Dynamics

Analysis of complex interconnected data

McGill
School of Computer Science

Outline

- Graphs and Time
- Diffusion Processes
  - Modelling Epidemics as Spreads
  - Contact Graphs Data Sources
  - Mobility Data and Population Dynamics
  - Classic compartment based models
  - Network-based variations
  - Covid examples: contact SEIR, flight SEIR
- Dynamic Graphs
  - Modelling Temporal Graphs
  - Dynamic network analysis: Patten example
  - Dynamic network analysis: Measure example
  - Dynamic network analysis: Module example

Slides mostly based on Introduction to network book, chapter 17 and network science chapter 6 and 10

Graphs and Time

- Diffusion Processes
    - propagates/transmits/commutes/spreads over the graph structure
- Cascading graphs
    - evolving graphs that trace propagation without a given underlying structure
- Dynamic Graphs
    - graphs that naturally change through time, nodes and edges are added/removed
- Streaming Graphs
    - Dynamic graphs that are too large to be considered at once

change on structure

structure as change

structure is changing

substructure is changing

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Diffusion Processes

- Graph structure provides the routes for dynamic processes
- An entity propagates/spreads over the graph
  - disease (epidemics on contact nets)
  - meme & news (social media)
  - traffic (transport nets)

Disease spread: infected, contagious, susceptible

Similar models can be applied to understand the **flow**

Information: news, rumors, or gossip

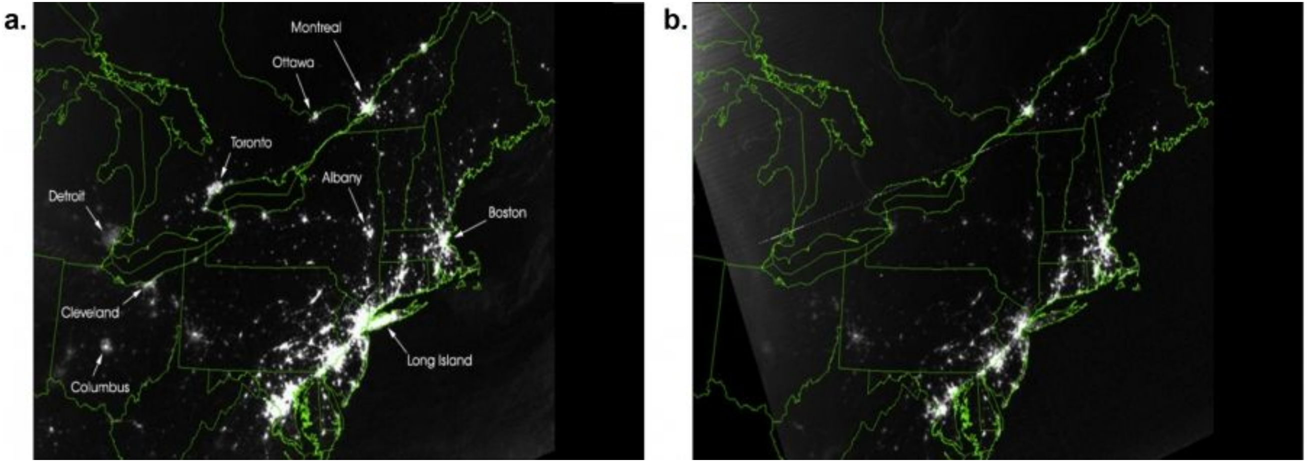
Exposed, believed, credulity

Diffusion Processes as flows

traffic (transport nets), population mobility, electricity

cascading failure as a contagious behavior

Transmission line failure in power grids, can overload other edges and lead to large power outages and blackouts



Percolation and network resilience Chapter 16 of NI

2003 North American Blackout
[from Network Science book]

Diffusion Processes example networks and agents

Phenomena	Agent	Network
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malwares, Digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social Network/Proximity Network
Bedbugs	Parasitic Insects	Hotel - Traveler Network
Malaria	Plasmodium	Mosquito - Human network

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Modelling Epidemics as Spreads

Infectious diseases spread when people come into close contact

droplet, touch, airborne (same room), etc.

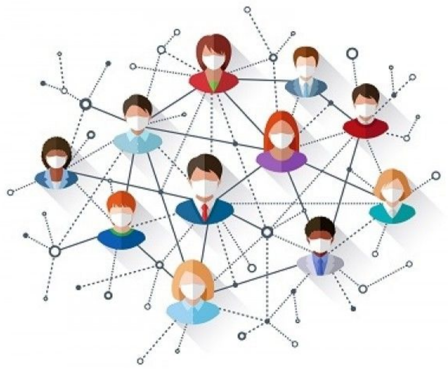
Close contact can be modeled as an edge in the graph
One of the reasons for interest in Network Science from early on but relevant now more than ever

- Understand and predict the outcomes of epidemics
- Decide on interference strategies (restrictions, vaccination, etc.)

Where can we get data on how people come into contact?

Contact Graphs Data Sources

- Mobile Carriers
  - cell-phone pings to towers
- Wifi providers
  - cell-phone connections to wifi hubs
- GPS tracking apps
  - Google location history
- Rfids
  - special purpose tracking devices



Contact Graphs from Mobile Carriers: example

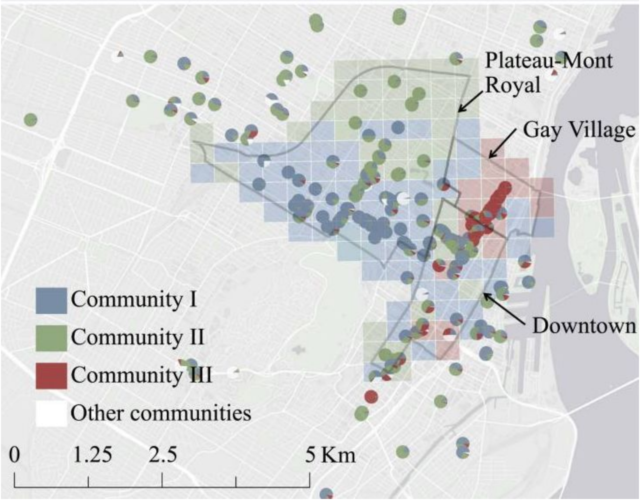
This model of West African regional transportation patterns was built using, among other sources, mobile-phone data for Senegal, released by the mobile carrier Orange.

