

PROTOCOL FOR:

Sex-assortativity and the spread of TB on contact networks

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Background:

TB is a respiratory-transmitted infectious disease that is heterogeneously distributed globally and concentrated in Africa and Asia. In addition, TB is heterogeneously distributed within populations; in particular, men face higher risk factors than women. The global male:female TB case ratio is 1.9, a pattern strikingly consistent across countries.

Male-bias in TB case reports is thought to be due to sex-specific differences in exposure to Mtb or susceptibility to disease following exposure, or a combination of the two. Exposure rates could be mediated by differences in behaviors and societal gender roles. For example men may have more contacts or be more central in social networks though previous studies have failed to substantiate this (Mossong et al. 2008, etc.). Alternatively, sex-specific exposure rates could be driven by differences in the types of contacts that men compared to women. Specifically, exposure could be higher in men due to assortative mixing which is where individuals tend to associate with others similar to them, creating sub-groups within a social network. However, we lack studies analyzing the role of hypothesized exposure mechanisms at driving male-bias.

The effects of assortativity (i.e., modularity) on aggregated (i.e., regardless of subgroup) epidemic dynamics (e.g., total outbreak size or equilibrium prevalence) depend on the infection process (SIR, SIS) and the distribution of subgroup size. Tuberculosis transmission is better represented by an SIR than an SIS process. In SIR systems, the total outbreak size of diseases with SIR dynamics decrease with increasing assortativity, perhaps due to a build-up of recovered nodes within-subgroups and transmission bottlenecks between subgroups (Nandini 2018). However, very high assortativity may be required to produce this “protective” effect of assortativity (Salathe & Jones 2015, Sah et al. 2017). In contrast, for SIS processes, infected nodes return to susceptible nodes and a build-up of recovered nodes does not occur, resulting in intensely connected subgroups which increase the equilibrium prevalence of infection (Nandini 2018). Subgroup size also affects disease spread: networks with larger subgroups increase epidemic size when compared with networks with constant subgroup size. Most prior studies have focused on networks with multiple (in the range of 10 to 100), highly connected subgroups. For our purposes, an open question remains about how disease spreads within lightly assorted networks with two subgroups (i.e., men and women) which potentially vary in their susceptibility to infection.

We wondered whether sex-assortativity in social networks could contribute to male-bias or if previously described differences in susceptibility between the sexes are necessary to explain male-bias.

Research questions:

1. Can sex-assortative mixing lead to male-bias by itself or is sex-specific susceptibility required to explain male-bias?
2. What are the effects of sex-assortative mixing on disease spread (peak size/time, variation in outbreak size/duration)?

Study design:

We will examine the effects of sex-assortativity and sex-specific susceptibility on the ratio of male to female cases using models of disease spread on simulated networks. In the simulated networks, each node will represent an individual and each link is a connection between individuals that infection can spread.

Network generation:

Simulated networks will vary in level of sex-assortativity, r , calculated according to Newman's discrete assortativity coefficient (Newman 2003) as

$$r = \frac{\sum_i e_{ii} - \sum_i (a(i)^2)}{1 - \sum_i (1 - a(i)^2)} = \frac{Tr\mathbf{E} - ||E^2||}{1 - ||E^2||}$$

where e_{ij} is the proportion of edges connecting nodes in subgroup i to subgroup j (undirected), $a(i) = \sum_j e_{ij}$. Alternatively, if \mathbf{E} is the matrix of e_{ij} and $||X||$ is the sum of all elements in a matrix \mathbf{X} , then assortativity can be calculated with the proportion of edges within-sex ($Tr\mathbf{E}$) and the proportion of edges that would be within groups if connections were random $||E^2||$. Here, if edges were distributed randomly, $Tr\mathbf{E} = ||E^2|| = 0.5$ and $r = 0$. Typically, r ranges from $-1 \gg r \geq 1$ because disassortative networks are much closer to random networks ($r=0$) than are assortative networks.

Note: Network modularity (Q) is a similar measure of non-random mixing in networks: $Q = \sum_i e_{ii} - a_i^2 = Tr\mathbf{E} - ||E^2||$ where e_{ij} is the proportion of edges in the network that link nodes in community i to community j and $a_i = \sum_j e_{ij}$ represents the proportion of edges in the network that link to nodes in subgroup i . The maximum value of Q is $1 - \frac{1}{K}$ where K is the number of modules (Sah 2014). Thus, the relationship between assortativity and modularity for networks with two subgroups is

$$assortativity = modularity / (1 - expected.prop.between.edges)$$

where the expected proportion of between edges is the proportion of nodes in that subgroup. Since groups have equal size, you would expect $1/2$ to occur between groups by chance. Thus, assortativity gets divided by 0.5 while modularity does not.

