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Spatial analysis of livestock disease data in sub-Saharan Africa: A scoping review

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ABSTRACT

Background: In livestock disease surveillance, spatial analysis methods play a major role in the identification of areas where the risk of disease could be higher. Though widely used in human health, their extent and depth of use are not well known in livestock health in sub-Saharan Africa and this has hindered their update in livestock disease modeling. This study set out to provide a comprehensive review of spatial analysis methods and their application in livestock disease data analysis in sub-Saharan Africa.

Methods: Articles were searched using keywords related to spatial and spatio-temporal analysis of livestock diseases in sub-Saharan Africa in PubMed, Web of Science, Embase, and Scopus. Articles were reviewed in terms of name of author, country of study area, study design, livestock species, livestock diseases, research tasks, and spatial epidemiological methods in terms of spatial statistics and models among others.

Results: A total of 56 articles were selected for review. Descriptive approaches such as simple maps of incidence and prevalence ($n = 22$) have been commonly used. Spatial scan statistics of the Kulldorff ($n = 15$) have also been the common spatial statistics employed. Model based spatial analysis has also been used ($n = 14$). Key research tasks that have been performed include investigating disease distribution, risk factors, space and time interaction and spatial risk prediction. The shortfalls of the reviewed studies include lack of exploration of irregularly shaped cluster scan statistics in case the actual disease clusters are irregular. There is also lack of use of multivariate scan and joint spatial models in case of multiple groups or diseases to show comorbidity. Model based spatial analysis has not accounted for space and time interaction. Machine learning niche models have failed to account for spatial autocorrelation in the data. Model based spatial risk prediction has mainly been retrospective as opposed to prospective for early warning.

Conclusion: Future research may consider the application of multivariate scan statistics and joint spatial models for disease comorbidity analysis. It may also explore the use of irregularly shaped cluster scan statistics to enable detection of irregular disease clusters. Research opportunities may also include the use of machine learning models that account for spatial autocorrelation. Future

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spatial prediction is another area worth exploring to show future disease risk trends for early warning.

Introduction

Spatial analysis methods play a vital role in livestock disease monitoring, prevention and control. The methods involve the use of quantitative approaches to analyze data collected at locations defined by geographical coordinates [1]. They are useful in describing and inferring the occurrence of a variable attribute in relation to geographical location [2]. The methods generate information on geographical distribution of diseases thereby highlighting areas with high disease burden needing immediate interventions for control. The disease distribution information is also used to hypothesize possible contextual factors [3] such as livestock and pastoral movements, limited sampling and climatic conditions.

Reviews on spatial analysis of livestock disease data have shown different analytical approaches [4–7]. The simplest approaches include the use of simple descriptive methods such as mapping of disease incidences and prevalence [8]. Spatial autocorrelation analysis commonly use the Khulldorff scan, Getis-Ord Gi* and Cuzick-Edwards' *k* nearest neighbor (*k*NN) statistic [4,5]. Other used spatial autocorrelation statistics are Moran's I and K function [7]. Model based spatial analysis of livestock diseases uses the conventional generalized linear model (GLM) approaches, for example, logistic, Poisson and geographically weighted regression and Bayesian approaches based on the conditional autoregressive (CAR) [4,5,9]. Other modeling approaches include kriging and ecological niche modeling based on method of maximum entropy (MaxEnt) and multicriteria decision analysis [4,5]. Different types of livestock spatial data are used, which include areal or lattice [9] and point referenced [10] data. The data is based on primary surveys and secondary sources such as national departments of animal health disease monthly and annual reports and world disease information systems such as World Organization for Animal Health Information System (WAHIS) and Emergency Prevention System (EMPRES-i) for Priority Animal and Plant Pests and Diseases of the Food and Agriculture Organization (FAO) [11]. Spatial analysis of these data uses either standalone software or add-in packages. The notable software includes SaTScan for scan statistics and GIS software for mapping. Bayesian spatial modeling while using conditional autoregressive regression is frequently done by INLA R package. MaxEnt software is commonly used to implement method of maximum entropy ecological niche modeling.

Challenges in spatial analysis of livestock diseases in poor resource settings such as those in sub-Saharan Africa mainly lie in data [12]. Data is usually limited due to poor surveillance systems characterized by under-reporting and storage of data on paper-based systems [13]. Livestock disease surveillance is also characterized by limited laboratories for diagnosis compared to human health [14], which results in unreliable data since diagnosis is based on clinical manifestation. 'One Health' disease surveillance between animals and humans is also minimal, which if done can permit joint spatial analysis of zoonotic diseases. Although there has been progress in 'One Health' initiatives in sub-Saharan Africa, countries still lack diagnostic capacity and coordinated surveillance [15]. Limited livestock data is also exacerbated by political and financial constraints facing livestock disease research, especially research about non-zoonotic diseases compared to human health [12,16]. Spatial analyses at national level require sub-national data, for example, farming system and livestock population and this data is obtained through livestock census studies which many African countries do not conduct in time [12]. Data for livestock diseases is also available for few diseases since not all diseases are considered a priority in reporting [12]. Livestock disease models at the global scale rely on large scale data and in most cases this data is not available and if available through the WAHIS and EMPRES-i, there are inconsistencies with national disease reports [17,18]. The other challenge of spatial analysis of livestock diseases is limited education and skills in animal related sciences in non-traditional statistics such as spatial statistics [19].

These challenges in turn may hinder the update, development and application of novel epidemiological methods in spatial analysis of livestock diseases. In particular, spatial analysis methods, if any, may be simple and non-novel. In this regard, a comprehensive review was conducted to find out the status of spatial analysis and modeling of livestock disease data in sub-Saharan Africa, more especially on the profile of spatial analysis methods, models employed and the research tasks considered. The main question guiding the scoping review was, what are the gaps in spatial statistics and models in spatial analysis of livestock disease data in sub-Saharan Africa? The specific objectives based on this research question were, (i) to determine common spatial statistical methods being used, and (ii) to identify research gaps in application of spatial statistics and models in spatial analysis of livestock disease data. The strength of this review is that it had a wider coverage in terms of review of spatial analysis methods applied in analysis of livestock disease data without being limited to a single disease. In this regard, a similar previous review in Africa has only considered a single disease [5], which has not given a comprehensive picture of the methods applied.

Methods

This review was done according to the guidelines of a scoping review [20] (Supplementary Table 1), namely, identifying research question and objectives, identification of studies, defining selection of studies criteria, and data extraction and presentation.

Research question and objectives

The main question guiding the scoping review was, what are the gaps in methods of spatial analysis of livestock disease data in sub-Saharan Africa? The specific objectives based on this research question were, (i) to determine common spatial analysis methods in

spatial analysis of livestock disease data in sub-Saharan Africa, and (ii) to identify research gaps in statistics and models that have been employed.