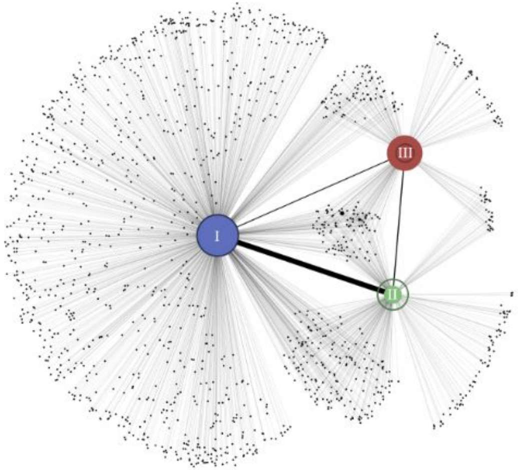
[Cell-Phone Data Might Help Predict Ebola's Spread]

Contact Graphs from Wifi providers: example

edges are formed between nodes (mobile phones) that are connected to the same public wifi hub at the same time

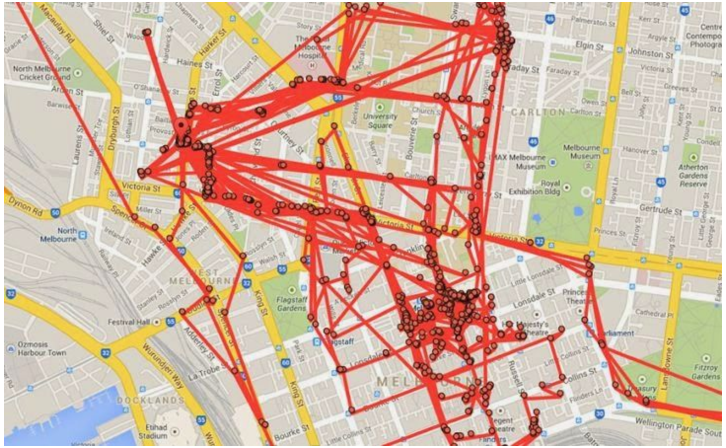
Île Sans Fil (ÎSF) is a not-for-profit organization established in 2004 in Montreal, Canada, that operates a system of public Internet hotspots. Hotspots are located in cafes, community and recreation centers, salons, markets, and other small businesses and public places.





[Epidemic Wave Dynamics Attributable to Urban Community Structure: A Theoretical Characterization of Disease Transmission in a Large Network]

Contact Graphs from GPS tracking: example



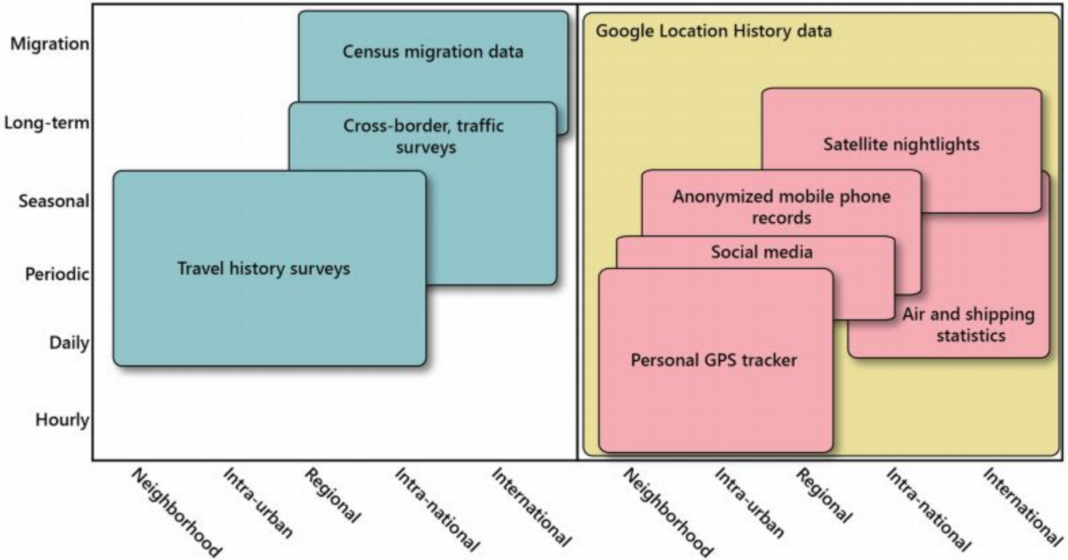
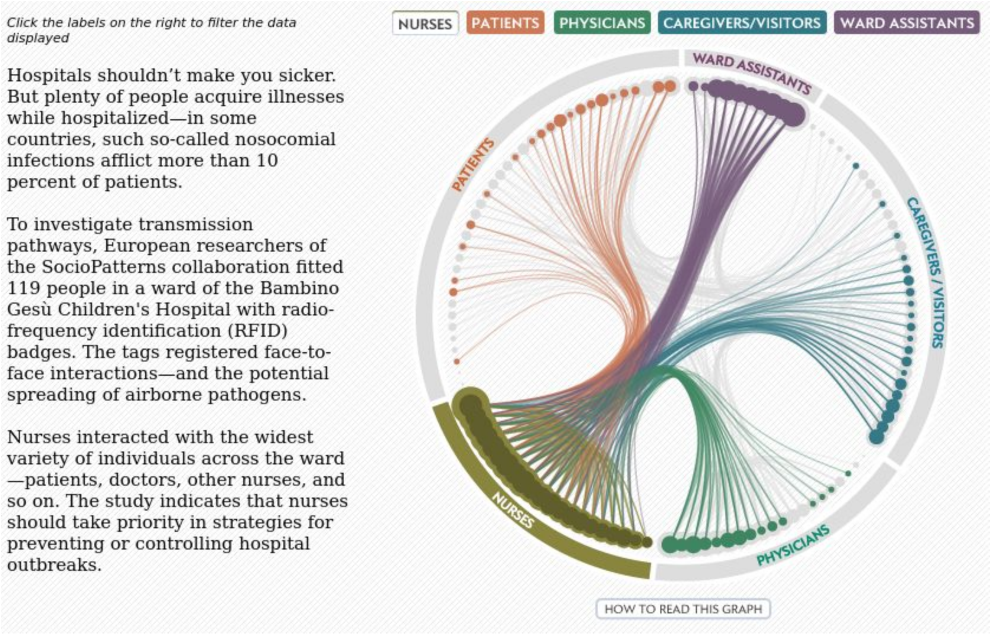


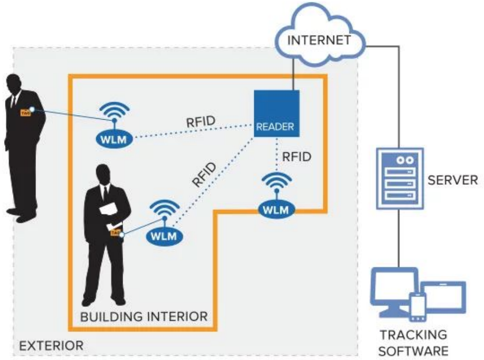
Fig. 1 The information niche that Google Location History occupies. Adapted from [9]; left includes traditional mobility data, right includes mobility data available with more recent technologies. Google Location History data (yellow) record location points similarly to GPS trackers, while spanning timescales similar to mobile phone data, and cover a breadth of time spans and spatial scales not possible in other datasets

All android devices, enabled on most
“GLH reporting disabled (as measured by a ‘No’ response to the question) ranged from 5.6% in Brazil to 17.5% in the UK”

[Using Google Location History data to quantify fine-scale human mobility]

Contact Graphs from rfid: example





https://www.scientificamerican.com/article/graphic-science-rfids-tags-track-possible-outbreak-pathways-in-hospital/

Hospital Acquired Infections

Common & Costly (money & lives)

Yearly	Cases	Deaths
US	**1.7M**	**200K**
Canada	**99K**	**8K**

CDC
CENTERS FOR DISEASE CONTROL AND PREVENTION

"The patient in the next bed is highly infectious. Thank God for these curtains."

