

Scale-free & Other Network Mean-field Models

(borrowed from Sayama
Ch (8))

- What if our network isn't Erdős-Rényi?

If we can assume a common connection probability p_c , it simplifies a lot of things - all nodes basically can be treated the same. But what if not?

Now we need to consider the degree distribution: $P(k)$
↑ degree

We can look at transition probabilities for all nodes of a given degree.

$P(k)$ = probability (fraction) of nodes w/ degree k .

$s(k)$ = probability (fraction) of nodes of degree k to be susceptible

$i(k)$ = probability (fraction) of nodes of degree k to be infected

Let's work this out for an SIS model (simpler)

Remember, our transition probability table for an SIS model was:

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

note we can just write in terms of i since $s = (1-i)$

But now - our transition probabilities need to break down by degree.

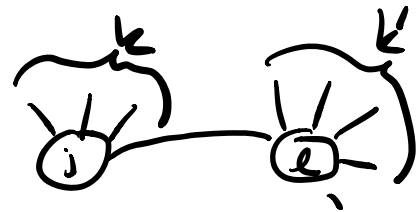
Note that $I \rightarrow S$ and $I \rightarrow I$ won't change, because they don't depend on interaction w/ any other nodes, i.e. degree doesn't matter for these.

But the transmission terms will change!

Let's look at $S \rightarrow S$ and $S \rightarrow I$.

- What is the probability of a susceptible node of degree k becoming infected by one of its neighbors?
 - depends on the degree of that neighbor! They will each have a different probability of being

infected, $i(k)$.



$$P(\text{svsc node } j \text{ is infected by neighbor } l) = \sum_{k'} P_n(k'|k) i(k') p_i$$

let k' be l 's degree (unknown)

Conditional probability that l is degree k' , given that j is degree k (the neighbor distribution)

fraction of nodes of degree k' that are infected

transmission probability

what is this going to be?

$P_n(k'|k)$ is tricky to sort out!

Is the network assortative/disassortative by degree? If yes, $P_n(k'|k)$ will depend on k . But if not, we can at

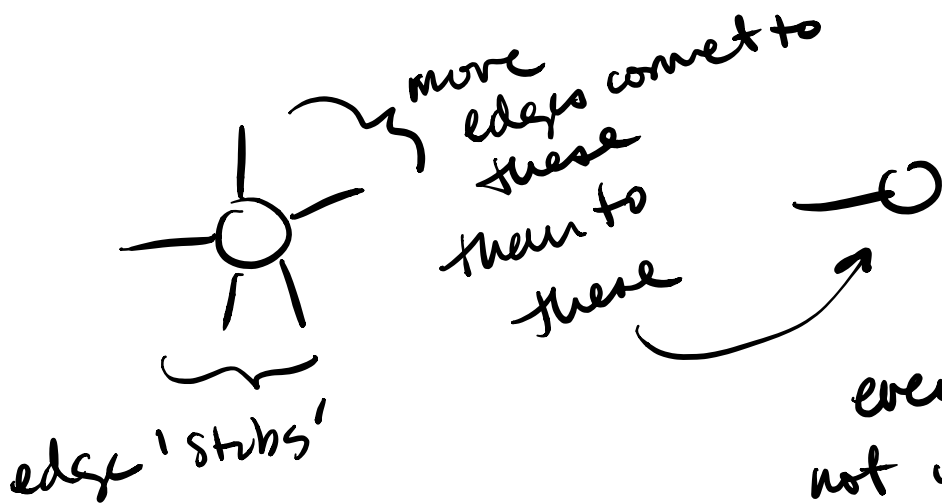
least simplify to $P_n(k')$ only!

Now, is $P_n(k') = P(k)$?

↗
neighbor degree
dist

↖
degree
dist

No! (Weirdly) High degree ppl are more likely to be neighbors.



even if not worried about assortativity

This is the "friendship paradox" ("your friends have more friends than you do.")

So, how to get $P_n(k')$?

What's the probability that node j connects to a 'stub' of degree k' ?

$$k' N \cdot P(k') = \text{total 'stubs' on } k' \text{ degree nodes}$$

each one has k' edges attached (stubs)

total nodes of degree k'

probability of choosing an initial node of degree k' (note this is degree dist! not neighbor list)

$$\sum_{k'} k' N P(k') = \text{total 'stubs' in the network}$$

If node j selects a stub randomly,
we get:

$$P_n(k') =$$

$$\frac{k' N P(k')}{\sum_{k'} k' N P(k')}$$

probability that node
attaches to a degree k'
node.
(i.e. probability that
node l is degree k')

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

denominator
= average
degree,
denoted
 $\langle k \rangle$

↑ this will be > 1 when
 $k' > \langle k \rangle$
and < 1 when
 $k' < \langle k \rangle$

so we upweight
neighbors when higher
degree.

