Complex Systems 530: Network Mean Field Models

2/20/19

# Network SIR Model

- **Network Structure**: Suppose individuals are connected randomly — Erdös-Renyi graph.
  - Can treat as a fixed Erdös-Renyi graph, or as a network where the edges are re-selected at each time step.
  - Let probability of each edge be $p_e$
- **Time step**: synchronous
- **Disease states**: susceptible, infectious, recovered (immune)
- **Rules**: at each time step
  - **Transmission**: if susceptible, can be infected by each infectious neighbor at the next time step w/ probability $p_i$
  - **Recovery**: if infectious, can recover at

next time step w/ probability Pr

We can write the network model as a difference equation system

$$x_{i,t+1} = \underbrace{f(x_{j,t} \in N(x_i))}_{\text{function of the states of the neighboring nodes}}$$

$x_{i,t+1}$: state of node $i$

However, this requires one variable for each node — very high-dimensional!

We can build a mean field model to reduce dimension.

↳ take advantage that nodes use same set of general rules, and are connected randomly.

# Building the mean field model

Let $N$ be total number of nodes.

$s = \frac{S}{N}$ = fraction of nodes who are susceptible

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

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

note $r = 1 - s - i$, since the total population is fixed.

Probability that a susc. node $j$ is infected by node $k$ is:

$$p_e \times i \times p_i$$

- $p_e$: probability that $j$-$k$ edge exists.
- $i$: probability node $k$ is infectious
- $p_i$: probability of transmission

Then $(1 - p_e i p_i)^{N-1}$ = probability that node $j$ remains susceptible at the next time step.

Probability of having a $S \to S$ transition in the next timestep, i.e. the fraction of nodes we expect to see go $S \to S$ is: $S(1 - p_e i p_i)^{N-1}$

- $S$: fraction $S$ to start
- $(1 - p_e i p_i)^{N-1}$: not infected by any other node

We can work out the probabilities of each transition as:

| Current state | Next state | Probability of transition |
|---|---|---|
| Susc. | Susc | $s(1 - p_e i p_i)^{N-1}$ |
| Susc. | Inf. | $s(1 - (1 - p_e i p_i)^{N-1})$ |
| Inf. | Inf. | $i(1 - p_r)$ |
| Inf. | Rec. | $i p_r$ |

Then we can write difference equations for the fraction of nodes in each state:

$S_{t+1}$ = only people who were S and stay S.

$$= S_t \left(1 - p_e i_t p_i\right)^{N-1}$$ (from table)

or can write:

$$= S_t - S \to I \text{ transitions}$$

current − loss

$$= S_t - S_t \left(1 - \left(1 - p_e i_t p_i\right)^{N-1}\right)$$

$$= S_t \left(1 - \left(1 - \left(1 - p_e i_t p_i\right)^{N-1}\right)\right)$$

$$= S_t \left(1 - p_e i_t p_i\right)^{N-1}$$

$i_{t+1}$ = incoming from S + stay sick (do not recover)

$$= S_t \left(1 - \left(1 - p_e i_t p_i\right)^{N-1}\right) + i_t \left(1 - p_r\right)$$

(note this is also same as $i_t$ + incoming − recovery)

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

(or we can write out similarly)

Note the eqns above are good, but we can simplify further — the binomial approx tells us that when $p_e i p_i$ is small (i.e. probability of connection and subsequent transmission w/ a node is small), then $(1 - p_e i p_i)^{N-1} \approx 1 - (N-1) p_e i p_i$.

Then we can rewrite as:

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

$$\approx s_t \left(1 - (N-1) p_e i_t p_i\right)$$

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

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

and similarly

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

$$\approx s_t \left(1 - \left(1 - (N-1) p_e i_t p_i\right)\right)$$

$$+ i_t(1-p_r)$$

$$= s_t (N-1) p_e p_i i_t$$

$$+ i_t (1-p_r)$$

$$= b s_t i_t \quad i_t(1-p_r)$$

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

And

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

$$= (1 - s_t - i_t) + p_r i_t$$

$r_t$: number we had

new recoveries

This looks a lot like the classic SIR model! (it is)

We can even go further and simplify to a set of ODE's.

