Spreading dynamics on small-world networks with wide connectivity fluctuations

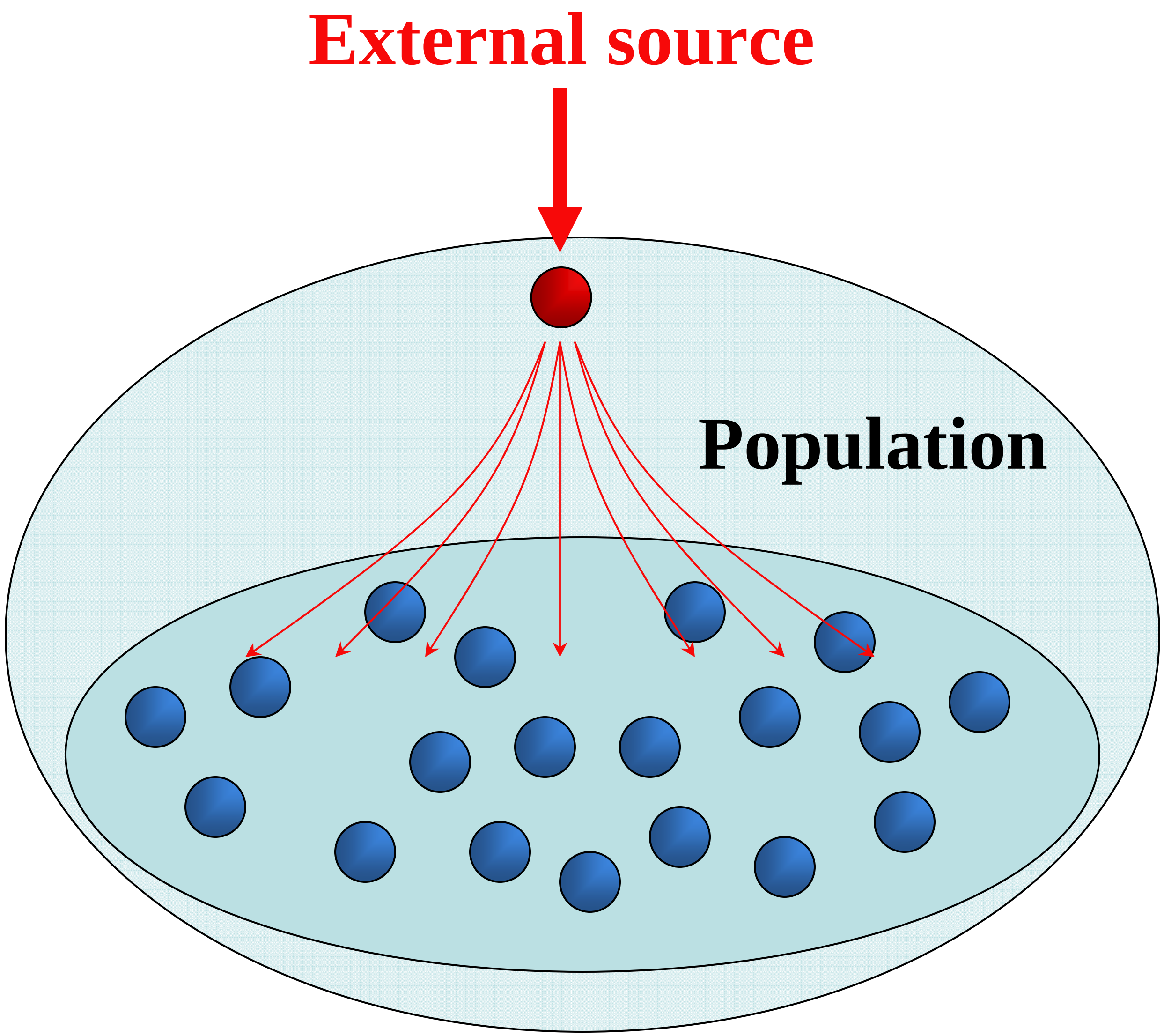
Alexei Vazquez

Center for Cancer Systems Biology,
Dana Farber Cancer Institute
Department of Physics and Center for Complex Networks Research
University of Notre Dame

Epidemic outbreak

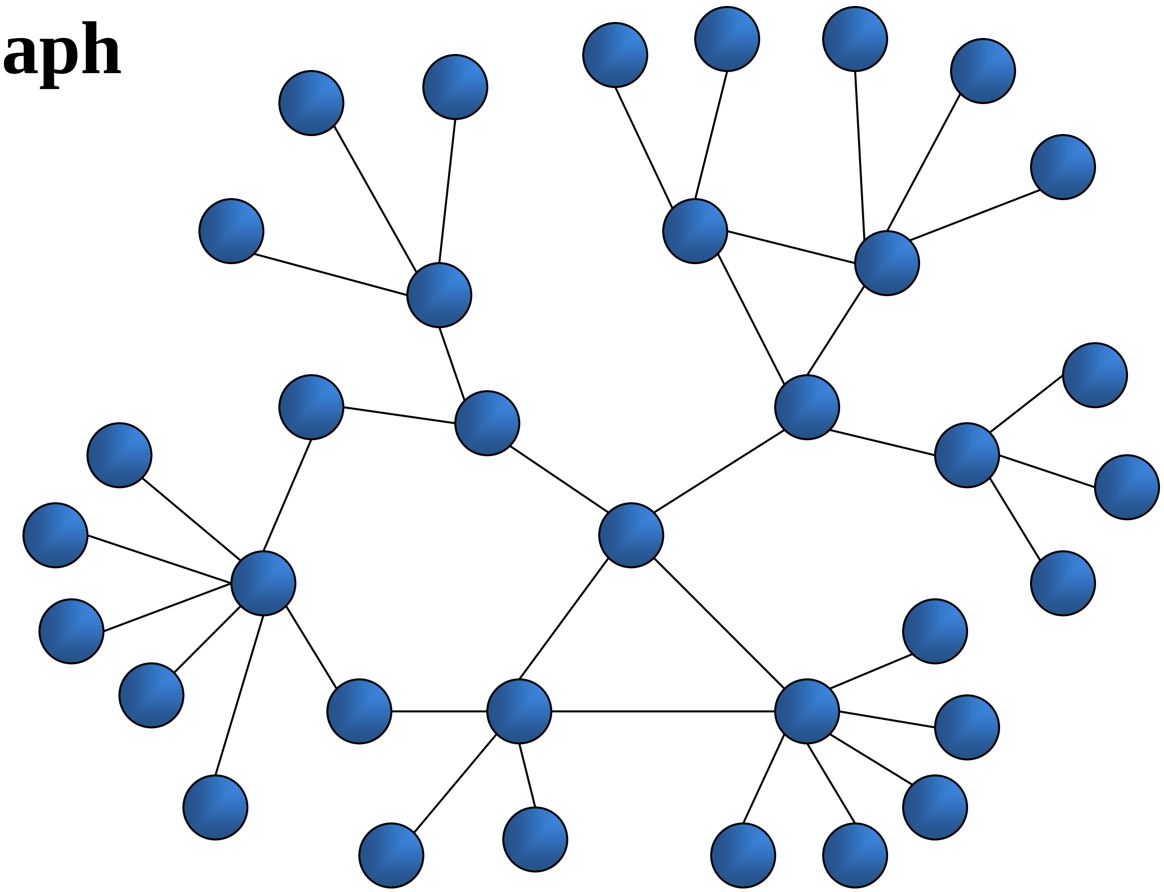
QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Model



