Time Evolution of Epidemics on Complex Networks

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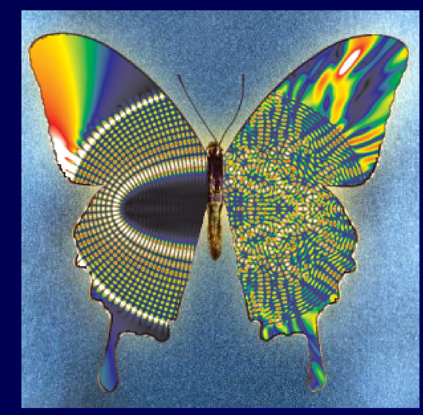


Motivation

Efficient tools are required by decision makers in matter of disease propagation to:

- ***predict*** and ***quantify*** risks;
- ***optimize*** prevention methods; and
- ***evaluate*** intervention scenario efficacy.

Only for diseases?

Not at all!
Almost anything that spread from neighbour to neighbour can be simulated with such formalisms.
For example: computer viruses, rumors, email chains...

Numerical simulations? Part of the solution. . .

Pros

- *Generality* } *Describe the dynamics,*
- *Availability* } *program what you have described!*

Cons

- *Computation time (some simulations "impossible").*
- *Lack of insight (compared to analytical solutions).*

*Our goal is to provide **analytical tools** that are as general and as close to the real-world system as possible.*

Fundamentals

*At a given time, each individual is in a specific **state**.*

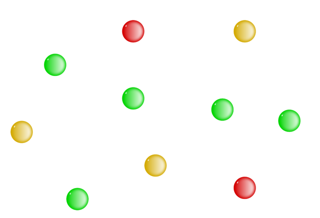
***S**usceptible individuals do not have the disease but can get infected by contact with infectious.*

***I**fectious individuals have the disease and can transmit it to susceptibles through contacts.*

***R**emoved individuals neither have nor can get the disease. This include death, quarantine and recovery by immunization.*

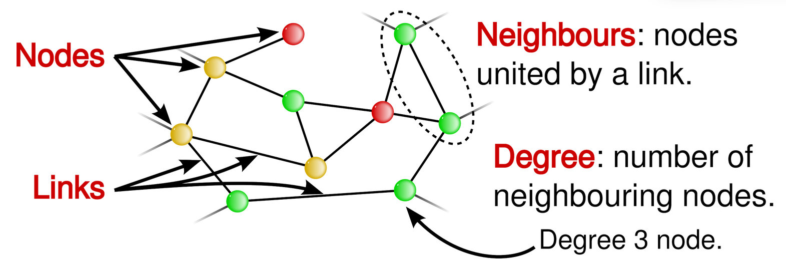
In traditional compartmental models, anyone can have contact with anyone (the fully-mixed approximation) and the dynamics is governed by "mass-action" ODE ($S + I + R = N$ = constant).

$$\dot{S} = -\beta S I$$
$$\dot{I} = \beta S I - \mu I$$
$$\dot{R} = \mu I$$



ODE?
Ordinary Differential Equation.
STI?
Sexually Transmitted Infections.
PGF?
Probability Generating Function.

*In network models, contacts are restricted by the **network structure**.*

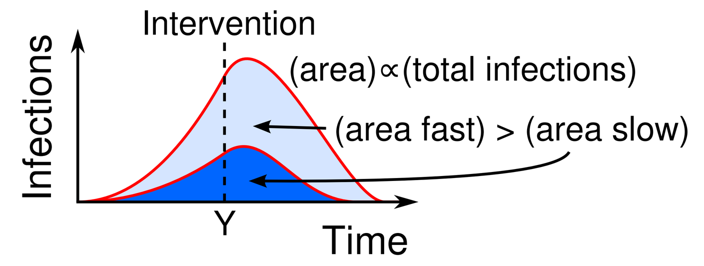


*Many real-world networks are highly **heterogeneous in degree** (e.g. STIs). The formalisms presented here hold for random networks with arbitrary degree distribution.*

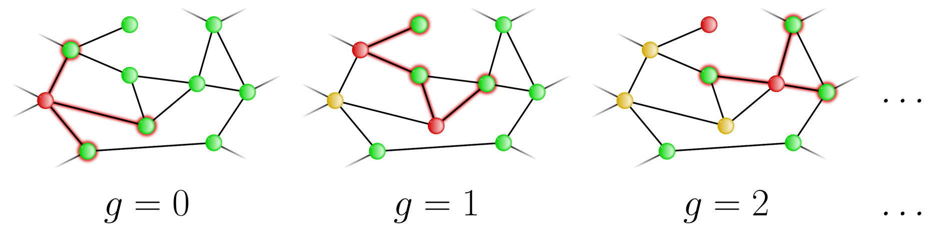
Generations and finite-size

[Noël *et al.* 2009]

