference to figure 83, a number of rooms did indicate higher abundance of *Proteobacteria*, e.g. Nebulisation. It cannot currently be confirmed that room types match in different healthcare buildings; however, the microbial composition of the two hospital were not invariant.

The data do not reflect statistical significance; however, the ventilation design caused cross distribution of outdoor biota in all rooms. Secondly, when reviewing the microbial data, each room type indicated the presence of indicator genera and phyla, but of varied relative abundance. The room type biomes differed from each other, and in addition, they differed seasonally. The BE factors do not show correlation at this time, but it is evident that there is a relationship amongst a multitude of factors. From the spatial analytical findings, it was observed that the following space logic is applied: both hospitals have a linear typology, high core flow and occupancy zones, and micro core zones that are less integrated in the global layout, but co-dependent at their core. An analysis on the OTU, ACH, airflow and occupancy was attempted (from Table 8.18 to Table 8.22 and Table 9.7), but no correlations were evident or unique in relation to the entire unit room type data. The author suggests that the spatial findings require focused investigation to determine the micro variable and biome factors. This thesis study cannot indicate which factors, besides ventilation and the presence of people, influence the composition of the indoor microbiome. Further focused research is needed to ascertain the factors and sampling threshold to achieve this answer.

The data indicate that, for the majority of factors, there were significant seasonal variations in the data observations. Occupancy dynamics in space and time analysis are key due to the dynamic nature of microbial communities. The study did find increased abundance with

relatively higher activity zones. Spatial network analysis could not determine the variant microbial communities between room types. This is most likely due to the global study level. A number of studies have noted niche focused research to elucidate microbial interaction with space and indoor environment.

**Primary research question 5) How can built environment data, microbiome data and spatial design data inform IPC processes, with the intentional focus on reducing the potential of HAI transmission?**

The objective of the thesis was to provide analysis tools and results that could be applied to improve IPC approaches and generate functional layout changes in building design. The application of models for bio informed design as postulated by the author in this thesis (ADMRM) still requires substantial data and investigation for application. However, the data and findings presented here can serve as empirical guide to informed design decision making in the health sector.

Spatial analytics: The methodology of modelling an existing base plan to elucidate flow patterns and focal space connectedness and levels of integration, then testing it with observational data, was shown to be highly effective. In the majority of the outcomes, the base plan analysis derived from Space Syntax methodology was correct. The observational data broaden understanding of social heuristics that develop in time and through operational and policy changes. The data shed light on both MPH and KDH rooms/zones that one would not perceive to be highly trafficked spaces and/or spatially connected with activity levels. Furthermore, the analytics elucidate the optimal planning of a hospital's central core. The findings offer insight into appropriate barriers and zone separation, and clarify the categorisation of spaces by function within a network of spaces. The data indicate potential zones of high integration and thus potential cores of interaction, providing insight into the number of people accessing spaces and moving within these spaces, when analysed within the framework of the entire system. Zones can be graded on use, occupancy and association with risk. From integrating microbial sampling data, genus species can be associated with room types and zones, and thereby functional activities in space can be associated with the typical biome, as found in this thesis. This allows for both localised IPC interventions and global network IPC interventions to reduce HAI. Critical to this is the relationship of program and IPC: The low correlations found between the observation flow data of space use for integration of spaces, evidenced by the observed patterns, and the spatial potential at both facilities consistently $R^2$ of 0.4 and less opposed to $R^2$ 0.58, in fact supports the notion of a strong building program dominant in both of these facilities. The building program (the manner in which it is used) often overrides the assigned space function (where function determines utilisation). This complicates space related IPC approaches and provides critical insight into approaching BE design choices. The author postulates that a stronger program will present a more temporal and dynamic microbial community not only determined by spaces but by the movement and activity between them.

