Epidemics on Hypergraphs

Márton Bálint Gyebnár

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Traditional models for epidemics on networks assume a graph structure of the network, where nodes represent individuals and disease spreads across edges between connected individuals. Each of the N nodes is assigned one of m distinct statuses, such as, in the case of SIS dynamics ($m = 2$), susceptible (S) or infected and infectious (I). The standard assumption that infections between infected and susceptible individuals as well as recovery of infected individuals occur according to independent Poisson processes leads to the description of the model as a continuous time Markov chain on a state space of size m^N, containing all possible system states given by the status of every node in the graph. Such a model offers meaningful insight into the evolution of epidemics on networks, yet it accounts only for pairwise interactions. However, many contagion processes, biological or otherwise, are further influenced by group interactions. A relatively new research area stems from generalizing the model described above by considering a hypergraph structure of the network, in an attempt to account for this added complexity. For the purpose of this project, I consider SIS epidemics on hypergraphs. In this report, I summarize essential aspects of the model for hypergraphs and introduce techniques for arriving at approximate differential equations, based on which a qualitative analysis can be conducted. This report is based on an unpublished draft of the second edition of [2]. Certain concepts discussed here also appear in the published first edition [1] for the case of graphs.

We begin with an overview of a general hypergraph structure. A hypergraph is a pair $(V, \mathscr{H})$, where $V = \{1, 2, \dots, N\}$ is the set of nodes and $\mathscr{H}$ is a set of $H \subset V$ hyperedges. The order of a hyperedge $H \in \mathscr{H}$ is simply $|H|$, the number of nodes within. The ℓ-uniform subhypergraph $\mathscr{H}^{(\ell)} = \{H \in \mathscr{H} : |H| = \ell\}$ contains the hyperedges of order ℓ, and $\mathscr{H}_i^{(\ell)} = \{H \in \mathscr{H}^{(\ell)} : i \in H\}$ denotes the set of hyperedges of order ℓ containing node $i \in V$. If $H \in \mathscr{H}$ implies $H' \in \mathscr{H}$ for all subsets $H' \subset H$, then we say that the hyperedge is a simplicial complex.

We now turn to the description of the dynamics considered. Given a state of the Markov chain, we wish to determine the rate of transitioning to another state. Because the probability of two events, be that infection or recovery of a node, occuring at the same time is zero, the chain transitions with positive rate only to states that differ in the status of exactly one node. The rate of transitioning to a state where node $i \in V$ is newly infected, otherwise refered to as the infection pressure felt by node i, is given by

$$\sum_{n=2}^{N} \sum_{H_j \in \mathscr{H}_i^{(n)}} r(n, m_j),$$

where m_j is the number of infected nodes in hyperedge H_j and $r(n, m_j)$ denotes the rate of infection across a hyperedge of order n with m_j infected nodes. For simplicity, we assume that

$$r(2, 1) = \tau \quad \text{and} \quad r(3, 2) = \beta$$

for $\tau, \beta > 0$ parameters and $r(n, m) = 0$ otherwise. As recovery is independent of the network, the rate of transitioning to a state where a node is newly

recovered is given by a single constant recovery rate $\gamma > 0$.

The above dynamics determine the generator of the continuous time Markov chain. Thus, one can analyze the evolution of the epidemic through the Kolmogorov forward equations, also called the master equations. This approach is called the top-down model. The solution of the master equations given a specific initial condition determines the probability of being in each state at any given time. However, this method is often unmanageable in practice, since the size of the system grows exponentially with the number of nodes in the network.

An alternative approach, called the bottom-up model, is to derive differential equations for the probability of a given state having a given status. Let $\langle I_i \rangle(t)$ and $\langle S_i \rangle(t)$ denote, respectively, the probabilities that node i is infected and susceptible at time t. Similar variables are introduced for the joint probability of multiple nodes having certain statuses at time t. For example, for two and three nodes these are denoted by $\langle A_i B_j \rangle(t)$ and $\langle A_i B_j C_k \rangle(t)$, where $i, j, k \in V$ and $A, B, C \in \{S, I\}$. Differential equations for the singles I_i and S_i depend on the variables for pairs and triples, depending on the hypergraph itself. For example, consider a complete hypergraph on $N = 3$ nodes. Then we have for instance that

$$\dot{\langle I_1 \rangle} = \tau(\langle S_1 I_2 \rangle + \langle S_1 I_3 \rangle) + \beta \langle S_1 I_2 I_3 \rangle - \gamma \langle S_1 \rangle.$$