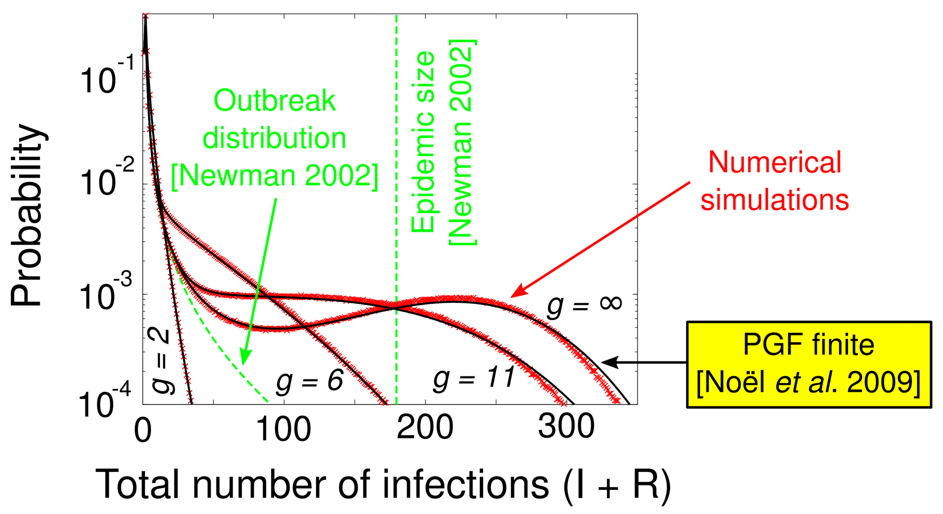
*Time is **crucial** for intervention scenarios. For example, what if a X% efficient vaccine is discovered after Y months?*



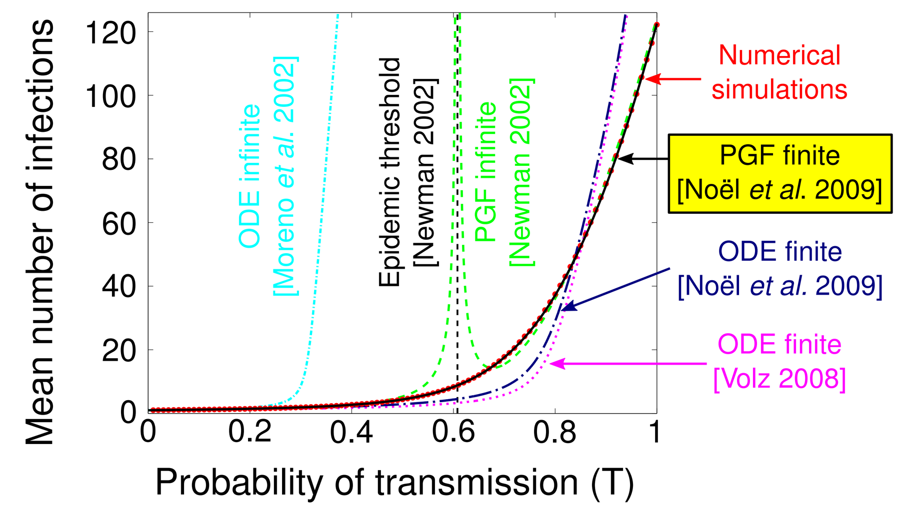
*Discrete time approach: **generations**.*



*We first use an infinite-size network approximation based on a **PGF** formalism [Newman 2002] adapted to include generations [Marder 2007] then add **corrections** for the **finite size** of the network.*



The results for the final state ($g = \infty$) of this finite-size algorithm also compares favourably with those of other formalisms.



Contribution A

*Formalism for **discrete time evolution** on **finite-size** networks with **heterogeneous degree distribution**.*

Information about the simulations

Network of $N = 1000$ nodes. Each node has probability $p_k \propto k^{-2} e^{-k/5}$ to be of degree k. In the first figure, the transmission probability is $T = 0.8$.

Types of nodes

[Allard *et al.* 2009]

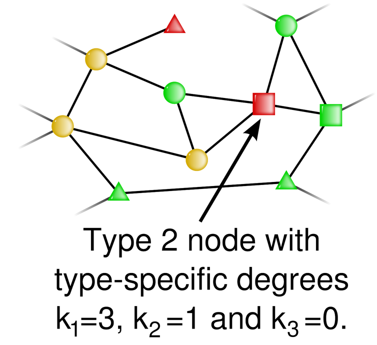
***Individuals differ** from one another (e.g. age, gender, sociocultural group, . . .). This affects the dynamics in two important ways by:*

- *introducing **correlations** on how the nodes are linked to one another (**network structure**) and*
- *modifying the **probability of transmission** between connected nodes.*

*We use a **PGF** formalism [Newman 2002] generalized for many different **types** of nodes.*

type 1: ●, *type 2:* ■, *type 3:* ▲, . . .

