

Fluctuations and Disease Dynamics: the roles of contact structure and of the recovery profile

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Abstract

Resonant fluctuations enhanced by spatial correlations are the dominant features of the long term dynamics of epidemic models on dynamic small world networks that represent the host population contact network structure. This mechanism is sensitive to all of the basic epidemiological parameters, and even the simplest stochastic models that include this ingredient are capable of reproducing the diversity of the temporal patterns of real diseases [1, 2].

Systematic simulations of dSIR dynamics for different values of the small world parameter p show that, for a wide range of values of p , the steady state densities follow the mean field relations for an effective (reduced) disease transmissibility. For the dSIR model with stochastic recovery, we show that, in this regime, the general mechanism of resonant amplification of demographic stochasticity proposed in [3] for the homogeneously mixed model can be used to model the fluctuation power spectrum.

We also study the role of the recovery profile by comparing the results obtained for stochastic and for deterministic recovery, at fixed average recovery time. The amplitude of the fluctuations is significantly larger in the case of deterministic recovery, for which recurrent epidemics with realistic levels of incidence can be obtained. We show that the homogeneously mixed dSIR model with deterministic recovery can be solved exactly in the limit of large populations, and use this result to model the fluctuation power spectrum in this case.

References

- [1] Verdasca et al, *Journal of Theoretical Biology* 233, 553-561 (2005)
- [2] Telo da Gama, Nunes A, *European Physical Journal B* 50, 205-208 (2006)
- [3] McKane AJ, Newman TJ, *Physical Review Letters* 94, 218102 (2005)