

# 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
$\beta$	Rate of transmission (exposure)
$\sigma$	Rate of infection (upon exposure)
$\gamma$	Rate of recovery (upon infection)
$\xi$	Rate of re-susceptibility (upon recovery)
$\mu_I$	Rate of infection-related death
$\mu_0$	Rate of baseline death
$\nu$	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  $\nu$ ,  $\mu_0$ , and/or  $\xi$  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
$\beta$	Rate of transmission
$\sigma$	Rate of infection (upon exposure)
$\gamma$	Rate of recovery (upon infection)
$\mu_I$	Rate of infection-related death
$\beta_D$	Rate of transmission (for individuals with detected infections)
$\sigma_D$	Rate of infection (upon exposure, for individuals with detected infections)
$\gamma_D$	Rate of recovery (upon infection, for individuals with detected infections)
$\mu_D$	Rate of infection-related death (for individuals with detected infections)
$\xi$	Rate of re-susceptibility (upon recovery)
$\mu_0$	Rate of baseline death
$\nu$	Rate of baseline birth
$\theta_E$	Rate of baseline testing (for exposed individuals)
$\theta_I$	Rate of baseline testing (for infectious individuals)
$\phi_E$	Rate of testing when a close contact has tested positive (for exposed individuals)
$\phi_I$	Rate of testing when a close contact has tested positive (for infectious individuals)
$\psi_E$	Rate of positive test (given exposed state)
$\psi_I$	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  $\theta_I$ , and may also be tested at an additional rate  $\phi_I$  if another individual in their close contacts (i.e.,  $j \in C_G(i)$ ) has tested positive. Infectious individuals test positively rate  $\psi_I$ , 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  $\theta_E, \phi_E, \psi_E$ , 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

$$\Pr(X_i = S \rightarrow E) = \left[ p \left( \frac{\beta I + q\beta_D D_I}{N} \right) + (1-p) \left( \frac{\beta \left[ \sum_{j \in C_G(i)} \delta_{X_j=I} \right] + \beta_D \left[ \sum_{k \in C_Q(i)} \delta_{X_k=D_I} \right]}{|C_G(i)|} \right) \right] \delta_{X_i=S}$$

$$\Pr(X_i = E \rightarrow I) = \sigma \delta_{X_i=E}$$

$$\Pr(X_i = I \rightarrow R) = \gamma \delta_{X_i=I}$$

$$\Pr(X_i = I \rightarrow F) = \mu_I \delta_{X_i=I}$$

$$\Pr(X_i = E \rightarrow D_E) = \left( \theta_E + \phi_E \left[ \sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_E \delta_{X_i=E}$$

$$\Pr(X_i = I \rightarrow D_I) = \left( \theta_I + \phi_I \left[ \sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_I \delta_{X_i=I}$$

$$\Pr(X_i = D_E \rightarrow D_I) = \sigma_D \delta_{X_i=D_E}$$

$$\Pr(X_i = D_I \rightarrow R) = \gamma_D \delta_{X_i=D_I}$$

$$\Pr(X_i = D_I \rightarrow F) = \mu_D \delta_{X_i=D_I}$$

$$\Pr(X_i = \text{any} \rightarrow S) = \xi \delta_{X_i=R} + \nu \delta_{X_i \neq F}$$

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.
- <https://andrewmellor.co.uk/blog/articles/2014/12/19/gillespie-epidemics/>