It is apparent, that in order to arrive at a closed set of equations, we need equations for all pairs and triples as well. This becomes intractable for larger networks, which is why often closures are applied. The simplest closure is to assume independence conditions $\langle A_i B_j \rangle = \langle A_i \rangle \langle B_j \rangle$ and $\langle A_i B_j C_k \rangle = \langle A_i \rangle \langle B_j \rangle \langle C_k \rangle$ for the joint probabilites for pairs and triples. Then, using $\langle S_i \rangle = 1 - \langle I_i \rangle$, the system simplifies greatly to the following three equations:

$$\begin{aligned}
\dot{\langle I_1 \rangle} &= \tau(1 - \langle I_1 \rangle)(\langle I_2 \rangle + \langle I_3 \rangle) + \beta(1 - \langle I_1 \rangle)\langle I_2 \rangle \langle I_3 \rangle - \gamma \langle I_1 \rangle, \\
\dot{\langle I_2 \rangle} &= \tau(1 - \langle I_2 \rangle)(\langle I_1 \rangle + \langle I_3 \rangle) + \beta(1 - \langle I_2 \rangle)\langle I_1 \rangle \langle I_3 \rangle - \gamma \langle I_2 \rangle, \\
\dot{\langle I_3 \rangle} &= \tau(1 - \langle I_3 \rangle)(\langle I_1 \rangle + \langle I_2 \rangle) + \beta(1 - \langle I_3 \rangle)\langle I_1 \rangle \langle I_2 \rangle - \gamma \langle I_3 \rangle.
\end{aligned}$$

By assuming $\langle I_1 \rangle(t) = \langle I_2 \rangle(t) = \langle I_3 \rangle(t) = x(t)$ for all t, the system can be reduced to

$$\dot{x} = 2\tau(1 - x)x + \beta(1 - x)x^2 - \gamma x.$$

In case the required equality of initial conditions is not met, the solution to the reduced system can be considered to be an approximation of the original variables. Aggregating multiple nodes to describe them using just one variable is a method called lumping, and it can be carried out when certain symmetries of the hypergraph are present. If our hypergraph on three nodes contained only two edges, say $\{1, 2\}$ and $\{2, 3\}$, we would have arrived at the two-dimensional system

$$\begin{aligned}
\dot{x} &= \tau(1 - x)y + \beta(1 - x)xy - \gamma x, \\
\dot{y} &= 2\tau(1 - y)x + \beta(1 - y)x^2 - \gamma y.
\end{aligned}$$

Systems such as the ones shown above allow for extensive qualitative analysis and often exhibit rich bifurcation landscapes. In this semester, I examined the bottom-up systems closed at the level of singles for all four possible hypergraphs on $N = 3$ nodes with the hyperedge of order three being present. For the case of two and three edges in the hypergraph, I showed that bistability between the disease-free steady state and an endemic steady state can occur. For the case of a single edge, using a Lagrange-multiplier method described in [3], I numerically determined two fold bifurcation curves and located a cusp bifurcation in the system, thereby showing that bistability can occur even between two endemic steady states. Going forward with the project, I aim to define scalable hypergraphs that reduce to an analytically tractable system and to describe the associated bifurcation diagram.

References

[1] István Z. Kiss, Joel C. Miller, and Péter L. Simon. Mathematics of Epidemics on Networks: From Exact to Approximate Models. Interdisciplinary Applied Mathematics 46. Cham: Springer International Publishing, 2017. https://doi.org/10.1007/978-3-319-50806-1.

[2] István Z. Kiss, Joel C. Miller, Grzegorz A. Rempała, and Péter L. Simon. Mathematics of Epidemics on Networks: From Exact to Approximate Models. Unpublished draft of the second edition, July 2025

[3] Owen, L., Tuwankotta, J.M. Computation of fold and cusp bifurcation points in a system of ordinary differential equations using the Lagrange multiplier method. Int. J. Dynam. Control 10, 363–376 (2022). https://doi.org/10.1007/s40435-021-00821-4