Network Analysis and Mining
11. Spreading phenomena

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Outline

About this section

Initially: from Part A (Complex Networks Analysis tools)
$\rightarrow$ to Part B (Graph mining)

- use our knowledge and tools to explore real networks
- adapt them to specific problems

$\rightarrow$ problem-oriented view

Illustration: a few Social Network Analysis concepts

Applying our tools to Social Network Analysis
Epidemic spreading models on graphs
The homophily phenomenon
Local density and community structure
Impact on social contagion

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What is homophily?

From Greek, *homo:* same, similar and *philos:* friend of, to like
$\rightarrow$ *"birds of a feather flock together"*

Observed for a long time in sociology:

- smoking habits, food habits
- residential segregation
- voting behavior
- ...

Do we observe this phenomenon in Social Networks Analysis?

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Do we observe this phenomenon in Social Networks Analysis?

Structural homophily, based on degree

Degree-based assortativity

Do high-degree nodes connect to high-degree nodes?

Measured using:

- q_k probability distribution of the remaining degree:
  if p_k is the degree distribution then $q_k = \frac{(k+1)p_{k+1}}{\sum_j j.p_j}$
- e_{jk} joint probability of remaining degree distribution (RDD),
  i.e. probability to pick an edge which ends have remaining degree j and k

We measure the assortativity coefficient r:

$$r = \frac{\sum_{j,k} j.k.(e_{jk} - q_j q_k)}{\sigma_q^2} \text{ with } \sigma_q^2 = \frac{1}{n} \sum_k q_k (k - \overline{k})^2$$

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- r measures if nodes connected together in the graph have more similar degrees than expected (if connected randomly)
- σ_q^2 is the variance of the remaining degree distribution (RDD) q_k
- r is a normalized quantity ($\in [-1:1]$)
- r: ratio between covariance across links of RDD and variance of RDD

Newman - *Phys. Rev. E, 2003*

Structural homophily, based on degree

Typical degree-assortativity on social networks:

- astrophysics coauthorship: $r = 0.235$ (Georgia Tech data)
- actor collaboration: $r = 0.227$ (Notre-Dame Univ data)
- friendship network: $r = 0.039$ (Livejournal data)

$\rightarrow$ social networks are usually degree-assortative

Note that all complex networks are not degree-assortative:

- Internet AS level: $r = -0.215$ (UCLA data)
- human protein network: $r = -0.126$ (Vidal data)
- US power grid network: $r = 0.003$ (Tore Opsahl data)

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Structural homophily: other kinds of assortativity

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r: ratio covariance across ties / variance of remaining degree k

General assortativity

$$\rho = \frac{\sum_{\lambda,\kappa} \lambda.\kappa.(\epsilon_{\lambda\kappa} - \chi_\lambda \chi_\kappa)}{\sigma_\chi^2} \text{ with } \sigma_\chi^2 = \frac{1}{n}\sum_\kappa \chi_\kappa (\kappa - \overline{\kappa})^2$$

ρ: ratio covariance across links / variance of characteristic κ
ϵ: joint probability across link of characteristic κ
χ: probability distribution of characteristic κ

examples for κ: age, salary, number of children. . .

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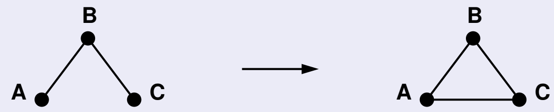
Transitivity and clustering

Reminder: social networks have a high average clustering

Triadic closure phenomenon

Old concept in sociology (Simmel, 1908).
Hypothesis on the growth dynamics of a network:



Consequences:

- high clustering
- large number of cliques (complete subgraphs)
- densification over time

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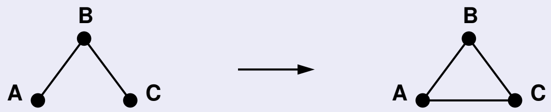