Microbial sampling data indicated that both air and surface sample environments shared unique and associated genus species, implying that to effectively apply IPC interventions, both sample types are needed. A core indicator of common organisms found in each room type and in both hospitals has been developed in the thesis. The data showed that both hospitals have similar biomes and thus a similar IPC approach can be followed. Whether this holds true for other health facilities in similar proximity is a worthwhile investigation towards standardisation

per sub-region, and will allow for focused “attack” IPC measures. Environmental measurement data revealed potential risks in various zones at both MPH and KDH. Applying the $CO_2$, occupancy, Ls pp and room volume data enables one to produce a risk scale for room types for TB and other airborne pathogens relying on mass balance equations. The data indicated that KDH had lower ACH and L/s pp per room with larger volume and rooms regardless of type, whereas MPH had a 50% increase in occupancy over the winter season, combined with a higher abundance of air-associated organisms unique to the two hospitals. These findings may guide IPC measures. The data revealed core indicator species associated with room type, and culture analyses were done to determine species viability. Based on USA HAI statistics, 60% of the top five HAI associated organisms were identified in culture, and sourced from the DNA genera found with other unique pathogenic species associated locally.

## 10.5 TESTING THE HYPOTHESES

*From the premise that all environments are ecosystemic and that each constitutes a unique biome, it is postulated in the thesis that the built environment microbiome is shaped by both ecological processes and interrelationships, but also by key factors within the BE, unique to indoor building environments. Furthermore, it is postulated in this thesis that the hospital environment would present a unique composition by nature of its source elements, with each composition being unique in different climates, environments, countries and social conditions.*

*The architectural layout of a building and its associated engineering aspects will impose differences in the biomes from one building to the next; however, the source/user would, as is the case with hospitals, be constant, but vary with burden of disease. By characterising the BE aspects and overlaying these with spatial analytics trends, the patterns of use, assemblies, and voids can be derived. In theory, this should lead to variations in the microenvironments of a building. As with all ecosystems, both macro- (department and whole building level) and microenvironments (room, table, keyboard) exist within, which also holds true for the built environment. In this thesis the macro biome environment of two A&E departments in the same region and climate are investigated with insight into the micro environment at room level only.*

**Primary research hypotheses:**

**Hypothesis A: Building typologies with associated typological planning layouts and room types can be distinguished through their microbiomes, thus elucidating potential risk in public health architectural design, based on the biome structure (abundance and richness) of the indicator organisms.**

The research found that the two hospitals studied are not dissimilar in their microbiome composition, but internal layout did show core spatial differences and global (at unit level) abundance and richness differences (based on OTUs); in addition a unique biome was associated with each room type and the common building types (two hospitals) had similar biomes. The indicator organisms were correlated with the HAI list and studies on healthcare associated infection. The presence of organisms cannot at this point define the status of a building, due to the fact that no significant association can be gathered from comparing microbial samples and BE factors. Ventilation, season, sample type (local environment) and hospital type are the only factors showing significant correlation; yet the data do show that BE factors also shift seasonally, as do biomes, adding a layer of complexity to biome factor identification.
Therefore…

**Hypothesis B: Social behavioural science studies which consider factors of human movement patterns, occupancy and functional use of space influencs the microbial composition of the built environment. Architectural spatial analytics with building ventilation systems provide insight into biome composition. Thus, the indoor environmental factors of hospitals MPH and KDH influence the composition of both the micro (room level) and macro biome (building level) environments.**

Most indoor biota (65%) were sourced from within the building and not present outdoors; of the organisms at least 25% were associated with human-sourced bacteria (skin and other) identified in the room by type samples. The biome of each room was unique and varied by composition and relative abundance, but similar in genus indicators. The spatial analysis factors did not show a significant correlation; however, the vector source (human) by occupancy and activity during time spent in a space must be a contributing factor, as seen in the abundance increase in winter seasons, related to occupancy increase in the same environment. At this time and with the current factors the thesis cannot confirm in which way social behaviour influences the indoor biome. Spatial analysis did reveal a space logic that is novel, i.e. core zones, micro networks OTU count and activity, and linear typologies for future investigation.Both hospitals employed an HVAC system. The study noted that they were working and functional - less or more so in each facility. Furthermore, windows were opened in similar rooms, providing natural ventilation. It was found that all rooms/spaces evidenced a similar distribution of outdoor biota comprising 35% of the microbes sampled, indoors. This included rooms with no external windows or access. The only ventilation system also had 80%-100% fresh air replacement; this implies that the only method by which microbes could be distributed in the manner they were, was through the ventilation system moving air from one space to the next, mixing the shared air between spaces not in duct. Other factors, including season, type of community (sample air and surface) and hospital, influenced the sampling data. When the factors (Table 9.7) were compared to the sampling data, no correlation between the indoor environmental factors (Table 60) and the micro- and macro biomes was found. The thesis data indicate that there are both micro- and macro biomes at play. These biomes are affected by BE factors but could not be identified within the current sample study and sample boundaries.