Identification of studies

Identification of studies involved searching for relevant documents using PubMed, Web of Science, Embase and Scopus database. The documents were also searched in Google Scholar. Identification of documents involved searching for phrases that used keywords such as "spatial", spatio-temporal", "analysis", "livestock", "diseases" and "Africa". Using these key words, a search phrase such as "spatial analysis of livestock diseases in Africa" would be implemented. The key word "spatial" would be replaced with "spatio-temporal" to make another search phrase. Alternatively, a single search phrase using Boolean operators "AND" and "OR" would be used to include the term "spatial" and "spatio-temporal". For example, the following was the search phrase with the terms "spatial" and "spatio-temporal" in PubMed: (((((spatial) OR (spatio-temporal)) AND (analysis)) AND (livestock)) AND (diseases)) AND (Africa).

Inclusion and exclusion criteria

The inclusion criteria involved selecting studies where, (i) spatial or spatio-temporal analysis of livestock disease data was done in sub-Saharan Africa, (ii) studies were published in journals, and (iii) spatial or spatio-temporal analysis was based on statistical approach. Studies were excluded if, (i) they involved wild or companion animals, (ii) zoonotic diseases were strictly about humans, (iii) disease vectors were residing outside the animal body such as tsetse flies, (iv) studies were conducted outside sub-Saharan Africa, (v) study area was entire Africa, and (vi) spatial analysis used mathematical models.

Data extraction and presentation

Data extraction involved the review of selected studies on selected variables. Data collected on each selected article included name of the author, country of study area, study design, nature of data, data source, spatial statistical methods, statistical software, name of livestock disease, livestock species, and research tasks or objectives. Data was entered in Microsoft Excel spread sheet and then presented descriptively by frequency tables and bar graphs.

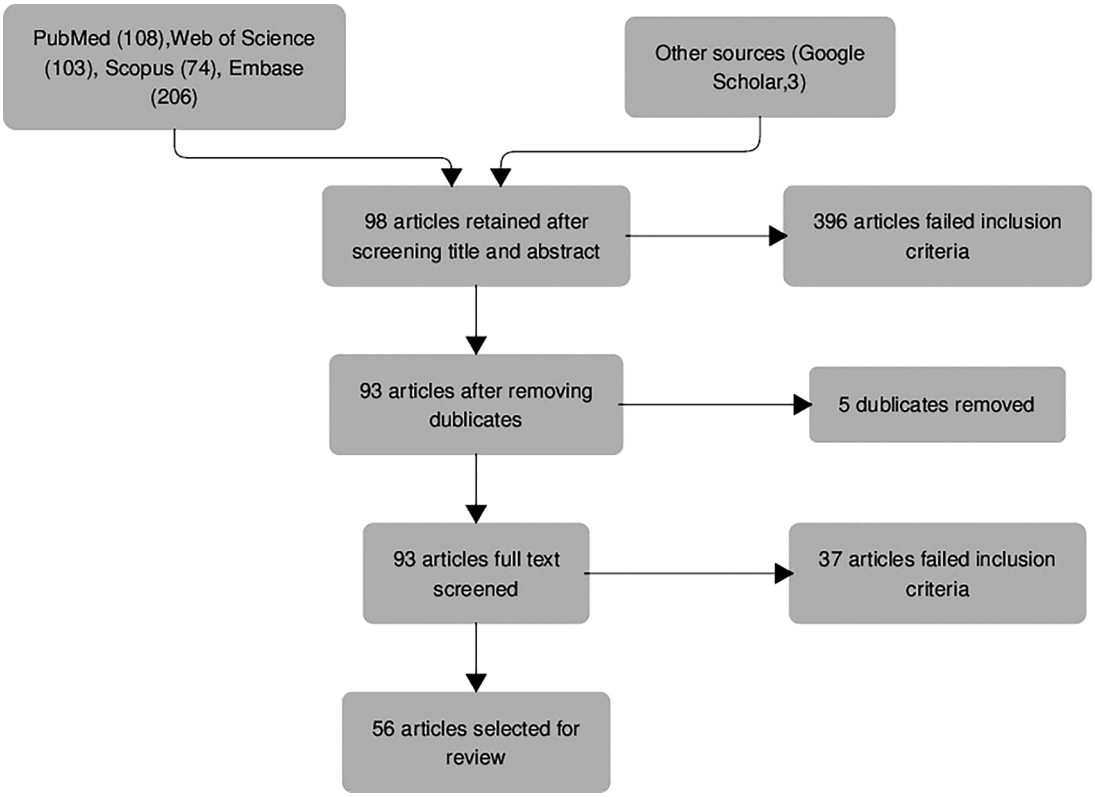

Fig. 1. Preferred reporting items for systematic reviews and meta-analyses (PRISMA) selection of articles.

Results

Study selection

Fig. 1 shows the selection process of the reviewed articles. A total of 494 articles were found and out of these 98 articles were eligible upon screening the title and abstract. Three hundred and ninety-six articles did not meet the selection criteria upon screening the title and abstract. Ninety-three articles were retained after removing 5 duplicates. After full text screening, 56 articles were finally selected for review and 37 articles failed the inclusion selection criteria.

Study country, livestock species and diseases

Supplementary Table 2 shows individual study characteristics. The distribution of the sampled studies by country shows a greater number of studies have been conducted in Tanzania ($n = 9$), Zimbabwe ($n = 8$), Ethiopia, ($n = 7$), Uganda ($n = 7$) and Kenya ($n = 6$) (Fig. 2). The distribution of studies by livestock species shows that most studies have been conducted in cattle ($n = 47$) (Fig. 3). Other studied livestock species include pigs, poultry and small ruminants such as sheep and goats. The studied diseases in cattle have been Foot and mouth disease, Anthrax, East Coast fever, Rabies, Lumpy skin disease, Anaplasmosis, Rift valley fever, Leptospirosis, Trypanosomiasis, Bovine tuberculosis, Crimean Congo hemorrhagic fever virus, Bovine dermatophilosis, Coxiella burnetii, Brucellosis and Cryptosporidiosis. The diseases studied in small ruminants have been Foot and mouth disease, Anthrax, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, Sheep and goats' pox, Rabies, Rift valley fever, Crimean Congo hemorrhagic fever virus, Coxiella burnetii, and Cryptosporidiosis. Porcine cysticercosis and African swine fever have been the studied diseases in pigs. The studied diseases in poultry include Newcastle disease and Avian influenza (HPAI H5N1). Overall, the frequently studied diseases have been Foot and mouth disease ($n = 15$), Anthrax ($n = 9$) and Rift valley fever ($n = 5$).