Population structure

Contact graph



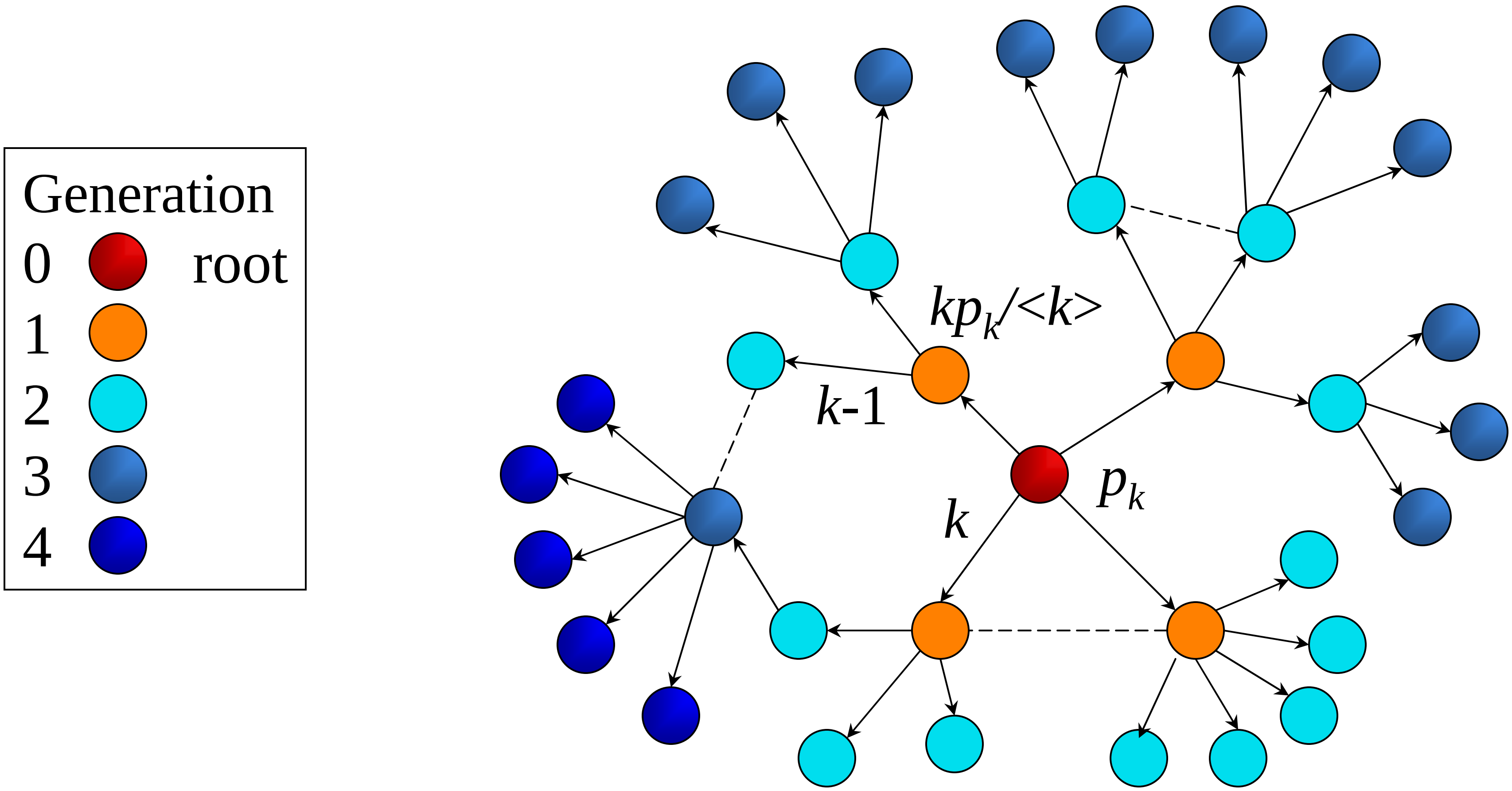
N agents

p_k connectivity distribution

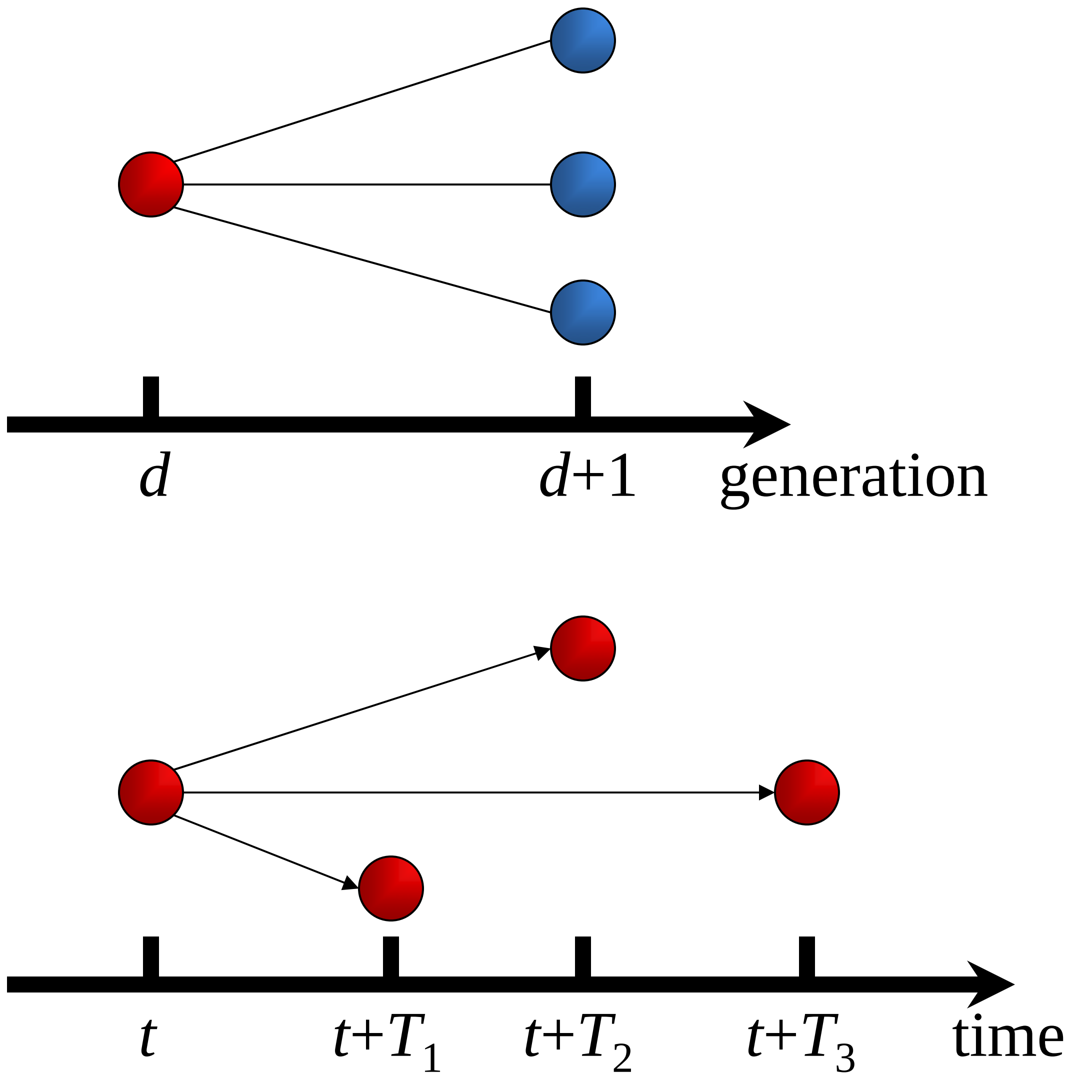
D average distance

Population structure

Spanning tree



Timming