(Side note - how does $\langle k \rangle$ (average degree)

Compare to average neighbor degree $\langle k_n \rangle$?

$$\langle k_n \rangle = \sum_{k'} k' P_n(k') = \sum_{k'} k' \frac{k' P(k')}{\langle k \rangle}$$

$$= \sum_{k'} \frac{k'^2 P(k')}{\langle k \rangle} = \frac{\langle k^2 \rangle}{\langle k \rangle}$$

$$= \frac{\langle k \rangle^2 + \sigma(k)^2}{\langle k \rangle} \leftarrow \text{variance of } P(k)$$

$$= \langle k \rangle + \underbrace{\frac{\sigma(k)^2}{\langle k \rangle}}_{\text{positive}}$$

so yes, on average $\langle k_n \rangle > \langle k \rangle$

Back to the topic
at hand...)

Ok, so now we can plug in for

$P_n(k')$:

$$P(\text{svsc node } j \text{ is infected by neighbor } l) = \sum_{k'} P_n(k'|k) i(k') p_i$$

$$= \sum_{k'} \frac{k'}{\langle k \rangle} P(k') i(k') p_i$$

\uparrow
average degree

probability that l is degree k'

probability that l is infected

probability of transmission

S \rightarrow S transition:

Now we need to make sure that

S doesn't get infected by any of its k neighbors.

fraction/probability of $S \rightarrow S$ transitions:

$$s(k) \left(1 - \sum_{k'} \frac{k'}{\langle k \rangle} P(k') i(k') p_i \right)^k$$

fraction/probability of nodes that are S

probability that node j doesn't get infected by any of their k neighbors.

$$= \underbrace{(1 - i(k))}_{\text{for SIS model, } s(k) = 1 - i(k)} \left(1 - \sum_{k'} \frac{k'}{\langle k \rangle} P(k') i(k') p_i \right)^k$$

Now we can rewrite our table as:

Current State	Next State	Probability of transition
Susc. of degree k	Susc. of degree k	$(1 - i(k)) \left(1 - \sum_{k' < k} \frac{k'}{k} P(k') i(k') p_i\right)^k$
Susc. of degree k	Inf. of degree k	$(1 - i(k)) \left(1 - \left(1 - \sum_{k' < k} \frac{k'}{k} P(k') i(k') p_i\right)^k\right)$
Inf. of degree k	Susc. of degree k	$i(k) p_r$
Inf. of degree k	Inf. of degree k	$i(k) (1 - p_r)$

from this, we can work out the difference equations! Note we'll get multiple difference eqns for each degree — we can see how

more complex networks add to the complexity of our mean-field model too!

If we use the same binomial approx again, we get:

$$i_{t+1}(k) = (1 - i_t(k)) (1 - (1 - k \text{ in } p_i)) + i_t(k) (1 - p_r)$$

$$= \underbrace{i_t(k)}_{\text{current } i} + \underbrace{(1 - i_t(k))}_{s(k)} \underbrace{k \text{ in } p_i}_{\text{new transmissions}} - \underbrace{i_t(k) p_r}_{\text{recoveries}}$$

where $i_n = \frac{\sum_{k'} k' P(k') i(k')}{\langle k \rangle}$



overall probability that
a neighbor is infected

Note that new new transmission
is a sum of things of the
form $b_{k'} i(k') s(k) \forall k'$
 \uparrow const.

You can do a similar analysis —
calculate equilibria, etc.

We can see that disease free equilibrium still exists, i.e.

$$\text{where } i(k) = 0 \quad \forall k$$

(since then $i_{\pm}(k) = i_{\pm}(k') = 0$
in the equation above)

But what about the endemic equilibrium?

Yes - requires some more

calculation, and we will need
to fill in the degree

distribution $P(k)$ (in in).

If we use the ER degree distribution
we get something roughly consistent
w/ previous mean field (although
w/ some nuance - see Sayama
Ch 18)

Scale free degree dist

for scale free, the degree dist
is known to be

$$P(k) = 2m^2 k^{-3}$$

where m is the number of
nodes each new node attaches
to.

If we plug in for $P(k)$ and solve for $i_{t+1}(k) = i_t(k)$, we get an endemic equilibrium!

$$i_n \approx \frac{pr}{\left(e^{\frac{pr}{mpi}} - 1\right) mpi}$$

Can check stability, and you end up finding that the endemic eq. is always stable! There is no actual threshold — you can always have an epidemic. But — stochasticity w/ small numbers means that you still won't always actually observe an

epidemic. Need to use large networks
to minimize stochastic effects (and
start w/ more than one infected
node) to see this.

(pause to
work w/
code)