Study design, nature and source of data

Table 1 is a summary of studies in terms of study design, nature and source of data. A large number of studies have used retrospective study design ($n = 34$) compared to cross-sectional design ($n = 22$). In retrospective design, studies have used historical disease outbreak or case records review. In this regard, either the outcome has been the number of outbreaks or cases. In some cases, the outcome has been the presence or absence of an outbreak or a case [21–23]. In most cases, the historical outbreak or case data has been collected from livestock health institutions such as the central animal health diagnostic laboratories, statistical and epidemiological units of the Ministry of Agriculture and Livestock. Historical animal data has also been collected from district and regional veterinary offices. Collection of the historical outbreak or case data has been through review of annual or monthly reports [24–26] and surveillance data bases [25,27]. Historical disease outbreak data has also been collected from peer reviewed journal articles and conference proceedings [28,29]. Historical record review has also seen the use of abattoir meat inspection records [30]. In other cases, the historical outbreak data has been collated from world disease information systems such as WAHIS [29,31,32]. Retrospective design studies have also used questionnaire surveys to collect retrospective disease outbreak data [22]. On the other hand, cross-sectional

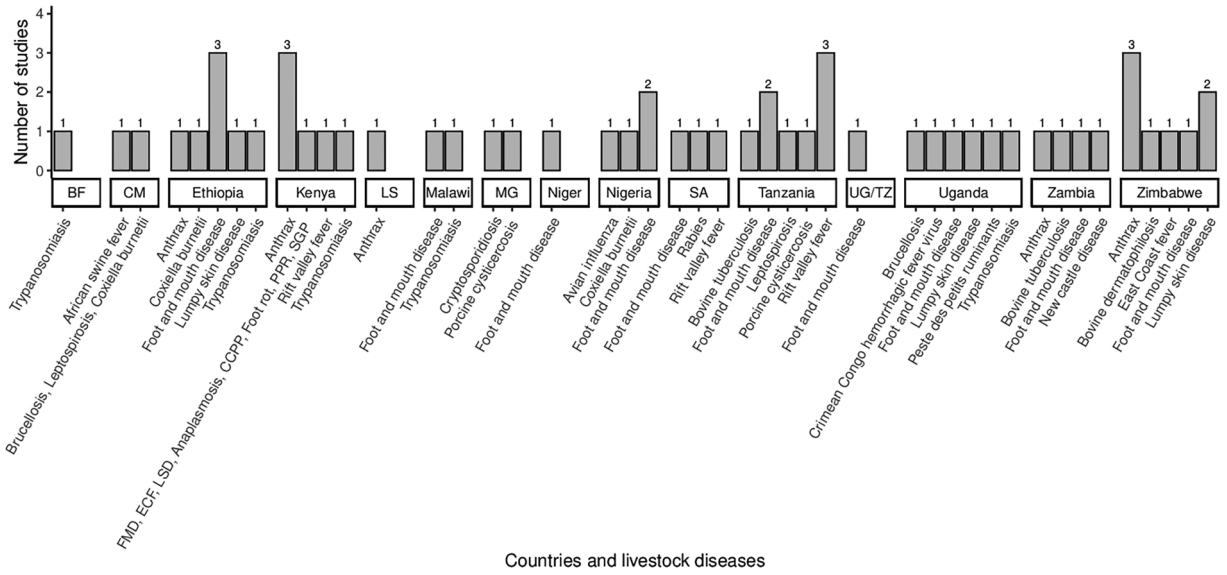

Fig. 2. Distribution of studies by country and diseases in sub-Saharan Africa. BF: Burkina Faso; CM: Cameroon; LS: Lesotho; MG: Madagascar; SA: South Africa; UG: Uganda; and TZ: Tanzania.

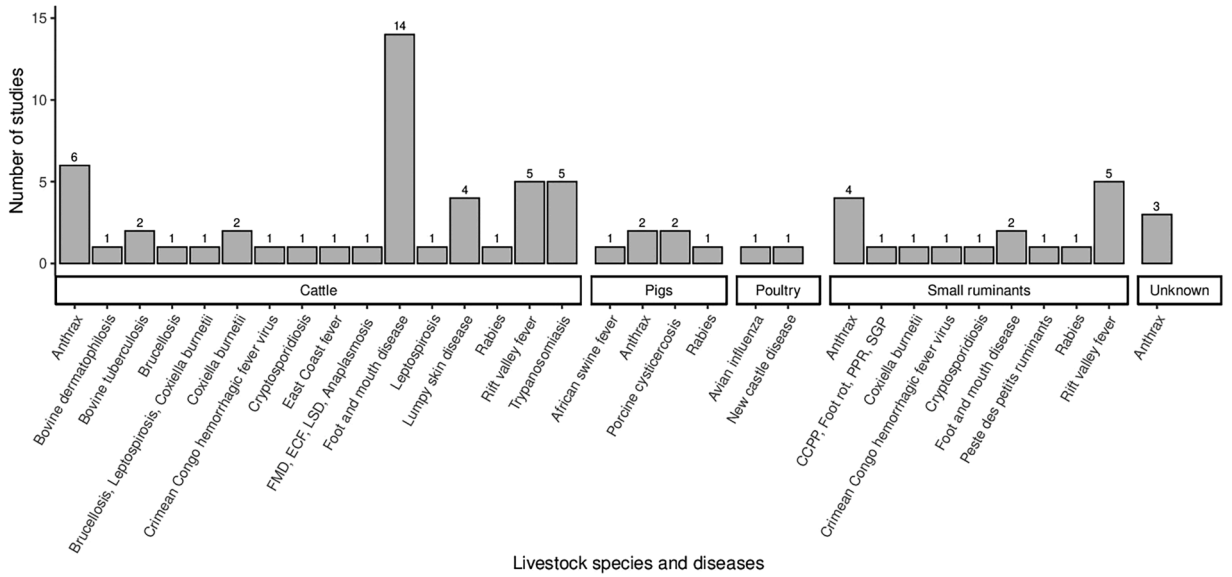

Fig. 3. Distribution of studies by livestock species and diseases. FMD: Foot and mouth disease; ECF: East Coast fever; LSD: Lumpy skin disease; CCPP: Contagious caprine pleuropneumonia; PPR: Peste des petits ruminants; and SGP: Sheep and goats' pox.

Table 1
Study design, nature and source of data.