Generation time
T

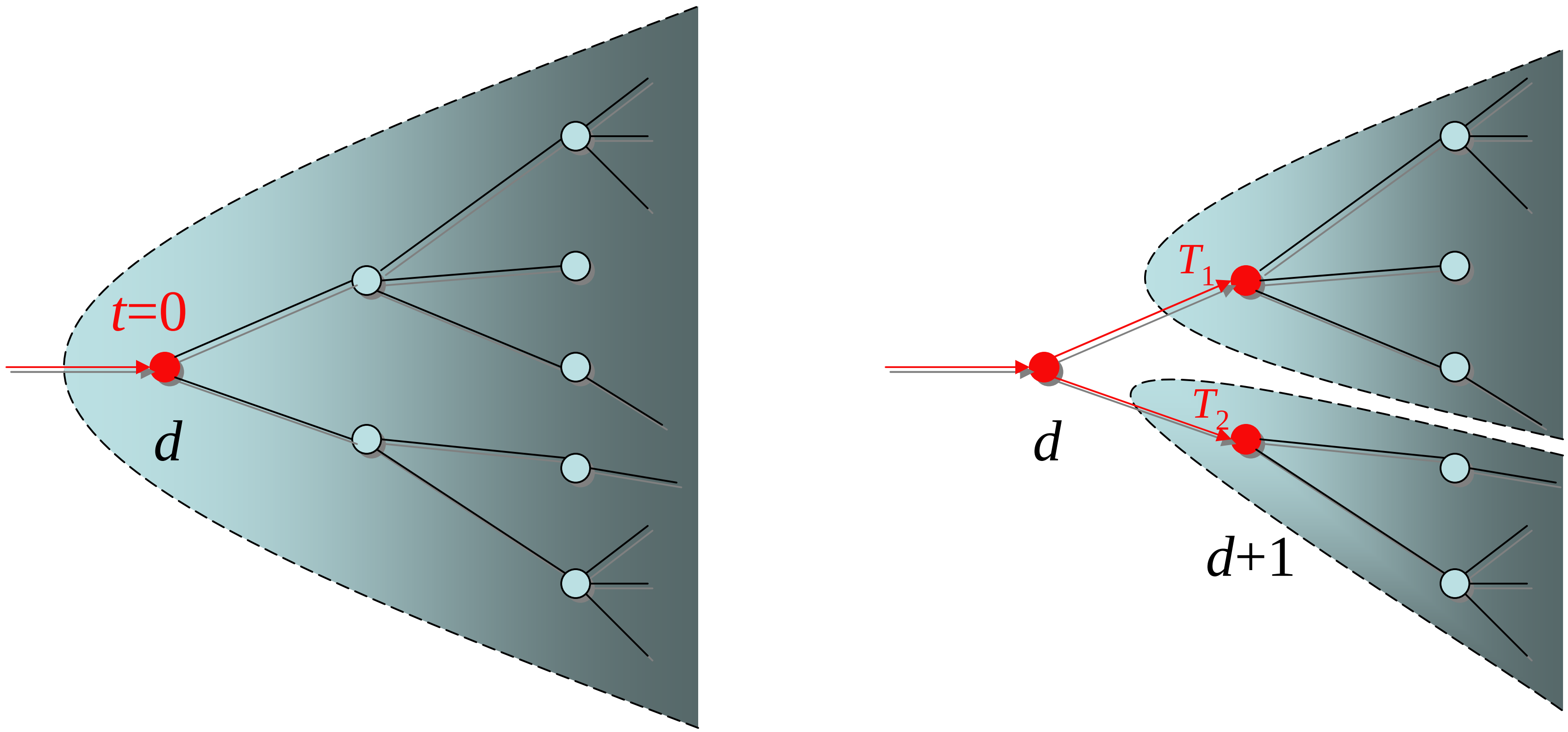
Distribution
$G(\tau)=\Pr(T\leq\tau)$

Branching process model

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 $kp_k/<k>$.
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