To do this, we will need to make our timestep smaller and smaller — currently $\Delta t = 1$. Let's rewrite w/ $\Delta t$ explicit:

$$i_{t+\Delta t} = i_t + b s_t i_t - p r_t$$

$$\underbrace{i_{t+\Delta t} - i_t}_{\text{change in } i} = b s_t i_t - p_r r_t$$

$$\Delta i$$

$$\frac{i_{t+\Delta t} - i_t}{\Delta t} = \frac{b s_t i_t - p_r r_t}{\Delta t}$$

$$\frac{\Delta i}{\Delta t} = \frac{b s_t i_t - p_r r_t}{\Delta t}$$

take the limit as $\Delta t \to 0$ and we get a derivative!

What about RHS? Need to think about how the

probabilities change as $\Delta t$ gets smaller. A few ways to do this — won't get into details now, but we can choose something "reasonable" (e.g. assuming constant rate of events etc.)

That will give us:

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

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

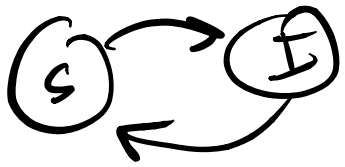
$$\frac{dR}{dt} = \gamma I$$

i.e. classic SIR.

But for now, lets stick w/ the differee eqns in above.

The differee eqns or ODE's that we get have a very standard form - if 2 (or more) nodes interact, usually get a product of the state variables, and if a node can independently do something w/ constant probability, typically turns out linear.

So, for example, if an SIS model, i.e.




recovery returns to S (not immune), then we would get:

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

$$i_{t+1} = i_t + b s_t i_t - pr\, i_t$$

note $s_t + i_t = 1$ so only need one eqn for this model.

How can the mean-field model help us?

- simpler to code
- easier to analyze

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## SIR equilibria

We can find equilibria by solving for where $s_{t+1} = s_t$,

$i_{t+1} = i_t$, $r_{t+1} = r_t$.

(Call of these must be true to be at eq.)

This gives us:

$$i_t = 0$$

$$s_t + r_t = 1$$

Note any of these s.t. $s_t + r_t = 1$ will work.

But this shows us that eventually the disease must die out.

## SIS Equilibria

Similarly, need $s_{t+1} = s_t$, $i_{t+1} = i_t$. But since $s = 1 - i$, one need to check for one eqn.

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

$$\| \quad \searrow$$

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

$$0 = (bs_t - \rho r) i_t$$

two possible equilibria:

| Disease free | Endemic |
| --- | --- |
| $i_t = 0$ | $s_t = \rho r / b$ |
| $s_t = 1$ | $i_t = 1 - \rho r / b$ |

We can look at stability at each of these equilibria -

Note that

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

if +, $i$ grows

if −, $i$ declines

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

this will control the sign

So, if we start @ disease free equilibrium (DFE) then we will grow more i's when $bs_t - pr > 0$ and we will lose i's when $bs_t \overset{\approx 1}{-} pr < 0$

If we lose i's then it will go back to DFE.

If we grow, it will go to endemic equil.

We can revisit this condition as:

$$\frac{b}{\rho r} < 1 \Rightarrow$$ DFE stable
EE unstable
disease dies out

$$\frac{b}{\rho r} > 1 \Rightarrow$$ ~~DFE~~ unstable
EE stable
disease persists

This is $R_0$!

$$b = \underbrace{(N-1)}_{\text{average degree}} \underbrace{P_e P_i}_{P(\text{infection})}$$

expected cases in next time step generated by 1 infected person in a fully susc. population

$(s \approx 1)$

$1/p_r$ = approximate number of steps we expect to stay infected.
(this comes from classic probability)*

$\frac{b}{p_r}$ = total cases generated by 1 infectious individual in a susc. pop.

Okay, so how does the mean field actually match up?

* take an infected node. probability of recovery @ next time = $p_r$

memoryless, so we can write:

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

- $E[X]$: time to recovery
- $1$: I have to take one step.
- $p_r \cdot 0$: stop if recovered
- $(1-p_r)$: keep going if didn't.
- $E[X]$: expected value next time is same as now given memoryless

Solve for $E[X]$:

$$E[X]\left(1-(1-p_r)\right) = 1$$

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