LIFE DATA EPIDEMIOLOGY

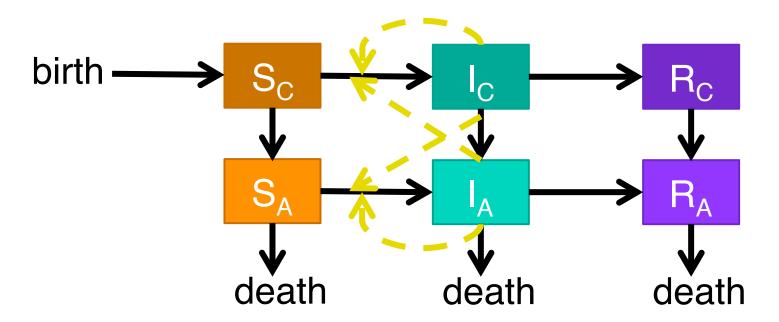
Lecture 6: Complex contagions

Leonardo Badia

leonardo.badia@unipd.it

Age structure

Other diseases have a different behavior at various ages, so consider population with (C)hildren and (A)dults



Age structure

□ We can still write WAIFW matrix β $\beta = \begin{pmatrix} \beta_{CC} & \beta_{AC} \\ \beta_{AC} & \beta_{AA} \end{pmatrix}$

- □ Hypotheses that are still reasonable □assortative mixing: $β_{ii} > β_{ij}$ with $i \neq j$ □symmetry $β_{AC} = β_{CA}$
- But now it is unclear what class is more at risk, and also class sizes change in time

Age structure

- We may actually be tempted to treat age as a continuous parameter
 but that makes the equations hard to solve
 and at the same time, we do not have this many parameters
- Better replicate compartments and divide the population in age classes
 model is more tractable and we can exploit standard assumptions (e.g. memoryless)

Control by vaccination

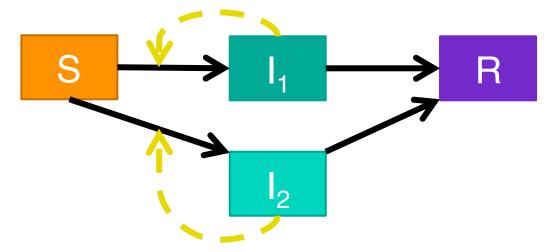
- For risk structure, it was more efficient to vaccinate or quarantine high-risk elements as this reduces the actual value of R₀
- In age structure, we do not have a class with "higher risk" (it can be both)
 individuals partake in the entire dynamics (we expect them to be C, then A in due time)
 yet, s_∞^(a) / n_∞^(a) ≥ s_∞^(b) / n_∞^(b) if a < b younger than

Control by vaccination

- This implies that to control the disease spread, most of the individual's lifespan should be immune; thus, it is generally best to vaccinate the **youngest** group □just a general rule, though (it depends on the numbers and also on waning immunity) \square If children are vaccinated, 1-1/R_o still well approximates the minimal vaccination rate
 - □often used for measles and baby-diseases

Multi-pathogen

 Consider an SIR with 2 (or more) strains of disease within the same population
 Cross-immunity relates to individuals becoming infected with only one strain.
 Simplest case is complete cross-immunity



Multi-pathogen

□ Class I_j only helps creating I_j members □we can write per-class $R_0^{(j)}$ as per definition □without loss of generality, say $R_0^{(1)} > R_0^{(2)}$

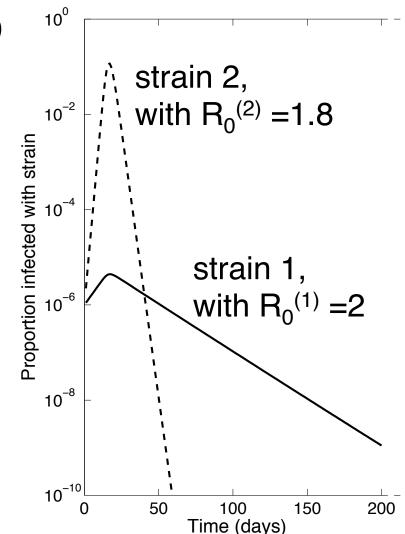
Now write + solve equations as usual or...
 use a principle: 2 infections cannot coexist!
 we can show that the equilibrium in case of complete cross-immunity, is the same as SIR with just one strain (because in the end only one strain is there)

