Session 30: Network modelling

Modelling and the Dynamics of Infectious Diseases

LSHTM

Outline

1. What are network models?
2. Some terminology
3. Modelling human social networks
4. Epidemics on networks
5. Pair approximation models
6. Limitations/assumptions

Mass action models

- Simplest model of population behaviour
- Everyone meets everyone else
- Meetings are instantaneous and not repeated

$$\frac{dS}{dt} = -\lambda S$$

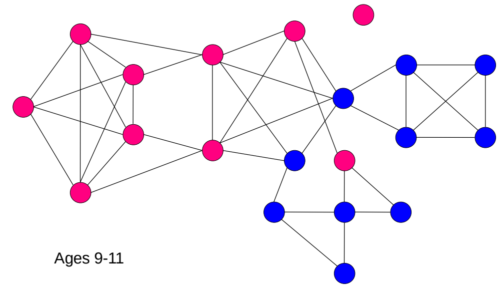
$$\frac{dI}{dt} = \lambda S - \gamma I$$

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

This is not realistic:

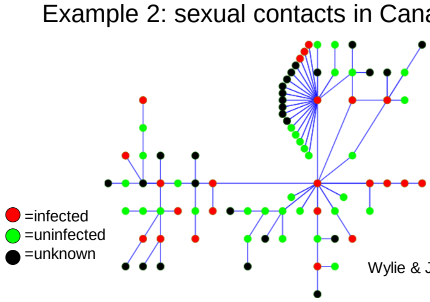
- We only ever meet a small fraction of the population
- Many of our contacts are repeated

Example 1: school contacts in Canterbury



- Entire class in school asked to name their social contacts.
- Plot all links that are confirmed by both individuals.

Example 2: sexual contacts in Canada

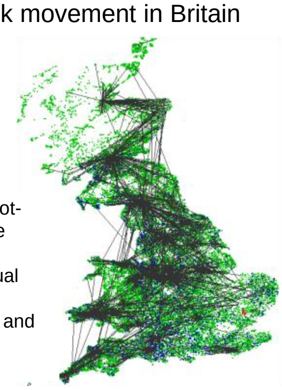


Wylie & Jolly, 2001

- Network data emerged from disease control efforts
- Seek sexual partners of anyone infected with Chlamydia
- Any found to be infected have their partners traced too

Example 3: livestock movement in Britain

- Following mad-cow and foot-and-mouth diseases, cattle movements are recorded.
- Data kept for each individual cow.
- Know date of movements, and place from/to which they occurred.



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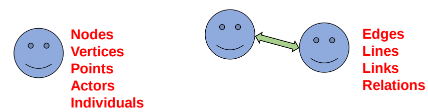
- A network is a set of items called nodes and connections between those items called links



- We'll mainly think of nodes as representing individual people and of edges representing a social interaction
- Edges are usually undirected: if A is linked to B, B is linked to A. They can be directed however: e.g. farms as nodes, and livestock movements as edges

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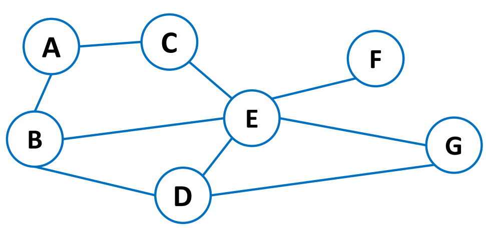
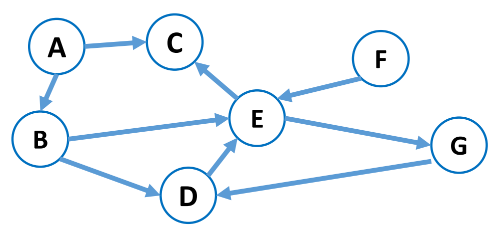


- Contacts/neighbours/partners: People with a link between them
- Degree: number of neighbours a person has



- Contacts/neighbours/partners: People with a link between them
- Degree: number of neighbours a person has
- In a directed graph, we can distinguish between indegree and outdegree

