

# Stochastic Network Models: Analytical Tools for STI Studies

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**Background:** We present a general modelling scheme particularly adapted for the epidemiology of sexually transmitted infections. Emphasis is placed on the complex interaction structure of the population and on the probabilistic nature of the dynamics.

**Methods:** We represent the interaction structure of the population with complex network models. Markov Stochastic Processes are used to consider the probabilistic time evolution of both the network structure and the epidemiological state of the population. Idealized epidemiological problems are considered: they are qualitatively inspired by real-world systems but no actual real-world data is fed to the models. All analytical results are systematically validated through Monte Carlo numerical simulations.

**Results:** By dedicating compartments to individuals with both similar epidemiological states and similar contact patterns, we observe great agreement between analytical results and Monte Carlo simulations. This is a special case of the general observation that compartmental models perform better when individuals within each compartment are very similar among themselves. Explicit examples are given for contact patterns changing through time as well as for the interactions of different infections in the same population.

**Conclusions:** By specifying the structure of the population through its local features, we successfully model the probabilistic evolution of complex epidemiological systems. Infection stages and/or behavioural groups are considered the same way they are in "classical" compartmental models. The generality of the approach facilitates its application to a vast array of epidemiological phenomena.

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