# **Stochastic Network Models**: Analytical Tools for STI Studies

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## Abstract

Models for transmission of infections on complex network structures are based on Markov stochastic processes. This general and analytical approach shows great potential in the context of STIs.

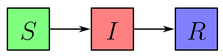
## Objectives

To obtain analytical STIs models considering:

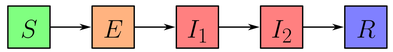
- elaborate epidemiological processes;
- complex and/or dynamic contact patterns; and
- stochasticity (*i.e.* non-determinism).

## Background

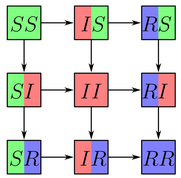
**Compartmental models** divide a population into compartments; two individuals in the same compartment are considered **indiscernible**.




In a SIR model, individuals may be **S**usceptible, **I**nfectious or **R**emoved. More compartments are added for infections with more elaborate stages.




**E**xposed compartments are added for incubation periods. Chains of infectious stages handle changes in infectiousness and improve timing.

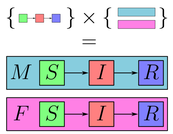



**Interacting infections**: one affects the transmission of another. Peer-exchanged information is an important special case.

**Numerous variations** include vaccination, loss of immunity and asymptomatic infection.

## Background (cont'd)

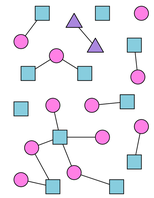
**Heterogeneity** of the individuals is handled by replicating the epidemiological compartments.




While two copies suffice for genders, more are required for behavioural groups, age groups, ethnic groups, *etc.*

**Mixing patterns** determine contact rates among groups; flow rates prescribe group transitions.

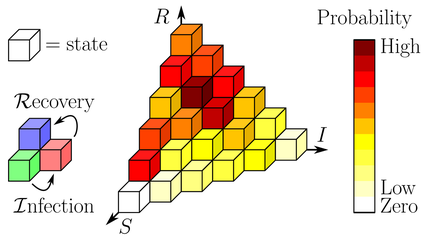
**Structure** matters: contacts are not "well mixed" but are instead constrained. In **network** models, a link (line) exists when a contact is possible. Structure may change in time.



**Deterministic** compartmental models provide mean values using ordinary differential equations.

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \qquad \frac{dI}{dt} = \frac{\beta SI}{N} - \mu I \qquad \frac{dR}{dt} = \mu I$$

**Stochastic** models give, for each possible future, the probability that it occurs. Benefits include accounting for variability about the mean value and allowing for random extinctions.




The master equation governing the above system is

$$\frac{dP(S,I,R|t)}{dt} = \mu\Big[(I+1)P(S,I+1,R-1|t) - IP(S,I,R|t)\Big] + \frac{\beta}{N}\Big[(S+1)(I-1)P(S+1,I-1,R|t) - SIP(S,I,R|t)\Big] \quad .$$

Using the general notation (defined later), this becomes

$$\mathbf{r}^{\mathcal{I}} = (-1,1,0) \qquad q_{\mathcal{I}}^{+}(S,I,R) = \frac{\beta SI}{N} \qquad q_{\mathcal{I}}^{-}(S,I,R) = 0$$
$$\mathbf{r}^{\mathcal{R}} = (0,-1,1) \qquad q_{\mathcal{R}}^{+}(S,I,R) = \mu I \qquad q_{\mathcal{R}}^{-}(S,I,R) = 0 \quad .$$

## Methods

- **Represent** the system with state vector $\mathbf{x}$.
- **Identify** and **quantify** the possible events.
- **Analyze** with standard stochastic tools.

If event $j$, which takes $\mathbf{x}$ to $\mathbf{x}+\mathbf{r}^j$, occurs at rate $q_j^{\pm}(\mathbf{x})$ in the forward/backward direction, then the master equation is

$$\frac{dP(\mathbf{x}|t)}{dt} = \sum_j \Big[q_j^+(\mathbf{x}-\mathbf{r}^j)P(\mathbf{x}-\mathbf{r}^j|t) - q_j^+(\mathbf{x})P(\mathbf{x}|t) + q_j^-(\mathbf{x}+\mathbf{r}^j)P(\mathbf{x}+\mathbf{r}^j|t) - q_j^-(\mathbf{x})P(\mathbf{x}|t)\Big] \quad .$$

For large systems, an estimate of the mean is obtained from

$$\frac{d}{dt}\langle\mathbf{x}(t)\rangle = \mathbf{a}\big(\langle\mathbf{x}(t)\rangle\big) \qquad a_i(\mathbf{x}) = \sum_j r_i^j\left[q_j^+(\mathbf{x}) - q_j^-(\mathbf{x})\right] \quad .$$