$$N_d(t) = 1 + \tilde{R}\int_0^t dG(\tau) N_{d+1}(t-\tau)$$

Results

Constant transmission rate λ, $G(\tau)=1-e^{-\lambda\tau}$

$$e^x = \sum_{d=1}^{\infty} \frac{x^{d-1}}{(d-1)!}$$

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

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

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

Vazquez, Phys. Rev. Lett. 2006

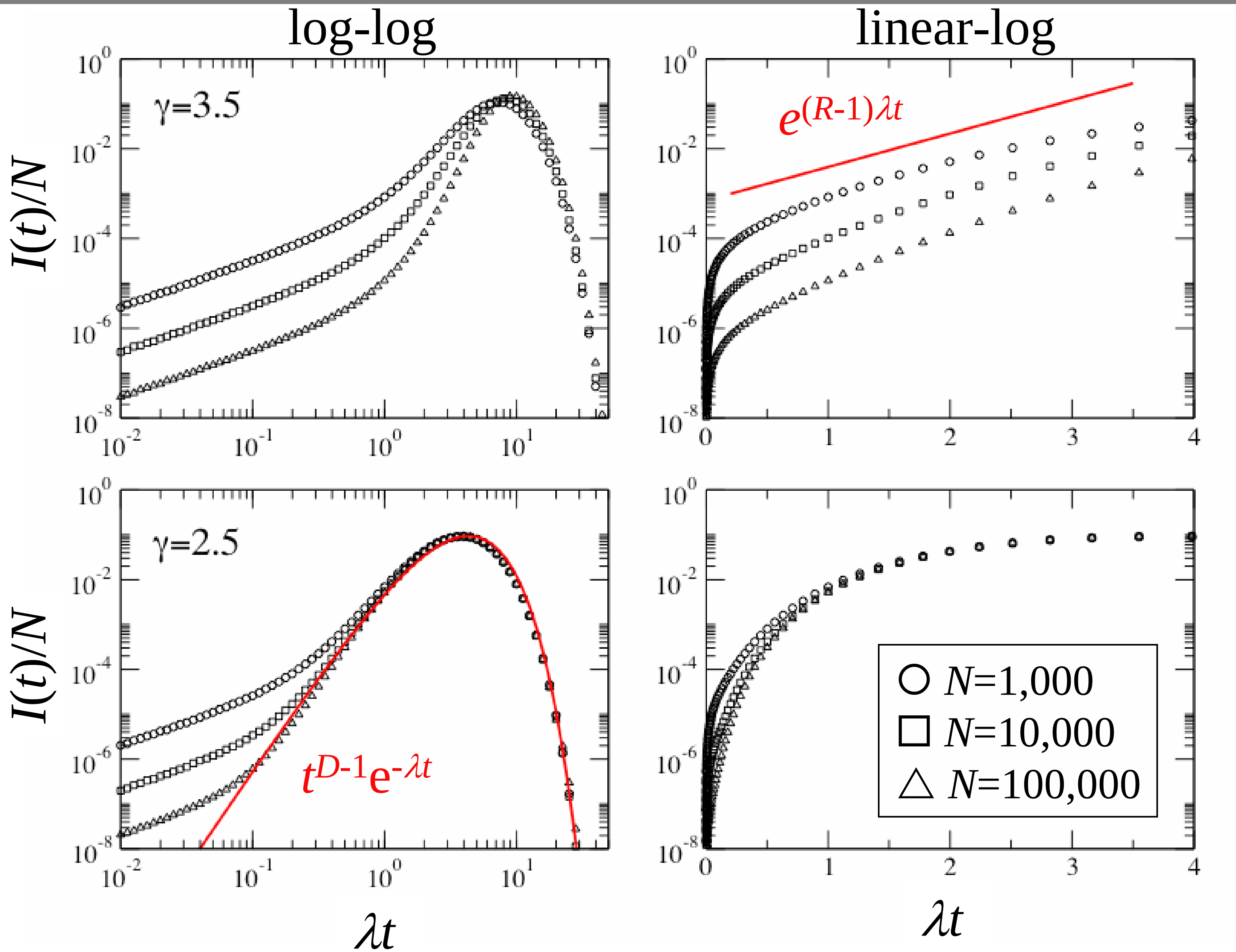