Method	Frequency	Disease	Reference
Study design			
Retrospective	34	Rift valley fever, Foot and mouth disease, Anthrax, Rabies, Peste des petits ruminants, Lumpy skin disease, Newcastle disease, East Coast fever, Bovine dermatophilosis, Bovine tuberculosis, Lumpy skin disease, Avian influenza, and African swine fever	[8,21–32,53–73]
Cross-sectional	22	Brucellosis, Leptospirosis, Trypanosomiasis, Coxiella burnetii, Foot and mouth disease, East Coast fever, Lumpy skin disease, Anaplasmosis, Sheep and goats' pox, Porcine cysticercosis, Leptospirosis, Bovine tuberculosis, Rift valley fever, Crimean Congo hemorrhagic fever virus, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, and Cryptosporidiosis	[10,33–52,74]
Nature of data			
Historical outbreaks /cases	33	Foot and mouth disease, Anthrax, East Coast fever, Lumpy skin disease, Rabies, Rift valley fever, Newcastle disease, Peste des petits ruminants, Bovine dermatophilosis, Bovine tuberculosis, Avian influenza, and African swine fever	[8,21–32,53–63,65–73]
Serological	19	Foot and mouth disease, Trypanosomiasis, Rift valley fever, Bovine tuberculosis, Crimean Congo hemorrhagic fever, Leptospirosis, Coxiella burnetii, Brucellosis, and Porcine cysticercosis	[10,33,34,36–49,61,74]
Case confirmation			
Suspected/clinical	9	Foot and mouth disease, Porcine cysticercosis, Bovine dermatophilosis, Bovine tuberculosis, and Lumpy skin disease	[22,30,50,53–58]
Confirmed/laboratory	26	Foot and mouth disease, Anthrax, Rabies, Rift valley fever, Leptospirosis, African swine fever, Trypanosomiasis, Bovine tuberculosis, Peste des petits ruminants, Crimean Congo hemorrhagic fever virus, Coxiella burnetii, Brucellosis, Leptospirosis, Avian influenza, and Cryptosporidiosis	[10,23,26,27,32–34,36–38, 40–49,51,52,61,70,71,74]
Suspected/clinical and laboratory	15	Foot and mouth disease, Anthrax, Lumpy skin disease, Rift valley fever, and Porcine cysticercosis	[8,24,28,29,31,39,60,62–67, 72,73]
Unknown	6	Anthrax, East Coast fever, Lumpy skin disease, Foot and mouth disease, Newcastle disease, Anaplasmosis, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, and Sheep and goats' pox	[21,25,35,59,68,69]
Data source			
Livestock health authorities	29	Foot and mouth disease, Anthrax, Lumpy skin disease, Rabies, African swine fever, Newcastle disease, Rift valley fever, Peste des petits ruminants, Bovine dermatophilosis, and Avian influenza	[8,23–29,53–73]
WAHIS	3	Foot and mouth disease, and Rift valley fever	[29,31,32]
Abattoir	2	Porcine cysticercosis, and Bovine tuberculosis	[30,50]
Journal articles	2	Foot and mouth disease	[28,29]

Table 2
Spatial analysis, models, software and research tasks.

Method	Frequency	Disease	Reference
Spatial analysis			
Spatial scan	7	Porcine cysticercosis, Foot and mouth disease, Bovine tuberculosis, Lumpy skin disease, and Cryptosporidiosis	[31,39,48,52,67,69,74]
Space-time scan	10	Foot and mouth disease, Rabies, Lumpy skin disease, Rift valley fever, Avian influenza, and Bovine dermatophilosis	[27–29,31,55,56,60,65,67,71]
Getis-Ord Gi*	2	Peste des petits ruminants, and Lumpy skin disease	[23,58]
Moran's I	4	Peste des petits ruminants, Bovine tuberculosis, Foot and mouth disease, and Trypanosomiasis	[23,30,48,49]
Cuzick-Edwards' *k*NN	5	Brucellosis, Leptospirosis, Coxiella burnetii, Avian influenza, Foot and mouth disease, Trypanosomiasis, and Cryptosporidiosis	[31,40,44,52,71]
Ripley's *K* function	1	Porcine cysticercosis	[39]
Space-time *K* function	2	Rift valley fever, and Foot and mouth disease	[32,55]
Space-time cube	1	Peste des petits ruminants	[23]
Kernel density estimation	1	Trypanosomiasis	[34]
Inverse distance weighting	1	Brucellosis	[46]
Ordinary kriging	3	Foot and mouth disease, and Trypanosomiasis	[29,31,44]
Semi-variogram	2	Crimean Congo hemorrhagic fever, and Coxiella burnetii	[10,47]
Conditional autoregressive	2	Foot and mouth disease, and Anthrax	[48,63]
Matern function	1	Crimean Congo hemorrhagic fever	[10]
Exponential function	1	Coxiella burnetii	[47]
Standard deviation ellipse	1	Anthrax	[62]
Descriptive statistics such as frequency tables, graphs and maps	22	African swine fever, Foot and mouth disease, East Coast fever, Lumpy skin disease, Anaplasmosis, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, Sheep and goats' pox, Anthrax, Porcine cysticercosis, Coxiella burnetii, Leptospirosis, Rift valley fever, Newcastle disease, and Trypanosomiasis	[8,22,24–26,33,35,36,38,41,42,43,45,50,51,53,54,57,62,68,72,73]
Model based risk prediction	12	Anthrax, Foot and mouth disease, East Coast fever, Trypanosomiasis, Rift valley fever, Peste des petits ruminants, Crimean Congo hemorrhagic fever, Coxiella burnetii	[10,21,23,29,47,49,59,61,63,64,66,70]
Spatial modeling			
Logistic	8	Rift valley fever, Foot and mouth disease, Crimean Congo hemorrhagic fever, Peste des petits ruminants, East Coast fever, Trypanosomiasis, and Coxiella burnetii	[10,21,23,29,31,47,49,61]
Negative binomial	1	Peste des petits ruminants	[23]
Zero inflated Poisson	1	Anthrax	[63]
Boosted regression trees	1	Anthrax	[62]
Ensemble	1	Anthrax	[59]
MaxEnt	2	Rift valley fever, and anthrax	[66,70]
Generalized estimation equations	1	Trypanosomiasis	[37]
Software			
QGIS	16	Foot and mouth disease, Anthrax, Rabies, African swine fever, Lumpy skin disease, Porcine cysticercosis, Bovine dermatophilosis, and Coxiella burnetii	[8,22,26,27,38,50,53,54,56,57,59,60,62–64,67]
ArcGIS	15	Foot and mouth disease, Anthrax, Rift valley fever, Bovine tuberculosis, Trypanosomiasis, and Coxiella burnetii	[28–31,34,41,44,47,51,61,65,66,69,72,74]
GIS Idrisi	1	East Coast fever	[21]
ArcMap	4	Foot and mouth disease, East Coast fever, Lumpy skin disease, Anaplasmosis, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, Sheep and goats' pox, Trypanosomiasis, and Brucellosis	[23,35,37,46]
ArcView	2	Porcine cysticercosis, and Anthrax	[24,39]
Epi Map	1	Newcastle disease	[25]
ILWIS	1	Anthrax	[70]
DIVA-GIS	1	Anthrax	[73]
MapInfo	1	Trypanosomiasis	[49]
biomod2 R package	1	Anthrax	[59]
SaTScan	14	Foot and mouth disease, Rabies, Bovine tuberculosis, Lumpy skin disease, Rift valley fever, Bovine dermatophilosis, Porcine cysticercosis, and Avian influenza	[27–29,31,39,48,55,56,60,65,67,69,71,74]
spatstat R package	2	Trypanosomiasis, and Cryptosporidiosis	[34,52]
splancs R Package	2	Rift valley fever, and Foot and mouth disease	[32,55]
INLA R package	1	Anthrax	[63]
SSTAT	1	Avian influenza	[71]
smacpod, sp, and ragdal R packages	1	Cryptosporidiosis	[52]
OpenBugs, and geoR R package	1	Coxiella burnetii	[47]
spdep, and CARBayes R packages	1	Foot and mouth disease	[48]

(*continued on next page*)

Table 2 (*continued*)