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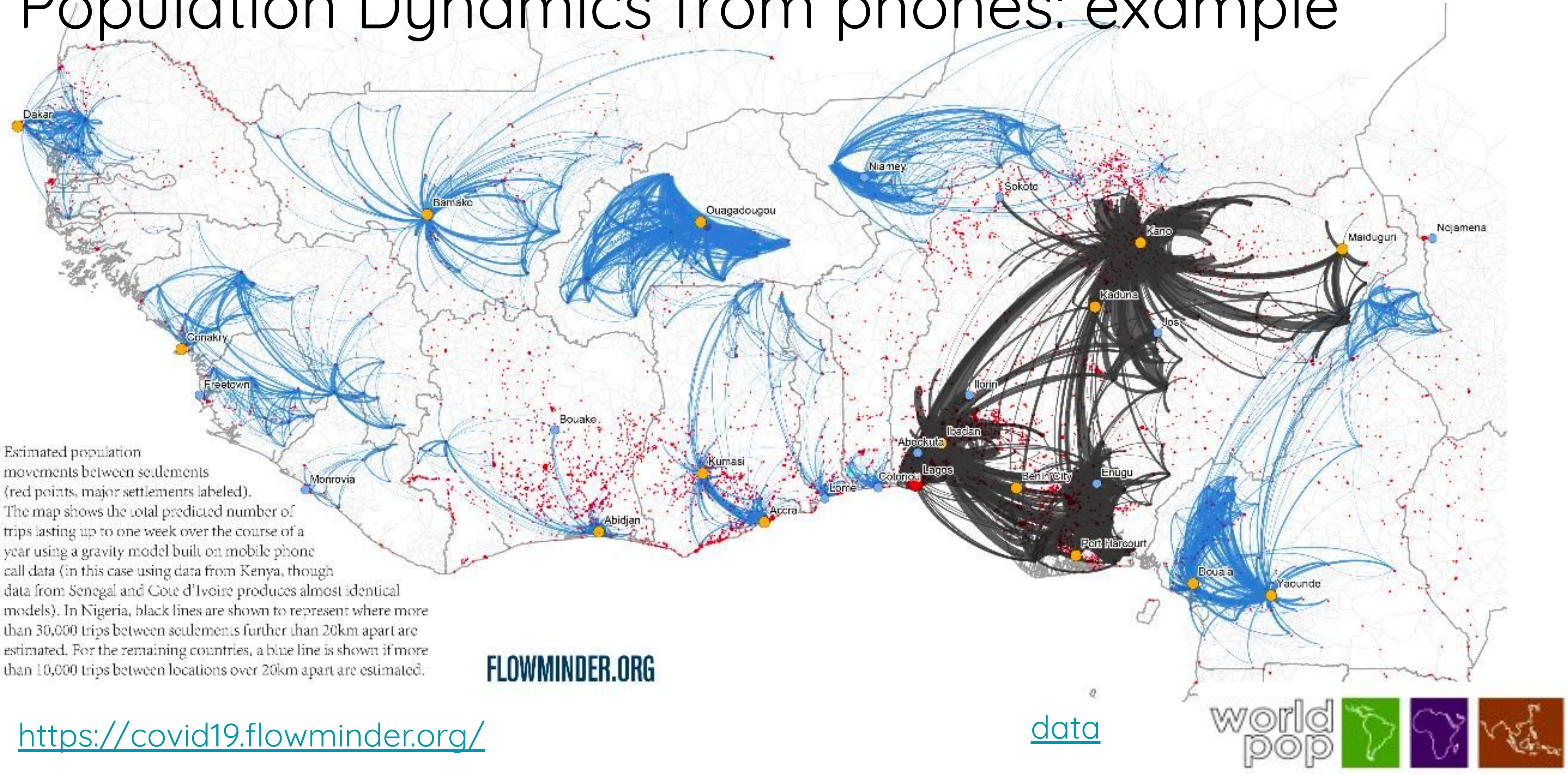
Mobility Data and Population Dynamics

Beyond modelling contact between individuals, we can model between population movements that are critical in global modelling of pandemic as well as disaster response, migration statistics, etc.

- Data sources:
    - All the sources for contact graphs
    - Border crossing records
        - https://www150.statcan.gc.ca/t1/tbl1/en/cv.action?pid=2410004101
    - Flight and rail records
        - https://www150.statcan.gc.ca/t1/tbl1/en/tv.action?pid=2310000201
    - Social Media
        - Use of Twitter social media activity as a proxy for human mobility to predict the spatiotemporal spread of COVID-19 at global scale

See the covid infected flights in and out of Canada: https://youtu.be/FJOUmINAg0I

Population Dynamics from phones: example

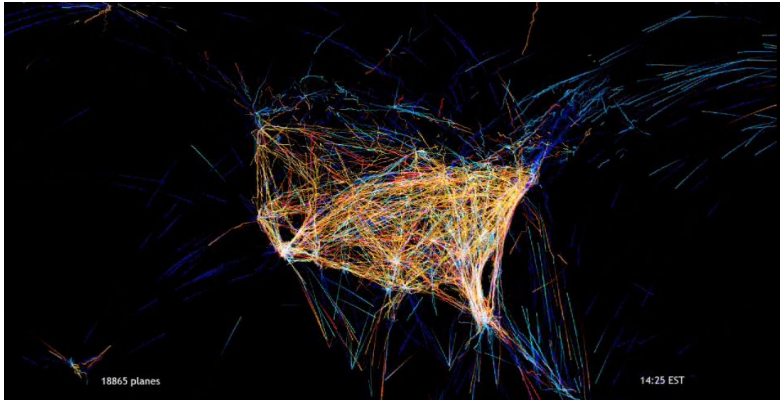


https://covid19.flowminder.org/

data

Population Dynamics from flights: example

North American Flight Patterns: https://vimeo.com/5368967



Global Epidemic and Mobility (GLEAM)
http://www.gleamviz.org/

captures the worldwide spread of the pandemic

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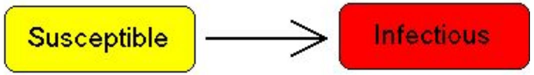
Compartmental Models of the spread of infection

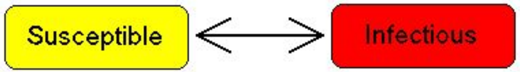
dynamics of the disease is reduced to changes between a few basic states

The SI model

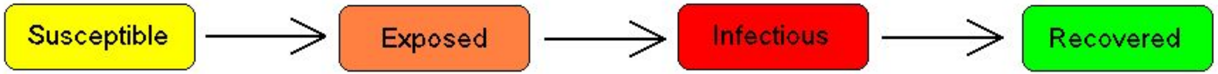


The SIR model

The SIS model



The SEIR model



Many more models

form [Wiki]

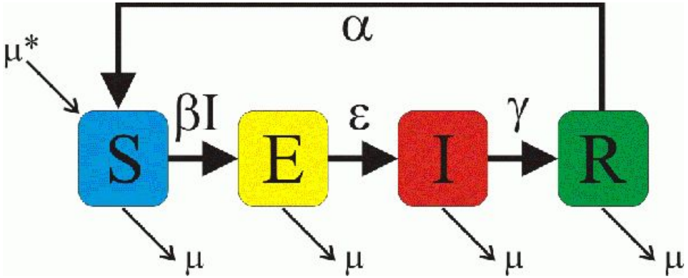
Compartmental Models: traditional models

- Population dynamics, mathematical modelling
- Kermack–McKendrick theory (1927) and Reed–Frost model (1928)
- Ignore the contact networks, assume people come into contact at random
- Only consider population size
  - S(t): [expected] number of susceptible individuals at time t
  - I(t): [expected] number of infected individuals at time t
  - R(t): [expected] number of recovered individuals at time t
  - E(t): [expected] number of exposed individuals at time t

$$\frac{dS(t)}{dt} = -\beta\left(\frac{S(t)}{P}\right)I(t) + \alpha R(t) + \mu(P - S(t))$$

$$\frac{dI(t)}{dt} = \beta\left(\frac{S(t)}{P}\right)I(t) - \gamma I(t) - \mu I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t) - \alpha R(t) - \mu R(t)$$



differential equations

Solve (analytically or numerically), or simulate

source

SIR model, example

What are S, I, R?