Numerical simulations

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

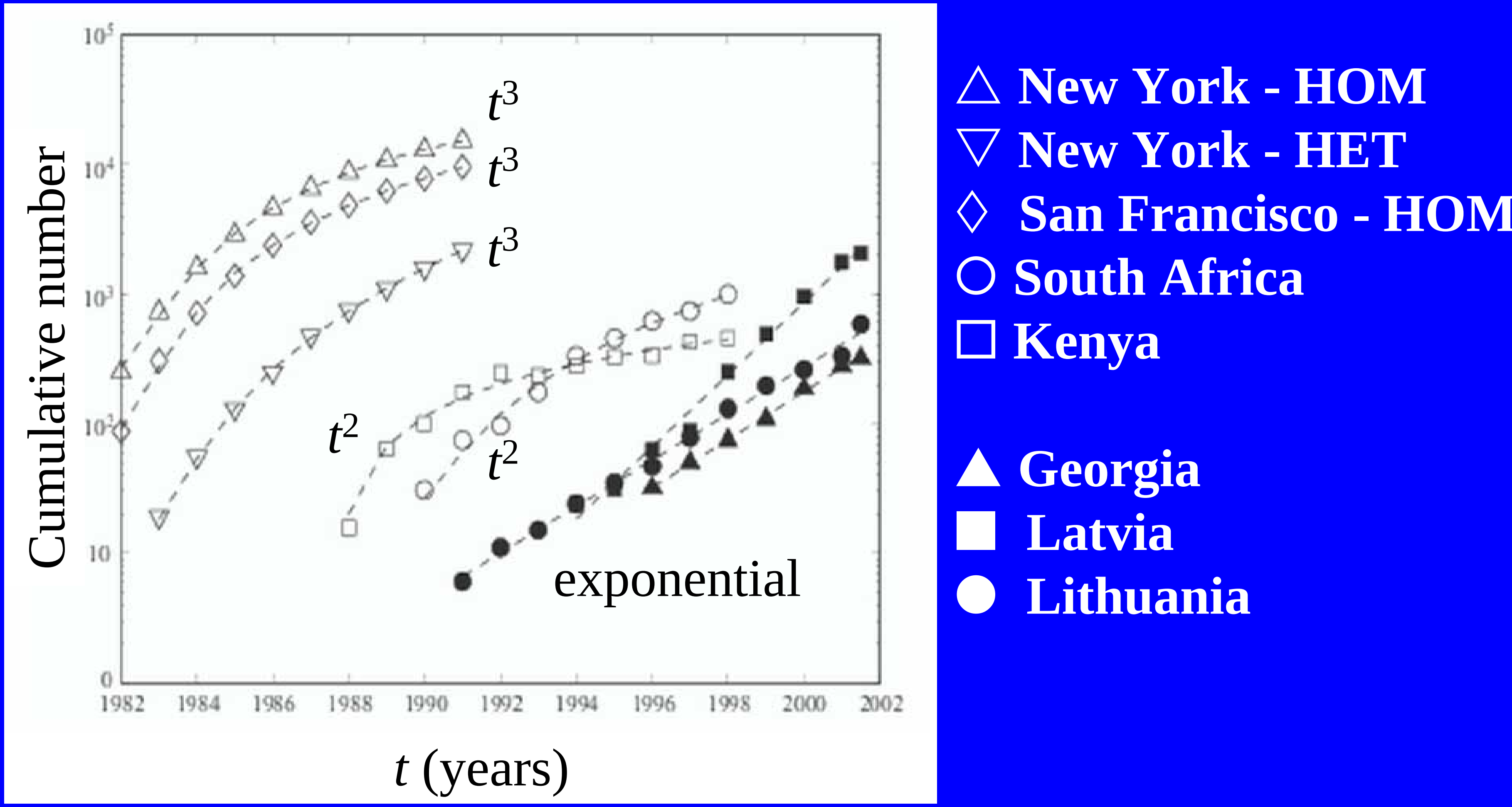
$$\tilde{R} = \frac{\langle k(k-1) \rangle}{\langle k \rangle} \sim \begin{cases} N^0 & \gamma > 3 \\ N^{(3-\gamma)/(\gamma-1)} & \gamma < 3 \end{cases}$$

$$\lambda t_0 \sim \begin{cases} \ln N & \gamma > 3 \\ \dfrac{\ln N}{N^{(3-\gamma)/(\gamma-1)}} & \gamma < 3 \end{cases}$$

