Epidemiological dynamics

In simple epidemiological models, there are three possible intrinsic node states.

- **Susceptible** nodes do not have the infection (but could acquire it).
- **Infectious** nodes have the infection and can transmit it.
- **Removed** nodes neither acquire nor transmit the infection.

Changes in node states during \([t, t+dt]\) depend on the specificity of the infection.

**SI**: S nodes become I with probability proportional to number of I neighbours.

**SIS**: As in SI, except that I nodes become S with constant probability.

**SIR**: As in SI, except that I nodes become R with constant probability.

**SIRS**: As in SIR, except that R nodes become S with constant probability. These changes correspond to the events of the birth-death process.

### Birth-death Markov process

The probability distribution \(P(x|t)\) is governed by the master equation:

\[
\frac{dP(x|t)}{dt} = \sum \frac{\partial \hat{a}_i(x)}{\partial x^i} P(x|t) + \sum \frac{\partial^2 \hat{a}_i(x) P(x|t)}{\partial x^i \partial x^j} + \hat{a}_i(x) P(x|t) - \hat{q}_i(x) P(x|t) + \hat{q}_i(x) P(x^i - x|t)
\]

For large systems, using a continuous approximation for the state vector leads to the **stochastic differential equation** (Fokker-Planck equation):

\[
\frac{\partial P(x|t)}{\partial t} = -\sum \frac{\partial}{\partial x^i} \left[ \hat{a}_i(x) P(x|t) \right] + \frac{1}{2} \sum \left[ \frac{\partial^2}{\partial x^i \partial x^j} \hat{a}_i(x) P(x|t) \right] - \frac{1}{2} \sum \left[ \frac{\partial^2}{\partial x^i \partial x^j} \hat{q}_i(x) P(x|t) \right]
\]

When the main contribution of \(P(x|t)\) is located around its mean value, using a mean-field approximation provides the ordinary differential equation:

\[
\frac{d}{dt} \langle x(t) \rangle = a(\langle x(t) \rangle).
\]

A Gaussian approximation determines how \(P(x|t)\) behaves around this mean value. Assuming deterministic initial conditions, this behaviour is given by

\[
P(x) \approx \frac{1}{\sqrt{2\pi d |\hat{C}(0)|^{1/2}}} \exp \left( -\frac{1}{2} \left( x - \langle x(t) \rangle - \hat{C}^{-1}(t)(x - \langle x(t) \rangle) \right) \right).
\]

where \(d\) is the dimensionality of \(x\), \(\hat{C}(t)\) is the covariance matrix of \(P(x|t)\), and \(\hat{a}(\langle x(t) \rangle)\) is the Jacobian matrix of \(a(\langle x(t) \rangle)\).


### Example: SIS pair model

- **State vector** based on node and pair motifs: \(x = \{x_S, x_I, x_R, x_{SI}, x_{IR}, x_{RS}, x_{ISR}\}\).
- **Events** \(\frac{dx}{dt} = \beta x_I (K-x)|S|\) depend on the first neighbourhood of the changing node. The **shift vectors** are \(r^{S-I} = (-1, 1, 1(k+1))\).
- **Inference terms** are required only for \(x\) and pair motifs.
- **Rates of occurrence** depend on these inference terms.

\[
q_{SI}(\beta) = \beta x_I \left( \langle S \rangle x_I |S| \right) \frac{|S|}{|S|+|I|} \text{ (random S-I link, x)}
\]

Although presented differently, the Gaussian approximation of this model for regular random graphs is equivalent to C. E. Dangerfield et al., J. R. Soc. Interface 6, 761 (2009).

### Example: SI on-the-fly assignment

For a configuration model network allowing for repeated links and self-loops, the following representation *exactly* corresponds to the full network model:

\[
x = (2, 1, 3, 4, 2) \Rightarrow x = (20, 1, 3, 4, 1, 0) \Rightarrow x = (18, 1, 3, 4, 1, 0)
\]

- **State vector** \(x = \{x_S, x_I, x_R, x_{SI}, x_{IR}, x_{RS}, x_{ISR}\}\) where \(x_S\) is the total number of unassigned stubs and \(x_{IR}\) are the number of SI-IR motifs. The total number of stubs belonging to infectious nodes is \(\lambda(x) = x_S - \sum_i x_{IR}\).
- **Events** occur when an I node's stub form a link with another stub. The event is of type \(j = 1\) if the other stub belongs to any I node and of type \(j \geq 2\) if it belongs to a S node with j unassigned stubs: \(r^j = (\lambda, 0, \delta_{j1} - 1)\).
- **Inference terms** are trivial in this case.
- **Rates of occurrence** \(q_{SI}^j = \beta x_I \left( \langle S \rangle x_I |S| \right) \frac{|S|}{|S|+|I|} \text{ (random I node, x)}\).

Using \(j = 1\). Initial condition \(k(0) = (520, 152, 76, 38, 19)\).

### Further examples

The following mean-field models are compatible with the philosophy presented here. As such, Gaussian approximations could be obtained for these models.

**Adaptive networks** V. Marceau et al. PRE 82, 056116 (2010)

Based on first neighbourhood motifs. A special SIS model where S nodes may disconnect from their I neighbours and reconnect to another S node instead.

**Community structure** L. Hébert-Dufresne et al. PRE 82, 056117 (2010)

SIS model tracking both first neighbourhood and clique motifs in the state vector.

**Interacting epidemics** V. Marceau et al. arXiv:1103.4059

On-the-fly model for two interacting SIR dynamics (total 9 intrinsic node states). Two overlaying networks are considered using intrinsic link states.