SIR model, example

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$

What are S, I, R?

SIR model, example

What are S, I, R? susceptible–infected–removed

What are β and γ?

SIR model, example

What are S, I, R? susceptible–infected–removed
What are β and γ?
β: number of contacts each individual has
γ: rate at which infected individuals recover (or die)

dS/dt = ?

SIR model, example

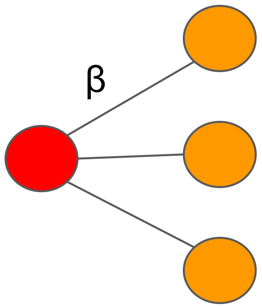
β: number of contacts each individual has

dS/dt = ?

Probability of meeting a susceptible person at random?

Given S + I + R = n (total population size)

SIR model, example



β: number of contacts each individual has

dS/dt = ?

Probability of meeting a susceptible person at random? S/n

How many susceptible people an infected person meets?

SIR model, example

β: number of contacts each individual has
dS/dt = ?

Probability of meeting a susceptible person at random? S/n
How many susceptible people an infected person meets? βS/n
Given X infected individuals, overall average rate of new infections is?

SIR model, example

β: number of contacts each individual has

dS/dt = ?

Probability of meeting a susceptible person at random? S/n

How many susceptible people an infected person meets? βS/n

Given X infected individuals, overall average rate of new infections is? βSX/n

SIR model, example

Given X infected individuals, overall average rate of new infections is? βSX/n

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta \frac{SX}{n}$$

$$s = \frac{S}{n}, \quad x = \frac{X}{n}$$

reformulating in terms of population ratios

$$s + x + r = 1$$

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta s x,$$

SIR model, example

$$\frac{ds}{dt} = -\beta s x, \qquad \frac{dx}{dt} = \beta s x - \gamma x, \qquad \frac{dr}{dt} = \gamma x.$$

other rate of changes, derived similarly

SIR model, example

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta s x, \qquad \frac{\mathrm{d}x}{\mathrm{d}t} = \beta s x - \gamma x, \qquad \frac{\mathrm{d}r}{\mathrm{d}t} = \gamma x.$$

$$\frac{1}{s}\frac{\mathrm{d}s}{\mathrm{d}t} = -\frac{\beta}{\gamma}\frac{\mathrm{d}r}{\mathrm{d}t}$$

$$s = s_0 \mathrm{e}^{-\beta r/\gamma}$$

we integrate both sides with respect to *t* to get

$$s + x + r = 1$$

$$\frac{\mathrm{d}r}{\mathrm{d}t} = \gamma(1 - r - s_0 \mathrm{e}^{-\beta r/\gamma}).$$

can’t evaluate the integral in closed form but we can evaluate it numerically

SIR model, example

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$

$$\frac{ds}{dt} = -\beta s x, \qquad \frac{dx}{dt} = \beta s x - \gamma x, \qquad \frac{dr}{dt} = \gamma x.$$

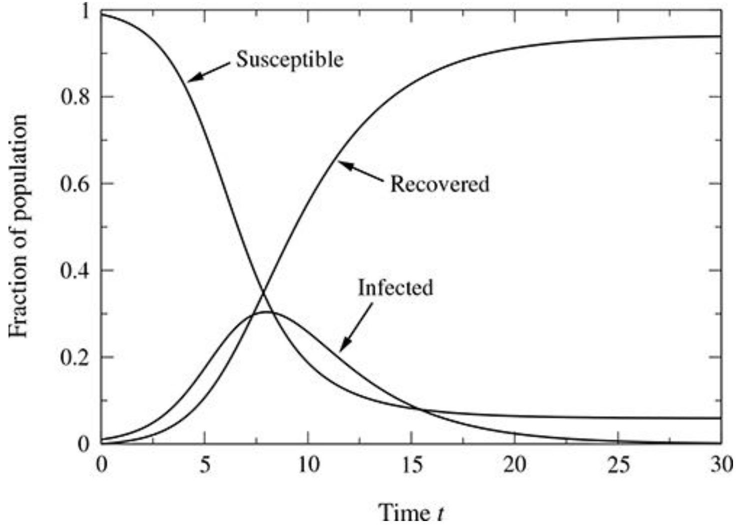
$$\frac{1}{s}\frac{ds}{dt} = -\frac{\beta}{\gamma}\frac{dr}{dt}$$

$$s = s_0 e^{-\beta r/\gamma}$$

$$s + x + r = 1$$

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\beta r/\gamma}).$$

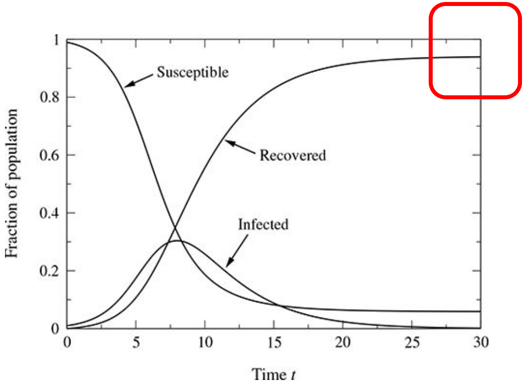
numerical solution of the SIR equations



Time evolution of the SIR mode
β=1, **γ**=0.4, s_0=0.99,x_0=0.01, and r_0=0
Newman's book

SIR model, example

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$



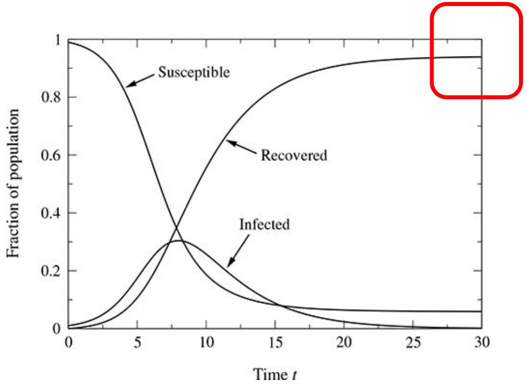
Time evolution of the SIR mode
β=1, γ=0.4, s_0=0.99,x_0=0.01, and r_0=0

$$\frac{\mathrm{d}r}{\mathrm{d}t} = \gamma(1 - r - s_0 \mathrm{e}^{-\beta r/\gamma}).$$

What does asymptotic value of r represent? (dr/dt = 0)

