

Q: what is this?

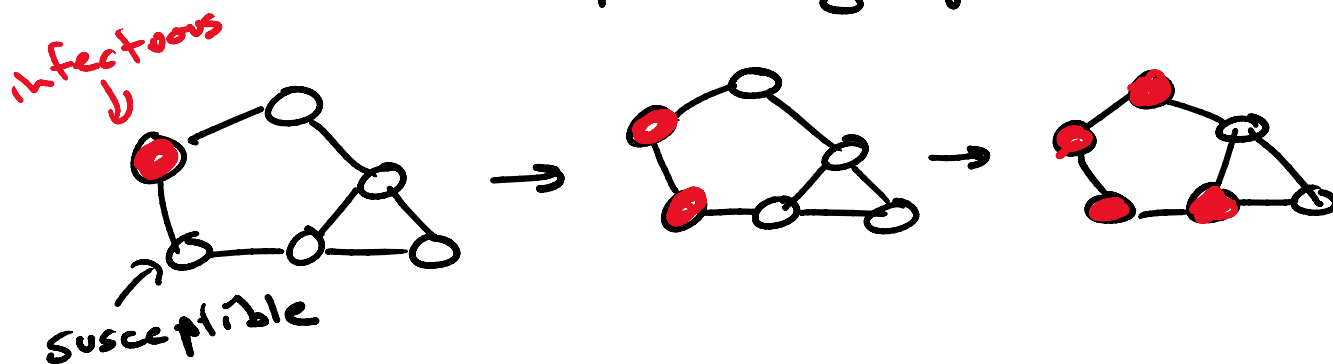
→ study of disease patterns in a population

→ analyzing how diseases spread

Q2: Why do "we" care?

→ Most models are implicitly defined on some underlying contact graph

→ simulations can also be run on an explicit graph



How do these graphs look?

Models → homogeneous (Erdős-Rényi)

→ heterogeneous (Chung-Lu)

... (...)

Simulations (agent based)

- arbitrary complexity
 - geographic/spatial considerations
 - work/school/home
 - movement patterns
-

Math O'clock



Mathematical models for the spread of disease

Classic model: compartmental model

→ population into compartments

→ spread is captured via changes in the populations of the compartments

Classic of the classics: SIR

S: susceptible, can be infected

I: infectious, can spread to S

R: removed, immune/non-contagious

Variations: SIS, SEIR

Model Dynamics of SIR

How does $S \rightarrow I \rightarrow R$ change over time?
 $S \rightarrow I$

$\frac{dS}{dt}$ = change in S over time

$\frac{dI}{dt}$ = " " I " "

$\frac{dR}{dt}$ = " " R " "

Parameters affecting the model

- Population N (often divided out)

- contact rate \rightarrow assume E-R

- probability of transmission

- $\beta = \frac{\text{contacts}}{\text{time}} * \frac{\text{prob. trans.}}{\text{contact}}$

$\beta = \frac{\text{prob. trans.}}{\text{time}}$

- duration of infection $\Rightarrow T$

$\rightarrow \nu = \frac{1}{T}$ \rightarrow rate of recovery

$$\rightarrow \gamma = \frac{1}{T} \rightarrow \text{rate of recovery}$$

Let's get combinatorics

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

possible I ↔ S interactions

↑
N
how many will an infectious infect

$$\frac{dI}{dt} = \frac{\beta I S}{N} - \gamma I$$

rate of recovery

↑
γ I
who recover

$$\frac{dR}{dt} = \gamma I$$

Model simplifications

- N = fixed, births & deaths (vital dynamics)
- ignore reinfectibility (SIS)
- homogeneous mixing
→ contacts more likely power-law
- assumes static behavior

population is constant

0 r 0 r 0 in -

population is constant

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

$$S(t) + I(t) + R(t) = N$$

Note: dynamics only depend on β, γ

↳ R_0 = new infections resulting from a single

$R_0 = \frac{\beta}{\gamma}$ aka basic reproductive number

$R(t) = R = R_{\text{eff}} \Rightarrow$ at same time
 $t \geq 0$

obviously $R(t) \leq R_0$

Let's look at our model dynamics considering the above

$$\frac{ds}{dt} = -\beta \overset{\leftarrow \text{little } s}{is} \quad s(0) \geq 0 \quad \text{IVP}$$

$$\frac{d\bar{i}}{dt} = \beta \bar{i}s - \gamma \bar{i} \quad \bar{i}(0) > 0$$

$$r(t) = 1 - s(t) - \bar{i}(t)$$

Let's consider the limit behaviors as $t \rightarrow \infty$

as $t \rightarrow \infty$

What can this tell us?

→ total infected: $r(\infty)$

$$\approx s(0) - s(\infty)$$

What else?

