Spreading Processes With Layer-Dependent Population Heterogeneity Over Multilayer Networks

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Abstract—**The study of spreading processes on complex networks has gained significant attention recently. For example, bond percolation models considering population heterogeneity have been used to provide insights into disease spread and misinformation control. However, most of these studies focus on single-layer contact networks. In our work, we examine how the spreading process is impacted by the existence of multiple contact network layers, considering layer-dependent population heterogeneity from a principled, mathematical perspective. Using SIR dynamics, we derive expressions for three key epidemiological measures: the probability of emergence, the epidemic threshold, and the expected epidemic size. Through extensive simulations, we demonstrate that our analytical results match the numerical results near-perfectly in the finite node regime. These findings reveal the interplay among the multi-layer network structures, transmission dynamics, and population heterogeneity in determining the final outcome of the spreading process. Furthermore, we investigate the impact of layer-dependent population heterogeneity and identify important factors for developing effective and economical layer-oriented spreading control strategies. Overall, our work provides insights into developing and analyzing mitigation and control strategies for disease spread and information diffusion across multi-layer complex networks.**

Index Terms—**Heterogeneous bond percolation, branching process, population heterogeneity, multi-layer networks.**

I. Introduction

The attention towards studies on spreading processes over complex networks has grown in recent years, driven by the impact of pandemics like COVID-19 and SARS, as well as concerns regarding misinformation diffusion [1]. Researchers have extensively examined mathematical models over complex networks to provide insights into the dynamics of spreading pathogens or information [2], [3], [4], [5]. The susceptible-infectious-recovered (SIR) compartmental model, in particular, has received significant interest due to its ability to capture the propagation of both pathogens and information [6], [7], [8]. Additionally, its steady-state analysis is closely linked to *bond-percolation* over networks [8], [9].

More recently, there has been interest on studying the SIR spreading process with increasing complexity of the underlying contact network (e.g., clustered networks [10], [11], [12] and multi-layer networks [7], [13], [14]) and the *heterogeneity* [8], [15] of the population. For example, Tian et al. [15] investigated a SIR model with population heterogeneity that manifest from different types of masks that the individuals in the population might be wearing. More broadly, population heterogeneity can also arise from factors such as age, gender, socio-economic status, and access to healthcare and other resources [16], [17], [18] in the population. In the context of information diffusion, population heterogeneity becomes relevant as individuals may exhibit different tendencies in accepting and transmitting information based on their personalities and fact-checking behaviors [1], [19]. Allard et al. [6] also studied the SIR model with population heterogeneity and showed that their steady-state can be analyzed through a *semi-directed* bond percolation model.

This paper is motivated by the fact that most studies on spreading processes with population heterogeneity consider single-layer networks. However, most real-world spreading processes take place over *multi-layer* networks. In viral spreading, different layers might represent viral spreading paths in different environments, e.g., community, school, workplace, etc, each with a different rate of viral transmissibility [20]. Similarly, (mis)information tends to spread over multiple social media platforms, each with different rates and dynamics of propagation. To the best of our knowledge, there have only been a few prior efforts [6], [21] on studying the SIR model while incorporating *both* population heterogeneity *and* the multi-layer nature of the contact network. Bongiorno and Zino [21] proposed a model that incorporates both population heterogeneity and a multi-layer contact network, but they do not provide mathematical analysis for the three epidemic quantities and instead rely on simulation results. The work by Allard et al. [6] considers multi-type networks with arbitrary joint degree distribution. However, their work does not provide a detailed analysis of the impact of multi-layer network structures and the associated multi-layer transmission dynamics on the final spreading results. Our preliminary work [22] studied the *multi-layer mask model*, which takes into account both population heterogeneity

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