

Network SIR Model - Meanfield.

- Erdős-Rényi graph
- synchronous time step
- Disease states: S - susceptible
I - infectious
R - recovered
- Processes:

- transmission probability p_i
- recovery: p_r (probability of transmitting at next time step)

We could write the network model explicitly:

$$x_{i,t+1} = f(x_{i,t}, x_{j,t} \in \mathcal{N}(x_i))$$

neighboring nodes

v/ high dimensional!

instead, lets make:

Mean field model

- reduces dimension

Take advantage of the fact that nodes are connected randomly.

let N be total number of nodes

Define variables:

$$s = \frac{S}{N} \quad \begin{array}{l} \text{number of} \\ \text{nodes} \\ \text{SUSC.} \end{array} = \text{fraction of nodes that are SUSC.}$$

$$i = \frac{I}{N} = \text{fraction of nodes that are infectious}$$

$$r = \frac{R}{N} = \text{fraction of nodes that are recovered}$$

note $r = 1 - s - i$ since the fractions
sum to 1
(population is fixed)

Probability that a susceptible node j
is infected by node k is:

$$P_{e \times i \times p_i}$$

probability that a $j-k$ edge exists probability that node k is infected probability of transmitting

Then $(1 - P_{e \times i \times p_i})^{N-1}$ is the probability
that node j remains susceptible
at the next time step.

Probability of having an $S \rightarrow S$ transition at the next time step, i.e. the fraction of nodes that go $S \rightarrow S$ is:

$$s (1 - p_e i p_i)^{N-1}$$

fraction of S

probability that they stay S

We can write out our transition probabilities as:
(note we dropped the t subscripts)

Current state	Next state	Probability of transition
S_{usc}	S_{usc}	$s(1 - p_e i p_i)^{N-1}$
S_{usc}	I_{nf}	$s(1 - (1 - p_e i p_i)^{N-1})$
I_{nf}	I_{nf}	$i(1 - p_r)$

Inf	P_{uc}	$i Pr$
P_{uc}	P_{uc}	$r \cdot 1$

Write out the difference equations:

$$s_{t+1} = s_t (1 - p_e i_t p_i)^{N-1}$$

or we could write:

$$s_{t+1} = \overset{\text{current}}{s_t} - \overset{\text{loss}}{\text{transitions to } i}$$

$$= s_t - s_t (1 - (1 - p_e i_t p_i)^{N-1})$$

$$= s_t (1 - (1 - (1 - p_e i_t p_i)^{N-1}))$$

$$= s_t (1 - p_e i_t p_i)^{N-1}$$

$$i_{t+1} = \text{incoming from } s + \text{stay inf. (don't recover)}$$

$$= s_t (1 - (1 - p_e i_t p_i)^{N-1})$$

$$+ i_t (1 - pr)$$

$$= i_t + \text{new transmissions} \\ - \text{recoveries}$$

$$r_{t+1} = i_t p r + r_t$$

$$= 1 - s_{t+1} - i_{t+1}$$

Pulling this all together:

$$s_{t+1} = s_t (1 - p_e i_t p_i)^{N-1}$$

$$i_{t+1} = s_t (1 - (1 - p_e i_t p_i)^{N-1}) \\ + i_t (1 - p r)$$

$$r_{t+1} = r_t + i_t p r$$

Binomial Approximation

$$(1+x)^p \quad \left(\begin{array}{l} x < 1 \\ \text{small} \end{array} \right. \left. \begin{array}{l} xp \ll 1 \end{array} \right)$$

$$\approx 1 + xp$$

Rewriting with the binomial approx
(assuming that $pe^i_t pi$ is small and
small $\times N-1$ also):

$$(1 - pe^i_t pi)^{N-1} \approx 1 - (N-1) pe^i_t pi$$

$$s_{t+1} = s_t (1 - pe^i_t pi)^{N-1}$$

$$= s_t (1 - (N-1) pe^i_t pi)$$

$$= s_t - \underbrace{\left((N-1) pe pi \right)}_b s_t i_t$$

$$s_{t+1} = s_t - b s_t i_t$$

$$i_{t+1} = s_t (1 - (1 - p_e i_t p_i)^{N-1}) + i_t (1 - p_r)$$

$$\approx s_t (1 - (1 - (N-1) p_e i_t p_i)) + i_t (1 - p_r)$$

$$= \underbrace{(N-1) p_e p_i}_{b} s_t i_t + i_t (1 - p_r)$$

$$= b s_t i_t + i_t - p_r i_t$$

$$s_{t+1} = s_t - b s_t i_t$$

$$i_{t+1} = i_t + b s_t i_t - p_r i_t$$

$$r_{t+1} = r_t + p_r i_t$$

This looks like an SIR model - it is!