$\max_t i(t) =$ peak infected over $t = 0 \dots \infty$

Can we get a "nice" solution for these in terms of $\bar{i}(0), \bar{i}(\infty), s(0), s(\infty)$

take $\frac{d\bar{i}}{dt} \Big/ \frac{ds}{dt}$

$$\Rightarrow \frac{d\bar{i}}{ds} = -1 + \frac{\gamma}{\beta s} = -1 + \frac{1}{R_0 s}$$

do same math ...

$$\bar{i}(\infty) - \bar{i}(0) = - (s(\infty) - s(0)) + \frac{\ln\left(\frac{s(0)}{s(\infty)}\right)}{R_0}$$

Let's assume:

$$\bar{i}(\infty) = 0$$

$$\dot{z}(\infty) = 0$$

$$\dot{z}(0) \approx 0$$

$$s(0) \approx 1$$

$$r(0) = 0$$

$$0 = -(s(\infty) - 1) + \frac{\ln(s(\infty))}{R_0}$$

$$0 = 1 - s(\infty) + \frac{\ln(s(\infty))}{R_0}$$

population infected is solely a function of R_0

to get $s(\infty)$ and therefore get $r(\infty) = 1 - s(\infty)$, find the roots

$$\text{If } R_0 = 2$$

$$0 = 1 - s(\infty) + \frac{\ln(s(\infty))}{2}$$

$$\hookrightarrow s(\infty) = 0.2 \rightarrow r(\infty) = 0.8$$

what about $\max_t \dot{z}(t)$

Note: probably depends on R_0

Note x2: if $R_0 \leq 1$ $i_{max} \approx i(0)$

if $R_0 > 1$

$\bar{i}(t)$ increases to a max

$R_0 < 1$ then decays to zero
 $R_0 > 1$



What is i_{max} ? (via math)

$$i_{max} = i(0) + s(0) - \frac{1}{R_0} - \frac{\ln(R_0 s(0))}{R_0}$$

assuming $i(0) = 0$
 $s(0) = 1$

$$i_{max} = 1 - \frac{1}{R_0} - \frac{\ln(R_0)}{R_0}$$

again, just a function of R_0

if $R_0 = 2$, then $i_{max} = 0.15$

if $R_0 = 2$, then $i_{max} = 0.15$

Finally, how can we estimate or calculate R_0 ?

We can consider at the end of an epidemic \rightarrow we can measure $s(\infty), s(0)$

if we assume $s(0) = 1$
 $i(0) = 0$
 $\bar{i}(\infty) = 0$

with ...

$$s(\infty) - 1 = \frac{\ln(s(\infty))}{R_0}$$

$$R_0 = \frac{\ln(s(\infty))}{s(\infty) - 1}$$

in reality, $s(0) \neq 1$

$$\rightarrow s(\infty) - s(0) = \frac{\ln\left(\frac{s(\infty)}{s(0)}\right)}{R_0}$$

solving for R_0

solving for R_0

$$R_0 = \frac{\ln\left(\frac{s(0)}{s(\infty)}\right)}{S(0) - s(\infty)}$$

Note: this is just an estimate as we might be able to infer or measure $s(0), s(\infty)$

what about non-homogeneous networks?
+ SIR models

Really: we can consider the pairwise behaviors between all degree classes

Recall: Chung-Lu graphs are just layered $G(n, p)$ E-R graphs where p is a function of degree-degree attachments

→ so our model is just described as the summation over all pairwise degree classes

dS_k ← big S
susceptibles with degree k ← attachment prob k, l
 n_i, c, r, u, s, \dots ← $T(t)$

$$\frac{dS_k}{dt} = - \underbrace{\beta k S_k(t)}_{\substack{\text{same } \beta \\ \text{as before}}} \underbrace{\sum_l p_{k,l} \frac{I_l(t)}{N_l}}_{\substack{\text{total contacts} \\ \text{probability of contact to an} \\ \text{infectious with degree } l}} \leftarrow \text{population with degree } l$$

$$\frac{dI_k}{dt} = \beta k S_k(t) \sum_l p_{k,l} \frac{I_l(t)}{N_l} - \gamma I_k(t)$$

$$\frac{dR_k}{dt} = \gamma I_k(t)$$

How might we ~~determine~~ estimate R_0 ?

$R_0 \approx \frac{I_2}{I_1}$ consider initially a single infected vertex of transmission per edge prob. degree k w/ prob $\frac{N_k}{N}$

$$I_{e,1} = \bar{\beta} \sum_k p_{e,k} \frac{N_k}{N}$$

$$= \bar{\beta} \sum_k \frac{2k}{2M} \frac{N_k}{N}$$

$$= \frac{\bar{\beta} l}{2M} \sum_k \frac{k N_k}{N}$$

$$= \bar{\beta} l \langle k \rangle$$

avg degree $\langle k \rangle$

... $2M$

$$= \frac{\bar{p} l \langle k \rangle}{2M}$$

$$N \langle k \rangle = \frac{2M}{N}$$

$$= \frac{\bar{p} l \langle k \rangle}{N \langle k \rangle} = \frac{\bar{p} l}{N}$$

Then for our second generation

$$I_{m,2} = \bar{p} \sum_l p_{n,l} I_{l,1}$$

of contacts with infected

we want to determine I_2/I_1 we can sum over all degrees and divide out...

"easy to show"

$$\frac{I_2}{I_1} \Rightarrow R_0 = \bar{p} \frac{\langle k^2 \rangle}{\langle k \rangle}$$

second moment of the degree distribution

For E-R $\Rightarrow R_0 \approx \bar{p} \langle k \rangle$
as $\langle k^2 \rangle \approx \langle k \rangle^2$

For more skewed distributions

$$\langle k^2 \rangle \gg \langle k \rangle^2$$

$\langle k^2 \rangle \gg \langle k \rangle^2$

due to the fat tail of
most real distributions
(super-spreader)

Interesting: fat-tailed sleep