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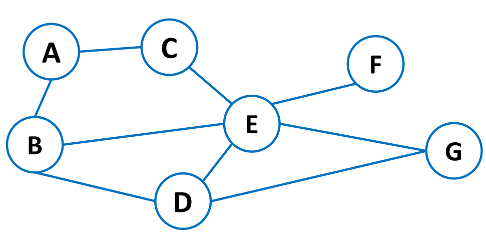
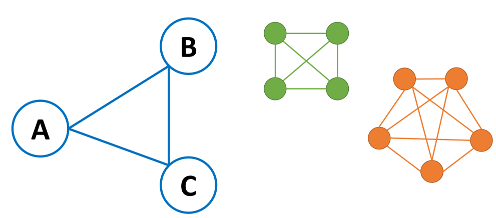


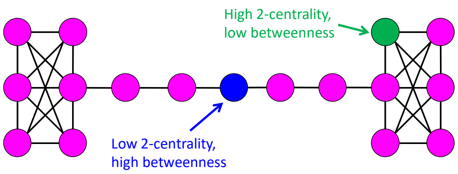
- If two nodes can be reached from each other by following links, they have a path between them.
- The distance between two points is the length of the shortest path between them.
- The diameter of a network is the largest distance (i.e. the longest shortest path).



- In social networks, often find that "the friend of my friend is my friend" (transitivity): shows up as triangles.
- Larger structures are also common: cliques of many people who all interact.
- Populations with many cliques (high transitivity) are said to be clustered.
- The clustering coefficient of a network is the probability that two randomly chosen contacts of a node will be connected

Centrality measures

- For any node *m* we can define:
  - s-centrality: number of nodes at distance ≤s from *m*; (N.B. 1-centrality=degree).
  - Betweenness: fraction of shortest paths between two nodes that go via node m.
- These provide ways to judge which nodes are "important", but don't always agree.



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Modelling human social networks

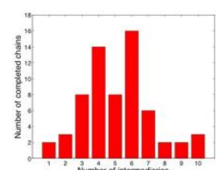
- Would ideally know the complete structure of the entire network, but this is rarely feasible
  - Vast data requirements
  - Not always clear what counts as a contact
  - Privacy issues
- Can avoid data problems by using idealised networks that only require a few parameters to describe
- Idealised networks need to capture two key characteristics of human social networks:
  - High levels of clustering, corresponding to social cliques.
  - Short path lengths – six degrees of separation.

A short aside: six degrees of separation

Experimental attempt in the 1960s to measure the diameter of American social networks, devised by sociologist Stanley Milgram.

- Participants had to transfer a letter from Nebraska to Boston.
- Letter was passed (or posted) only via personal connections.

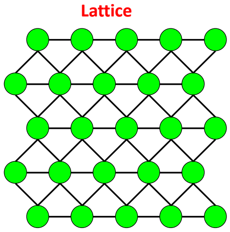
- Of 296 chains, 64 arrived.
- Much easier than one might expect; mean number of intermediaries was 5.2.



Recent studies using e-mail give similar results.

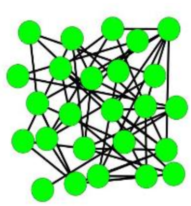
How should we model human social networks?

Lattice



High clustering,
but long paths

Random

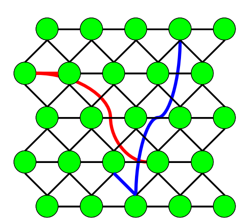


Short paths,
but low clustering

Neither of these matches observed network properties.

In a paper in 1998, Watts and Strogatz observed that we can turn a lattice into a random network by rewiring links:

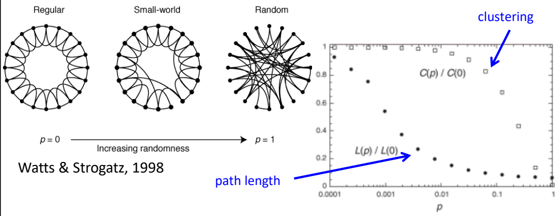
Procedure:
1. Pick a link.
2. Break it off at one end.
3. Reattach somewhere else at random.
4. Continue until proportion *p* of links rewired.



