

# Efficient simulation of infection processes

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Studying virus marketing Domingos and Richardson [1] introduced the so-called Independent Cascade model. Kleinberg, Kempe and Tardos have proven in [2] that this model is an equivalent form of Granovetter's Linear Threshold model [3]. In that model a small set, the initial adopters (infected vertices) infect neighboring vertices with prescribed probabilities in stages. This model has been extended and applied to many other real-world examples with considerable success [4].

The computation of a single infection process may not be difficult, but very often we are faced with the task of predicting the possibility of nodes (or the network as a whole) getting infected. This task can be solved by running the infection process multiple times resulting in an *a posteriori* probability distribution over the network. Due to the nature of infection dynamics the complexity of this simulation is demanding.

Another way of solving this task is to design an algorithm that is able to compute the *a posteriori* distribution directly, omitting the simulation. Unfortunately, this task is also very difficult. In this talk we will describe alternative ways of simulating infection processes with improved performance. We will also describe an algorithm, that is able to compute the desired distribution directly. Finally we will compare the results of these methods considering both accuracy and time complexity.

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