Threshold for Virus Spread on Networks

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Joint work with:

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What are the features of the topology that determine how virulent the epidemic is?

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Large outbreak and existence of the giant component

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- Ball et al. (1997) Structured networks with two levels of mixing: local (within a household) and global (between households)

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Eventually there are no more infectives in the population: How many nodes are removed?

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If we assume that the graph is connected, then the spectral radius $\lambda_1(A)$ has multiplicity one

Theorem Suppose $\beta \lambda_1(A) < 1$. Then

$$\mathbb{E}[|Y(\infty)|] \le \frac{1}{1 - \beta \lambda_1(A)} \sqrt{n|X(0)|}$$

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Moreover, if the graph G is regular (i.e., each node has the same number of neighbours), then $\mathbb{E}[|Y(\infty)|] \leq \frac{1}{1-\beta\lambda_1(A)}|X(0)|$

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To infect node v at t, there must be a chain of distinct nodes $u_0, u_1, \ldots, u_t = v$ along which the infection passes from some initial infective u_0 to v

$$\mathbb{P}(X_v(t) = 1) \le \sum_{u_0, \dots, u_{t-1}} \beta^t X_{u_0}(0),$$

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Consequently, for $\beta \lambda_1(A) < 1$,

$$\mathbb{E}[|Y(\infty)|] = \sum_{v \in V} \mathbb{P}(Y_v(\infty) = 1) \leq \sum_{v \in V} \sum_{t=0}^{\infty} \sum_{u \in V} (\beta A)_{uv}^t X_u(0)$$

$$= \sum_{t=0}^{\infty} \mathbf{1}^T (\beta A)^t X(0)$$

$$= \mathbf{1}^T (I - \beta A)^{-1} X(0)$$

$$\leq \|\mathbf{1}\| \|(I - \beta A)^{-1}\| \|X(0)\|$$

$$\leq \frac{1}{1 - \beta \lambda_1(A)} \sqrt{n|X(0)|}$$

Regular graphs: Using the spectral decomposition and the fact that the positive vector $\frac{1}{\sqrt{n}}(1,\ldots,1)^T$ is an eigenvector of A corresponding to the eigenvalue $\lambda_1(A)=d$, we have

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Using the same ideas, one can prove that $\mathbb{E}[|Y(\infty)|] \leq \frac{1}{1-\beta\lambda_1(A)} \frac{x_{\max}^1}{x_{\min}^1} |X(0)|$, for general graphs.

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General infectious periods: If $(1-\mathbb{E}[e^{-\lambda I}])\lambda_1(A)<1$ then the Theorem holds.

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■ Thus the upper bound of the theorem is close to the best possible. Moreover this
illustrates the effect of initial conditions

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if $\beta < 1/\log_2 n$, then the final size of the epidemic is bounded by a constant multiple of the number of initial infectives.

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Let C_u denote the component containing u in the random subgraph of the complete graph obtained by retaining each edge with probability β : C_u is the set of infected nodes in the epidemic (F. Ball 1983, A. Barbour & D. Mollison 1990)

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- By classical result on Bernoulli random graphs, the final size of the epidemic satisfies

$$\mathbb{P}\big(|Y(\infty)|>(1+o(1))\gamma n\big)=\gamma,\quad \mathbb{P}\big(|Y(\infty)|=O(\log(n)\big)=1-\gamma$$
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Threshold c=1 for the final size of the epidemic starting with a constant number of initial infectives, the final size is a constant independent of n if c<1, and a fraction of n if c>1.

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Define $c_n=(n-1)\beta p_n.$ Consider an SIR epidemic on such a graph starting with one node initially infected

Consider the graph $G(n,p_n)$ where $np_n >> \log(n)$, which leads to a connected graph with high probability

Since the node degrees are $Binom(n-1,p_n)$, Perron-Frobenius and the Chernoff bound yield $\lambda_1(A)=(1+o(1))np_n$ w.h.p.

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The size of the epidemic is stochastically dominated by a (subcritical) branching process with offspring distribution $Binom(n-1,\beta p_n)$

Lemma If $\limsup_{n\to\infty} c_n = c < 1$, then for all n sufficiently large, $\mathbb{E}[|Y(\infty)|]$ is bounded by a constant that does not depend on n.

On the other hand, if $\liminf_{n\to\infty}c_n=c>1$, then $\mathbb{E}[|Y(\infty)|]\geq (1+o(1))\gamma^2n$ where $\gamma>0$ solves $\gamma+e^{-\gamma c}=1$ (Giant component).

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 - Internet AS graph: $\gamma=2.1$ (Faloutsos, Faloutsos, Faloutsos 1999) (biased by traceroute?)
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Models for power law graphs: preferential attachment, Yule branching processes

Let G(w) be a graph and $w=(w_0,w_1,\ldots,w_{n-1})$ the sequence of its average degrees. The edge between the pair of vertices (i,j) is present with probability

$$p_{ij} = \frac{w_i w_j}{\sum_{k=1}^n w_k}, \qquad w_i = c(i_0 + i)^{-\frac{1}{\gamma - 1}}$$

where

$$c = \frac{\gamma - 2}{\gamma - 1} dn^{\frac{1}{\gamma - 1}}, \qquad i_0 = n \left(\frac{d(\gamma - 2)}{m(\gamma - 1)}\right)^{\gamma - 1}$$

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By Chung, Lu and Vu 2004, under mild conditions the spectral radius of the graph is

$$\lambda_1(A) = \begin{cases} (1+o(1))\sqrt{m}, & \gamma > 2.5, \\ (1+o(1))Cm^{3-\gamma}, & 2 < \gamma < 2.5. \end{cases}$$

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By Theorem, if $\beta\lambda_1(A)<1$, then the size of the epidemic is bounded by \sqrt{n} times the size of the initial infective population

Theorem (Chung, Lu 2002) For a random graph G(w) with expected degree sequence having average expected degree d>1, there is a unique giant component C such that $\sum_{i\in C} w_i \geq (1-c_\delta) \sum_{i\in V} w_i$, where $c_\delta\in(0,1)$ is a constant that depends only on δ .

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Fix k (as a function of n) and consider the subgraph induced by the k nodes with the largest weight in the random graph $G(\beta w)$. The average expected degree of this subgraph is easily seen to be

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Suppose first that $\gamma>3$. Then d_k is a non-decreasing function of k, and its maximum value, attained at k=n, is βd . This only yields the weak result that there is a large epidemic if $\beta d>1$.

 d_k is a decreasing function of k. Fix $\delta>0$. Defining N_δ to be the largest value of k for which $d_k>1+\delta$, we see that

$$N_{\delta} = \left\lfloor \left(\frac{\beta d}{1+\delta} \right)^{\frac{\gamma-1}{3-\gamma}} n \right\rfloor + 1,$$

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- $ightharpoonup 2 < \gamma < 3$, studying the epidemic on the subgraph of high degree nodes (close to an Erdös-Rényi graph) and using above result one can show that there is a large epidemic with high probability.

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- Conjecture: the right threshold appears to be $\tilde{d} = \frac{\sum_i w_i^2}{\sum_i w_i}$.
- Duration of such the epidemic (in the supercritical case) until it reaches an absorbing state (diameter is a trivial lower bound)