As *p* increases:
- Average path length falls.
- Average clustering falls.
- Lattice becomes a random network.

Small-world networks

- p=0: regular lattice.
- p=1: random network.

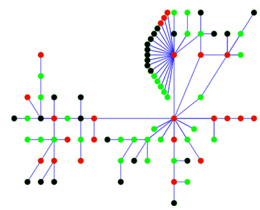


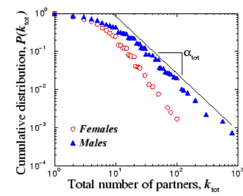
Watts & Strogatz, 1998

- For intermediate values of rewiring, we observe networks with high clustering but short paths: **small-world** network.
- Simple model captures important properties.

Scale-free networks

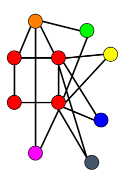
- Some networks (sexual partners, Internet) have more high degree nodes than these models allow.
- **Scale-free** networks have these dominant high degree **hubs**.





Liljeros et al, 2001

- Scale-free networks can be *dynamically* generated by **preferential attachment**.
- Probability of connecting to a node is proportional to that node's degree: "the rich get richer".



- Original four nodes end up with degrees of 2, 3, 6, and 7

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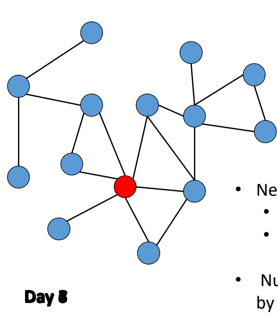
Epidemics on networks



- Susceptible
- Infected
- Recovered

- Need to know:
  - Recovery rate = r
  - Transmission rate along a link = τ
- Number of contacts, k, specified by the network

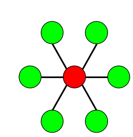
Networks v. mass-action: R_0

- On networks, epidemics are slowed "spatially" – long paths – and "locally" – depletion of susceptibles.
- Previously defined R_0 as "the mean number of secondary cases if the population was entirely susceptible".

Recall: mass-action approximation gives $R_0 = \frac{bN}{r}$

N = population size;
β = transmission parameter
r = recovery rate

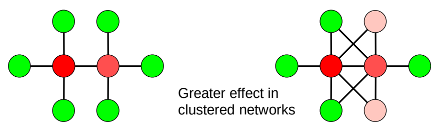
- In a mass-action model, R_0 can be increased indefinitely by increasing the transmission rate, infectious period, or population size.
- The same cannot happen on a network - limited by neighbourhood size.



= infected
= susceptible

"… if the population was entirely susceptible"

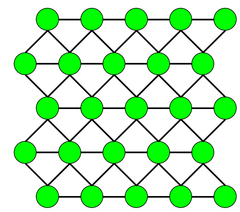
- Any secondary cases mean that the population is no longer entirely susceptible.
- In the mass-action model this doesn't matter - the first few cases behave independently because they hardly interact.
- This is no longer true on a network:



- Early cases are clustered and infection quickly becomes locally saturated.
- The "classic" definition of R_0 is no longer as useful

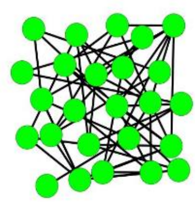
Epidemic behaviour: lattice network

- Epidemic spread is strictly local
- The epidemic proceeds as a wave
- Initial growth is slow due to local depletion of susceptibles
- Epidemic progress is slow



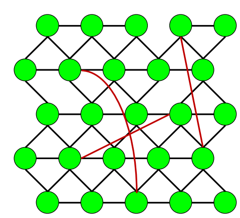
Epidemic behaviour: random

- Growth rate slower and final size smaller than equivalent mass action models
- Nevertheless, behaviours more similarly to mass action models than most network structures