Multi-pathogen

 \square Proof: we expect x(t) to grow and reach a peak (when $s R_0 = 1$) and then go down \Box as we have 2 different R₀s, if we believe to be at the endemic point for $R_0^{(2)}$, we still have a higher $R_0^{(1)}$ causing x to still grow $\Box \rightarrow$ thus, we cannot be at equilibrium The only possibility is that at equilibrium, one strain survived, the other is eliminated

Implications

Relationship R₀⁽¹⁾ > R₀⁽²⁾ does not mean that strain 2 cannot have faster dynamics (being stronger than strain 1 in the short term)



Evolutionary implications

- Why do not we have a single dominant disease with extremely high R₀?
 that would be the limit of a spotted equilibrium where mutants keep appearing with higher R₀
 also this would be a harmless disease (why it has to be harmful to the host?)
- Biologists would answer that there is a natural tradeoff of transmission (how contagious) vs virulence (how deadly)

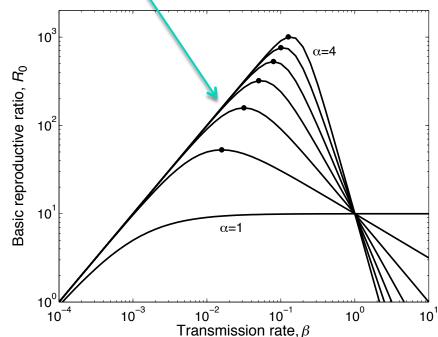
Evolutionary implications

If a disease produces many pathogens, it spreads rapidly but is also harmful to the host; thus, we cannot have very high β without μ being very high too
 e.g., STDs have long infected time 1/μ but also are not very contagious, compared to measles (high β, but 1/μ is short)

A power law?

The tradeoff between β and μ is generally taken as a power law μ = k β^α
 If this holds, R₀ cannot grow arbitrarily it can only reach these peaks
 Why power law?

□easy (but hard to validate choice of α)
 □other functions may fit better

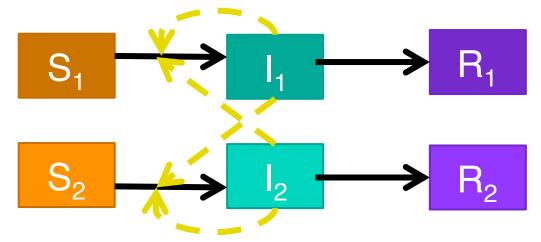


Without cross-immunity

This situation has two extreme cases simultaneous infections are frequent, and in the end it is just two separate strains evolving orthogonally on same population □or multiply infected individuals are rare (e.g., because when you are sick you control yourself and avoid further infections) \rightarrow this is just like a single infection

Multi-host

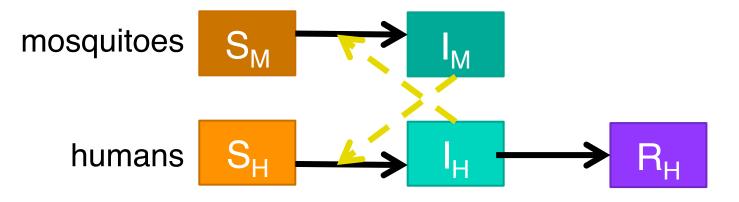
We can connect this to risk-structure



 main difference: now we have two distinct populations (of different species! so, we will not require symmetry of WAIFW)
 some special cases are notable

Vectored transmissions

This is the case for many diseases carried by mosquitoes (or similar insects)
 S_M→I_M: susceptible mosquito bites infected
 S_H→I_H: infected mosquito bites susceptible

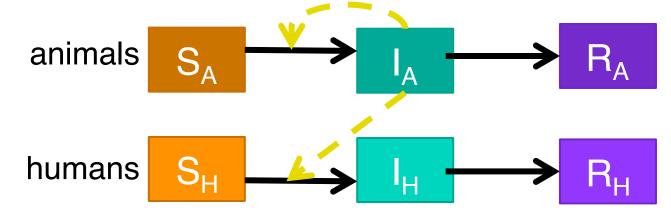


Vectored transmissions

- No intra-species infection, thus WAIFW is $\beta = \begin{pmatrix} 0 & \beta_{MH} \\ \beta_{HM} & 0 \end{pmatrix} = can be related to$ "bite rate" of mosquitoes r = bites per sec/ N_H
- Usually, transmission mechanism is:
 frequency-dependent for human population
 density-dependent for mosquitoes
 i.e. mosquitoes bite at same rate, humans get bitten more often if mosquito-density 1