Numerical simulations



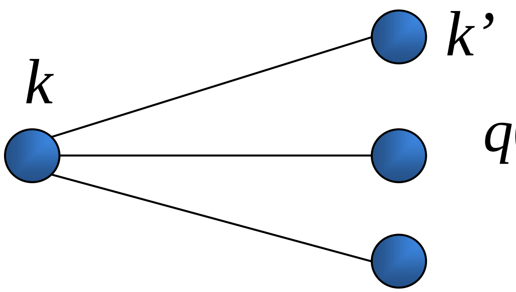
AIDS epidemics



Szendroi & Czanyi, Proc. R Soc. Lond. B 2004

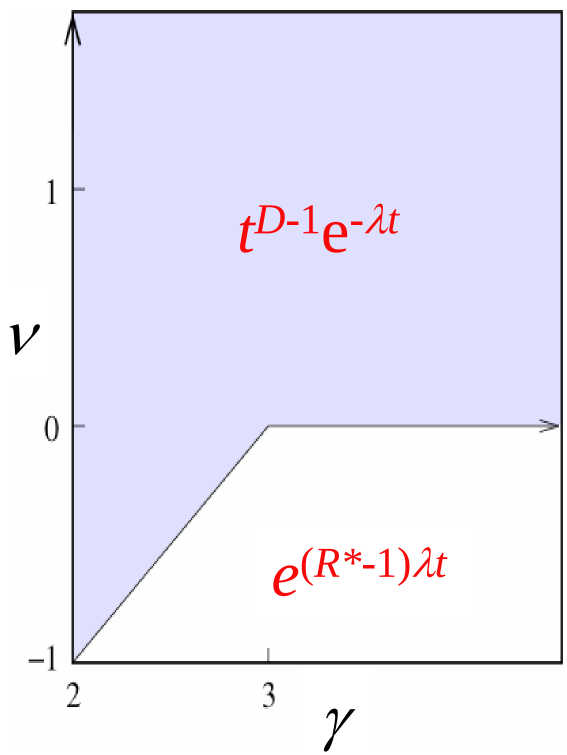
Generalizations

Connectivity correlations



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

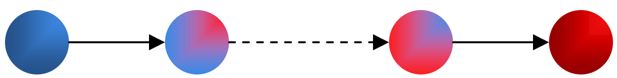
$$\tilde{R}_k = \sum_{k'} q(k' \mid k) k' \sim k^{\nu} \rightarrow \begin{cases} \nu < 0 & \text{disassortative} \\ \nu = 0 & \text{uncorrelated} \\ \nu > 0 & \text{assortative} \end{cases}$$



Vazquez, q-bio.PE/0603010

Generalizations

Intermediate states

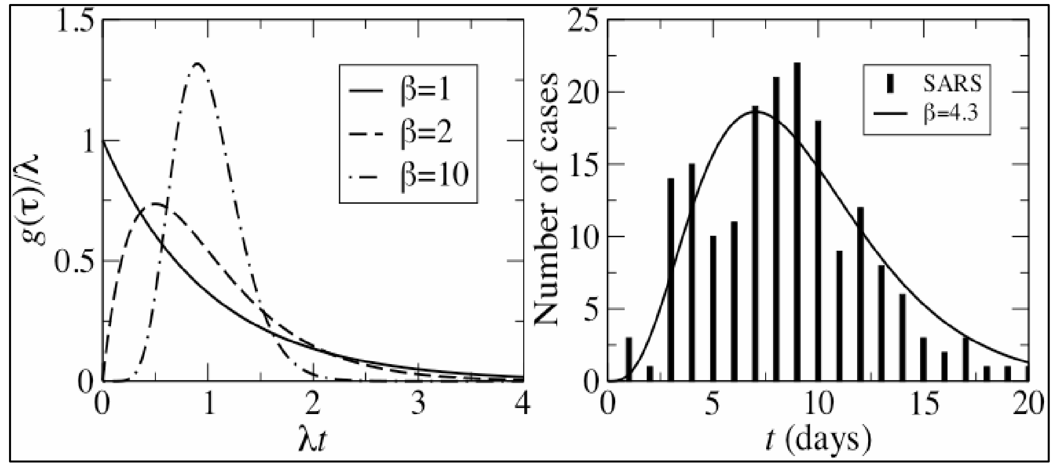


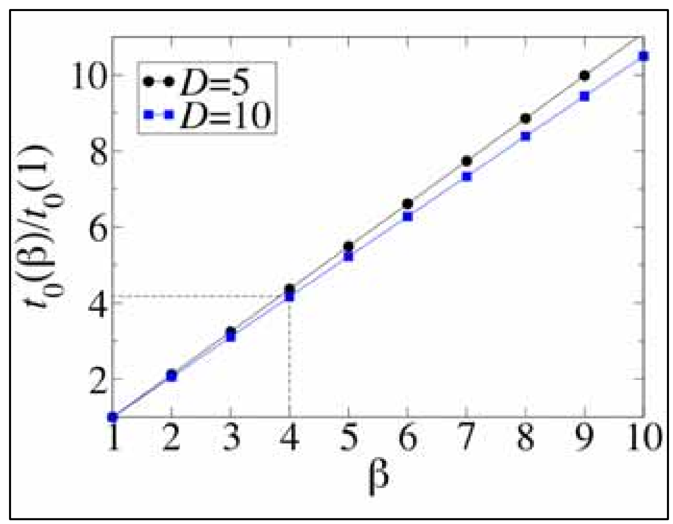
$$g(\tau) = \dot{G}(\tau) = \frac{\lambda(\lambda\tau)^{\beta-1}e^{-\lambda\tau}}{\Gamma(\beta)}$$

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

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

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





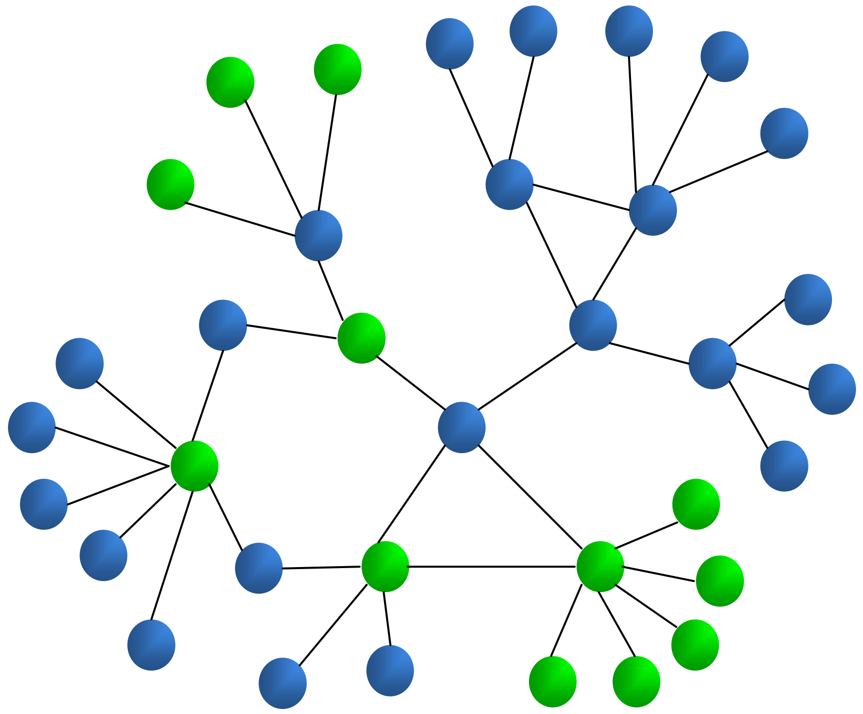
Vazquez, AMS-DIMACS 2006

Generalizations

Multi-type

i=1,…,M types

N_i	number of type *i* agents
$p^{(i)}_k$	type *i* degree distribution
e_{ij}	mixing matrix
D	average distance