**Secondary research hypotheses:**
**Sub-hypothesis A: The source of ventilation (either mechanical or hybrid) uniquely influences the composition of the microbial community and/or richness in a room.**

Both hospitals employed an HVAC system. The study noted that they were working and functional - less or more so in each facility. Furthermore, windows were opened in similar rooms, providing natural ventilation. It was found that all rooms/spaces evidenced a similar distribution of outdoor biota comprising 35% of the microbes sampled, indoors. This included rooms with no external windows or access. The only ventilation system had 80%-100% fresh air replacement. Microbial distribution was equitable by OTU count and unique by diversity and richness. The study confirms that sub-hypothesis A holds true: The ventilation system did influence the composition of microbiome, as seen in the presence of outdoor biota indoors,

&

**Sub-hypothesis B: The levels of social exchange and interaction (measured by gateway crossings and internal movement) uniquely influence the composition of the microbial community, evidenced through OTU count, abundance and/or richness in a room.**

The study confirms that the null hypothesis holds true only in part for sub-hypothesis B: This investigation found that neither limited median room level activity indicating social interaction had an impact on the OTU count, abundance and/or richness of a room (space), irrespective of type. It could not be determined, and statistical tests on occupancy and gate crossing factors showed no correlation.

## 10.6 PERTINENT FINDINGS

In summary, the pertinent findings are described below.

10.6.1. In the spatial analysis, all aspects of spatial relationships were considered, including spatial integration and spatial connectivity, as well as the identification of potential zones of congregation and zones of isolation. Spatial analyses indicated that observation data closely matched the simulation data. In future, this may assist in determining microbial associations. The spatial analysis findings established the following space logic as applied in A&E units: both hospitals have linear typologies, core high user flow and occupancy zones, and micro core zones that are less integrated in the global layout, but co-dependent in their micro core. The author suggests that the spatial findings require focused investigation to determine the micro variables and biome factors. This investigation found that the composition of the majority of organisms in the hospital biome (65%) was human- sourced. A 90% correlation was found between the gate counts and internal movement counts of the spaces analysed. When considering the assessment of spatial activity, gate counts can provide valuable association data and support the use and application of SS in building planning analytics.

10.6.2. Both hospitals experienced seasonal variation in occupancy and internal user flow, suggesting that MPH is preferred over KDH in winter by the local community, as the summer occupancy rates are similar but the winter occupancy rate is 30% more than at KDH. A number of factors across all three areas of investigation were influenced by seasonal change (BE and microbial) – refer to Table 46 for details. These findings indicate that the built environment is not a static environment but is continuously influenced by external conditions. This fact potentially contributed to the negative hypothesis result showing that no direct BE factors influence the indoor microbiome, except ventilation.

10.6.3. MPH experienced a 50% increase in occupancy in the winter season, while a variation was found between the summer and winter microbial sampling, with an increase in indicator species related to air source. Considering the species identified in the indicator list, it could be attributed to an increased “illness” rate over the winter season (assumed, based on the increased occupancy or patient visits in winter). What is of value is the microbiome change between MPH and KDH in winter versus summer. The data showed seasonal variation in BE factors and seasonal change in the indoor microbiome of both hospitals, but not significant correlation between either.

10.6.4. The investigation found that the indoor rooms are representative of indoor human-sourced bacteria, as is shown by the Gamma diversity per room type and per season and sample type. However, from the thesis study data, data set for indicator organism by room, the corresponding genera were identified. They include Propionibacterium, Corynebacterium, Staphylococcus, Streptococcus and Acinetobacter. They were

globally reported and not by type (air or surface) or by season (winter and summer), but by room. Due to the number and complexity of spaces sampled, source tracking was not technically feasible for this investigation. From the data in Table 8.14 and Table 8.15, as noted previously, the indoor spaces contained on average 35% shared organisms from the outdoors; therefore, 65% of the organisms found are sourced from within the building, of which an estimated 25% are potentially human-sourced biota based on the organism identified and abundance count; however, it is noted that physical transport of soil and other environmental organisms into the sampled rooms, followed by resuspension of dust particles, also represents a potential route for "human-sourced" microorganisms. Nevertheless, in this discussion, the principal focus is on organisms which are human-associated (skin, hair, etc.) rather than vicariously associated (with shoes, clothing, etc). Adams et al. (2016: 227) indicate through various study reviews that human-sourced bacteria found indoors equate to up to 40% indoors; data varies by study.

