

Supplementary Material

Supplemental Equation 1.

$$\text{Eq. 1. } \Pr(Y = y) \equiv (1/\kappa) \exp\{\sum_A \eta_A g_A(y)\}$$

$g_A(y)$ = any possible network statistic, where A indexes the multiple statistics included in a model vector $g(y)$

η_A = coefficients for model terms; their value reflects the change in the conditional log odds of a tie for each unit increase in g_A that the tie would create

κ = normalizing constant, the sum of $\exp\{\sum_A \eta_A g_A(y)\}$ over all possible networks with n actors

Supplemental Table 1. Characteristics of networks with alternate genomic link definitions

Genomic link definition	Number of edges (total links) in network	Cases with at least one link (%)	Mean number of links per case	Maximum number of links
≤ 3 pairwise SNPs, undirected	240	116 (34)	0.45	22
Undirected RFLP/WGS (≤ 3 pairwise SNPs) combined	353	100 (29)	2.1	20
≤ 10 pairwise SNPs, directed	4704	181 (53)	39.3	95

Supplemental Table 2. Associations between infectiousness and network position in model without cough

	Undirected \leq 5 SNPs			
	Odds Ratio	95% CI		p
Cough duration				
No cough reported	Ref			
1 month	-	-	-	-
2 months	-	-	-	-
3 months	-	-	-	-
\geq 4 months	-	-	-	-
Smear status				
Smear - negative	Ref			
Smear +, scanty +	1.00	0.76	1.25	1.00
Smear +, grade 1	0.74	0.52	0.97	0.01
Smear +, grade 2	0.84	0.62	1.06	0.013
Smear +, grade 3+	0.64	0.43	0.85	<0.0001
HIV status				
HIV-negative	Ref			
HIV-positive, undetectable VL	1.11	0.91	1.31	0.31
HIV-positive, detectable VL	0.86	0.65	1.06	0.13
Sex				
Male	Ref			
Female	0.90	0.75	1.05	0.17
Age category				
\leq 15	Ref			

16-34	0.69	0.33	1.04	0.04
35-54	0.80	0.44	1.16	0.23
≥ 55	1.13	0.73	1.52	0.55

Supplemental Table 3. Associations between infectiousness and network position in models with collapsed variables for cough duration, smear status

	n (%) Total n = 344	Odds Ratio	95% CI		p
Cough duration					
No cough reported	128 (37)	Ref			
1 month	60 (17)	0.51	0.37	0.70	<0.0001
2 months	51 (15)	2.59	2.12	3.16	<0.0001
3 months	72 (21)	2.28	1.88	2.76	<0.0001
≥ 4 months	33 (10)	1.06	0.78	1.45	0.72
Smear status					
Smear -	109 (32)	Ref			
Smear +	235 (68)	0.65	0.55	0.76	<0.0001
Cavitary disease					
No cavitary disease	284 (83)	Ref			
Cavitary disease	60 (17)	1.50	1.25	1.81	<0.0001
HIV status					
HIV-negative	78 (23)	Ref			
HIV-positive, undetectable VL	133 (39)	1.17	0.95	1.42	0.14
HIV-positive, detectable VL	133 (39)	1.02	0.83	1.25	0.87
Sex					
Male	142 (41)	Ref			
Female	202 (59)	0.92	0.80	1.07	0.28
Age category					

≤ 15	12 (3)	Ref			
16-34	171 (50)	0.76	0.53	1.09	0.14
35-54	134 (39)	0.84	0.58	1.21	0.36
≥ 55	27 (8)	1.25	0.84	1.86	0.27

Supplemental Table 4. Model including cavitory disease, restricted to cases with chest x-rays (n = 233)

	Undirected ≤ 5 SNPs			
	Odds Ratio	95% CI		p
Cough duration				
No cough reported	Ref			
1 month	0.98	0.74	1.28	0.863
2 months	2.17	1.72	2.72	<0.0001
3 months	1.87	1.49	2.34	<0.0001
≥ 4 months	1.07	0.78	1.48	0.666
Smear status				
Smear - negative	Ref			
Smear +, scanty +	0.74	0.53	1.03	0.077
Smear +, grade 1	0.88	0.69	1.12	0.304
Smear +, grade 2	0.78	0.60	1.01	0.061
Smear +, grade 3+	0.93	0.75	1.16	0.525
Cavitory disease				
No cavitory disease	Ref			
Cavitory disease	1.10	0.91	1.33	0.303
HIV status				
HIV-negative	Ref			
HIV-positive, undetectable VL	1.77	1.41	2.23	<0.0001
HIV-positive, detectable VL	0.95	0.74	1.21	0.657
Sex				
Male	Ref			

