Spreading dynamics on small-world networks with wide connectivity fluctuations

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Epidemic outbreak

QuickTime™ and a TIFF (Uncompressed) decompressor are needed to see this picture.
Population structure

Contact graph

$N$ agents

$p_k$ connectivity distribution

$D$ average distance
Spanning tree

- Generation
  - 0: root
  - 1
  - 2
  - 3
  - 4

- $kp_k/\langle k \rangle$
- $k-1$
- $k$
- $p_k$
Timming

Generation time $T$

Distribution $G(\tau) = \Pr(T \leq \tau)$
1. The process start with a node \((d=0)\) that generates \(k\) sons with probability distribution \(p_k\).

2. Each son at generation \(1<d<D\) generates \(k-1\) new sons with probability \(kp_k/\langle k \rangle\).

3. Nodes at generation \(D\) does not generate any son.

4. The generation times are independent random variables with distribution function \(G(\tau)\).

Note: Galton-Watson, Newman, Bellman-Harris, Crum-Mode-Jagers
Iterative approach

\[ N_d(t) = 1 + \tilde{R} \int_{0}^{t} dG(\tau)N_{d+1}(t - \tau) \]
Constants transmission rate $\lambda$, $G(\tau)=1-e^{-\lambda \tau}$

$I(t) = \frac{dN_0(t)}{dt} = \lambda \tilde{R} e^{-\lambda t} \sum_{d=1}^{D} \frac{(\lambda \tilde{R} t)^{d-1}}{(d-1)!} \approx \begin{cases} e^{(\tilde{R}-1)\lambda t} & t << t_0 \\ t^{D-1} e^{-\lambda t} & t >> t_0 \end{cases}$

$\tilde{R} = \frac{\langle k(k-1) \rangle}{\langle k \rangle}$ Excess degree/reproductive number

$t_0 = \frac{D-1}{\tilde{R}} \frac{1}{\lambda}$ Characteristic time scale

Numerical simulations

• Random graphs with a power law degree distribution: $p_k \sim k^{-\gamma}$

\[
\tilde{R} = \frac{\langle k(k-1) \rangle}{\langle k \rangle} \sim \begin{cases} 
N^0 & \gamma > 3 \\
N^{(3-\gamma)/(\gamma-1)} & \gamma < 3
\end{cases}
\]

\[
\lambda t_0 \sim \begin{cases} 
\ln N & \gamma > 3 \\
\frac{\ln N}{N^{(3-\gamma)/(\gamma-1)}} & \gamma < 3
\end{cases}
\]
Numerical simulations

\[ \frac{I(t)}{N} = \begin{cases} \lambda t, & \gamma = 3.5 \\ t^{D-1} e^{-\lambda t}, & \gamma = 2.5 \end{cases} \]

\[ e^{(R-1)\lambda t} \quad \text{for all } \gamma \]

\[ N = 1,000, \quad N = 10,000, \quad N = 100,000 \]
AIDS epidemics

![Graph showing cumulative number of cases over time for different locations with different growth models: exponential, linear, quadratic, and cubic. The graph includes data points for New York - HOM, New York - HET, San Francisco - HOM, South Africa, Georgia, Latvia, Lithuania, and Kenya. The reference is Szendroi & Czanyi, Proc. R Soc. Lond. B 2004.](image)
Generalizations

Connectivity correlations

\[ \tilde{R}_k = \sum_{k'} q(k' \mid k) k' \sim k^{\nu} \rightarrow \begin{cases} \nu < 0 & \text{disassortative} \\ \nu = 0 & \text{uncorrelated} \\ \nu > 0 & \text{assortative} \end{cases} \]

\[ q(k' \mid k) = \begin{cases} \frac{k' p_{k'}}{\langle k \rangle} & \text{uncorrelated} \\ \neq \frac{k' p_{k'}}{\langle k \rangle} & \text{correlated} \end{cases} \]

Vazquez, q-bio.PE/0603010
Generalizations

Intermediate states

\[ g(\tau) = \frac{\lambda (\lambda \tau)^{\beta-1} e^{-\lambda \tau}}{\Gamma(\beta)} \]

\[ I(t) \sim \begin{cases} 
  e^{(\tilde{R}-1)\lambda t} & t << t_0 \\
  t^{\beta D-1} e^{-\lambda t} & t >> t_0
\end{cases} \]

\[ \tilde{R} = \beta \left( \frac{\langle k(k-1) \rangle}{\langle k \rangle} \right)^{1/\beta} \]

\[ t_0(\beta) \approx \left[ \frac{\beta (\beta D - 1) \cdots (\beta D - \beta)}{\tilde{R}} \right]^{1/\beta} \frac{1}{\lambda} \]

Vazquez, AMS-DIMACS 2006
Generalizations

**Multi-type**

\(i = 1, \ldots, M\) types

\(N_i\) number of type \(i\) agents

\(p^{(i)}_k\) type \(i\) degree distribution

\(e_{ij}\) mixing matrix

\(D\) average distance

**Reproductive number matrix**

\[
\tilde{R}_{ij} = \frac{\langle k_i (k_i - 1) \rangle}{\langle k_i \rangle} e_{ij}
\]

Vazquez, q-bio.PE/0605001
Patient isolation (at rate $\mu$)

$$I(t) \approx \begin{cases} e^{(\tilde{R} - 1)(\lambda + \mu)t} & t << t_0 \\ t^{D-1} e^{-(\lambda + \mu)t} & t >> t_0 \end{cases}$$

$$t_0 = \frac{D - 1}{\tilde{R}} \frac{1}{\lambda + \mu}, \quad \tilde{R} = \frac{\lambda}{\lambda + \mu} \frac{\langle k(k-1) \rangle}{\langle k \rangle}$$

Final outbreak size

$$N_1 = R \frac{\tilde{R}^D - 1}{\tilde{R} - 1}$$
Conclusions

- Truncated branching processes are a suitable framework to model spreading processes on real networks.
- There are two spreading regimes.
  - Exponential growth.
  - Polynomial growth followed by an exponential decay.
- The time scale separating them is determined by $D/R$.
- The small-world property and the connectivity fluctuations favor the polynomial regime.
- Intermediate states favor the exponential regime.
- The final outbreak size is determined by $R$ and $D$. 
Outbreak size dynamics

\[ N_1(t) = 1 + \sum_{d=1}^{D} z_d \Pr(\sum_{l=1}^{d} \tau_l \leq t) \]

mean number of nodes at generation \( d \)

prob. of reaching a node at generation \( d \) before time \( t \)

Incidence

\[ I(t) = \frac{dN_1(t)}{dt} \]

Example: constant transmission rate \( \lambda \), \( G(\tau) = 1 - e^{-\lambda \tau} \)

\[ I(t) = \lambda \langle k \rangle e^{-\lambda t} \sum_{d=1}^{D} \frac{(\lambda K t)^{d-1}}{(d-1)!} \]

Current models vs reality

Current models

- few secondary cases
- several generations

Reality

- Super-spreading
- few generations

- Infected
- Infected/super-spreader
- Infected/recovered
Epidemic outbreak
**Annealed spanning tree (AST)**

1. The process starts with a node \((d=0)\) that generates \(k\) descendants with probability distribution \(p_k\).
2. Each descendant at generation \(1<d<D\) generates \(k-1\) new descendants with probability \(kp_k/k\).
3. Nodes at generation \(D\) do not generate any descendant.

Approximations

1. Tree structure
2. Annealed average
3. Sharp truncation

Note: Galton-Watson, Newman