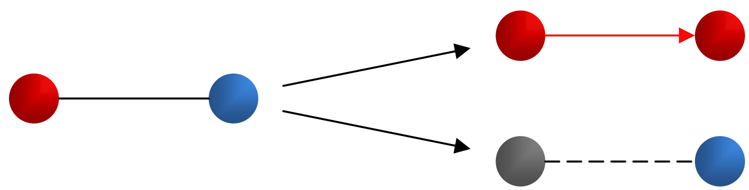
Reproductive number matrix

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

Vazquez, q-bio.PE/0605001

Generalizations

Patient isolation (at rate μ)

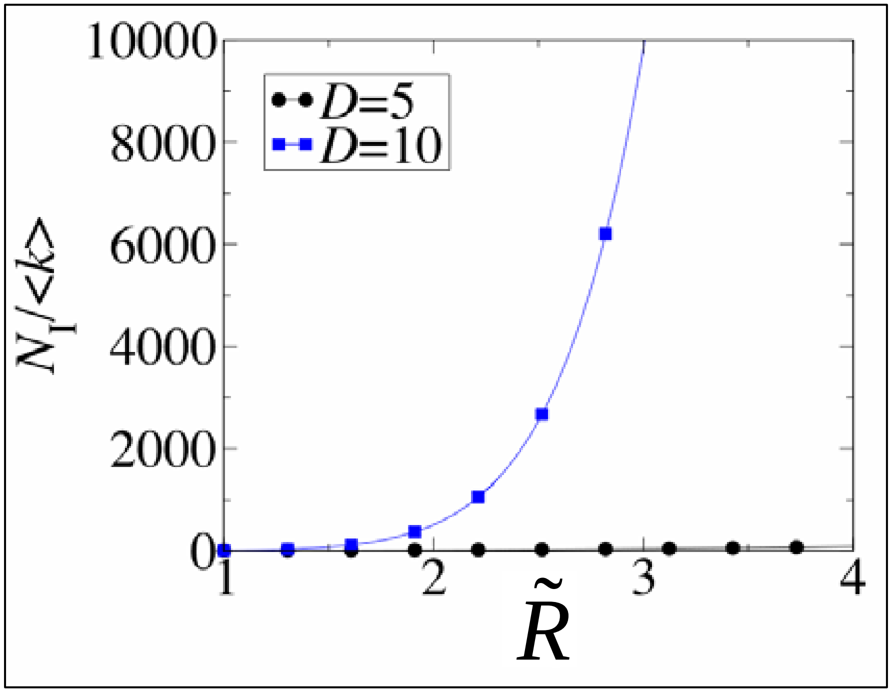


$$I(t) \approx \begin{cases} e^{(\tilde{R}-1)(\lambda+\mu)t} & t << t_0 \\ t^{D-1}e^{-(\lambda+\mu)t} & t >> t_0 \end{cases}$$

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

Final outbreak size

$$\boxed{N_{\mathrm{I}} = R\frac{\tilde{R}^D - 1}{\tilde{R}-1}}$$



Conclusions

- Truncated branching processes are a suitable framework to model spreading processess on real networks.
- There are two spreading regimes.
  - Exponential growth.
  - Polynomial growth followed by an exponential decay.
- The time scale saparating 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.

Results

Outbreak size dynamics

$$N_{\mathrm{I}}(t) = 1 + \sum_{d=1}^{D} z_d \ \Pr\left(\sum_{l=1}^{d} \tau_l \le t \right)$$

mean number of nodes at generation *d* (refers to z_d)

prob. of reaching a node at generation *d* before time *t* (refers to $\Pr\left(\sum_{l=1}^{d} \tau_l \le t \right)$)

Incidence

$$I(t) = \frac{dN_{\mathrm{I}}(t)}{dt}$$

$$z_d = \langle k \rangle K^{d-1} \qquad K = \frac{\langle k(k-1) \rangle}{\langle k \rangle}$$

$$\Pr\left(\sum_{l=1}^{d} \tau_l \le t \right) = G^{*d}(t)$$

average excess degree (refers to K)

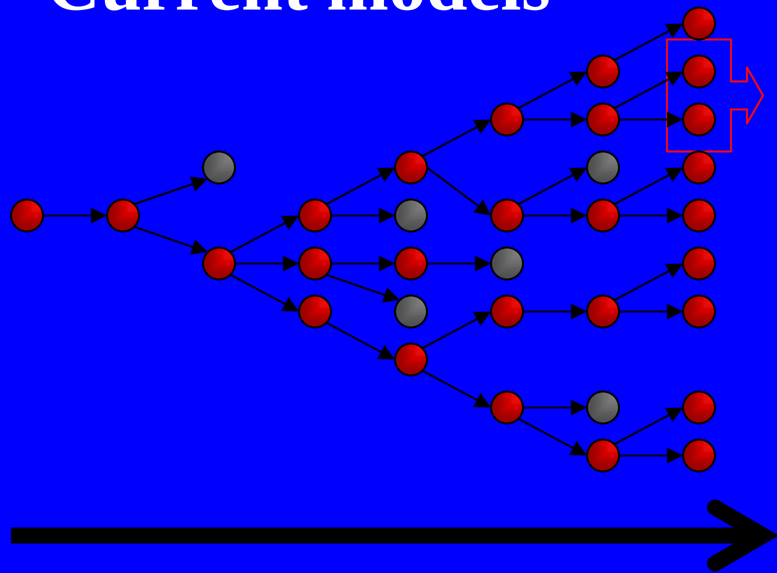
Example: constact transmission rate λ, $G(\tau)=1-e^{-\lambda\tau}$