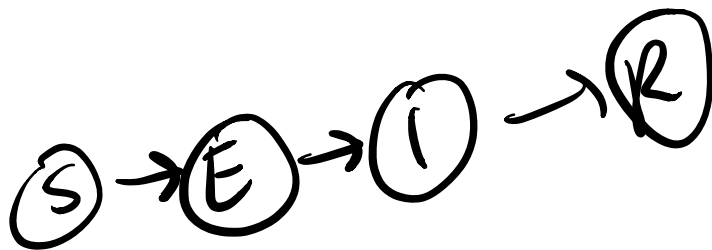
Also looks like a discretization
of the standard ODE
version:

$$\frac{dS}{dt} = -\beta SI$$

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

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

a different model:



$$s_{t+1} = s_t - b s_t i_t$$

$$e_{t+1} = b s_t i_t - p e e$$

$$i_{t+1} = p e e - p r i \quad \text{etc.}$$

SIR Equilibria

How can the mean field model help us?

Solve for where:

$$s_{t+1} = s_t$$

$$i_{t+1} = i_t$$

$$r_{t+1} = r_t$$

} this is an equilibrium point for our model

This gives us:

$$i_t = 0$$

$$s_t + r_t = 1$$

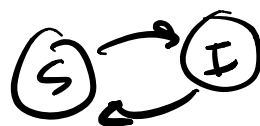
any set of values for s, r that fit this condition will work.

SIR model can't have long term

eventually the disease must die out.

$\bar{i} \neq 0$ as steady state

SIS model equilibria



$$s_{t+1} = s_t - b s_t i_t + p r i_t$$

$$i_{t+1} = i_t + b s_t i_t - p r i_t$$

Note w/ fixed pop. size:

$$s_t + i_t = 1 \quad s_t = 1 - i_t$$

We can write the model as 1 equation:

$$i_{t+1} = i_t + b(1 - i_t)i_t - p r i_t$$

Solve for equilibria by setting $i_{t+1} = i_t$:

$$0 = b s_t i_t - p r i_t$$

$$0 = \underbrace{(b s_t - p r)}_{=0} i_t \rightarrow s = p r / b$$

} mean field
for ER network
w/ SIS
dynamics

Two possible equilibria:

Disease free EQ.

$$i_t = 0$$
$$s_t = 1$$

Endemic Eq.

$$s_t = pr/b$$

$$i_t = 1 - pr/b$$

We can look at stability by noting

that $i_{t+1} - i_t = \text{change in } i$

if + then i will grow

if - then i will decline

$$i_{t+1} - i_t = (bs_t - pr) i_t$$

controls whether
the RHS is + or -

If we start near the DFE then if

$b s_t - p r > 0$ then the epidemic will grow

if $b s_t - p r < 0$ it will decline

at DFE $i_t = 0$ $s_t = 1$

So near DFE:

$$b s_t - p r \approx b - p r > 0 \quad \text{vs } < 0$$

≈ 1

$$b > p r$$

that will control growth of disease

$$R_0 = \boxed{\frac{b}{p r}} > 1$$

R_0

$R_0 > 1$ the disease \uparrow

$R_0 < 1$ the disease \downarrow

$$R_0 = b \cdot \frac{1}{p r}$$

d. null -

mean

$$b = (N-1) p_e p_i$$

average
degree

prob
of transmission

expected number of cases
1 person generates in 1 time
step

$\frac{1}{pr}$ = approximate number of time
steps we expect to
stay infected.

Why? (comes from basic probability
will post notes)

But anyhow -

together

$$R_0 = \frac{b}{pr}$$

= total cases generated
by 1 infected person
over the time
we

try to
infectious.

Extra note on why $1/pr =$ expected number of steps until recovery (we didn't have time in class for this so I figured I'd add it on)

* take an infected node. probability of recovery @ next time = pr
memoryless, so we can write:

$$E[X] = 1 + pr \cdot 0 + (1-pr) E[X]$$

time to recover I have to take one step. keep going if didn't. expected value next time is same as now since memoryless

Solve for $E[X]$:

$$E[X] (1 - (1-pr)) = 1$$

$$E[X] = \frac{1}{pr}$$