

SEIRS+ Network Model

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1 SEIRS Model

Deterministic SEIRS Model Equations:

$$\begin{aligned}\dot{S} &= \frac{-\beta SI}{N} + \xi R + \nu N - \mu_0 S \\ \dot{E} &= \frac{\beta SI}{N} - \sigma E - \mu_0 E \\ \dot{I} &= \sigma E - \gamma I - \mu_I I - \mu_0 I \\ \dot{R} &= \gamma I - \xi R - \mu_0 R \\ \dot{F} &= \mu_I I \\ N &= S + E + I + R\end{aligned}$$

Variables & Parameters:

| | Description |
|----------|---|
| S | Number of susceptible individuals |
| E | Number of exposed individuals |
| I | Number of infectious individuals |
| R | Number of recovered individuals |
| F | Number of infection-related fatalities |
| N | Total number of living individuals |
| β | Rate of transmission (exposure) |
| σ | Rate of infection (upon exposure) |
| γ | Rate of recovery (upon infection) |
| ξ | Rate of re-susceptibility (upon recovery) |
| μ_I | Rate of infection-related death |
| μ_0 | Rate of baseline death |
| ν | Rate of baseline birth |

Setting $\nu = \mu_0$ maintains constant population size (excluding infection-related fatalities) with corresponding rate of birth-death turnover introducing new susceptible individuals. Setting ν , μ_0 , and/or ξ to 0 removes vitality and/or re-susceptibility terms, respectively, and reduces the model to basic SEIR dynamics (with mortality).

Stochastic SEIRS Model on a Network:

Consider a graph G representing individuals (nodes) and their interactions (edges). Each individual is adjacent to a set of nodes that defines its set of "close contacts" $C_G(i) = \{j : (i, j) \in G\}$. At a given time, individual i makes contact with a random individual from their set of close contacts ($j \in C_G(i)$) with probability $1 - p$ or with a random individual from anywhere in the network with probability p . The latter global contacts represent individuals interacting with the population at large (i.e., individuals outside their social circle, such as on public transit, at an event, etc) with some probability. The parameter p defines the locality of the network: for $p = 0$ an individual only interacts with their close contacts while $p = 1$ represents a uniformly mixed population. Social distancing interventions may increase the locality of the network (i.e., decrease p) and/or decrease local connectivity of the network (i.e., decrease the degree of individuals, $d_i = |C_G(i)|$).

Each individual i has a state $X_i \in \{S, E, I, R, F\}$. State transitions corresponding to the SEIRS dynamics are

$$\begin{aligned}\Pr(X_i = S \rightarrow E) &= \left[p \frac{\beta I}{N} + (1 - p) \frac{\beta \sum_{j \in C_G(i)} \delta_{X_j=I}}{|C_G(i)|} \right] \delta_{X_i=S} \\ \Pr(X_i = E \rightarrow I) &= \sigma \delta_{X_i=E} \\ \Pr(X_i = I \rightarrow R) &= \gamma \delta_{X_i=I} \\ \Pr(X_i = I \rightarrow F) &= \mu_I \delta_{X_i=I} \\ \Pr(X_i = \text{any} \rightarrow S) &= \xi \delta_{X_i=R} + \nu \delta_{X_i \neq F}\end{aligned}$$

where $\delta_{X_i=A} = 1$ if the state of X_i is A , or 0 if not. When $p = 1$ and $N \rightarrow \infty$, this stochastic model approaches the same dynamics as the deterministic SEIR model.

2 SEIRS+ Model with Testing

Deterministic SEIRS+ Model with **Testing**:

$$\begin{aligned}\dot{S} &= -\frac{\beta SI}{N} - q \frac{\beta_D S D_I}{N} + \xi R + \nu N - \mu_0 S \\ \dot{E} &= \frac{\beta SI}{N} + q \frac{\beta_D S D_I}{N} - \sigma E - \theta_E \psi_E E - \mu_0 E \\ \dot{I} &= \sigma E - \gamma I - \mu_I I - \theta_I \psi_I I - \mu_0 I \\ \dot{D}_E &= \theta_E \psi_E E - \sigma_D D_E - \mu_0 D_E \\ \dot{D}_I &= \theta_I \psi_I I + \sigma_D D_E - \gamma_D D_I - \mu_D D_I - \mu_0 D_I \\ \dot{R} &= \gamma I + \gamma_D D_I - \xi R - \mu_0 R \\ \dot{F} &= \mu_I I + \mu_D D_I \\ N &= S + E + I + D_E + D_I + R\end{aligned}$$