We will generate scale-free networks according to the parameters listed in Table 1 using the classic BA-algorithm. Following network generation, we will update the networks as following:

1. Assign nodes randomly as male (0) or female (1).
2. Calculate temporary value of sex-assortativity in the network (r_t).
3. If r_t is not within ϵ of r , randomly choose a proportion α of 0-1 edges (i.e, a male-female edge) if $r \geq 0$ and re-wire them or if $r < 0$, choose a proportion α of 0-0 and 1-1 edges and re-wire them.
4. Repeat step 3 until $|r_f - r_t| \leq \epsilon$.

Network will be generated with parameters shown in Table 1.

Table 1: Network parameters.

Variable	Value
Sex-assortativity, r	(-0.9, 0.9) by 0.1
Degree distribution, $p(K)$	$\frac{k^{-\alpha}}{\zeta(\alpha)}$
Mean degree, $\langle K \rangle$	10
Network size, N	500, $1 \cdot 10^3$, $2 \cdot 10^3$, $5 \cdot 10^3$
Tolerance, ϵ	0.035
Rewiring proportion, α	0.2
Replicates	100

Disease transmission modeled as SIR:

Nodes can exist as either susceptible, infected, or recovered (Table 2).

We will model disease spread on networks as a continuous time Markov chain with infection spreading along an edge at rate τ and recovery happening at rate γ .

An infected node transmits to each of its uninfected neighbors independently with probability $p(T) = 1 - e^{-\tau T}$ where T is the duration of infection for the infected node.

We will use an event-driven algorithm for simulations on synthetic networks implented in the python module EoN (Kiss, Miller & Simon 2017).

We will assume SIR dynamics as our model of disease spread (Table 2).

Table 2: Disease parameters.

Variable	Value
Initial susceptible, S_0	$N - 0.05 \cdot N$
Initial infected, I_0	$0.05 \cdot N$
Infection rate, τ	0.125, 0.25, 0.375
Recovery rate, γ	1
Estimated R_0	$[\frac{\tau}{\tau+\gamma}][\frac{<K^2-K>}{<K>}]$

Analysis:

Network structure:

- Relationship between network structure (clustering, degree assortativity, diameter, degree variation) and assortativity

Case ratio:

- Relationship between assortativity and M:F case ratio
- Variation by network size and R_0

Disease spread:

- Relationship between assortativity and epidemic peak size, peak time, variation in outbreak size, variation in epidemic duration
- Variation by network size and R_0

Checklist:

- X Understand the relationship between measures of community structure (Q vs. r) for K=2 modules
- X Run study across larger parameter grid and more replicates
- Analyze and interpret results from extended simulations
- Understand and relate results to Salathe and Sah research
- Decide on next steps which could be: (1) Seed epidemics disproportionately in one module; (2) Incorporate sex-specific susceptibility; (3) Incorporate latent class of individuals; (4) Sample epidemics according to COHSONET and validate results

Important background papers:

Kiss, I Z, J C Miller, and PL Simon Cham Springer. 2017. “Mathematics of Epidemics on Networks.” Springer.

Newman, MEJ. 2003. “Mixing Patterns in Networks.” *Physical Review E* 67 (2). American Physical Society. doi:10.1103/PhysRevE.67.026126.

Nhamoyebonde, Shepherd, and Alasdair Leslie. 2014. “Biological Differences Between the Sexes and Susceptibility to Tuberculosis.” *Journal of Infectious Diseases* 209 (suppl 3): S100–S106. doi:10.1093/infdis/jiu147.

Pastor-Satorras, R, and A Vespignani. 2001. “Epidemic Dynamics and Endemic States in Complex Networks.” *Physical Review. E, Statistical, Nonlinear, and Soft Matter Physics* 63 (6 Pt 2): 066117. doi:10.1103/PhysRevE.63.066117.

Perkins, S E, M F Ferrari, and P J Hudson. 2008. “The Effects of Social Structure and Sex-Biased Transmission on Macroparasite Infection.” *Parasitology* 135 (13): 1561–69. doi:10.1017/S0031182008000449.

Sah, Pratha, Stephan T Leu, Paul C Cross, Peter J Hudson, and Shweta Bansal. 2017. “Unraveling the Disease Consequences and Mechanisms of Modular Structure in Animal Social Networks..” *Proceedings of the National Academy of Sciences of the United States of America* 114 (16). National Academy of Sciences: 4165–70. doi:10.1073/pnas.1613616114.

Sah, Pratha, Lisa O Singh, Aaron Clauset, and Shweta Bansal. 2014. “Exploring Community Structure in Biological Networks with Random Graphs.” *BMC Bioinformatics* 15 (220). BioMed Central. doi: 10.1186/1471-2105-15-220.

Salathé, Marcel, and James H Jones. 2010. “Dynamics and Control of Diseases in Networks with Community Structure.” Edited by Christophe Fraser. *PLoS Computational Biology* 6 (4). Public Library of Science: e1000736. doi:10.1371/journal.pcbi.1000736.

CHANGE-LOG:

- [bullet list of changes to protocols with reasons for each change]