10.6.5. A common distributor of the indoor biome was the ventilation system. The equitable distribution of organisms from outdoors in all rooms (even those without windows and access to the outside) indicates that ventilation is a common source, as with humans as vector. Associating the data with the spatial analytics sheds light on the other 65% of organisms prevalent indoors. The sample study showed no correlation between BE factors and the abundance or richness of indoor organisms, due to the "few" microbial samples compared to the large BE factor set. The data did, however, indicate that the core area at both MPH and KDH averaged 850 operational taxonomic units (OTUs) in winter, versus 510 OTUs in summer. Similarly, the core triage area in MPH and KDH averaged 890 OTUs in winter, versus 550 OTUs in summer – refer to Table 8.18 to Table 8.22. The winter season had a much higher relative abundance of OTU genera taxa than summer. In this study, it is proposed that additional local focused room-based studies be undertaken to inform on the micro factors and interactions.

10.6.6. The comparison between fully mechanically ventilated spaces and hybrid ventilated spaces did not show a correlation; however, when analysing the sample data, up to 35% of outdoor-sourced organisms are represented in the samples, which suggests that the ventilation system plays a direct critical role in the composition of the indoor biome. It not only circulates outdoor biota but also the prominent indoor human-sourced biota, as is evident from the similarity in composition between rooms. The data tables indicate relatively stable HVAC performance. Please note: HVAC filters were not sampled and sequenced.

10.6.7. The gate crossing data for KDH did not vary between summer and winter. The total occupancy can be considered constant during both seasons; the BE factors varied, but spatially KDH by observation indicated similar use and flow activity for both seasons. This finding implies that the season did not in fact influence the room functions at KDH. There was an observed variation in use and flow at MPH, with a 30% increase in occupancy from summer to winter. Of all room types, 69% correlated with gate crossing in winter for both hospitals, and 73% in summer. The MPH spatial data indicated that the activity levels between zones vary greatly seasonally with only a 40% similarity between seasons. One can conclude that the seasons did play a role in activity levels within zones. The Nurses' Station was the highest use zone in both hospitals in all seasons, and the Procedure room the least active space, which could

suggest under-utilisation. The occupancy correlation with gate crossing and internal flow was less than 35%, which suggests that hospital environments, specifically A&E units, are fluid, transitory spaces, and that the level of activity varies greatly from the level of occupancy. Thus, it can be accepted that the occupancy did not correlate with either the internal activity or the function of the rooms; it did, however, correlate with the CO2 values measured, which are surrogate indicators for re-breathed air and airborne infections. The use of spatial analytics provides a viable option for simulating potential space use and activity, as was confirmed through the observed data and the correlation between VGA and axial mapping through integration, and connectivity analyses of base plans, observation overlays on base plans, and GIS data overlay on both base plan and base plan observation overlays.

10.6.8. The spatial analysis indicates integrated and connected environments. Similarly, it predicts spaces of clustering. With the observed flow data of people moving and people entering and exiting spaces it gives insight and enables modelling verification. The gate counts and internal flow measures in many respects were strongly associated with the potential predicted simulations of where one would expect to find congregation and reduced people numbers. When considering IPC transmission models (ventilation, congregation settings, people distribution), the analytics provide insight for localised IPC approaches; it highlights potential rooms of higher risk. Combining spatial data with environmental data, appropriate approaches and IPC selections can be proposed. The overlay of microbial biome data per room type and the relationship between rooms could provide another layer of data for, and insight into, this potential. Spatial planning and typology (linear at KDH and MPH) can influence IPC outcomes, guide IPC decision making, guide IPC selection, and recommend focused interventions at a local and global unit level.

10.6.9. Important note: The findings of the longitudinal study by Lax et al. (2017) executed for a year in a hospital environment and sampling 12 rooms, found no universal pattern of transmission between patient rooms. In addition, it reported that the vast majority of indoor microbes were sourced from people and, secondly, specifically from the nurses. Similarly, this thesis study indicates no direct correlation between BE factors and biota distribution. The thesis study utilised 16S sequencing technology with similar results; it did not incorporate clinical data, but did include additional environmental and social data.