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

Vazquez, Phys. Rev. Lett. 2006

Current models vs reality

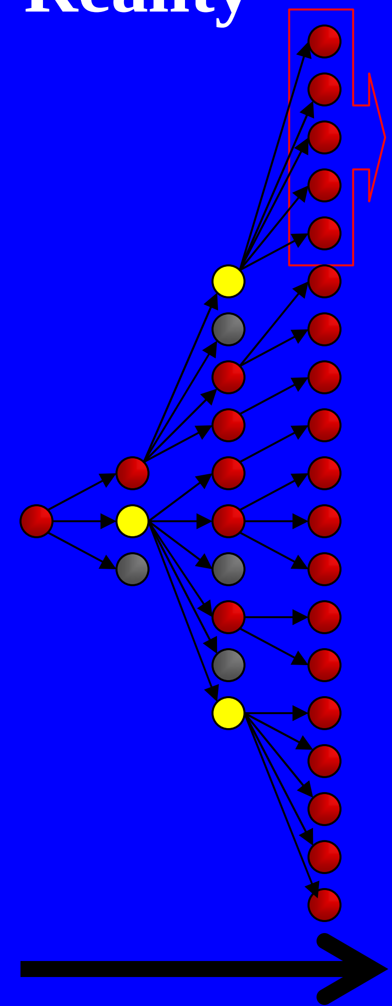
Current models



few secondary cases

several generations

Reality

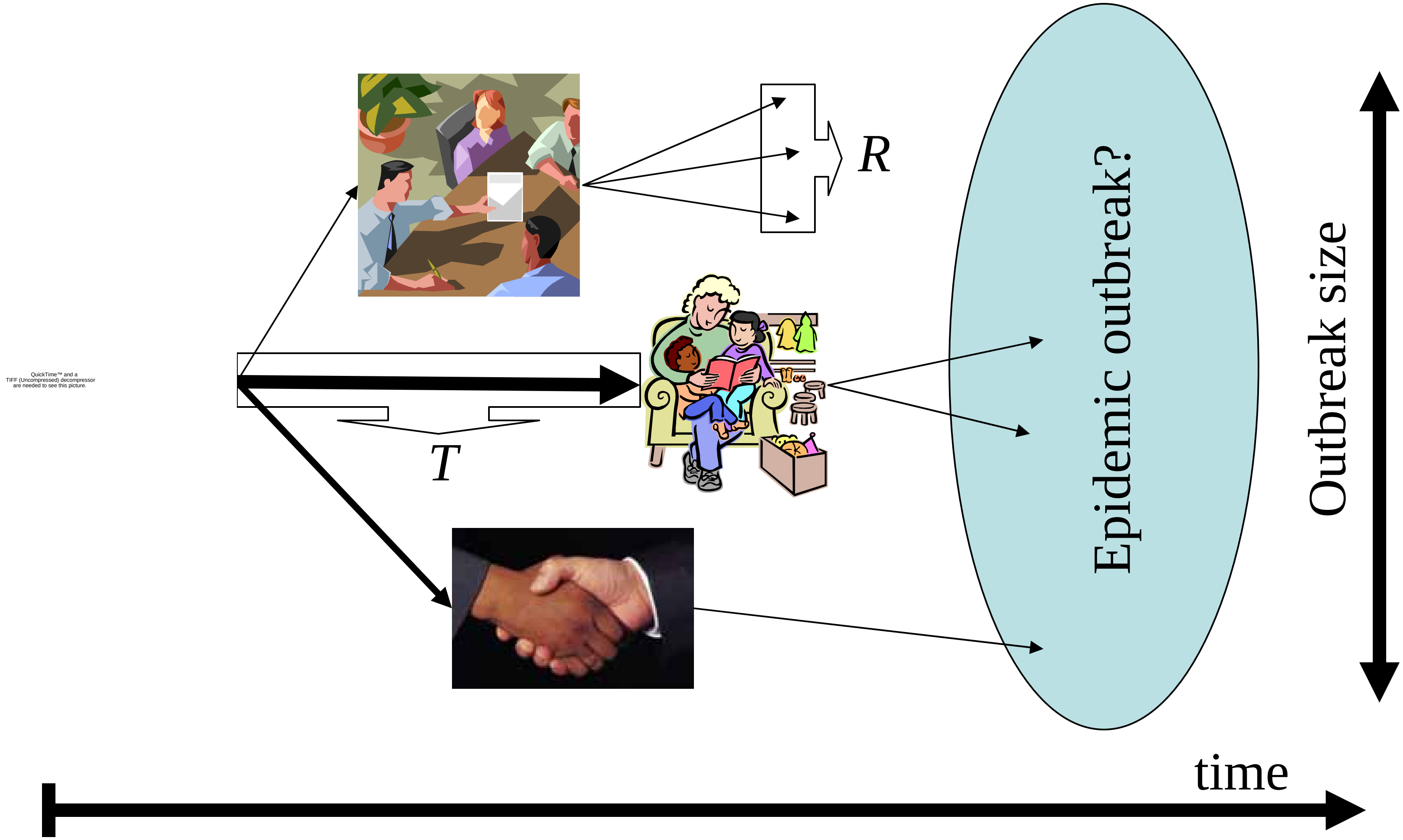


Super-spreading

few generations

- Infected
- Infected/super-spreader
- Infected/recovered

Epidemic outbreak



Annealed spanning tree (AST)

1. The process start with a node (d=0) that generates k decendants with probability distribution p_k.
2. Each decendant at generation $1<d<D$ generates k-1 new decendants with probability $kp_k/<k>$.
3. Nodes at generation D does not generate any decendant.

Approximations

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

Note: Galton-Watson, Newman