SIR model, example

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$



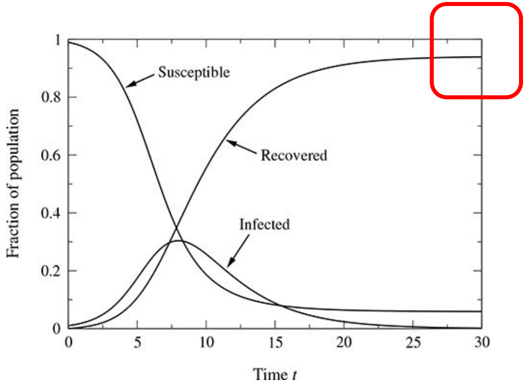
Time evolution of the SIR mode
β=1, γ=0.4, s_0=0.99,x_0=0.01, and r_0=0

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\beta r/\gamma}).$$

Asymptotic value of r (dr/dt = 0) :
total number of individuals who ever catch the disease
total outbreak size, final attack rate

$$r = 1 - e^{-\beta r/\gamma}$$

SIR model, example



Time evolution of the SIR mode
β=1, γ=0.4, s_0=0.99,x_0=0.01, and r_0=0

$$\frac{\mathrm{d}r}{\mathrm{d}t} = \gamma(1 - r - s_0 \mathrm{e}^{-\beta r/\gamma}).$$

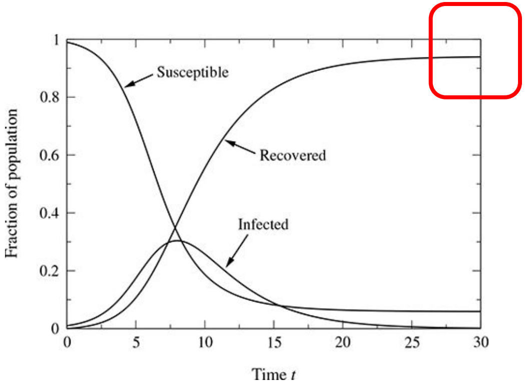
Asymptotic value of r (dr/dt = 0) :
total number of individuals who ever catch the disease
total outbreak size, final attack rate

$$r = 1 - \mathrm{e}^{-\beta r/\gamma}$$

When do we have outbreak?

SIR model, example

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$



Time evolution of the SIR mode
$\beta=1$, $\gamma=0.4$, $s_0=0.99$,$x_0=0.01$, and $r_0=0$
Newman's book

$$r = 1 - e^{-\beta r/\gamma}$$

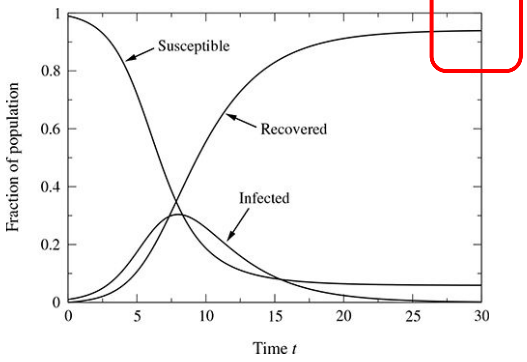
Asymptotic value of r, total outbreak size ⇒ **epidemic threshold (β=γ)**

β≤γ ⇒ no epidemic at all

"infected individuals recover faster than susceptible individuals become infected, so the disease cannot get a toehold in the population"

SIR model, example

$$r = 1 - e^{-\beta r/\gamma}$$



Time evolution of the SIR mode
β=1, γ=0.4, s_0=0.99,x_0=0.01, and r_0=0
Newman's book

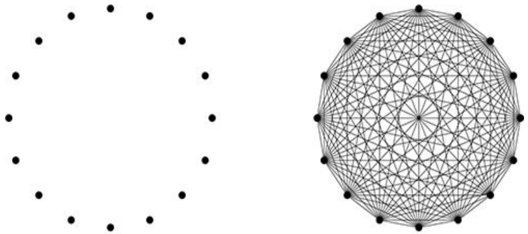
Asymptotic value of r, total outbreak size ⇒ **epidemic threshold (β=γ)**

B≤γ ⇒ no epidemic at all

"infected individuals recover faster than susceptible individuals become infected, so the disease cannot get a toehold in the population"

Any relation to graphs?

Emergence of a giant component in ER graphs

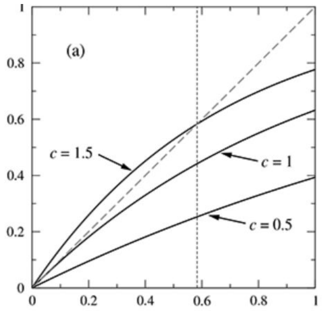


(a) $p = 0$ (b) $p = 1$

At which point we see a giant component?
(NG/N is finite; NG grows in proportion to N)

G(n,p) ⇒ <k> = 1

(Erdos and Renyi, 1959)



$c = \beta/\gamma$

$S = 1 - e^{-cS}$ fraction of nodes that are in the giant component

$r = 1 - e^{-\beta r/\gamma}$ fraction of nodes that are infected

SIR model, example

probability that the individual is still infected after a total time ***τ*** is given by?

$$\lim_{\delta\tau \to 0} (1 - \gamma\delta\tau)^{\tau/\delta\tau} = e^{-\gamma\tau}$$

γ δτ: probability of recovering in any time interval **δτ**

$\lim_{x \to 0}\left((1-ax)^{\frac{b}{x}}\right)$

Apply exponent rule: $a^x = e^{\ln(a^x)} = e^{x \cdot \ln(a)}$

$(1-ax)^{\frac{b}{x}} = e^{\frac{b}{x}\ln(1-ax)}$

$= \lim_{x \to 0}\left(e^{\frac{b}{x}\ln(1-ax)}\right)$

Apply the Limit Chain Rule: e^{-ba}

$= e^{-ba}$

$\lim_{x \to 0}\left(\frac{1}{x}\ln(1-ax)\right) = -a$

Steps

$\lim_{x \to 0}\left(\frac{1}{x}\ln(1-ax)\right)$

Simplify $\frac{1}{x}\ln(1-ax)$: $\frac{\ln(1-ax)}{x}$

$= \lim_{x \to 0}\left(\frac{\ln(1-ax)}{x}\right)$

Apply L'Hopital's Rule

$= \lim_{x \to 0}\left(\frac{-\frac{a}{1-ax}}{1}\right)$

Simplify

$= \lim_{x \to 0}\left(-\frac{a}{1-ax}\right)$

Plug in the value $x = 0$

$= -\frac{a}{1-a \cdot 0}$

Simplify

$= -a$

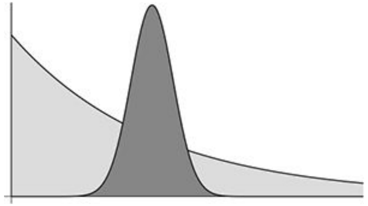
SIR model, example

probability that the individual is still infected after a total time τ is given by

$$\lim_{\delta\tau \to 0} (1 - \gamma\delta\tau)^{\tau/\delta\tau} = e^{-\gamma\tau}$$

probability the individual remains infected for time τ and then recovers in the interval between τ and τ+dτ

$$p(\tau)\mathrm{d}\tau = \gamma e^{-\gamma\tau}\mathrm{d}\tau.$$



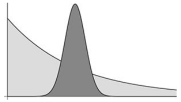
“an infected person is most likely to recover immediately after becoming infected, but might in theory remain in the infected state for quite a long time”