10.6.10. Comparing the room types with the OTU count and relative abundance did not indicate a significant correlation. When reviewing the data per indicators, a variation in genera and diversity was found between the rooms; also, a variation was found between seasons, and between sample types in rooms. It is evident that the sample types have a relationship effect on each other; therefore, each room did present a unique surface and air biome. This unique biome differs in winter and summer; refer to Figure 83 and Figure 84. Further spatial study overlays and additional correlation measures with BE factors will provide a more informed outcome. At this stage, no correlation has been found – refer to 7.1.5 for the analysis. The author proposes that a large sample set per room type is required (thus, more room samples should be taken).

## 10.7 CONTRIBUTIONS TO THE FIELD

From the pertinent findings of this study, this research makes the following contributions to the MoBE and architecture study field:

10.7.1. The building microbiome varies by season with the community structure defined by both air and surface communities, further to that, Built Environment factors indicate dynamic seasonal variations, combined with localised occupancy and spatial patterns.

10.7.2. These indoor environments are unique biomes at room space level, but they are similar by building typology from examening the two case studies.

10.7.3. Hospital building designs consist of either weak or strong programmes. Hospitals are often considered to require strong programs, but have the tendency to shift between weak and strong. This study found that both hospitals showed consistently strong building programs (the manner in which they are used in both seasons) which overrides the assigned space function (where function determines utilisation). This finding reveals a new layer of infection prevention and control (IPC) complexity in the built environment form the results it is suggested that a stronger programme will in fact present a more temporal and dynamic microbial community, which is not only determined by the physical spaces but also by the movement and activity between them. Considering that humans spend up to 85% of their time indoors, this is critical considerstion for user health.

10.7.4. The dynamic nature of the indoor built environment is reflected in the variety of biomes and the variation due to occupancy, season and ventilation. This finding indicates that niche areas exist within indoor environments and dynamic and temporal factors are at play, which require focused research attention.

10.7.5. Spatial analytics is fundamental to understanding building user pathways, and building use, tracked by Operational taxonomic unit (OTU) abundance and diversity. The influence of building design decisions ranging from operations, layout, planning, to hardware and systems have a direct effect on the microbial composition and structure of the indoor built environment.

It is currently not possible to define exactly what a good and or healthy indoor environment should be, however, every contribution to this field takes us one step closer to understanding the role architecture plays in the creating and supporting an indoor building microbiome in South African healthcare facilities.

# CHAPTER 11 PERTINENT CONSIDERATIONS AND FUTURE INVESTIGATIONS

## 11.1 PERTINENT CONSIDERATIONS

Various goals and objectives were set for this thesis, aimed at improving the quality of the indoor built environment, contributing to the MoBE research agenda, and stimulating a public health centred architectural response. In pursuit of gaining insight and testing the spatial relationship of indoor environments and the biome composition and distribution, a methodology is proposed towards IPC building assessment and operational guidance.

11.1.1. Architectural and engineering design decisions for a public health centred outcome should consider the built environment decision making factors and their influence on microbial environments, which in turn affect the building user.

11.1.2. The application of spatial analytics in room and space analysis overlaid with risk determinants outlined in this study support a novel BE risk assessment for early design analysis, primed for future development as a guide towards bio-informed design. The role of building programs and risk application is critical and requires further investigation.

11.1.3. This study has managed to characterise the first South African hospital biome, which would be representative of the developing world for future meta data studies. It contributes to MoBE data sets and enables future meta data analysis for future MoBE studies.

11.1.4. The study characterises a hospital biome for a developing world country such as South Africa, and specifically for the Western Cape, Cape Flats region. It also contributes to the development of HAI research and a pathogen species list, through the identification of microbial genera indicators and viable pathogens associated with the hospital biome and cross-matched with international HAI lists, and confirms that the sequencing of biota is viable through culture analysis.

11.1.5. There is supporting evidence in the research field that the outcome of this study will stimulate renewed interest in public health centred building design. It represents a first step towards realising bio-informed design guidelines for healthcare, in architecture and engineering.