Female	1.36	1.14	1.62	0.001
Age category				
≤ 15	Ref			
16-34	0.85	0.54	1.33	0.471
35-54	1.07	0.68	1.69	0.761
≥ 55	1.33	0.81	2.18	0.257

Supplemental Table 5. Associations between infectiousness and node outdegree in undirected networks and using alternate SNP thresholds

	Undirected ≤ 5 SNPs				Directed ≤ 10 SNPs				Undirected RFLP/WGS (≤ 3 SNPs) combined			
	Odds Ratio	95% CI		p	Odds Ratio	95% CI		p	Odds Ratio	95% CI		p
Intercept		-4.18				-3.14				-6.44		
Cough duration												
No cough reported	Ref				Ref				Ref			
1 month	1.27	1.12	1.45	0.00	0.51	0.45	0.57	<0.0001	0.70	0.54	0.89	0.00
2 months	1.67	1.47	1.90	<0.0001	1.92	1.77	2.08	<0.0001	1.53	1.24	1.88	<0.0001
3 months	1.69	1.51	1.90	<0.0001	1.84	1.71	1.99	<0.0001	1.37	1.13	1.67	0.00
4 months	0.88	0.68	1.12	0.29	0.63	0.52	0.77	<0.0001	0.49	0.30	0.81	0.01
≥ 5 months	0.80	0.62	1.04	0.10	1.11	0.95	1.29	0.20	0.82	0.54	1.24	0.35
Smear status												
Smear - negative	Ref				Ref				Ref			
Smear +, scanty +	1.26	1.10	1.45	0.00	0.78	0.70	0.87	<0.0001	1.51	1.16	1.95	0.00
Smear +, grade 1	0.66	0.57	0.76	<0.0001	0.63	0.57	0.69	<0.0001	1.17	0.92	1.48	0.20
Smear +, grade 2	0.89	0.78	1.02	0.09	0.65	0.60	0.72	<0.0001	1.02	0.79	1.32	0.87
Smear +, grade 3+	0.80	0.71	0.90	0.00	0.61	0.56	0.66	<0.0001	1.35	1.10	1.67	0.00
Cavitory disease												
No cavitory disease	Ref				Ref				Ref			
Cavitory disease	1.31	1.17	1.46	<0.0001	1.50	1.39	1.61	<0.0001	1.46	1.21	1.75	<0.0001
HIV status												
HIV-negative	Ref				Ref				Ref			
HIV-positive, undetectable VL	1.20	1.06	1.35	0.00	1.41	1.30	1.54	<0.0001	1.29	1.04	1.61	0.02

HIV-positive, detectable VL	1.07	0.95	1.21	0.26	1.19	1.10	1.30	<0.0001	1.45	1.17	1.80	0.00
Sex												
Male	Ref				Ref				Ref			
Female	1.01	0.93	1.11	0.75	1.12	1.05	1.19	0.00	1.00	0.86	1.16	0.98
Age category												
≤ 15	Ref				Ref				Ref			
16-34	0.77	0.62	0.97	0.02	0.66	0.57	0.76	<0.0001	1.15	0.72	1.82	0.57
35-54	0.82	0.65	1.03	0.08	0.75	0.65	0.86	<0.0001	1.02	0.64	1.64	0.93
≥ 55	1.08	0.84	1.39	0.53	1.14	0.97	1.33	0.11	1.63	0.97	2.72	0.06

Supplemental Table 6. Associations between infectiousness and network position in full and parsimonious models

