Epidemic spreading on hypergraphs

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Introduction

Graphs provide a formalism to represent dyadic interactions occurring in real-life networks - for instance, online social networks, such as Facebook, can be represented as networks with links corresponding to friendship on Facebook. Hypergraphs generalise graphs by allowing edges of different cardinalities. Hypergraphs can represent complex interactions, such as co-authorship hypernetworks. We generalize existing contagion models on 2-simplicial complexes to higher orders.

Definition: Hypergraphs

Hypergraphs are mathematical structures, introduced by the mathematician Claude Berge in the 1970s, that generalise graphs in the sense that an edge can have any number of vertices. Formally, a hypergraph H is a pair $H = (V, E)$, where V is a set of vertices and E is a set of non-empty subsets of V called hyperedges.

Definition: Simplicial complex

Simplicial complexes are a particular type of hypergraphs: if a hyperedge σ is present then all the subsimplices $v \subset \sigma$ are also contained in E. By convention, an ω-simplex contains $\omega + 1$ nodes.

Interest

Generalisations of SIS models to hypergraphs are interesting because both theoretical analyses and numerical simulations show the emergence of a discontinuous transition induced by higher-order interactions. The analysis showing the possibility of a discontinuous transition is realised (for 2-simplicial complexes only) via the microscopic Markov chain approach (MMCA) in [MGA20]. We show that the analysis carries to higher-orders, which doesn't seem to appear anywhere in the literature. Higher-order interactions also lead to the appearance of a bi-stable region where both susceptible and infectious asymptotic states co-exist. The asymptotic state depends on the the initial proportion of infectious nodes - a critical mass is needed to reach the endemic state. This was demonstrated for 2-simplicial complexes in [IPBL19]. We conducted simulations on 3-simplicial complexes and showed that one can obtain tri-stable regions as well as the bi-stable region.

SIS model

In the classical SIS model on a connected undirected graph, the vertices represent individuals who are either infectious (I) or susceptible (S) [Luc13]. To each vertices, we assign a binary value from the set $\{0, 1\}$ - 0 model susceptible individuals, and 1 models infectious individuals. We let $s_i(t) \in \{0, 1\}$ represent the state of individual i at time t. The infection propagates, through pairwise interactions, from infectious individual to susceptible individuals with probability β_{S_1} (we use S_1 to indicate that we consider 1-simplicial complexes), and infectious nodes recover with probability μ. For 2-simplicial complexes, we can consider as well triangular interactions as in [MGA20]. We extend the model to higher-order simplicial complexes: nodes also interacts within the ω-simplices with the ω neighbours at unison, with an infection probability β_{S_ω}.

MMCA equations

One can define a system of discrete-time MMCA equations to describe the evolution over time of the probability p_i of node i being infectious at time t as:

$$p_i(t+1) = (1 - p_i(t))(1 - \prod_{\omega=1}^{D} q_i^{S_\omega}(t)) + p_i(t)(1 - \mu)$$

$q_i^{S_\omega}(t)$ denotes the probability that node i is not infected by any ω simplex it participates in. If node i is infectious it will recover with probability μ. Otherwise the node is susceptible and could get infected through interaction in ω-simplices it takes part in. The probability that the node will become infectious is $(1 - q_i^{S_1}(t) \dots q_i^{S_D}(t))$. Indeed, the node is not infected if it's not infected through any ω-simplex. The probability that node i is not infected by pairwise relations is:

$$q_i^{S_1}(t) = \prod_{j \in S_1} (1 - \beta_{S_1} p_j(t))$$

where S_1 is the set of neighbours (via links) of node i. Similarly, the probability that node i is not infected by any ω-simplex interaction is:

$$q_i^{S_\omega}(t) = \prod_{n_1, \dots, n_\omega \in S_\omega} (1 - \beta_{S_\omega} p_{n_1}(t) \dots p_{n_\omega}(t))$$

where S_ω is the set of ω-simplices (from which we exclude i) containing node i.

Expanding the MMCA equations

Expanding the MMCA equations up to second order in p, and developing the equation at the stationary state, we arrive at:

$$0 \approx (1-p)\left[k_{S_1}\beta_{S_1}p + \left(k_{S_2}\beta_{S_2} - \beta_{S_1}^2\binom{k_{S_1}}{2}\right)p^2\right] - \mu p$$

Simplicial Contagion Model (SCM): Mean Field

One can write a MF expression for the temporal evolution of the density of infectious nodes $\rho(t)$:

$$d_t\rho(t) = -\mu\rho(t) + \sum_{\omega=1}^{D} \beta_{S_\omega}\langle k_{S_\omega}\rangle \rho^\omega(t)[1 - \rho(t)]$$

where, for each $\omega = 1, \dots, D$, $\langle k_{S_\omega}\rangle$ is the average number of ω-simplices incident to a node. To derive this equation, we note that infectious nodes become susceptible with rate per unit time μ, and the susceptible nodes (their density is $(1 - \rho(t))$) can be infected by any simplices, ranging from links to D-simplices. Contagion happens through a ω-simplex, by definition with rate β_{S_ω}, if and only if all other nodes are infectious, hence the term $\rho^\omega(t)$ [IPBL19].

