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The effect of clumped population structure on the variability of spreading dynamics

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Abstract

Processes that spread through local contact, including outbreaks of infectious diseases, are inherently noisy, and are frequently observed to be far noisier than predicted by standard stochastic models that assume homogeneous mixing. One way to reproduce the observed levels of noise is to introduce significant individual-level heterogeneity with respect to infection processes, such that some individuals are expected to generate more secondary cases than others. Here we consider a population where individuals can be naturally aggregated into clumps (subpopulations) with stronger interaction within clumps than between them. This clumped structure induces significant increases in the noisiness of a spreading process, such as the transmission of infection, despite complete homogeneity at the individual level. Given the ubiquity of such clumped aggregations (such as homes, schools and workplaces for humans or farms for livestock) we suggest this as a plausible explanation for noisiness of many epidemic time series.

Keywords: epidemics, continuous-time Markov chain, offspring distribution,

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