	n (%) Total n = 344	Parsimonious model (excluding sex)				Full model (including TB strain and year)			
		Odds Ratio	95% CI		p	Odds Ratio	95% CI		p
Cough duration									
No cough reported	128 (37)	Ref				Ref			
1 month	60 (17)	0.51	0.37	0.71	<0.0001	0.74	0.53	1.04	0.08
2 months	51 (15)	2.67	2.18	3.26	<0.0001	2.15	1.75	2.64	<0.0001
3 months	72 (21)	2.35	1.94	2.85	<0.0001	1.96	1.61	2.39	<0.0001
4 months	16 (5)	0.97	0.63	1.48	0.89	1.25	0.81	1.93	0.32
≥ 5 months	17 (5)	1.17	0.77	1.78	0.46	0.82	0.54	1.24	0.35
Smear status									
Smear -	109 (32)	Ref				Ref			
Smear +, scanty +	37 (11)	0.96	0.75	1.22	0.72	1.13	0.87	1.47	0.37
Smear +, grade 1	59 (17)	0.65	0.51	0.81	0.00	0.80	0.62	1.01	0.06
Smear +, grade 2	51 (15)	0.70	0.56	0.88	0.00	0.73	0.57	0.93	0.01
Smear +, grade 3+	88 (26)	0.55	0.44	0.68	<0.0001	0.59	0.47	0.74	<0.0001
Cavitary disease									
No cavitary disease	284 (83)	Ref				Ref			
Cavitary disease	60 (17)	1.52	1.26	1.83	<0.0001	1.72	1.41	2.09	<0.0001
HIV status									
HIV-negative	78 (23)	Ref				Ref			
HIV-positive, undetectable VL	133 (39)	1.19	0.97	1.45	0.10	1.32	1.06	1.63	0.01
HIV-positive, detectable VL	133 (39)	1.00	0.81	1.23	0.98	1.06	0.86	1.32	0.57
Sex									

Male	142 (41)					Ref				
Female	202 (59)			-		0.83	0.71	0.97	0.02	
Age category										
≤ 15	12 (3)	Ref				Ref				
16-34	171 (50)	0.81	0.56	1.17	0.27	0.67	0.47	0.97	0.04	
35-54	134 (39)	0.91	0.62	1.31	0.60	0.63	0.44	0.92	0.02	
≥ 55	27 (8)	1.37	0.92	2.04	0.12	1.03	0.68	1.55	0.89	
Strain										
HP	259 (75)					Ref				
Non-HP	85 (25)	-	-	-	-	37.76	17.89	79.68	<0.0001	
Year										
2011	58 (17)					Ref				
2012	107 (31)	-	-	-	-	0.43	0.36	0.51	<0.0001	
2013	82 (24)	-	-	-	-	0.36	0.29	0.44	<0.0001	
2014	97 (28)	-	-	-	-	0.14	0.10	0.20	<0.0001	

Supplemental Table 7. Associations between social mixing measures and network position in full and parsimonious models

	n (%) Total n = 344	Parsimonious model (excluding sex)				Full model (including TB strain and year)			
		Odds Ratio	95% CI		p	Odds Ratio	95% CI		p
Contact with urban areas									
0 urban settings	149 (43)	Ref				Ref			
1 urban settings	147 (43)	2.66	2.23	3.16	<0.0001	2.13	1.78	2.56	<0.0001
2 urban settings	39 (11)	1.65	1.21	2.25	0.00	1.07	0.78	1.46	0.68
3 urban settings	9 (3)	3.85	2.53	5.87	<0.0001	2.88	1.78	4.64	<0.0001
Duration in hospital									
0 - 2 months	113 (33)	Ref				Ref			
3 - 5 months	81 (24)	0.90	0.75	1.08	0.25	0.89	0.74	1.08	0.23
≥ 6 months	59 (17)	0.36	0.27	0.47	<0.0001	0.43	0.33	0.58	<0.0001
Named close contacts									
0 - 4 contacts	108 (31)	Ref				Ref			
5 - 9 contacts	144 (42)	1.19	0.99	1.44	0.07	0.97	0.80	1.18	0.74
10 - 14 contacts	72 (21)	1.49	1.21	1.83	0.00	1.39	1.11	1.74	0.00
≥ 15 contacts	13 (4)	0.98	0.66	1.44	0.91	1.33	0.89	1.99	0.17
Cough duration									
No cough reported	128 (37)	Ref				Ref			
1 month	60 (17)	0.43	0.31	0.59	<0.0001	0.68	0.48	0.95	0.02
2 months	51 (15)	2.39	1.95	2.93	<0.0001	1.82	1.47	2.25	<0.0001
3 months	72 (21)	2.32	1.91	2.83	<0.0001	1.88	1.53	2.31	<0.0001
4 months	16 (5)	1.02	0.66	1.57	0.94	1.30	0.82	2.06	0.27
≥ 5 months	17 (5)	1.43	0.94	2.18	0.10	1.00	0.65	1.52	0.99