Method	Frequency	Disease	Reference
MaxEnt	2	Rift valley fever, and Anthrax	[66,70]
gbm R package	1	Anthrax	[64]
PrevMap R package	1	Crimean Congo hemorrhagic fever virus	[10]
Research tasks			
Distribution	34	African swine fever, Foot and mouth disease, Anthrax, Trypanosomiasis, East Coast fever, Lumpy skin disease, Anaplasmosis, Contagious caprine pleuropneumonia, Foot rot, Peste des petits ruminants, Sheep and goats' pox, Porcine cysticercosis, Coxiella burnetii, Rift valley fever, Leptospirosis, Bovine tuberculosis, Newcastle disease, and Bovine dermatophilosis	[8,22,24–26,28,30–39,41–43,45,50,51,53,54,56,57,59,62,63,67,68,72–74]
Cluster analysis	21	Brucellosis, Leptospirosis, Coxiella burnetii, Anthrax, Foot and mouth disease, Porcine cysticercosis, Rabies, Bovine tuberculosis, Rift valley fever, Lumpy skin disease, Peste des petits ruminants, Bovine dermatophilosis, Avian influenza, Trypanosomiasis, and Cryptosporidiosis	[23,27–31,39,40,44,48,50,52,55,56,59,60,65,67,69,71,74]
Interaction	2	Rift valley fever, and Foot and mouth disease	[32,55]
Risk factors	25	Rift valley fever, African swine fever, Foot and mouth disease, Anthrax, Porcine cysticercosis, Coxiella burnetii, Leptospirosis, Crimean Congo hemorrhagic fever, Peste des petits ruminants, East Coast fever, Bovine tuberculosis, and Trypanosomiasis	[8,10,21–23,26,29,30,36,38,43,45,48–51,54,61–66,21,63,6469,70]
Prediction	12	Rift valley fever, Anthrax, Foot and mouth disease, Peste des petits ruminants, East Coast fever, Crimean Congo hemorrhagic fever, Newcastle disease, Coxiella burnetii, and Trypanosomiasis	[10,21,23,25,29,47,49,59,61,64,66,70]
Emergence of hot spots	1	Peste des petits ruminants	[23]
Dispersion and direction	1	Anthrax	[62]

design studies have mainly employed serum surveys to collect data [10,26,33–49]. Some cross-sectional studies have used abattoir meat inspection [50]. Cross-sectional study of biological and environmental samples such as bones, soil and animal feces has also been done [51,52]. Cross-sectional design has also seen the use of participatory epidemiology, where selected key informants have been asked to rank livestock diseases based on prevalence in each study site [35]. The status of case confirmation shows that most studies have used confirmed cases ($n = 26$) and a combination of suspected/clinical and laboratory confirmed cases ($n = 15$). Most of the studies that have used purely suspected/clinical cases have been retrospective design studies while using historical record review or survey ($n = 8$) [22,30,53–58].

Spatial statistics, models and software

Table 2 shows a summary of studies in terms of spatial analysis methods, software and research tasks. The common spatial analysis approaches in spatial analysis of livestock diseases in sub-Saharan Africa have been the use of the exploratory statistics such as frequency tables, graphs and simple maps ($n = 22$) [8,22,24–26,33,35,36,38,41–43,45,50,51,53,54,57,62,68,72,73]. Exploratory spatial analysis has also seen the use of analysis of variance (ANOVA) to test for significant differences between regions [68]. The use of exploratory statistics has limited these studies not to dive deep into spatial epidemiology. In this regard, these studies have been limited in testing for significant spatial autocorrelation or clustering. Furthermore, the studies have been limited in taking into account disease risk factor information in the spatial distribution. Nevertheless, the advantage of exploratory analysis is in the ease of its implementation and that it offers a quick overview of disease distribution.

Kulldorff spatial scan statistics have been the other frequently used methods of spatial analysis, mainly to search and test for significant disease clusters ($n = 15$) [27–29,31,39,48,52,55,56,60,65,67,69,71,74]. The search for disease clusters has been purely in space or time [31,39,48,52,67,69,74]. In some cases, other studies have performed the search for disease clusters in both space and time [27–29,31,55,56,60,65,67,71]. With the Kulldorff scan statistics, a search window is imposed over the disease outbreak region or time period. The method detects a region or time frame as a cluster if the disease risk within the window is greater than outside. For the purely spatial scan, the window is usually a circle or an ellipse, while for a space-time scan, the search window is usually a cylinder where the base represents the space and the height represents time. Depending on the nature of the data, different surveyed studies have used different scanning models. Some studies have used the Bernoulli model where the outcome data is assumed to be either the case or control [29,31,39,48,52,69,71]. The Poisson model has been used when the outcome data has been the number of cases and the population at risk has been known [27,39,67]. The permutation model has also been used in case of the presence of cases data only without the base population at risk [28,55,56,60,65]. While the Kulldorff scan statistics are able to adjust for confounders [28], none of the surveyed studies have controlled for confounders. The other limitation of the surveyed studies is that the Kulldorff scan statistics have been limited to detecting regularly shaped circular clusters only. Furthermore, while it is known that multivariate Kulldorff scan statistics can be applied to multiple disease outcomes simultaneously to investigate commodity [75,76], the potentially sampled studies to do so have not investigated multiple disease comorbidity while using multivariate scan statistics [27,52,60]. This if it was done, would ensure unraveling comorbidity risk between animals and humans [52] or between different animal species [27,60]. Similar to space-time scan statistic, the other study used the space-time cube statistic to detect and test for significant clustering [23]. The space-time cube uses a regular three-dimensional structure with x and y coordinates representing space and height representing

time dimension to search for clusters. To test for significant clustering in each space-time window, a Getis-Ord Gi* statistic is used, and to test for the cluster trend, a Mann-Kendall statistic is employed [77]. The strength of the study by Nkamwesiga et al. [23] was its ability to show the increasing or decreasing trend of the cluster. Thus, the advantage of the space-time cube over the space-time Kulldorff scan is that it can show the growth and shrinkage of a disease cluster over time.

The other used spatial autocorrelation statistic has been the Moran's I [23,30,49]. In this case, the Moran's I has been used to test for the presence of spatial autocorrelation. A positive value of the Moran's I means the presence of clustering and a negative value means the presence of dispersion. The use of the Moran's I in these studies failed to show high and low value clusters. This might be the reason why Nkamwesiga et al. [23] also used the Getis-Ord Gi* statistic in addition to the Moran's I which is capable of separating low from high value clusters [78]. The Cuzick-Edwards' *k*NN statistic has been another used cluster statistic in spatial analysis of livestock diseases in sub-Saharan Africa [31,40,44,52,71]. It is used to test for clustering of point process case-control data. The statistic defined as $T_k = \sum_{i=1}^{n} \delta_i d_i^k$ is based on the total number of cases d_i^k which are in the k nearest neighbor of each case and control. The parameter δ_i is a binary indicator of a case ($\delta_i = 1$) and a control ($\delta_i = 0$). While the Cuzick-Edwards' *k*NN test is capable of adjusting for the base population at risk including the known and unknown confounding factors [79], the surveyed studies did not control for the confounding factors. The other used spatial cluster statistic has been the Ripley's K function, $K(h)$ [39] coined by Ripley [80]. This is similar to the Cuzick-Edwards' *k*NN test which is used to test for clustering of point level case and control data. It measures the 'intensity' of incidences within the distance h of a randomly selected event. It tests the hypothesis that cases are more clustered than the controls. Other studies have used the bivariate K function to investigate the interaction of space and time in disease clustering, $K(s,t)$ [32,55]. In this regard, $K(s,t)$ defines disease 'intensity' within the distance s and time t of the randomly selected event. Specifically, the significance of the space-time interaction and the presence of excess risk due to space and time interaction has been investigated. In the absence of space-time interaction, $K(s,t) = K_1(s)K_2(t)$. The use of K function in these studies has shown limitation in explicitly showing the location of disease hot spots. Kernel density estimation (KDE) has been another spatial analysis method in spatial analysis of livestock diseases in sub-Saharan Africa [34]. In this approach, the probability of a disease event occurring at location s called 'density' was calculated using a kernel and mapped. A kernel is basically a function which is symmetric about the mean such as the Gaussian distribution. In the KDE approach, the kernel is estimated at each data location and then the overall KDE is the sum of separate kernel functions. The advantage of the KDE is that it creates a smooth and continuous map surface without considering boundaries, which is visually impressive. Furthermore, the KDE can evaluate both clustering and location of clusters which is not the case with the K function [81]. Nevertheless, its disadvantage is that the specification of a band width for the kernel that determines smoothness of the estimate may give inconsistent results for different values [82].