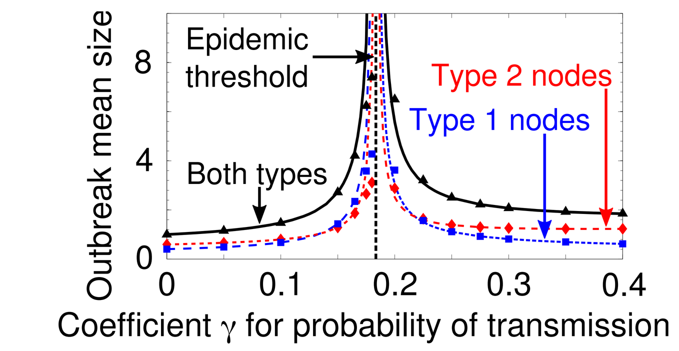
*This allows for new **network structures** where the degree k_j of a node must be specified for each possible type j.*



	●	■	▲	…
●	T_{11}	T_{12}	T_{13}	⋯
■	T_{21}	T_{22}	T_{23}	⋯
▲	T_{31}	T_{32}	T_{33}	⋯
⋮	⋮	⋮	⋮	⋱

*Different **probability of transmission** are considered for each ordered pair of infectious and susceptible node types.*

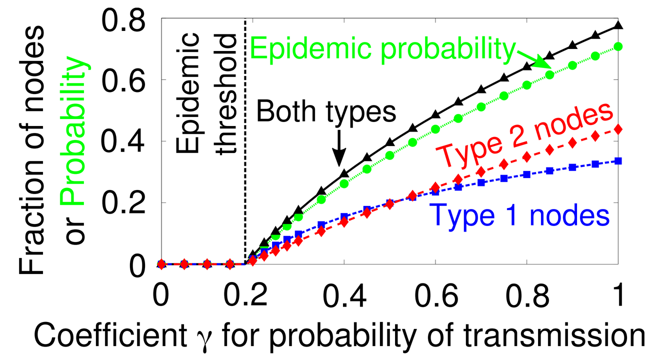
Using a 2 types network, simulations (symbols) confirm analytical results (lines) for outbreaks. . .



Outbreak?

In arbitrarily large networks, an outbreak's size (number of individuals affected) does not scale with the network size (e.g. unchanged by increasing network size by a factor 10). Outbreaks can occur both below and above the epidemic threshold.

. . . as well as for large-scale epidemics!



Epidemics?

Epidemics affect a fraction of the network: the total number affected scale with network size (e.g. 10 times more affected in a 10 times larger network). In addition to the fraction affected, epidemics are also characterized by their probability of occurrence.

Contribution B

*Formalism for dynamics on networks of **multiple types of nodes** with **heterogeneous degree distribution**.*

Information about the simulations

Network of $N = 10^5$ nodes (see paper for degree distribution). The transmission probability matrix is $\mathbf{T} = \gamma \begin{bmatrix} 0.95 & 0.98 \\ 0.48 & 1.00 \end{bmatrix}$.

Work in progress

Mapping generations to continuous time

*This is an add-on to **Contribution A** aiming at mapping this **discrete-time generation based formalism** to **observables varying continuously in time**.*

Basically, we get the infected proportion of each generations at any given time then translate this to the desired observable. Complications occur when one introduces finite-size.

Genuine continuous-time formalism

*This is an alternative to **Contribution A** aiming for a true **continuous time evolution** formalism on **finite-size** networks with **heterogeneous degree distribution**.*

We have designed a high-dimensional ODE system that fulfil these requirements. Some properties of the formalism indicate that an analytical solution might be possible for important special cases.

Types of links

*We extend the **PGF** formalism of **Contribution B** in order to include different **types of links**.*

Similarly to the "type of nodes" approach of Contribution B that needs a list of degrees for every node type, this approach requires a list of degrees for every link type (types of nodes are a special case of this formalism). In addition to allow new network structures, this could make the formalism particularly well adapted for survey data.

Future directions

- *Inclusion of clustering.*
- *Dynamical networks that evolve in time.*
- *Co-evolution of networks and dynamics (retroaction of process dynamics on network topology).*
- *Co-infection (interaction of more than one disease).*
- *Networks of networks.*

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