

SEIR Graph Model

March 22, 2020

1 SEIRS Model

Deterministic SEIR(S) Model:

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

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 SEIR(S) Model on a Graph:

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.

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.

2 SEIRS Model with Testing

Deterministic SEIR(S) Model with Testing:

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

Variables & Parameters:

	Description
S	Number of susceptible individuals
E	Number of exposed individuals
I	Number of infectious individuals with undetected cases
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 (exposure, for individuals with undetected infections)
β_D	Rate of transmission (exposure, for individuals with positively detected infections)
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
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 SEIR(S) Model with **Testing** on a Graph:

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 , and may be tested at a higher rate ϕ if another individual in their close contacts (i.e., $j \in C_G(i)$) has tested positive. Exposed and infectious individuals test positively rate ψ_E or ψ_I , respectively, which moves them into the D_E or D_I state representing a detected case.

Now we also consider another graph Q which represents the interactions that each individual has if they test positively for the disease and enter into a form of quarantine. That is, individuals in the D_E or D_I states. 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, such as dropping a random fixed percentage of a node's edges). 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

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

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