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Disease Spread on Networks using Percolation Methods and Edge-Based Modeling

Bond percolation methods can be used to model disease transmission on complex networks and accommodate social heterogeneity while keeping tractability. Here we review the seminal works on this field by Newman (2002, 2003, 2010), and Miller, Slim & Volz (2011) and present a more clear and systematic discussion about the theoretically background, assumptions, derivation and development of the percolation method. We also present a new R package based on these papers that take epidemic and network parameters as input and generates estimates of the epidemic trajectory and final size. This allows us to investigate the interaction between different community structures and disease control strategies, leading to interesting new research directions.