Here, the disease is mostly active in animals, but can affect humans yet, negligible contagion rate from humans



e.g. brucellosis, Ebola, rabies, toxoplasmosis

Zoonoses

- Now the WAIFW matrix is β = (β_{AA} β_{AH} 0 0)
 yet, epidemics hard to eradicate as we estimate R₀ and enact countermeasures in humans but spreading happens in animals
 Also, combined cases: vectored zoonosis
 - spreading in animals (birds/mammals) can extend to humans via insects bites: Lyme, Chagas, leishmaniasis, bubonic plague

Temporal forcing

It has been observed that some diseases have a cyclic behavior (seasonal flu, outbreak of measles/smallpox in schools) the oscillatory pattern of the endemic equilibrium of classic SIR model is insufficient to explain these trend Some models introduce a temporal forcing to explain these phenomena

Temporal forcing

 A simple example
 we have birth rate λ and recovery rate μ but we neglect deaths in classes S and I

$$\frac{ds}{dt} = \lambda - \beta(t) sx$$
$$\frac{dx}{dt} = \beta(t) sx - \mu x$$

□β(t) represents seasonal variability in the contact rate (e.g., school time of children)
 □ E.g., β(t)=constant term + sinusoid β(t) = β₀ [1+β₁ cos(2πf₁ t)]

Temporal forcing

If
$$X = X_{\infty}(1+\chi)$$
, $\chi = \text{small perturbation}$, we get

$$\frac{d^{2}\chi}{dt^{2}} + \lambda R_{0} \frac{d\chi}{dt} + \lambda \beta_{0}(t)\chi = -\omega_{1}\beta_{1}\mu \sin(\omega_{1}t)$$

□ Oscillatory with frequency f_1 and amplitude $M = \omega_1 \beta_1 \mu \left[(\lambda \beta_0 - \omega_1^2)^2 + (\lambda R_0 \omega_1)^2 \right]^{-0.5}$

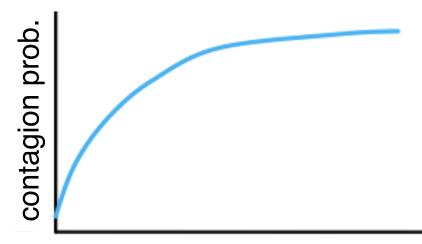
□ Generally, $M \gg \beta_1$ so natural oscillations are highly amplified (**resonance**)

Complex contagion

- What if infection occurs after exposure to multiple sources? → complex contagion
- Diseases (a single contact is enough) vs:
 adoption of innovation
 - consensus over a policy
 - spreading of a news (or urban legend)
 these usually requires multiple sources!
- No consolidated analytical models how can we quantify this anyways?

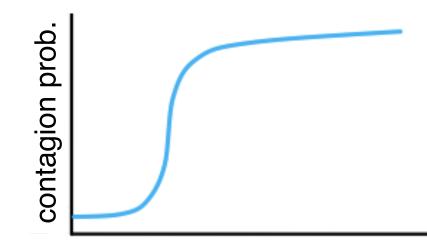
Exposure

Driving process=exposure (passive influence) → expect a monotonic increasing trend



number of infected friends

diminishing law (prob \rightarrow 1 but saturates)

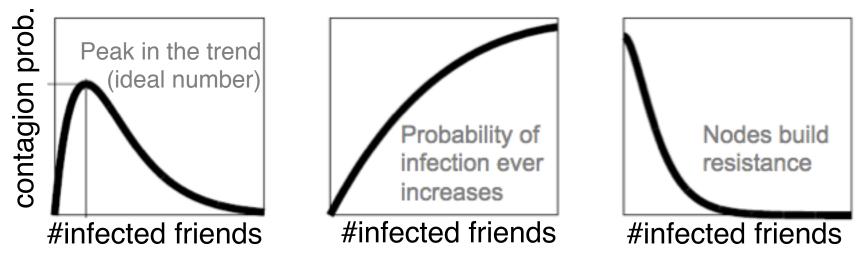


number of infected friends

activation threshold (min #infected neighbors)

Adoption

Or we require an active agreement to accepts the contagion (adoption)