SIR model, example

probability that the individual is still infected after a total time τ is given by

$$\lim_{\delta\tau \to 0} (1 - \gamma\delta\tau)^{\tau/\delta\tau} = e^{-\gamma\tau}$$

probability the individual remains infected for time τ and then recovers in the interval between τ and τ+dτ $\gamma e^{-\gamma\tau} d\tau$,



expected number of others they will have contact with during that time is $\beta\tau$

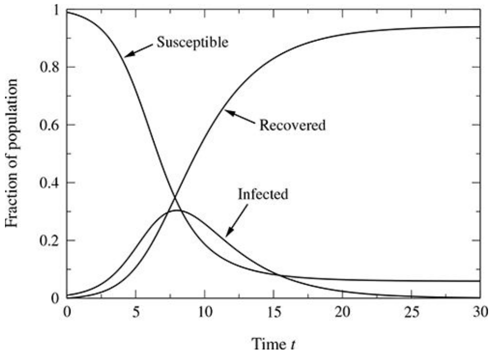
Basic reproduction number

"average number of additional people that a person passes the disease on to before they recover"

$$R_0 = \beta\gamma \int_0^\infty \tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}.$$

R_0=1 ⇒ **epidemic threshold (β=γ)**

SIR model, example



Time evolution of the SIR mode
β=1, γ=0.4, s_0=0.99,x_0=0.01, and r_0=0

Asymptotic value of r (dr/dt = 0) ⇒ **epidemic threshold (β=γ)**

B≤γ ⇒ no epidemic at all

"infected individuals recover faster than susceptible individuals become infected, so the disease cannot get a toehold in the population"

Basic reproduction number (R_0=1) ⇒ **epidemic threshold (β=γ)**

"average number of additional people that a person passes the disease on to before they recover"

Dynamics- Quick recap

- Graphs & Time: diffusion on graph, cascade as the graph, dynamic graph, streaming graph
- Diffusion on Graphs
  - An entity that spreads/flows over the graph: disease, meme & news (social media), etc.
  - Epidemic modelling with contact graphs & between population dynamics
  - Classic compartment based models
    - Differential equations of compartment size changes (S, I, E, R)
    - Total outbreak size (asymptotic value of R) relates to the size of giant component in ER graph
      - We have an outbreak with the similar condition as having a giant component
    - Assume full mixing (= ER contact graph)

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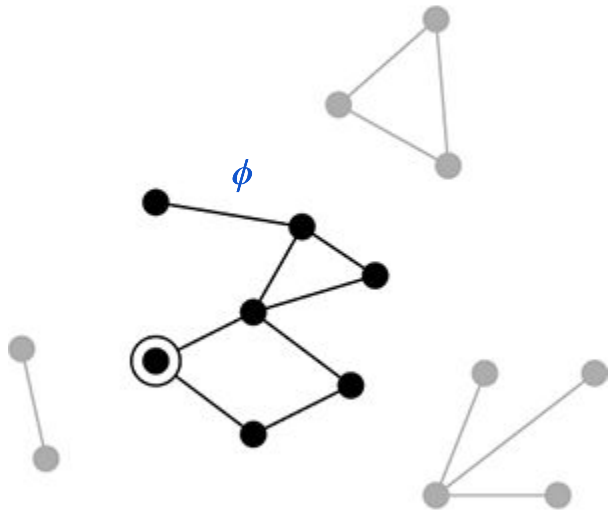
Epidemic models on networks

generalized to the network case considering transmission rate for edges

Instead of **full mixing** anyone could contact/infect anyone



infected nodes spread the disease to their susceptible neighbors

Epidemic models on networks

generalized to the network case considering transmission rate for edges

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full mixing
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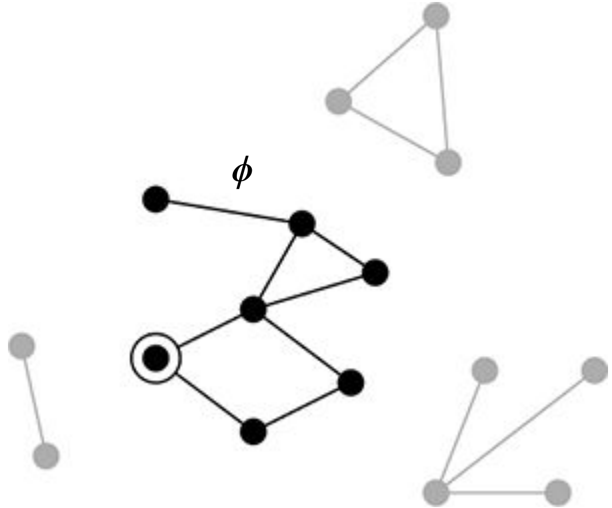


infected nodes spread the disease to their susceptible neighbors

Would we always have an outbreak?

Depends on the network structure and on the position in the network of the first infected individual

Epidemic models on networks

an individual's probability of infection at early times is proportional to **eigenvector centrality :** higher ⇒ infected sooner

the position of the epidemic threshold depends on the **leading eigenvalue** of the adjacency matrix. If the leading eigenvalue is small, then the probability of infection β must be large, or the recovery rate γ small, for the disease to spread

$$\frac{\beta}{\gamma} = \frac{1}{\kappa_1}.$$

Epidemic models on networks

connecting outbreak sizes and percolation

SIR model, transmission probability $\phi = 1 - e^{-\beta\tau}$

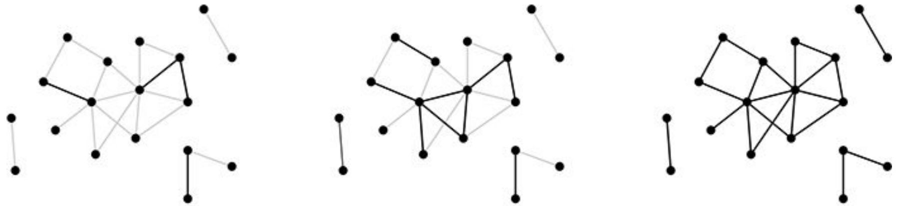
Bond percolation: a fraction ϕ of edges are occupied uniformly at random

represent those along which disease will be transmitted if it reaches either of the nodes at the ends of the edge

percolation transition ⇒ epidemic threshold

count the nodes in the appropriate percolation cluster

As ϕ increases, S also increases and hence both the probability and the size of an epidemic increase with ϕ.