Defining the matrices

$$\widehat{A}(t,t') = \exp\left[\int_{t'}^{t} \widehat{J}_{\mathbf{a}}\big(\langle\mathbf{x}(t'')\rangle\big)dt''\right] \qquad B_{ij}(\mathbf{x}) = \sum_j r_i^j r_{i'}^j\left[q_j^+(\mathbf{x}) + q_j^-(\mathbf{x})\right]$$
$$\widehat{C}(t) = \int_0^t \widehat{A}(t,t')\cdot\widehat{B}\big(\langle\mathbf{x}(t')\rangle\big)\cdot\widehat{A}(t,t')^T dt' \quad ,$$

the probability distribution may be approximated as Gaussian

$$P(\mathbf{x}|t) = \frac{1}{\sqrt{(2\pi)^d|\widehat{C}(t)|}}\exp\left(-\frac{1}{2}\big(\mathbf{x}(t)-\langle\mathbf{x}(t)\rangle\big)^T\cdot\widehat{C}(t)^{-1}\cdot\big(\mathbf{x}(t)-\langle\mathbf{x}(t)\rangle\big)\right).$$

C. W. Gardiner, *Handbook of Stochastic Methods*, Springer (2004).

**State vector** $\mathbf{x}$ should encode epidemiological state, individual characteristics and structure.

$\mathbf{x} = \{\quad\} \times \{\quad\} \times \{\quad\}$

Since the amount of information is **huge**, focus is placed on what **matters** epidemiologically.

**Pair** approximations are models where structural information is limited to linked pairs.

$\mathbf{x} = \{\quad\} \times \{\quad\} \times \{\quad\}$

Example: there are $k$ links between SM and SF, $l$ links between SM and IF, $m$ links between...

C. E. Dangerfield *et al.*, J. R. Soc. Interface **6**, 761 (2009).
T. House *et al.*, Bull. Math. Biol. **71**, 1693 (2009).

**First neighbourhood** approximations track all the links of a single node (**concurrency**).

$\mathbf{x} = \{\quad\} \times \{\quad\} \times \{\quad\}$

Example: there are $k$ isolated SM, $l$ SM linked to one SF, $m$ SM linked to two SF, $n$ SM linked...

P.-A. Noël *et al.* arXiv:1102.0987.
V. Marceau *et al.* PRE **82**, 036116 (2010).
L. Hébert-Dufresne *et al.* PRE **82**, 036115 (2010).
V. Marceau *et al.* accepted for PRE, arXiv:1103.4059.

## Results

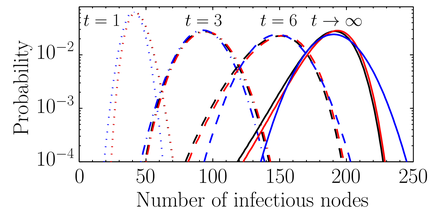
**Case study 1**: SI with first neighbourhood.

$\mathbf{x} = \{\quad\} \times \{\quad\}$

The network structure is static.

| Number of contacts | 1 | 2 | 3 | 4 |
|---|---|---|---|---|
| Number of individuals | 160 | 80 | 40 | 20 |

Total 300 individuals, 5% initially infectious.



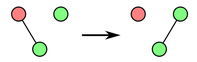

**Red**: Monte Carlo simulations (numerical).
**Black**: full Markov process (analytical).
**Blue**: Gaussian approximation (analytical).

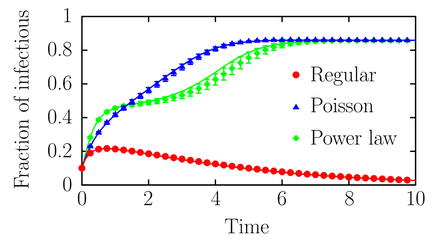
P.-A. Noël *et al.* arXiv:1102.0987.

**Case study 2**: SIS with first neighbourhood.

$\mathbf{x} = \{\quad\} \times \{\quad\}$

The network structure is **dynamic**: S individuals may switch a contact with an I for one with a S.






Color: different initial contact distribution (all 3 have the same average number of contacts).
Symbols: Monte Carlo simulations (numerical).
Lines: mean values from ODE system (analytical).

V. Marceau *et al.* PRE **82**, 036116 (2010).

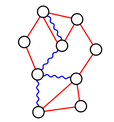
Different mechanisms could be implemented.

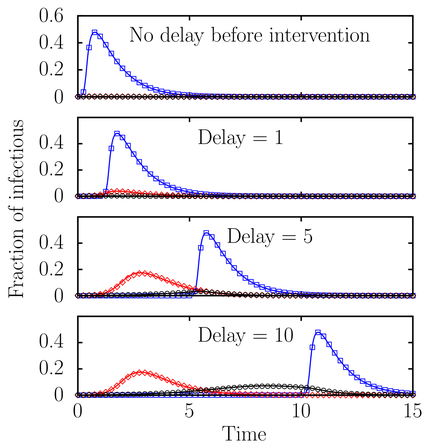
## Results (cont'd)

**Case study 3**: two interacting infections (each SIR) with first neighbourhood and types of links.

$\mathbf{x} = \{\quad\} \times \{\quad\} \times \{\quad\}$

Two static networks are overlaid: a pathogen spreads on the first while a fully immunizing intervention against the pathogen spreads on the second.






First network: **Poisson** or **power law**.
Second network: **power law**.
Symbols: Monte Carlo. Curves: ODE.

V. Marceau *et al.* accepted for PRE, arXiv:1103.4059.

## Conclusion

Network models naturally consider concurrency and a large variety of dynamical contact patterns.

As in standard compartmental models, Gaussian approximations are often available at low cost.

Stochastic network models are sufficiently mature: a new tool is available for STI applications.

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