Variables & Parameters:

| | Description |
|------------|---|
| S | Number of susceptible individuals |
| E | Number of exposed individuals |
| I | Number of infectious individuals |
| D_E | Number of exposed individuals with detected cases |
| D_I | Number of exposed individuals with detected cases |
| R | Number of recovered individuals |
| F | Number of infection-related fatalities |
| N | Total number of living individuals |
| β | Rate of transmission |
| σ | Rate of infection (upon exposure) |
| γ | Rate of recovery (upon infection) |
| μ_I | Rate of infection-related death |
| β_D | Rate of transmission (for individuals with detected infections) |
| σ_D | Rate of infection (upon exposure, for individuals with detected infections) |
| γ_D | Rate of recovery (upon infection, for individuals with detected infections) |
| μ_D | Rate of infection-related death (for individuals with detected infections) |
| ξ | Rate of re-susceptibility (upon recovery) |
| μ_0 | Rate of baseline death |
| ν | Rate of baseline birth |
| θ_E | Rate of baseline testing (for exposed individuals) |
| θ_I | Rate of baseline testing (for infectious individuals) |
| ϕ_E | Rate of testing when a close contact has tested positive (for exposed individuals) |
| ϕ_I | Rate of testing when a close contact has tested positive (for infectious individuals) |
| ψ_E | Rate of positive test (given exposed state) |
| ψ_I | Rate of positive test (given infectious state) |
| q | Rate of individuals with detected infection interacting with population |

Stochastic SEIRS+ Model with Testing on a Network:

Consider a graph G representing individuals (nodes) and their interactions (edges) as before. Each individual i has a state $X_i \in \{S, E, I, D_E, D_I, R, F\}$, where the new states D_E and D_I represent individuals who have tested positively for infection (exposed and infectious, respectively). Infectious individuals (state I) are tested at a baseline rate θ_I , and may also be tested at an additional rate ϕ_I if another individual in their close contacts (i.e., $j \in C_G(i)$) has tested positive. Infectious individuals test positively rate ψ_I , which moves them into the D_I state representing a detected case. Infectious individuals (state I) are tested in the same way, with corresponding parameters θ_E , ϕ_E , ψ_E , and move into state D_E when testing positive.

Now we also consider another graph Q which represents the interactions that each individual has if they test positively for the disease (i.e., individuals in the D_E or D_I states) and enter into a form of quarantine. The quarantine has the effect of dropping some fraction of the edges connecting the quarantined individual to others (according to some rule to be specified elsewhere). The edges of Q for each individual are then a subset of the edges of G for that individual. The set of nodes that are adjacent to a quarantined individual define their set of "quarantine contacts" $C_Q(i) = \{j : (i, j) \in Q\}$. At a given time, a quarantined individual i may come into contact with another individual in this quarantine contact set. A quarantined individual i may also be accessible to contact with a random

individual from anywhere in the network with rate q .

State transitions corresponding to the SEIRS+ dynamics with testing are

$$\begin{aligned}
\Pr(X_i = S \rightarrow E) &= \left[p \left(\frac{\beta I + q\beta_D D_I}{N} \right) + (1-p) \left(\frac{\beta \left[\sum_{j \in C_G(i)} \delta_{X_j=I} \right] + \beta_D \left[\sum_{k \in C_Q(i)} \delta_{X_k=D_I} \right]}{|C_G(i)|} \right) \right] \delta_{X_i=S} \\
\Pr(X_i = E \rightarrow I) &= \sigma \delta_{X_i=E} \\
\Pr(X_i = I \rightarrow R) &= \gamma \delta_{X_i=I} \\
\Pr(X_i = I \rightarrow F) &= \mu_I \delta_{X_i=I} \\
\Pr(X_i = E \rightarrow D_E) &= \left(\theta_E + \phi_E \left[\sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_E \delta_{X_i=E} \\
\Pr(X_i = I \rightarrow D_I) &= \left(\theta_I + \phi_I \left[\sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_I \delta_{X_i=I} \\
\Pr(X_i = D_E \rightarrow D_I) &= \sigma_D \delta_{X_i=D_E} \\
\Pr(X_i = D_I \rightarrow R) &= \gamma_D \delta_{X_i=D_I} \\
\Pr(X_i = D_I \rightarrow F) &= \mu_D \delta_{X_i=D_I} \\
\Pr(X_i = \text{any} \rightarrow S) &= \xi \delta_{X_i=R} + \nu \delta_{X_i \neq F}
\end{aligned}$$

where $\delta_{X_i=A} = 1$ if the state of X_i is A , or 0 if not.

References:

- Dottori, M. and Fabricius, G., 2015. SIR model on a dynamical network and the endemic state of an infectious disease. *Physica A: Statistical Mechanics and its Applications*, 434, pp.25-35.
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