Epidemic behaviour: small world

- Transmission mainly local
- Long-range links allow rapid transmission to new areas, increasing epidemic synchronisation



Epidemic behaviour: scale-free

- Hubs act as super-spreaders
- Small diameter leading to rapid spread through network
- Target interventions at hubs for maximum impact

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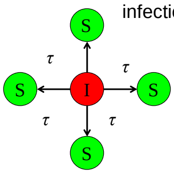
Pair approximation model

- A deterministic approximation of spread on a network.
- Allows long-lasting contacts and allows correlations to build up between connected individuals.

Rate of new infections $= \tau \times$ number of contacts between an S and an I



Here, rate of new infections = 4τ

- Notation: let [SI] be **number of links** between an S and an I:

$$\Rightarrow \frac{dS}{dt} = -\tau[SI]$$

- In the mass-action model we would approximate [SI]:

$$[SI] \approx S \times k \times \frac{I}{N}$$

number of contacts

probability a contact is infected

- Giving the familiar: $\frac{dS}{dt} = -\frac{\tau k}{N} \times SI$

mass-action λ

- This ignores all the network information so, instead, we leave the pairs term in the equations:

$$dS/dt = -\tau[SI]$$

$$dI/dt = \tau[SI] - rI$$

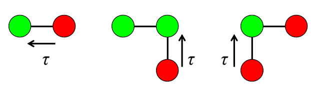
- We now need to know how the number of S-I pairs changes.

$$d[SI]/dt = ?$$

Pair dynamics

- Simple to calculate: all that can happen is recovery and transmission.
- Recovery only matters if it takes place within the pair.
- Transmission can **either** happen within a pair **or** infection can enter the pair from outside.

$$\Rightarrow d[SI]/dt = -r[SI] \quad - \tau[SI] \quad + \tau[SSI] \quad - \tau[ISI]$$



- Can do the same thing for other pair types ([SS], [IR], etc.)

Triples approximation

For a network where each node has degree k:

$$[ABC] \approx [AB] \times (k-1) \times \frac{[BC]}{kB}$$

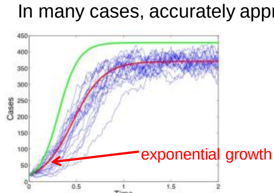
number of other partners of a B in an A-B pair

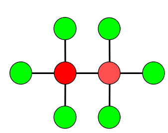
probability that neighbour of a B is a C

- This allows us to close the system at the level of pairs and to iterate the differential equations.
- Can be simply adapted to model any network: just need to know how nodes of different degrees interact.

Properties of pair approximation model

- Models the long-lasting connections described by networks.
- Easy to parameterise: uses same data as mass-action model.
- In many cases, accurately approximates network spread.





Question: why k-2?

- Can determine "R_0" using the initial epidemic growth rate:
  - pair approximation model: "R_0" = (k-2) τ/r.
  - compare with mass-action: $R_0 = k\tau/r$.
- As expected, local saturation slows spread on networks.

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Major assumptions (and adaptations)

- Assumes that all links are the same
  - Often untrue, e.g. more likely to transmit flu to family member than casual acquaintance
  - Can use weighted links, e.g. based on duration of contact
  - Requires additional data

Major assumptions (and adaptations)

- Assumes that all links are always present
  - May be acceptable if contacts are sufficiently frequent relative to duration of infectious period
  - Less realistic for other types of contact, e.g. STIs
  - Dynamic networks – links form and dissolve over time
  - As networks become more dynamic, then approach mass action models

Summary

- Can use networks to describe how a population interacts.
- Observed social networks often have low path lengths and high clustering: lots of interconnected cliques.
- Epidemics are fundamentally different on networks.
- Can use a range of models to represent disease spread on networks.
  - Stochastic approach allows the role of each node to be assessed.
  - Deterministic approximations are available.
- As with all models, some major assumptions are made. It’s important to consider the effect of those assumptions on your research questions.