Expanding the MF equations for $D = 2$

We can expand the case $D = 2$ and solve $d_t\rho(t) = 0$ - the steady state equation. This has three acceptable solutions in the range $[0, 1]$. The solution $\rho_1^* = 0$ corresponds to the usual absorbing epidemic-free state, in which all the individuals recover and the spreading dies. The two other solutions are:

$$\rho_{2\pm}^* = \frac{\lambda_{S_2} - \lambda_{S_1} \pm \sqrt{(\lambda_{S_2} - \lambda_{S_1})^2 - 4\lambda_{S_2}(1 - \lambda_{S_1})}}{2\lambda_{S_2}}$$

where $\lambda_{S_j} := \beta_{S_j}\langle k_{S_j}\rangle/\mu$, $j = 1, 2$ [IPBL19].

Expanding the MF equations for $D = 4$

For $\langle k_{S_1}\rangle \approx 43$, $\langle k_{S_2}\rangle \approx 17$, $\langle k_{S_3}\rangle \approx 5$ and $\langle k_{S_4}\rangle \approx 1$. We use the re-scaled parameters $\lambda_{S_j} = \beta_{S_j}\langle k_{S_j}\rangle/\mu$ for $j = 1, \dots, 4$, with $\lambda_{S_1} = 0.999$, $\lambda_{S_2} = 1.065$, $\lambda_{S_3} = 0$ and $\lambda_{S_4} = 5$. We get roots approximately equal to $\rho_2^* \approx 0.02244$, $\rho_3^* \approx 0.06978$, $\rho_4^* \approx 0.17407$ and $\rho_5^* \approx 0.73371$, as well as the root $\rho_1^* = 0$. ρ_1^*, ρ_3^* as well as ρ_5^* are stable roots. We thus get a tri-stable region when we allow contagions on pentagons, squares, triangles and links.

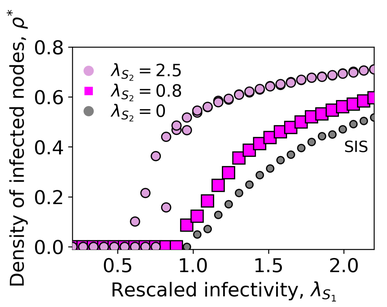
Synthetic hypergraphs

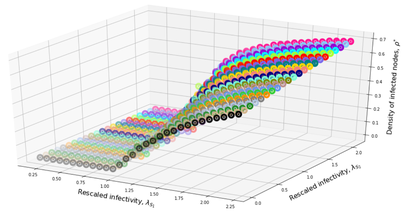
It is possible to construct random simplicial models of dimension D via the Random Simplicial Complexes (RSC) model. It has $D + 1$ parameters, the number of vertices N and D probabilities $\{p_1, \dots, p_D\}$, with $p_\omega \in [0, 1]$ to control the creation of ω-simplices up to dimension D [IPBL19]. It is a direct generalisation of the Erdös-Rényi model for random graphs. When we want to create D-simplicial complexes with targets for the average degree $\langle k_{S_1}\rangle$ and the average number of ω-simplices $\langle k_{S_\omega}\rangle$ any node participates in, we use:

$$p_i = \frac{\langle k_{S_i}\rangle - (i+1)\langle k_{S_2}\rangle}{\binom{N-1}{i} - (i+1)\langle k_{S_2}\rangle}, \text{ for } 1 \le i < D \quad (1)$$

$$p_D = \frac{\langle k_{S_D}\rangle}{\binom{N-1}{D}} \quad (2)$$

Example on 2-simplicial complexes





SCM on a RSC with $\langle k_{S_1}\rangle \approx 23$, $\langle k_{S_2}\rangle \approx 7$ and $\mu = 0.06$. We plot ρ^* against λ_{S_1} for different values of λ_{S_2}. We observe a discontinuous transition at a value approximately equal to $\lambda^c = 2\sqrt{\lambda_{S_2}} - \lambda_{S_2}$ when $\lambda_{S_2} = 2.5$.

References

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[IPBL19] Iacopo Iacopini, Giovanni Petri, Alain Barrat, and Vito Latora. Simplicial models of social contagion. Nature communications, 10(1):1–9, 2019.

[Luc13] Adam R Lucas. A fixed point theorem for a general epi- demic model. Journal of Mathematical Analysis and Applications, 404(1):135–149, 2013.