Inverse distance weighting (IDW) has been another spatial analysis technique in spatial analysis of livestock disease data in sub-Saharan Africa [46]. This is a method of spatial interpolation, where a value at unobserved location s_0 is estimated by the weighted sum of the sampled values s_i denoted by $z(s_0) = \sum_{i=1}^{n} \lambda_i z(s_i)$, where λ_i are weights of the sampled values. The weights λ_i are the inverse of the distance of the sampled point to the predicted point. The disadvantage of IDW is that it does not account for statistical properties of the data, since the method is more of mathematical than geostatistical. A statistical approach to spatial interpolation has been kriging [29,31,44]. This is similar to IDW, only that the method uses the weights based on the semi-variogram model rather than been assigned by the user. Thus, the method is more of geostatistical than deterministic. Kriging is also capable of accounting for directional bias in spatial autocorrelation which is not the case with IDW. While kriging by Chimera et al. [29] was based on disease risk values adjusted by confounders in the model, Sirdar et al. [31] and Chimera et al. [44] kriging was based on the unadjusted disease incidence and prevalence respectively. The standard deviation ellipse (SDE) has been another used statistic in spatial analysis of livestock diseases in sub-Saharan Africa [62]. This has been used to show the central tendency, dispersion and orientation of a disease cluster. It uses the ratio of long axis to short axis to measure orientation effects. If the ratio is more than 1, it entails the presence of orientation in the cluster and if the ratio is 1, it implies absence of orientation.

Model based spatial analysis has been another method of spatial analysis of livestock diseases in sub-Saharan Africa ($n = 14$) [10,21,23,29,37,47–49,59,61,63,64,66,70]. In this approach, a model of the disease outcome has been fitted on the predictor variables and in most cases, based on the fitted model, the disease risk has been predicted and mapped. To take into account spatial autocorrelation in the data, spatial autocorrelation statistics are employed. Different models have been fitted depending on the nature of outcome data. The logistic regression has been used in case the outcome data has been the presence or absence of the disease [10,21,23,29,47–49,61]. Of these studies, only Munsey et al. [48], Proboste et al. [47] and Telford et al. [10] took into account spatial autocorrelation of the outcome data by modeling location as spatially correlated random effect. Both Proboste et al. [47] and Telford et al. [10] used the geostatistical approach, where location was assigned the Gaussian distribution with zero mean and variance covariance matrix. To capture spatial dependency, the covariance matrix was specified as a Matern [10] or an exponential function [47], where in both cases spatial autocorrelation was a function of the distance between two points. Parameters of these covariance functions were dependent on the semi-variogram model of the residuals. In this regard, a semi-variogram is an exploratory plot of simi-variance of all pairs of points for different values of separating distance in geostatistical modeling. It serves to depict the extent of spatial autocorrelation. The problem of geostatistical models is that they are more often limited to point referenced data. On the other hand, Munsey et al. [48] used the conditional autoregressive (CAR) distribution to account for spatial autocorrelation. In this case, the random effect of location s_i was modeled on the values of immediate neighbors. In this way, the smooth pattern is estimated within the immediate neighborhood. The problem of the study by Munsey et al. [48] however was that it did not use the model to estimate the overall risk which would then be mapped. The CAR approach is usually appropriate in dealing with areal data as opposed to geostatistical approaches. In case the outcome data has been the number of disease outbreaks or cases, count data models have been employed [23,63]. In this case, Ndolo et al. [63] are using a Poisson hurdle model, which is a two staged model of the presence and absence and incidence of anthrax data.

The presence and absence data use the logistic regression and the incidence data is using the zero inflated Poisson (ZINP) distribution model. Location and year were modeled as spatial and temporal components respectively. Spatial autocorrelation was captured by the CAR model through the Besag, York and Mollié specification [83], where location was considered to be spatially correlated and uncorrelated. The correlated temporal component was modeled by the random walk prior and the uncorrelated temporal component was modeled by independent normal distribution with zero mean. The advantage of ZINP model is that it is capable of taking into account extra variation due to excess zero counts which is common in livestock disease data. The model however did not evaluate the space-time interaction. Nkamwesiga et al. [23] used the negative binomial (NB) distribution regression with the aim of accounting for overdispersion in the data. The model did not model location as a spatial parameter.

Machine learning models in the context of ecological niche modeling have also been employed. Boosted regression trees [64], method of maximum entropy (MaxEnt) [66,70] and ensemble [59] are some of the observed machine learning approaches. The studies aimed at predicting probability of habitat suitability of the livestock diseases based on environmental variables. The advantage of boosted regression trees is that they can model complex nonlinear terms and interactions and their challenge is that they tend to overfit the data in case of too much noise. On the other hand, ensemble approach uses a set of machine learning algorithms with the aim of outperforming individual algorithms [59]. The use of machine learning has not accounted for spatial autocorrelation of disease suitability probability, where probability of nearby locations could be considered similar. The use of generalized estimation equations (GEE) has been another approach in spatial modeling of livestock diseases in sub-Saharan Africa [37]. In this case, they were used to estimate apparent disease prevalence with the aim of adjusting for correlation within communities. The method was not explicit in adjusting for other confounders.