Exposure - Adoption

 We can also combine two behaviors
 the higher #infected neighbors, the higher the number of contagious interactions
 this is taken as the input for adoption

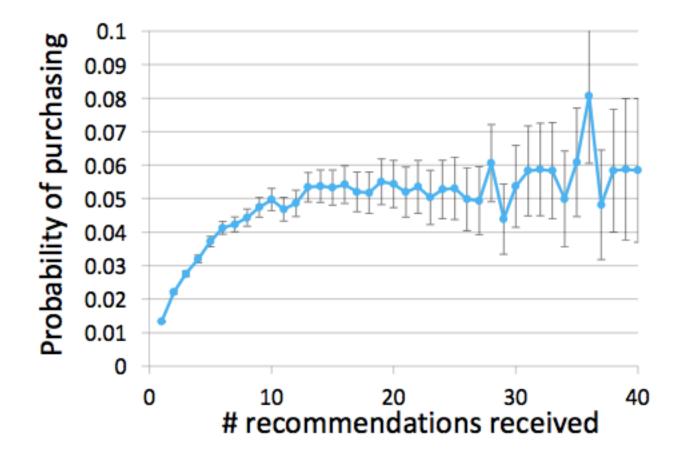
Applications

some friends of yours are joining a social network: do you join it too?

how many ads needed to trigger a buy?how many views to check a viral video?

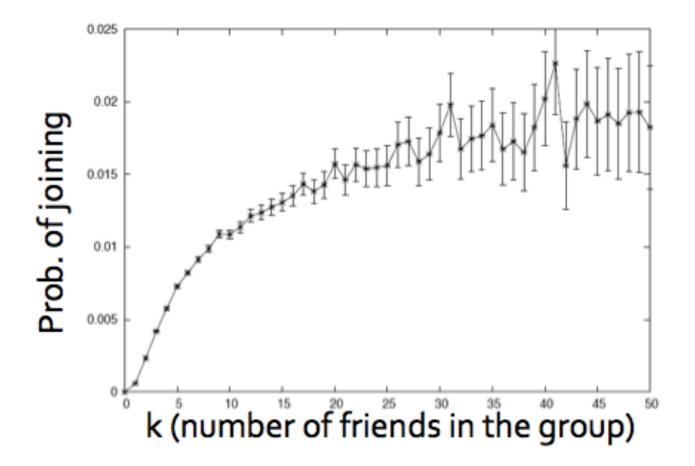
Example of application

DVD Recommendations



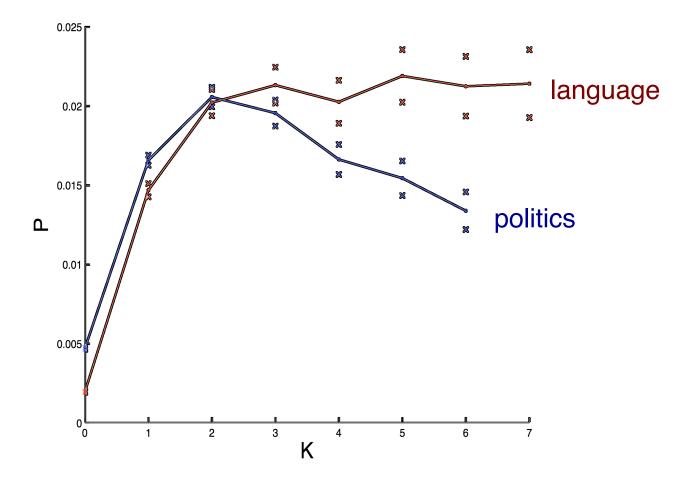
Example of application

LiveJournal membership



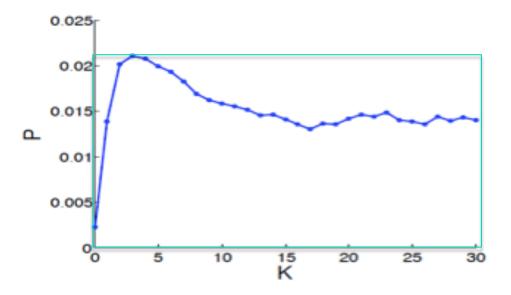
Example of application

Retweeting probability



Spreading on Twitter

Persistence: ratio $\int_0^{k_{max}} curve / \int_0^{k_{max}} peak$



Stickiness: just the peak (assumes we exploit contagion at its top strength)