LIFE DATA EPIDEMIOLOGY

lect. 4: application of metapopulation models Chiara Poletto <u>polettoc@gmail.com</u>

SIR metapopulation model: markovian mobility

 $\frac{dS_i}{dt} = -\beta \frac{I_i(t)S_i(t)}{N_i} + \Omega_i^S$ $\frac{dI_i}{dt} = \beta \frac{I_i(t)S_i(t)}{N_i} - \mu I_i(t) + \Omega_i^I$ $\frac{dR_i}{dt} = \mu I_i(t) + \Omega_i^R$ $\Omega_i^X = \sum_j \frac{w_{ji}}{N_j} X_j - \frac{w_{ij}}{N_i} X_i$

SIR metapopulation model: markovian mobility

What can I do with that?

- analytical understanding
 - spatial propagation & predictability
 - global invasion threshold
- computer simulations

global invasion threshold



which are the conditions for a local outbreak to spread at global proportion?

global invasion threshold



coarse graining

following the spread from one subpopulation to another

mapping the spreading dynamics among subpopulation into the spreading on a network



[Colizza & Vespignani, PRL 2007, JTB 2008; Cross, et al. JRSoc Interface 2007]

global invasion threshold



- Invasion dynamics at the subpopulation level
- branching process approximation

Dⁿ: diseased subpopulations at generation n



- W_0 travellers along each link
- $\langle k
 angle$ # connection of each subpopulation
- $N\,$ population of each subpopulation
- lpha epidemic attack rate

total # infectious individuals sent from i to j during the local outbreak



probability of early extinction $~P_{\epsilon}$

$$\mathbf{ext} = \left(\frac{1}{R_0}\right)^{\lambda_{ij}}$$



- $w_0 \,$ travellers along each link
- $\langle k
 angle$ # connection of each subpopulation
- $N\,$ population of each subpopulation
- lpha~ epidemic attack rate

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probability of early extinction I

extinction
$$P_{\text{ext}} = \left(\frac{1}{R_0}\right)^{\lambda_{ij}}$$

$$D^{n} = (\langle k \rangle - 1) \left(1 - P_{\text{ext}}\right) \left(1 - \sum_{m=0}^{n-1} \frac{D^{n}}{V}\right) D^{n-1}$$

$$D^{n} = \left(\langle k \rangle - 1\right) \left(1 - P_{\text{ext}}\right) \left(1 - \sum_{m=0}^{n-1} \frac{D^{n}}{V}\right) D^{n-1}$$

$$R_* = \left(\langle k \rangle - 1\right) \left(1 - P_{\text{ext}}\right)$$

$$1 - P_{ext} = 1 - \left(\frac{1}{R_0}\right)^{\lambda_{ij}} \simeq \lambda_{ij}(R_0 - 1) = \frac{\alpha w_0}{\mu}(R_0 - 1)$$

$$R_* = (\langle k \rangle - 1) \frac{\alpha w_0}{\mu} (R_0 - 1)$$

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invasion potential growing function of :

- *R*₀

- over all traffic rescaling
- average number of connections
- infectious duration

Real systems are highly heterogeneous. E.g.: air transportation network



Good news :)



- scaling relations:
 approximate laws that
 make possible calculations
 and justify the degree block description
- number of connections and travellers along the connections is heterogeneous
- average quantities are not good representative of the properties of patches
- homogenous approximation is bad

Degree-block description:

we group patches according to their degree and consider patches within the same degree-class homogeneous

$$N_{k} = N_{0}k^{\phi}$$
$$w_{kk'} = w_{0}(kk')^{\theta}$$
$$p_{kk'} = \frac{w_{0}}{N_{0}}\frac{(kk')^{\theta}}{k^{\phi}}$$



 D_k^n : diseased subpopulations at generation n, with k mobility connections



P(k)

Degree distribution

 $N_k = N_0 k^{\phi}$ $w_{kk'} = w_0 (kk')^{\theta}$ $p_{kk'} = \frac{w_0}{N_0} \frac{(kk')^{\theta}}{k^{\phi}}$

[Pastor-Satorras & Vespignani PRL 2001, review :Pastor Satorras et al. Rev Mod Phys 2015]





what is the probability that an infected patch with degree k is connected to a disease-free patch of degree k'?