The use of software for spatial analysis of livestock diseases has fallen into standalone and add-in packages software. The commonly used standalone software include the familiar GIS related software such as QGIS ($n = 16$) and ArcGIS ($n = 15$). Other used GIS related software have been ArcView, ArcMap, MapInfo and Epi Map. The studies have also employed ILWIS, Diva GIS and GIS Idris. The GIS related software have mainly been used in mapping. SaTScan ($n = 14$) has been another commonly used standalone software, especially for disease cluster detection analysis [27–29,31,39,48,55,56,60,65,67,69,71,74]. The less used standalone software include OpenBugs [47] and MaxEnt [66,70]. The OpenBugs is designed to estimate Bayesian models via Markov chain Monte Carlo (MCMC) while using the Gibbs sampling algorithm. On the other hand, MaxEnt software is convenient in estimating ecological niche models while using the machine learning approach called method of maximum entropy. The use of add-in packages has seen the use of R and non R related packages. The R package *smacpod* has been used to implement cluster scanning using the Kulldorff scan statistics [52]. The other used R package has been *spatstat* for density estimation [34] and performing Cuzick-Edwards' *k*NN test [52]. The Cuzick-Edwards' *k*NN test has also been done by the Microsoft Excel add-in package known as SSTAT [40,71]. The use of R packages has also seen the use of *splancs* for computing the *K* functions [32,55] and *sp* and *ragdal* for drawing maps [52]. The R package *geoR* [47] and *PrevMap* [10] have been used in geostatistical modeling. The *spdep* and *CARbayes* R packages have been employed to test and account for spatial autocorrelation using the Moran's I and CAR model respectively [48]. The implementation of the CAR model has again been done by the INLA R package. Machine learning models have seen the use of the *gbm* R package to implement boosted regression trees [64] and *biomod2* [59] R package to implement ensemble modeling. While the use of add-in packages offers additional functionalities and flexibility over standalone software such as most of the familiar GIS software, they are not user friendly, especially those that are added in R programming software due to the use of coding to make commands.

Research tasks

Various research tasks have been performed in spatial analysis of livestock disease data in sub-Saharan Africa (Table 2). Some studies have merely investigated the distribution of disease incidence or prevalence through exploratory spatial analysis while using simple maps of disease prevalence or incidence [8,22,24,26,33,35–38,41–43,45,51,53,54,57,62,63,68,72,73]. Other studies have investigated disease clustering while using cluster statistics [23,27–31,39,40,44,48,50,52,55,56,58–60,65,67,69,71,74]. Nevertheless, Porphyre et al. [50] cluster analysis was exploratory basing on the size of apparent prevalence to define a cluster. The other research objective has been spatial prediction [10,21,23,29,47,49,59,61,63,64,66,70]. In this regard, in most cases, model based prediction has been used. The other form of prediction has been spatial interpolation while using cluster statistics such as KDE [34], IDW [46], and kriging [29,31,44]. The main aim of spatial interpolation has been smoothing. The shortfall of these studies however with exception to Chimera et al. [29] is that they implemented interpolation while using covariate unadjusted prevalence values. In general, spatial prediction has been retrospective rather than prospective. Mubamba et al. [25] attempted future prediction while using first order moving average time series model, but it is was not spatial prediction either. Determination of risk factors has been another research objective [8,10,21–23,26,29,36,38,43,45,48–51,54,59,61–66,69,70]. The shortfall of some of these studies though is that the risk factors were not used for spatial risk prediction [8,22,26,30,36,38,43,45,48,50,51,54,62,65,69]. Other studies have looked at investigation of space and time interaction while using the space-time *K* function [32,55]. In this regard, the investigation of space-time interaction while using the spatio-temporal model has been limited. Detection of emerging disease clusters has been another research task that has been performed in spatial analysis of livestock diseases [23] while using the Mann–Kendall statistic. The other research task that has been performed has been dispersion, direction and orientation of a disease cluster [62] while using the standard deviation ellipse.

Key findings and research gaps

The review has found most studies employing exploratory approaches to spatial analysis compared to cluster statistics and models. The review has found lack of adjustment for confounders in the use of cluster statistics which are explicitly capable of adjusting for confounders such as the Cuzick-Edwards' *k*NN and spatial scan statistics. The study has also found lack of use of irregularly shaped cluster scan statistics other than Kulldorff spatial scan statistics which are known to be limited in detecting irregular clusters. The use of cluster statistics has failed to explore disease comorbidity while using multivariate scan statistics [27,52,60]. Spatial modeling has revealed a few of the model based studies taking into account spatial autocorrelation in the data by modeling location as a spatial random effect [10,47,48,63]. In this regard, a special concern is on studies employing machine learning approaches which have not considered spatial autocorrelation in disease risk prediction. The investigation of space-time interaction has been limited to the use of cluster statistics such as space-time *K* function [32,55] as opposed to the use of spatio-temporal models. Model based spatial prediction has also been limited to retrospective prediction instead of prospective prediction so as to unravel future trends. Model based spatial analysis has also lacked evidence of comorbidity disease clustering between groups. For example, one interesting case would be Ndolo et al. [63] in using a joint spatial model to investigate comorbidity of anthrax between livestock and wildlife. Key research opportunities therefore include the adjustment for cofounders in the use of cluster statistics. It also includes the use of scan statistics that can detect irregular disease clusters. The use of cluster analysis also calls for exploration of multivariate scan statistics to investigate disease comorbidity between groups. Spatial modeling research opportunities include the incorporation of space and time interaction in disease modeling. It further includes the prospective spatial prediction to unravel future trends. Joint spatial modeling to unravel disease comorbidity between groups may also be explored.

Discussion

This review aimed at determining the status of spatial analysis of livestock diseases in sub-Saharan Africa, more especially on the spatial statistics and models that have been employed. The strength of the review has been a wider coverage of livestock diseases than in previous reviews. This has given a comprehensive picture of the spatial analysis methods that are commonly used as far as all livestock diseases are concerned in sub-Saharan Africa. The research gaps found will thus help biostatisticians in veterinary epidemiology to know areas that need application or development of novel spatial analysis approaches.

The study has found a greater usage of retrospective design than cross-sectional survey design. The greater use of retrospective design may be attributed to the easiness in data collection, especially if historical record review is employed, since in this scenario, data is readily available from animal health institutions. The other advantage of retrospective designs is that they can cover a wide geographical area, especially if the record review is based on a regional or world disease information system such as the EMPRES-i of the FAO [11]. Nevertheless, retrospective record review suffers the problem of data quality, due to missing records for some periods of time. Also, if the historical case notification was based on suspicion, there is no option to have confirmed cases. To circumvent the problem of missing data in historical record review, a retrospective questionnaire survey may be administered to animal health officers, asking them about the occurrence of the disease in the past as done by Jemberu et al. [22]. Nonetheless, the disadvantage of this approach lies in the difficulty for animal health officers to remember when they had an outbreak in the past. Most of the reviewed cross-sectional design studies have employed serum surveys. Although disease cases are usually confirmed, serum surveys are expensive to implement and hence forth tend to cover a small geographical area. The use of participatory epidemiology [35] cross-sectional design ensures that sufficient information is collected in areas where data is hard to find, which is the case with most livestock data, especially in developing countries such as in sub-Saharan Africa. The problem of this approach might be the use of wrong clinical experience in disease listing from some key informants with poor disease clinical experience.