Smear status									
Smear - negative	109 (32)	Ref				Ref			
Smear +, scanty +	37 (11)	0.89	0.69	1.14	0.34	1.04	0.80	1.36	0.75
Smear +, grade 1	59 (17)	0.63	0.50	0.81	0.00	0.80	0.62	1.03	0.09
Smear +, grade 2	51 (15)	0.63	0.50	0.79	<0.0001	0.70	0.55	0.89	0.00
Smear +, grade 3+	88 (26)	0.59	0.48	0.74	<0.0001	0.64	0.51	0.80	<0.0001
Cavitary disease									
No cavitary disease	284 (83)	Ref				Ref			
Cavitary disease	60 (17)	1.43	1.26	1.63	<0.0001	1.48	1.29	1.69	<0.0001
HIV status									
HIV-negative	78 (23)	Ref				Ref			
HIV-positive, undetectable VL	133 (39)	1.22	1.00	1.49	0.05	1.35	1.09	1.68	0.01
HIV-positive, detectable VL	133 (39)	0.95	0.78	1.16	0.63	1.07	0.86	1.32	0.56
Sex									
Male	142 (41)					Ref			
Female	202 (59)					0.79	0.68	0.93	0.01
Age category									
≤15	12 (3)	Ref				Ref			
16-34	171 (50)	0.86	0.59	1.25	0.43	0.78	0.54	1.14	0.20
35-54	134 (39)	0.88	0.60	1.28	0.49	0.66	0.45	0.96	0.03
≥ 55	27 (8)	1.17	0.78	1.74	0.45	1.14	0.76	1.72	0.52
Strain									
HP	259 (75)					Ref			
Non-HP	85 (25)	-	-	-	-	35.50	16.79	75.05	<0.0001

Year								
2011	58 (17)					Ref		
2012	107 (31)	-	-	-	-	0.52	0.43	0.63 <0.0001
2013	82 (24)	-	-	-	-	0.47	0.37	0.60 <0.0001
2014	97 (28)	-	-	-	-	0.16	0.11	0.22 <0.0001

Supplemental Table 8. Associations between social mixing measures and network position in networks with alternate genomic link definitions

	Undirected ≤ 5 SNPs				Directed ≤ 10 SNPs				Undirected RFLP/WGS (≤ 3 SNPs) combined			
	Odds Ratio	95% CI		p	Odds Ratio	95% CI		p	Odds Ratio	95% CI		p
Intercept		-4.60				-3.49				-6.90		
Contact with urban areas												
0 urban settings	Ref				Ref				Ref			
1 urban settings	1.49	1.35	1.65	<0.0001	1.83	1.71	1.96	<0.0001	1.35	1.14	1.61	0.00
2 urban settings	1.77	1.52	2.06	<0.0001	1.47	1.31	1.64	<0.0001	1.11	0.84	1.48	0.46
3 urban settings	1.89	1.47	2.43	<0.0001	1.16	0.93	1.44	0.19	1.24	0.77	1.99	0.38
Duration in hospital												
0 - 2 months	Ref				Ref				Ref			
3 - 5 months	0.97	0.87	1.08	0.57	0.83	0.77	0.90	<0.0001	0.95	0.79	1.15	0.61
≥ 6 months	0.41	0.35	0.48	<0.0001	0.57	0.52	0.63	<0.0001	0.71	0.56	0.90	0.00
Named close contacts												
0 - 4 contacts	Ref				Ref				Ref			
5 - 9 contacts	1.10	0.98	1.22	0.09	1.26	1.17	1.36	<0.0001	1.18	0.98	1.43	0.08
10 - 14 contacts	1.42	1.25	1.60	<0.0001	1.32	1.21	1.44	<0.0001	1.59	1.29	1.96	<0.0001
≥ 15 contacts	0.70	0.55	0.88	0.00	0.80	0.68	0.94	0.01	0.74	0.48	1.15	0.18
Cough duration												
No cough reported	Ref				Ref				Ref			
1 month	1.10	0.96	1.25	0.17	0.86	0.81	0.92	<0.0001	0.68	0.53	0.88	0.00
2 months	1.57	1.38	1.78	<0.0001	1.47	1.38	1.56	<0.0001	1.46	1.18	1.80	0.00
3 months	1.68	1.49	1.89	<0.0001	1.18	1.11	1.25	<0.0001	1.38	1.13	1.68	0.00
4 months	0.81	0.63	1.04	0.09	0.84	0.75	0.95	0.00	0.49	0.29	0.81	0.01

