Disease Transmission and Epidemic Thresholds on Generalized Random Hypergraph Models

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Due to the grave danger that epidemics hold to our health and way of life, there has always been a dire need for models that predict the onset and severity of an epidemic. This is emphasized in a Southampton study which found that early action by just a week could've cut COVID-19 cases by 66%. Previous research has focused on random graph settings for modeling disease spread, but this method provides an oversimplified outlook on epidemic progression as they only allow for pairwise interactions. This study addresses this limitation by proposing random hypergraphs as an improved approach for modeling disease transmission. Hypergraphs are generalized graphs, in which hyperedges are groups of vertices, rather than pairs. Due to their ability to model group interactions, they are invaluable for accurately representing real-world processes, such as epidemics. This project presents three random hypergraph models: d-uniform, non-uniform, and extra-realistic. After examining the SIR epidemic models (nodes transition between Susceptible, Infected, Removed) on hypergraphs generated using these models, epidemic thresholds for the hypergraph structures were determined. Equations that solve for the probability of infection were derived using eigenvalues of the hypergraphs' adjacency matrices. This was then used to provide an upper bound on the magnitude of the probability vector, giving us frameworks for predicting outbreak severity. Additionally, random and targeted vaccinations were modeled to analyze effectiveness of containment strategies. By utilizing the complexity of hypergraphs, this study gives deeper and more precise insights into disease propagation and how epidemics occur in the real world.

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