

Epidemiology: Networks and Disease Spread

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Types of Biological Networks [New10]

- Biochemical Networks
 - Metabolic Networks
 - Protein-protein interaction networks
 - Genetic regulatory networks
- Neural Networks
- Ecological Networks
 - Food webs
 - Host-parasite networks
 - Mutualistic networks

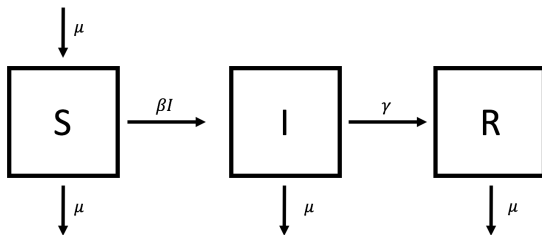
Types of disease models

- SI
- SIR
- SIS
- SIRS
- SIWR
- SEIR

Epidemics on networks [New10]

- population mixing
- transmission rate
- pair-approximations
- Late-time Properties

SIR Model (including vital dynamics)



$$\frac{dS}{dt} = \mu N - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

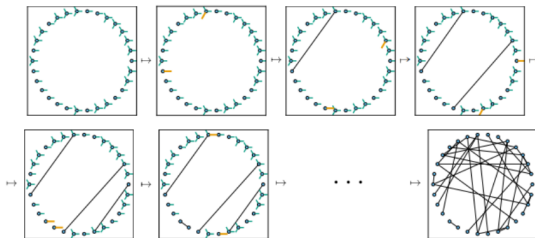
$$\frac{dR}{dt} = \gamma I - \mu R$$

Incorporating Networks [JCM13]

- edge-based compartmental modeling (EBCM)
 - proved exact for static Configuration Model populations
- mechanistic infection-spread models
 - mass-action model
 - does not depend on the duration of a relationship
 - Probability any two individuals will interact is the same
 - network-based
 - assume partnerships are permanent
 - pair approximation

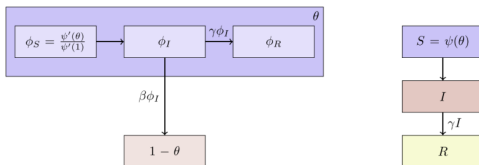
Configuration Model network construction I

- node has assigned number of edges
- edges connect randomly using proportional mixing
- $S(t)$: susceptible proportion of the population at time t
- $I(t)$: infected proportion of the population at time t
- $R(t)$: recovered proportion of the population at time t
 - S, I, T change deterministically at the population scale



Sample generation of a Configuration Model network [JCM13]

Configuration Model network construction II



Flow Diagram for Configuration Model networks [JCM13]

$$\dot{\theta} = -\beta\theta + \beta \frac{\psi'(\theta)}{\psi'(1)} + \gamma(1 - \theta)$$

$$\dot{R} = \gamma I \quad S = \psi(\theta) \quad I = 1 - S - R$$

Configuration Model network construction III

$$\dot{\theta} = -\beta\theta + \beta \frac{\psi'(\theta)}{\psi(1)} + \gamma(1 - \theta)$$

$$\dot{R} = \gamma I \quad S = \psi(\theta) \quad I = 1 - S - R$$

- θ : probability that v has not transmitted to u
- S : probability that u is susceptible
- I : probability that u is infected
- R : probability that u is susceptible
- $\psi(x) = \sum_k P(k)x^k$
- β : infection rate within a partnership
- γ : recovery rate of an individual

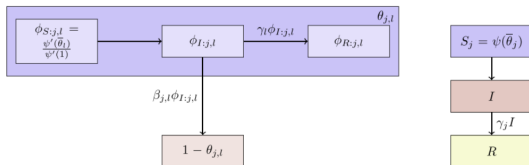
CM Network Model analysis/expansion

Implicit assumption that the epidemic is started by a small initial condition

$$\text{As } t \rightarrow -\infty : \quad \theta \rightarrow 1, \quad \phi_S \rightarrow 1, \quad \phi_I \rightarrow 0, \quad \phi_R \rightarrow 0$$

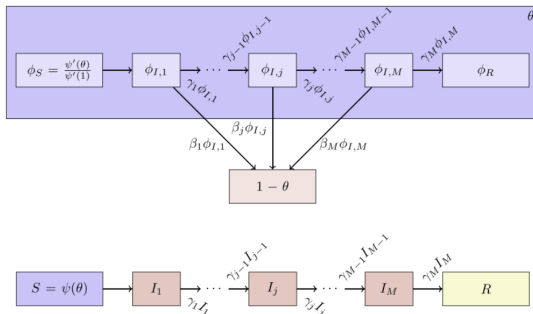
If any value in $\begin{bmatrix} 1 - \phi_S \\ 1 - \theta \\ \phi_I \\ \phi_R \end{bmatrix}$ is known at $t = 0$, we can find the others.

Other CM Network Models I



Heterogeneous infectiousness/susceptibility model [JCM13]

Other CM Network Models II



Multiple infectious stages model [JCM13]

Other CM Network Models III

- Directed networks
- Populations with assortative mixing by type
- Multiple modes of transmission

References

Erik M. Volz Joel C. Miller. Incorporating disease and population structure into models of SIR disease in contact networks. *PLOS*, 2013.

Mark Newman. *Networks: An Introduction*. Oxford University Press, 2010.