≥ 5 months	0.86	0.66	1.12	0.27	0.82	0.73	0.92	0.00	0.84	0.55	1.28	0.43
Smear status												
Smear - negative	Ref				Ref				Ref			
Smear +, scanty +	1.23	1.07	1.42	0.00	0.97	0.90	1.04	0.35	1.56	1.20	2.04	0.00
Smear +, grade 1	0.67	0.58	0.78	<0.0001	0.60	0.56	0.65	<0.0001	1.18	0.92	1.50	0.19
Smear +, grade 2	0.86	0.75	0.98	0.03	0.78	0.73	0.83	<0.0001	1.00	0.77	1.30	0.98
Smear +, grade 3+	0.83	0.73	0.93	0.00	0.81	0.77	0.86	<0.0001	1.37	1.11	1.70	0.00
Cavitary disease												
No cavitary disease	Ref				Ref				Ref			
Cavitary disease	1.41	1.26	1.57	<0.0001	1.27	1.20	1.34	<0.0001	1.51	1.25	1.82	<0.0001
HIV status												
HIV-negative	Ref				Ref				Ref			
HIV-positive, undetectable VL	1.25	1.11	1.41	0.00	1.18	1.11	1.25	<0.0001	1.30	1.05	1.62	0.02
HIV-positive, detectable VL	1.07	0.95	1.21	0.26	0.97	0.92	1.03	0.35	1.46	1.17	1.81	0.00
Sex												
Male	Ref				Ref				Ref			
Female	0.91	0.83	1.00	0.05	1.13	1.08	1.18	<0.0001	0.92	0.79	1.08	0.31
Age category												
≤ 15	Ref				Ref				Ref			
16-34	0.78	0.62	0.98	0.03	0.82	0.73	0.91	0.00	1.17	0.73	1.86	0.52
35-54	0.81	0.64	1.02	0.07	0.98	0.87	1.09	0.66	1.02	0.64	1.65	0.92
≥ 55	1.01	0.78	1.30	0.97	1.07	0.95	1.21	0.28	1.57	0.94	2.64	0.09

Code Appendix (see also: <https://github.com/kbratnelson/tb-ergms>)

```
---
title: "tb network clinical and social mixing ergms"
author: "author: kristin"
date: "started 10/5/2017"
most recent edit: "1/8/2019"
output: html_document
---

```{r setup and call packages, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
library(GGally)
library(network)
library(sna)
library(statnet)
library(tidyverse)
library(EpiModel)
```

```{r, create networks, include=FALSE}

#####
CREATE NETWORK
#####

#create directed network objects (shown for directed network with 5 SNP threshold - main model)

dnet_le5_pMDRdxdiff <- as.network(x = mat_dxdiffpMDR5snp, # the network object
 directed = TRUE, # specify whether the network is directed
 loops = FALSE, # do we allow self ties (should not allow them)
 matrix.type = "adjacency" # the type of input
)

```

_create network with vertex (node) attributes_
```{r, add vertex attributes to network}

#####
```

```

ADD VERTEX ATTRIBUTES
#####

#add vertex attributes to networks (shown for directed network with 5 SNP threshold - main model)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "coughdur_mo", t2_order$co_dur_mo)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "coughdur_mowk", t2_order$co_dur_mowk)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "cluster", t1_order$Cluster)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "rflp", t1_order$rflp)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "hp", t1_order$hp)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "smgrade", t2_order$smgrade_num)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "smstat", t2_order$smstat)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "cav", t2_order$cav_num)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "HIV", t1_order$HIV_all)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "hiv_arv", t1_order$hiv_arv)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "sex", t1_order$Female_sex)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "age_cat", t1_order$age_cat)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "resdis", t4_order$District_num)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "prevMDR", t1_order$prevMDR_all)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "yr", t1_order$year)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "hp", t1_order$hp)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb", t6_order$allurbcomb)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb2", t6_order$allurbcomb2)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb_predst", t6_order$allurbcomb_predst)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb2_predst", t6_order$allurbcomb2_predst)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "tothospmos", t6_order$tothospmos)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "totcon", t6_order$total.contacts)

...

ergms, in directed and non-directed networks
```{r, ergms}

model.0 <- ergm(net_le10~edges)
summary(model.0)

#####
#
# CLINICAL INFECTIOUSNESS VARIABLES (Aim 2)
#
#####