(a) $\phi = 0.2$ (b) $\phi = 0.5$ (c) $\phi = 1$

Epidemic models on networks

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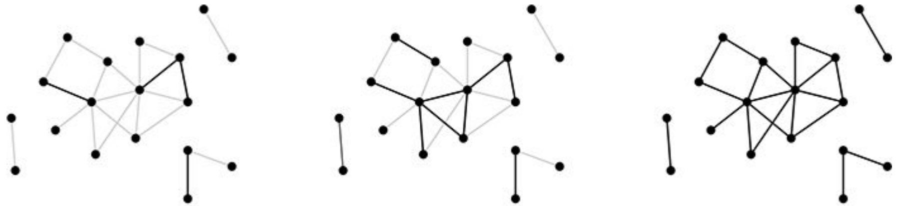
count the nodes in the appropriate percolation cluster

Can measure the long-time behavior, about the overall total number of individuals infected by the disease
But not the temporal evolution of the disease outbreak
⇒ simulate instead



(a) $\phi = 0.2$ (b) $\phi = 0.5$ (c) $\phi = 1$

Network Modelling

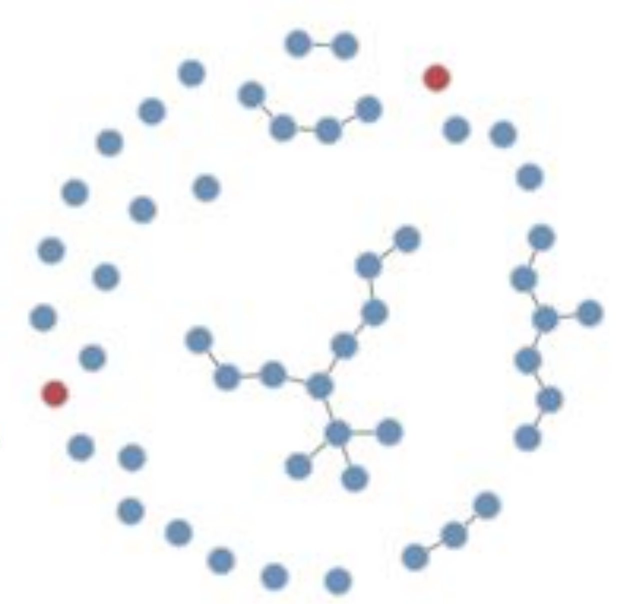
We can model/simulate it!

- More accurate
- Enables further analysis
  - Contact tracing
  - Finding super-spreaders
- Enables comparing interventions
  - Vaccination
  - Social distancing
  - Quarantine
  - Wearing masks

$$\frac{\mathrm{d}s_i}{\mathrm{d}t} = -\beta s_i \sum_i A_{ij} x_j,$$

$$\frac{\mathrm{d}xi}{\mathrm{d}t} = \beta s_i \sum_i A_{ij} x_j - \gamma x_i,$$

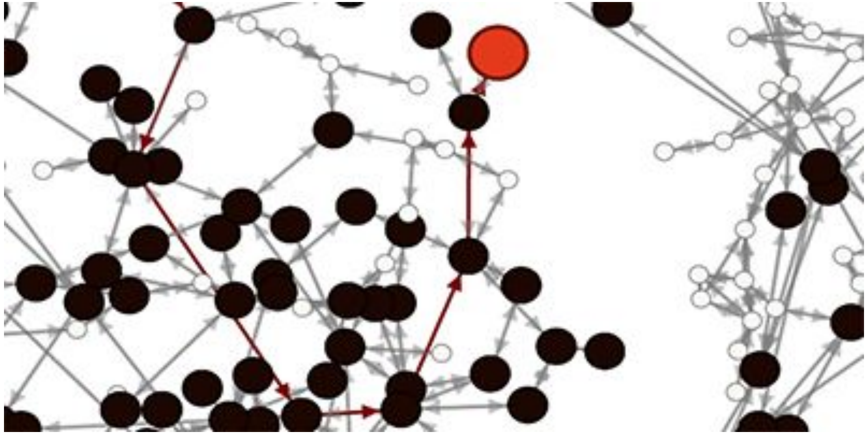
$$\frac{\mathrm{d}r_i}{\mathrm{d}t} = \gamma x_i,$$



$s_i(t)$, $x_i(t)$, and $r_i(t)$ to be the probabilities that node i is susceptible, infected, or recovered respectively at time t.

Epidemic models on networks

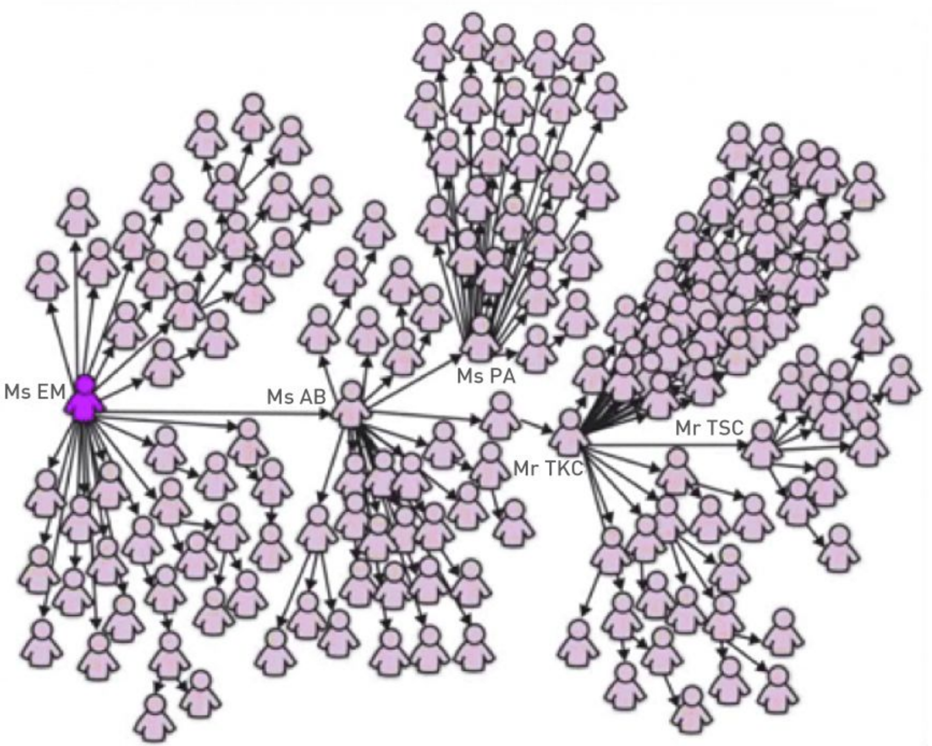
Network structure and patient zero are both important



[Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations]

Contact Tracing

One-hundred-forty-four of the 206 SARS patients diagnosed in Singapore were traced to a chain of five individuals that included four **super-spreaders**. The most important of these was **Patient Zero,** the physician from Guangdong Province in China, who brought the disease to the Metropole Hotel.