Building types can be distinguished through their microbiomes. Longitudinal studies will indicate the community dynamics over time for BE biome environments, whereas focused studies will define the temporal dynamics in community structure. The unique biomes associated with each room type reflect this fact. The factors that determine these biomes are still unclear but represent future possibilities for research investigation. The study finds that two hospitals, in relatively close proximity and serving a similar burden of disease, with matching climates and microclimates, will present similar microbiomes. At this time, the community composition cannot define the status of the health quality of a building for its user. Indoor environments are less diverse than outdoor environments, but no significant association could be gathered from BE factors. However, occupancy, ventilation, season, sample type (local environment) and hospital type (building typology) are factors that show significant correlation. The thesis study reveals that, similar to seasonal variation in the microbiota of a hospital, BE factors also shift seasonally, adding a layer of complexity to biome factor identification, especially for hybrid environments

## 11.2 RECOMMENDATIONS FOR FUTURE INVESTIGATIONS

11.2.1. The research shows that a sample size threshold needs to be established between the different disciplines to address the following questions: What is too much data or too little for each discipline? How much data is required to achieve significant outcomes? This investigation finds that 288 DNA 16SrRNA sequenced samples and 160+ culture samples were still not sufficient to answer the questions concerning the association of BE factors, but were able to provide inferred results where appropriate. The study recommends increasing the number of outdoor samples to align more closely with the quantity of indoor samples, as this will allow more robust sample comparisons and provide data support for future studies. However, for this study it is noted that the number of samples and the sampling duration differ between outdoor and indoor sampling sites, and as such a direct comparison of microbial biomass between the two areas is not strictly valid. Identification and quantification of shared biota was the motivation.

11.2.2. The author concurs with recommendations made by Kelley and Gilbert (2013) for future niche focused investigations; this is obvious considering the temporal dynamics of microbial communities. Future study should focus on room type and increase sampling with full BE sampling. Spatial measures of space in relation to other spaces should be recorded. This should also include further focused research to understand how temperature, humidity, building materials and the integrity of the building structure affect the interchange between the indoor and human bacterial microbiomes.

11.2.3. Future study contributions based on the findings of this investigation could have far reaching effects, appraising each built form setting that we dwell in or have contact with indoors, ranging from hospital environments to surfaces, and rooms in which we process and package food to rural huts and informal shacks. It is worth considering that related studies are being conducted on the home biome, gut biome, human biome and even the space station biome. In this thesis a theory for further investigation is put forward, i.e. that through the design and spatial separation of room types or categories, microbial contamination can be prevented.

11.2.4. Furthermore, individual air filtration per room is required to prevent the spread of microbial contamination. It is postulated that by implementing such a process, the cross distribution of organisms will be reduced throughout an indoor environment and the biota localised, thus enabling effective IPC protocols. This is an indication of the growing importance of ventilation strategies in indoor environments caused by increased urbanisation, indoor living, densification, and public health and social services requirements. In response to natural ventilation applications, the study did establish that the extent to which natural ventilation was applied in both hospital environments did not influence the composition of the indoor microbial community.

11.2.5. Additional South African hospitals must be studied to test and understand the reproducibility and generalisability of the findings of the study and add to the dataset for future meta data analysis; this should include full BE factors with spatial metrics for comparison of sampling types and methodologies.

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# ADDENDA

The following documents are available as addenda to the study. The documents are in an electronic format, and accessible from an online download platform provided by the University of Pretoria (UP) library services. In addition, the addenda are also accessible via a two compact disks (CD) from the Library of the Department Architecture, University of Pretoria (UP)

The list of digital addenda is:

1. Addendum 1 Master data base (Excell spreadsheet)
2. Addendum 2.1 (Master Microbiology data bases) Data set_Genera_Frequency
3. Addendum 2.2 (Master Microbiology data bases) Data set_Indicators per Room
4. Addendum 2.3 (Master Microbiology data bases) Data set_Metadata 175
5. Addendum 2.4 (Master Microbiology data bases) Data set_Shared OTU's (Excell spreadsheet)
6. Addendum 2.5 (Master Microbiology data bases) 97_OTUS.FASTA
7. Addendum 2.6 (Master Microbiology data bases) ALL-SEQ-292.FNA
8. Addendum 3 Master microbiology culture results (PDF)
9. Addendum 4 Ethics approvals and applications 2014 (PDF)
10. Addendum 5 Master Questionnaire data base (Excell spreadsheet)
11. Addendum 6 Mechanical characterisation 2016 (Excell spreadsheet)