```

```

#####
# UNDIRECTED networks
#####

model.1.u <- ergm(net_le5 ~ edges + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.1.u)

#####
# DIRECTED networks
#####

#Main model
model.1.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodefactor("coughdur_mo") + nodefactor("smgrade") +
nodefactor("cav") + nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.1.d)

#Alternative model 1
#parsimonious model, directed networks (no sex)
model.3.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodefactor("coughdur_mo") + nodefactor("smgrade") +
nodefactor("cav") + nodefactor("hiv_arv") + nodefactor("age_cat"))
summary(model.3.d)

#Alternative model 2
#full model (including hp (strain) and year enrolled)
model.4.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodefactor("coughdur_mo") + nodefactor("smgrade") +
nodefactor("cav") + nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat")) +
nodefactor("yr") + nodefactor("hp"))
summary(model.4.d)

#Alternative model 3
#alternate variables (collapsed cough duration)
model.5.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodefactor("coughdur_mored") + nodefactor("smstat") +
nodefactor("cav") + nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.5.d)

##Alternative edge definition 1
#different SNP threshold (3SNP)
model.6.d <- ergm(dnet_le3_pMDRdxdiff ~ edges + nodefactor("coughdur_mo") + nodefactor("smgrade") +
nodefactor("cav") + nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.6.d)

```

```

##Alternative edge definition 2
#different SNP threshold (10SNP)
model.7.d <- ergm(dnet_le10_pMDRdxdiff ~ edges + nodeofactor("coughdur_mo") + nodeofactor("smgrade") +
nodeofactor("cav") + nodeofactor("hiv_arv") +nodeofactor("sex") + nodeofactor("age_cat") +
nodeofactor("yr") + nodeofactor("hp"))
summary(model.7.d)

##Alternative edge definition 3
#WGS + RFLP cluster (clust_le3)
model.8.d <- ergm(dnet_clust_le3 ~ edges + nodeofactor("coughdur_mo") + nodeofactor("smgrade") +
nodeofactor("cav") + nodeofactor("hiv_arv") +nodeofactor("sex") + nodeofactor("age_cat"))
summary(model.8.d)

#####
#
# SOCIAL MIXING VARIABLES (Aim 3)
#
#####

set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb_red", t6_order$allurbcombred)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "urbcomb2_red", t6_order$allurbcomb2red)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "totcon_cat", t6_order$total.contacts_cat)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "totcon_catred", t6_order$total.contacts_catred)
set.vertex.attribute(dnet_le5_pMDRdxdiff, "tothomos_cat", t6_order$tothomos_cat)

#####
# UNDIRECTED networks
#####

model.1.u <- ergm(net_le5 ~ edges + nodefactor("urbcomb") + nodefactor("tothomos_cat") +
nodefactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.1.u)

#####
# DIRECTED networks
#####

```

```

#Main model
#urban contact var 1 - number of domains (range: 0-3)
model.1.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.1.d)

#Alternative model 1
#parsimonious model, directed networks (no sex)
model.2.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") + nodefactor("age_cat"))
summary(model.2.d)

#Alternative model 2
#full model (including hp (strain) and year enrolled)
model.3.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodeofactor("coughdur_mo") + nodeofactor("smgrade") + nodefactor("cav") +
nodeofactor("hiv_arv") +nodeofactor("tothomos_cat") + nodeofactor("age_cat") + nodeofactor("hp") +
nodeofactor("yr"))
summary(model.3.d)

#Alternative model 3
#urban contact variable 2 - number of locations (range: 0-15)
model.4.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodeofactor("urbcomb2_red") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.4.d)

#Alternative model 4
#alternative vars (reduced number of categories for urban contact, close contacts)
model.5.d <- ergm(dnet_le5_pMDRdxdiff ~ edges + nodeofactor("urbcomb_red") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_catred") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("tothomos_cat") + nodefactor("age_cat"))
summary(model.5.d)

##Alternative edge definition 1
#different SNP threshold (3SNP)
model.6.d <- ergm(dnet_le3_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))

```

```
summary(model.6.d)

##Alternative edge definition 2
#different SNP threshold (10SNP)
model.7.d <- ergm(dnet_le10_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat") +
nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.7.d)

##Alternative edge definition 3
#WGS + RFLP cluster (clust_le3)
model.8.d <- ergm(dnet_clust_le3_pMDRdxdiff ~ edges + nodeofactor("urbcomb") + nodeofactor("tothomos_cat")
+ nodeofactor("totcon_cat") + nodefactor("coughdur_mo") + nodefactor("smgrade") + nodefactor("cav") +
nodefactor("hiv_arv") +nodefactor("sex") + nodefactor("age_cat"))
summary(model.8.d)

...

```