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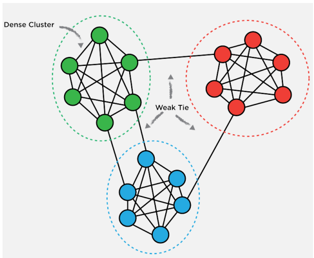
Transitivity and clustering

$\Rightarrow$ schematic picture of social networks

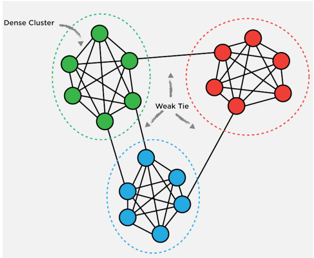


credits image: V.Gauthier

Disclaimer: only a schematic representation
misses overlaps in clusters, groups hierarchy, core/periphery...

Transitivity and clustering

⇒ schematic picture of social networks



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About weak ties ...

Hypothesis of the strength of weak tie (link) Granovetter - *1973*

A "weak tie" is a link in a social network which represents a relation which is not frequently maintained

It is argued that weak ties play an essential role as they ensure connections between groups

What is a measure of strength of a tie in social sciences?

- frequent contacts
- strong affinity (if measurable)
- structural criterion: many mutual neighbors

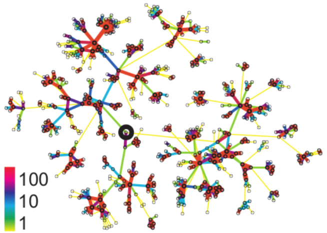
About weak ties ...

Onnela et al. - *2007*

Experimental validation on a phonecall network
→ are weaker links between clusters?

- strength of a relationship = cumulative duration of calls
- link between groups measured with link betweenness

weight (color) = cumulative duration of calls



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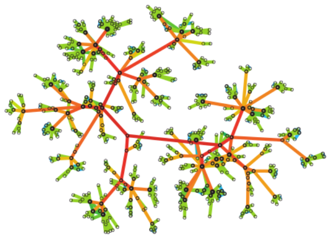

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Quiz: what could you plot to check the correlation ?

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e.g.: link strength vs. link betweenness, correlation coefficient

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Effects on spreading in a social network

Examples: innovation spreading, rumor spreading, adversiting. . .

What can we expect from the previous observations?

- fast spreading within a community
- use of weak links to spread from a group to another

In practice hard to measure experimentally:

- "contagion" hard to track and isolate
- spreading rarely reaches a large part of a network

$\rightarrow$ active field of research

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Outline

From social networks to epidemic spreading

In SNA, innovation spreading dates back to the 50s

In parallel, epidemic modeling developed

Late 90s, data availability $\Rightarrow$ take into account the social network that supports the spreading

Networks and epidemic models - *Keeling and Eames, 2005*

Traditional (simplified) approach of epidemic model

Compartmental models

Basic assumption:

- random mixing hypothesis
  each individual has an equal chance to come into contact with anyone
- $\Rightarrow$ homogeneous description of individual behaviors

Infection and population complexity $\rightarrow$ compartments

- **S**: susceptible
- **I**: infected
- **R**: recovered
- **E**: exposed
- **M**: maternally-immune ...

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Equations

Model: set of transition rules from a compartment to another

- when S encounters I, uniform probability of contamination
- after being contaminated, I has uniform probability of recovery
- etc.

Example: SIR model

$$\begin{cases} \frac{dS}{dt} = -\beta \frac{IS}{N} \\ \frac{dI}{dt} = +\beta \frac{IS}{N} - \gamma I \\ \frac{dR}{dt} = +\gamma I \end{cases}$$

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- $N = S + I + R$: size of the population
- β : infection rate (parameter)
- γ : recovery rate (parameter)

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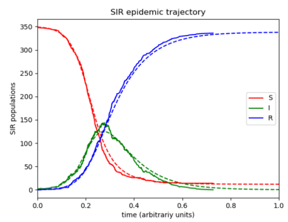

Classic models

- SIR:
  - 3 compartments S, I, R
  - used for disease with lifelong immunity
    ex: measles (rougeole) , whooping cough (coqueluche)
- SIS:
  - 2 compartments S, I
  - used for disease with possible reinfections
    ex: STD such as chlamydia
  - equations

$$\begin{cases} \frac{dS}{dt} = -\beta\frac{IS}{N} + \gamma I \\ \frac{dI}{dt} = +\beta\frac{IS}{N} - \gamma I \end{cases}$$

- SEIS, SEIR, SEIRS, MSEIR, ...