number of mobility connections through which the seeding may potentially occur:

X

probability that contact has degree *k*':

P(k'|k)

number of disease-free patches within the *k*'class:



k – 1

$$P(k'|k) = k' \frac{P(k')}{\langle k \rangle}$$

If I make a connection at random I will do it more likely with a node that is well connected (more stubs)



Friendship paradox:

my friends have more friends than me!

$$D^{n} = (\langle k \rangle - 1) (1 - P_{\text{ext}}) \left(1 - \sum_{m=0}^{n-1} \frac{D^{n}}{V} \right) D^{n-1}$$
$$D^{n} \rightarrow D^{n}_{k}$$
$$D^{n}_{k} = \sum_{k'} D^{n-1}_{k'} (k'-1)P(k \mid k') \left(1 - \sum_{m=0}^{n-1} \frac{D^{m}_{k}}{V_{k}} \right) (1 - P_{\text{ext}}(\lambda_{k'k}))$$

$$D_{k}^{n} = \sum_{k'} D_{k'}^{n-1} \underbrace{(k'-1)P(k \mid k')}_{k'} \underbrace{\left(1 - \sum_{m=0}^{n-1} D_{k'}^{m}\right)}_{m=0} \underbrace{(1 - P_{ext}(\lambda_{k'k}))}_{k'k} \underbrace{\left(1 - P_{ext}(\lambda_{k'k})\right)}_{k'k} \underbrace{1 - P_{ext}(\lambda_{k'k})}_{k'k} = 1 - \left(\frac{1}{R_{0}}\right)^{\lambda_{k'k}} \simeq \lambda_{k'k}(R_{0} - 1)$$

$$\underbrace{\left(\sum_{k' \in \mathbb{R}} \frac{w_{0}(kk')^{\theta}}{\mu}}_{homogenous case} \lambda_{k'k} = \frac{w_{0}(kk')^{\theta}}{N_{0}k^{\phi}} \frac{\alpha}{\mu}(N_{0}k^{\phi})$$

$$D_k^n = \sum_{k'} D_{k'}^{n-1} (k'-1) P(k \mid k') \left(1 - \sum_{m=0}^{n-1} \frac{D_k^m}{V_k} \right) \left(1 - P_{ext}(\lambda_{k'k}) \right)$$

$$\begin{split} D_k^n &= (R_0 - 1) \frac{\alpha w_0}{\mu} \frac{k^{1+\theta} P(k)}{\langle k \rangle} \underbrace{\sum_{k'} D_{k'}^{n-1} (k' - 1) k'^{\theta}}_{k'} \\ \Theta^n &= (R_0 - 1) \frac{\alpha w_0}{\mu} \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} \Theta^{n-1} \end{split}$$

$$R_* = (R_0 - 1) \frac{\alpha w_0}{\mu} \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} > 1$$

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invasion potential growing function of :

- *R*₀

- over all traffic rescaling
- average number of connections
- infectious duration
- moments of the degree distribution and its fluctuations

$$\begin{split} \langle k^{2+2\theta} \rangle &- \langle k^{1+2\theta} \rangle \simeq 7 \ 10^4 \\ \langle k \rangle &\simeq 10 \end{split}$$





[Colizza & Vespignani, PRL 2007, JTB 2008]

competition between two strains at the spatial level



the model: 2strain transmission

▶same R₀

▶different infectious period → $au_s > au_f$

▶full cross-immunity



[Poletto, PLOS Comp Biol PRL 2007, JTB 2008]

the model: 2strain transmission

▶same R₀

▶different infectious period → $au_s > au_f$

▶full cross-immunity



stochastic numerical simulations



the 2 strains originate from different locations
 markovian dynamics
 probability of traveling: p

results: simulations





$$\begin{split} R_* &= \left(\bar{k} - 1\right) \left[1 - \left(\frac{1}{R_0}\right)^{\frac{pS_{\infty}}{\mu \bar{k}}} \right] \\ R_* \text{ increasing function of } \mu^{-1} \square R_*^s > R_*^f \end{split}$$

large p:

$$R_*^s$$
 and $R_*^f >> 1$

fast strain reaches more rapidly new patches



 $R^s_* > R^f_* \Longrightarrow \ \mbox{more able to percolate}$





