Exact analytical solution of binary dynamics on networks

Edward Laurence[1], Jean-Gabriel Young[1], Sergey Melnik[2] & Louis J. Dubé[1]

[1] *Département de Physique, de Génie Physique, et d'Optique, Université Laval, Québec, Qc, Canada*

[2] *MACSI, Department of Mathematics & Statistics, University of Limerick, Ireland*

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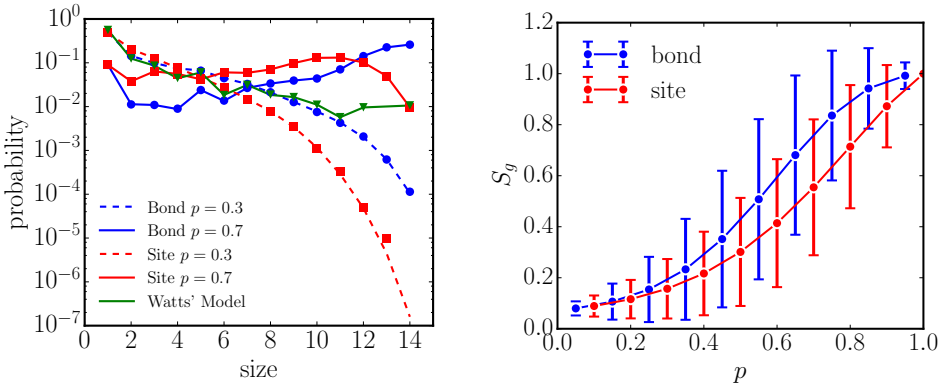
We present an exact analytical approach for solving a class of binary cascade dynamics on arbitrary graphs, where each node can be in one of the two possible states called active and inactive. This approach allows us to calculate the exact probability of any possible configuration of active/inactive nodes. Our method relies on a set of recursive equations [1] and can be applied, for example, to bond and site percolation problems, to the Watts threshold model, and used for calculating k-core sizes [2]. Our approach gives exact results even for configurations that occur so rarely that their numerical evaluation using Monte-Carlo simulations is virtually impossible.

Additionally, we develop two practical ways of using our method. The first one yields the exact probability of a single configuration of active/inactive nodes in a minimal number of iterative steps, while the second one uses an algorithm that mimics the cascade dynamics process and returns the probability of every possible final configuration, also in an optimal number of steps.

By knowing the exact probability of each configuration of active/inactive nodes one can calculate, for example, the size distribution of connected components and the mean size of the giant component, including its variance (see Fig. 1). Besides opening the way to the theoretical prediction of cascade dynamics on arbitrary graphs, we argue that our results can greatly improve existing classes of motif-based methods for solving dynamics on networks.

[1] Allard A, Hébert-Dufresne L, Noël PA, Marceau V and Dubé LJ, Exact solution of bond percolation on small arbitrary graphs, *Europhys. Lett.* **98**, 16001, (2012)

[2] Gleeson JP, Cascades on correlated and modular random networks, *Phys. Rev. E* **77**, 046117, (2008)



(a) (b)

FIGURE 1 | (a) Size distribution for the IEEE 14 Bus network under different dynamical processes; bond percolation (blue), site percolation (red) and Watts's threshold model (green). Symbols are the results of 5×10^6 Monte-Carlo simulations, and curves show the exact probability given by our approach. Note that we omitted Monte-Carlo results for $s = 14$ under site percolation with probability $p = 0.3$, because convergence is extremely slow in that case. (b) Exact mean size of the giant component S_g for bond and site percolations, and analytical prediction of the variance (error bars).