Structure matters: bipartite contact networks and vaccination

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Extended Abstract

Mathematical epidemiology models are incredibly valuable for helping to understand the spread of disease and supporting public health policy [1]. However, traditional epidemiology models typically assume that populations are "well-mixed", with everyone having equal likelihood of having contact with everyone else. In the real world, infectious diseases spread through highly structured contact networks. It is an established result that the structure of the contact network has significant implications for disease transmission dynamics [2], [3].

In this research, we simulate the spread of disease on a bipartite contact network with individuals linked via group nodes. This captures an important feature of real-world contact networks: our contacts are mediated through groups, such as households, classrooms, workplaces, and social groups.

First, we show how different structural features of the contact network affects the spread of disease by comparing the spread of disease on bipartite networks with null model graphs with the same densities (using Erdős–Rényi graphs), degree distributions (configuration models), and clustering coefficients (Watts-Strogatz), as well as traditional "well-mixed population" models. We find that the timing and magnitude of the epidemic peak for a group-based bipartite network differs to those of the null models.

We then consider the implications of the bipartite network structure for vaccination. We consider three different vaccination approaches: randomly vaccinating individuals, vaccinating all individuals in randomly selected groups, and vaccinating a proportion of individuals in randomly selected groups. For each approach we assume that vaccination is 100% effective and that we have the same number of vaccines to allocate. We then simulate the spread of disease over the remaining unvaccinated individuals.

For each simulation, we calculate epidemic metrics such as the height and timing of the infection peak, and the total size of the outbreak. We find that the group-based and random vaccination approaches produce different disease dynamics. Specifically, for the same proportion of the population vaccinated, group-based vaccination reduces the size of the epidemic wave more than random vaccination of individuals. This effect becomes larger when partially vaccinating groups. This is likely due to a bipartite version of the "friendship paradox, where group-based vaccination is more likely to vaccinate people who are in more groups. This means that the people who remain unvaccinated were in fewer groups on average in the first place. Consequently, despite group-based vaccination leading to networks with higher clustering, the way that the vaccines are allocated results in unvaccinated people having fewer unvaccinated contacts than random vaccination. Furthermore, compared to random vaccination, group-based vaccination reduces the size of the largest connected component of the contact network of unvaccinated individuals, breaking the network up into smaller, isolated pieces, and reducing the likelihood of large outbreaks.

These findings show that infectious disease models that explicitly represent individuals and their contact network are important for more accurately representing the highly structured interactions between individuals and the impacts of public health interventions.

References

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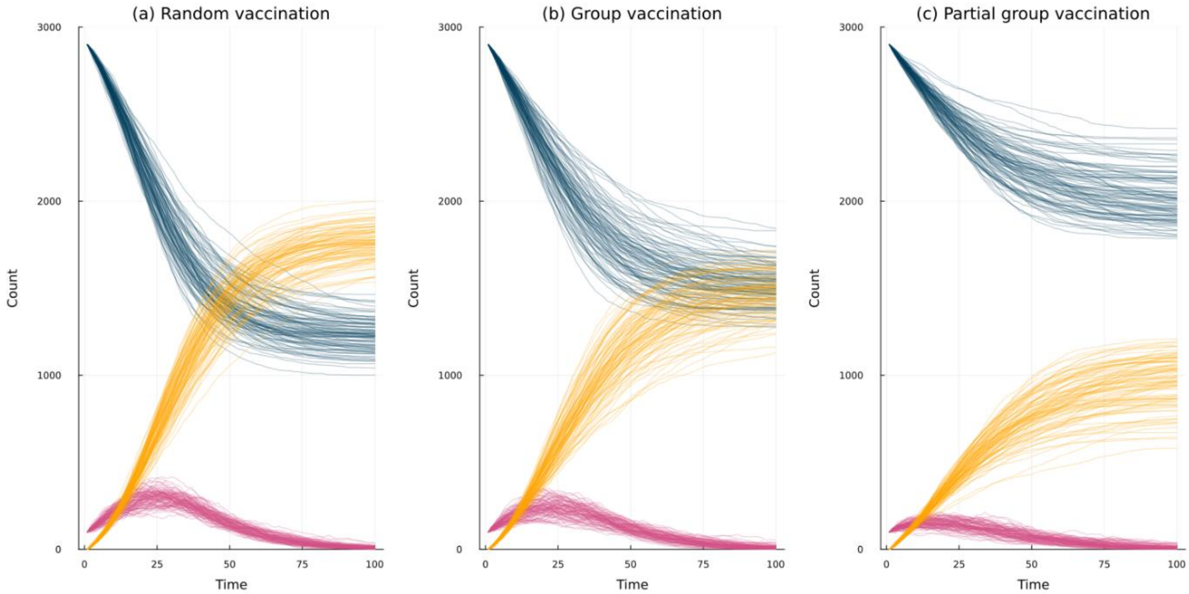

Figure 1. **Simulation results for 100 simulations of disease spread** on bipartite contact networks with 70% of the population vaccinated using: (a) Random individual vaccination (b) Group-based vaccination. (c) Partial (60%) group-based vaccination. Counts of individuals are shown for susceptible (blue), infected (pink), and recovered (orange) states for an SIR contagion process.

Table 1. **Network and epidemic metrics with different vaccination approaches.** All metrics are means across 100 simulations. The number of groups is calculated after removing group nodes with degree zero or one.

	Random vaccination	**Group-based vaccination**	**Partial group vaccination**
Outbreak size	1,670	1,383	876
Number of individuals	3,000	3,000	3,000
Bipartite network			
Individual degree	3.0	2.3	1.9
Number of groups	3,247	2,417	2,156
Group degree	2.8	2.8	2.7
Projected network			
Individual degree	6.7	5.2	4.1
Density	0.00092	0.00093	0.00089
Clustering coefficient	0.27	0.33	0.36
Largest connected component	2882	2750	2560
Number of components	113	221	380