A few useful concepts in epidemiology

- Basic reproductive number R_0: expected number of new infections from a single infection if everyone is susceptible
  ex: for SIR with random mixing, $R_0 = \frac{\beta}{\gamma}$
  some estimated values (without intervention):
  - *measles: 12–18*
  - *seasonal flu: 1–2*
  - *covid-19: 3.3–5.7*
- k value: shape parameter, dispersion parameter, related to the inverse of the dispersion
  random mixing ⇒ homogeneous behavior ⇒ high values of k
  some estimated values (without intervention):
  - *measles: 0.22*
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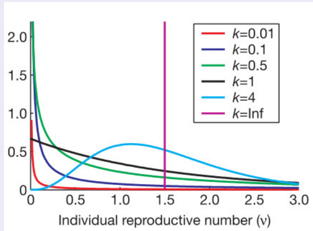
More about the k value

Superspreading and the effect of individual variation on disease emergence -
Lloyd-Smith et al., 2005

Origin

Model for the individual reproductive number distribution: negative binomial distribution



Average $\mu = R_0$, variance $\mu + \frac{\mu^2}{k}$

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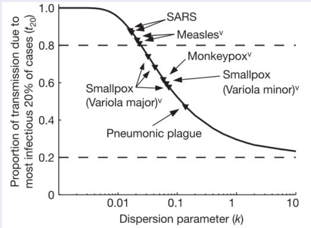
Another interpretation



∗ error of a factor 10 on the X-axis range

More about the importance of k for Covid-19 pandemic:
`https://www.theatlantic.com/health/archive/2020/09/k-overlooked-variable-driving-pandemic/616548/`

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Compartmental models in epidemiology
What networks bring to the models

What networks bring

Random mixing assumption implies uniform contact patterns
we know it is not true

Network-based models

- keep the compartments (S, I, R, E, . . .)
- spreading occurs on the contact network
- at each step, nodes may change compartment:
  - I may contaminate S (or E) neighbors
  - I may recover and turns R
  - . . .
- more details: *see practical work*

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Data collection and issues

Network-based epidemiology develops because of data
but how available and reliable are the data?

What is the meaning of an edge?

- *potentially* infectious contact
  disease specific: relatively clear for some diseases (STDs), but airborne diseases?
  ex: TousAntiCovid definition of a contact
- $\Rightarrow$ some degree of arbitrariness

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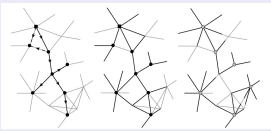
What are the data collection methods?

- infection tracing: look for infectious individuals that have transmitted the disease
- contact tracing: interview individuals to collect their potentially infectious contacts
- diary-based: based on day-to-day collection by individuals
  ex: cattle breeders in Europe since the 90s



credits image: M.Keeling, K.Eames

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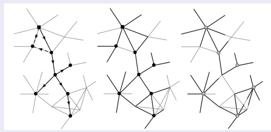
Issues with data collection methods

- infection tracing: focus on infectious contacts not all contacts, costly
- contact tracing: individual bias, sensitive data, subjective evaluation of danger, heterogeneity of data, costly
- diary-based: individual bias, sensitive data, disconnected network, heterogeneity of data



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Modeling on artificial networks

Difficult data collection
⇒ large use of network models

A few key-results in this field:

- "shortcuts" (e.g. air connections) break the locality of spreading and geographic wave-like patterns
- hubs (superspreaders) have a dramatic effect on an epidemic, can re-ignite the spreading
- large variability of spreading simulations: heterogeneity of networks ⇒ fluctuations

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