The study has found a greater proportion of studies employing exploratory approaches in spatial analysis of livestock diseases compared to modeling in sub-Saharan Africa [8,22,24–26,33,35,36,38,41–43,45,50,51,53,54,57,62,68,72,73]. Some studies have not used risk factor information in predicting spatial risk while using models [8,22,26,30,36,38,43,45,48,50,51,54,62,65,69]. In either case, this may be related to challenges facing livestock health including lack of expertise in modeling due to lack of well-trained biostatisticians at veterinary related institutions. In this regard, the so-called biostatisticians at most veterinary institutions have their background not related to statistics. Also, lack of modeling skills might arise due to absence of postgraduate programs in biostatistics at veterinary institutions. Although, there are biostatistics programmes in non-agriculture training institutions, these tend to focus much of application in human health compared to animal health, thereby limiting advanced application in livestock health. It is high time that non-agriculture institutions biostatistics programmes strike a balance between different fields of application including animal health. Lack of data is another problem facing modeling in livestock diseases [12]. This is due to the poor surveillance systems characterized by under-reporting, absence of electronic data base systems and inadequate laboratories for diagnosis. Limited livestock data is also attributed to political and funding constraints facing livestock disease research, especially that about non-zoonotic diseases [12,16].

The use of spatial autocorrelation or cluster statistics has shown lack of controlling for confounders, and that the Kulldorff scan statistics have been limited to regular circular shapes. Adjusting for cofounders can allow the depicting of spatial autocorrelation without the contribution of nuisance factors. In this regard, it has been documented in the literature that the cluster statistics such the Cuzick-Edwards' *k*NN can adjust for the base population at risk, unknown and known confounders by the wise choice of controls [79]. Similarly, the Kulldorff scan statistics are also capable of adjusting for confounders [28]. For example, Alton et al. [84] were able to use covariate adjusted space-time scan on bovine pneumonic lung and parasitic liver condemnation data in Ontario, Canada. In this case, four different methods of adjustment were employed and the results had shown substantial difference. The observed limited

application of covariate adjustment spatial scan statistics in sub-Saharan Africa may also be attributed to the poor data quality due to poor surveillance systems to capture all data variables including the confounders. It may also be attributed to lack of technical know-how in implementation of the adjustment methods. The problem that arises when using the regularly shaped cluster scan statistic is that in case the true disease cluster is irregular, circular scan statistics tend to underestimate or overestimate the clusters [85], resulting in false alarms in case of overestimation. Irregular cluster scan statistics are available which biostatisticians need to explore [86]. Investigating disease comorbidity between groups while using autocorrelation and cluster statistics is another interesting area that has also been lacking. In this case, it would be vital to see if disease outcomes between groups are correlated over space which would aid in hypothesis formulation about common risk drivers. Investigation of disease comorbidity between groups may also enhance 'One Health' approaches, especially if comorbidity is between livestock, wildlife and humans. In this regard, outside sub-Saharan Africa, some studies have attempted to use multivariate scan statistics to simultaneously investigate spatial distribution of livestock disease outcomes [75,76]. Aleuy et al. [76] are using a multinomial model where the infectious bronchitis virus genotypes are considered as nominal levels. On the other hand, Jonsson et al. [75] are using the multiple data set adjustment approach to simultaneously study clusters of Campylobacteriosis in humans and broiler flocks.

Model based spatial analysis has shown limitation in taking into account spatial autocorrelation in disease distribution [10,48,63]. Spatial autocorrelation in livestock data is likely due to limited sampling in some areas. In this case, some veterinary officers are not diligent enough to consistently record and report disease cases. Livestock disease spatial autocorrelation may also be caused by livestock and pastoral movements [87], land use, climatic and environmental factors [11]. Non accounting for spatial autocorrelation can results in biased parameter estimation and decreased model predictive performance [88]. The greater concern is with the studies that have used ecological niche machine learning approaches, where not even one study has considered the issue of spatial autocorrelation in the data. In this case, the literature has shown that spatial autocorrelation also affects ecological niche models. In this regard, the presence of spatial autocorrelation in the data tends to inflate the significance values [89]. It also tends to inflate measures of model accuracy such as the area under the curve (AUC) of the receiver operating characteristic (ROC) [90]. According to Segurado et al. [89], two methods can be used to deal with spatial autocorrelation in niche models, namely, sub-sampling original data to eliminate certain data cells, and including an auto-covariate in a spatial model. The other problem in model based spatial analysis of livestock diseases has been lack of investigation of the interaction of space and time. This if done can allow the taking into account extra variability due to space and time interaction in overall risk estimation. This is possible as Bekara et al. [9] in France used a Bayesian model which incorporated the space and time interaction. Model based risk prediction has also been retrospective as opposed to prospective. This is an important limitation since prospective spatial risk prediction would enable visualization of future risk trends by space, which would be vital for early warning. Similar to limitation in disease comorbidity investigation by cluster statistics, joint spatial disease modeling needs to be enhanced for elucidation of common spatial trends between disease groups. This is possible, more especially in the frame work of Bayesian disease modeling. An important scenario where joint modeling can be useful would be modeling zoonotic diseases to understand comorbidity between humans and animals. In this case, joint models would be useful in understanding divergent and shared risk of zoonotic diseases between wild animals, livestock and humans [91]. It may also be used to correlate animal host population with human disease incidence [92]. Joint modeling may also be used to collate animal and human data to inform risk of zoonoses [93].

The following are the weaknesses of this study. The first weakness is that the review might have missed some important studies in other languages since the review was done in English. The other shortfall is that the study did not widen the scope to look at the entire world. This would have offered an opportunity to compare spatial analysis methods in sub-Saharan Africa with other continents. The study also focused on statistical methods rather than widening the scope to even look at mathematical approaches to spatial analysis. Future similar studies may thus explore the world-wide review and incorporate mathematical approaches in spatial analysis to compare with statistical approaches.

Conclusion and recommendation

The review has found majority of studies employing exploratory tools in spatial analysis of livestock diseases in sub-Saharan Africa. It has also found limited usage of risk factor information in estimating disease risk. The study has also found lack of usage of irregular shape cluster scan statistics. There is also no adjustment for nuisance factors in the usage of spatial cluster statistics. Disease comorbidity spatial scanning and modeling has also been lacking. Model based spatial analysis has not investigated the interaction of space and time. Most model based spatial analysis, especially machine learning approaches, have not explored the issue of spatial autocorrelation in the data. Model based spatial prediction has not considered future prediction for early warning. Future research can consider application of irregular cluster scan statistics in detection of disease clusters. It can also consider adjustment for cofounders and investigation of disease comorbidity while using the multivariate spatial scan statistics. Future research should consider development and application of joint spatial models for multiple diseases or groups to show disease comorbidity. The use of machine learning in niche models should consider exploring the effect of spatial autocorrelation in the data. Lastly, future research can consider prospective spatial prediction as opposed to retrospective prediction to aid in early warning.

Ethics

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CRediT authorship contribution statement

Alfred Ngwira: Conceptualization, Writing – review & editing. **Samuel Manda:** Investigation, Writing – review & editing. **Esron Daniel Karimuribo:** Investigation, Writing – review & editing. **Sharadhuli Iddi Kimera:** Investigation, Writing – review & editing. **Christopher Stanley:** Investigation, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

The original contributions presented in this study are included in the supplementary material.

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Supplementary materials

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