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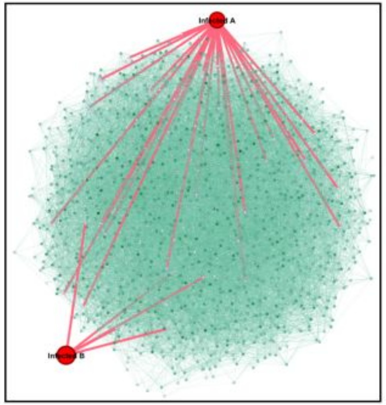
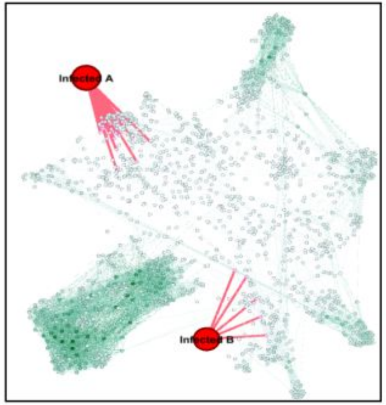
Contact Graph Epidemic Modelling of COVID-19 example

for Transmission and Intervention Strategies



ER Graph Contact Network



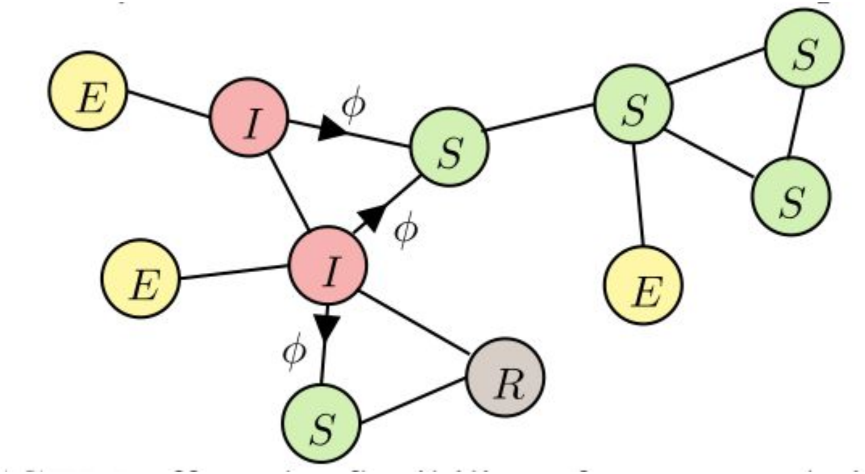
Montreal Wifi Contact Network

Date	Location	Event(s)
Mar. 11	[Worldwide]	WHO declares global pandemic
Mar. 12	[QC]	returning travellers to self-isolate
	[ON]	close public schools
Mar. 13	[ON, AB]	cancel events > 250
	[BC, MB]	cancel events > 250
	[NS, NB]	discourage gatherings > 150
Mar. 14	[QC, ON]	ban visits to long term care facilities
Mar. 15	[NS]	close schools, childcare, casinos
		ban visits to long term care facilities
		ban gatherings over 150
Mar. 16	[Canada]	close borders, excluding US.
	[Canada]	mandatory 14 days quarantine
	[QC]	close schools, universities, and daycares
Mar. 17	[ON, AB]	ban public events of over 50
	[BC]	close schools, restaurants, and bars
Mar. 19	[NB]	close most businesses, gatherings ≤ 10
Mar. 20	[Canada]	close boarder with US
Mar. 23	[NS]	quarantine for domestic travellers
	[Canada]	social distancing enforced
	[ON, QC]	close all non-essential workplace
Apr. 6	[Canada]	advise to wear masks
May 22	[MTL]	allow outdoor gatherings ≤ 50
		ease social distancing for some
May 25	[MTL]	reopen shops with exterior entrance
	[QC]	reopen manufacturers without restrictions
June 15	[MTL]	reopen personal and aesthetic care
June 22	[MTL]	reopen restaurants
June 28	[MTL]	reopen educational childcare facilities
July 18	[QC]	reopen offices
Aug. 1	[QC]	allow indoor gathering ≤ 250
Aug. 5	[QC]	allow outdoor gathering ≤ 250

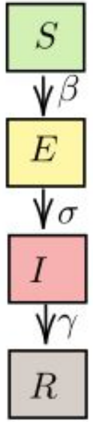
Table 1: Timeline of Canada COVID-19 selected NPI events based on (Vogel 2020; Trevor Lawson 2020)

Read more here & here

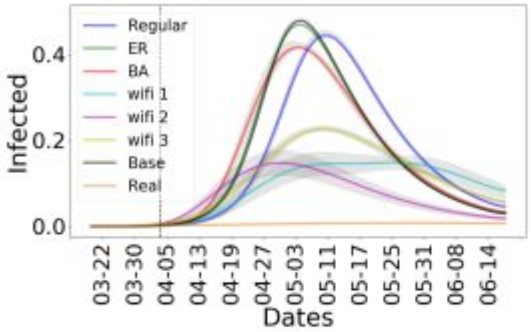
Contact Graph Epidemic Modelling of COVID-19 example



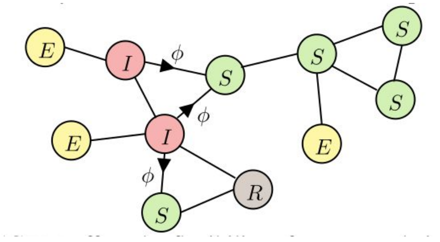
$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$
$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E$$
$$\frac{dI}{dt} = \sigma E - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

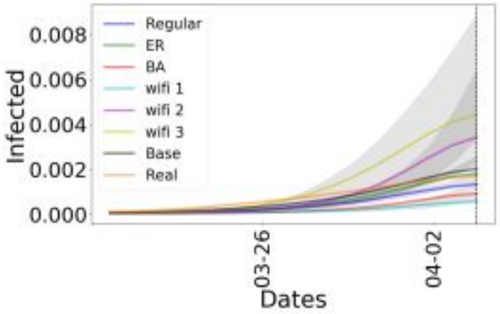


Contact Graph Epidemic Modelling of COVID-19 example



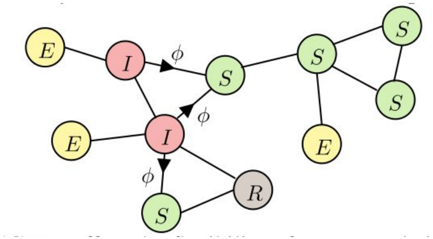
CGEM closely approximates the base SEIR model when the contact network is assumed to be Erdős-Reńyi graph.

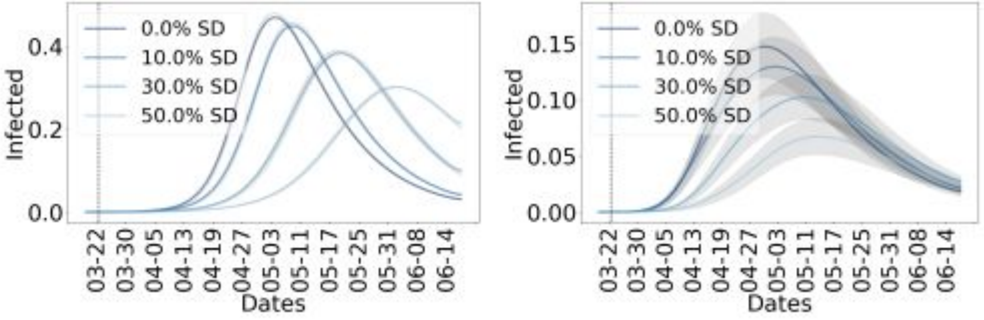




Assuming an Erdős-Reńyi graph as the contact network overestimates the impact of COVID-19 by more than a factor of 3 when compared with more realistic structures.

Contact Graph Epidemic Modelling of COVID-19 example

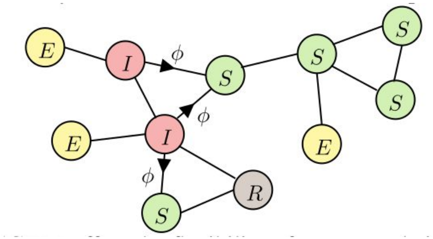




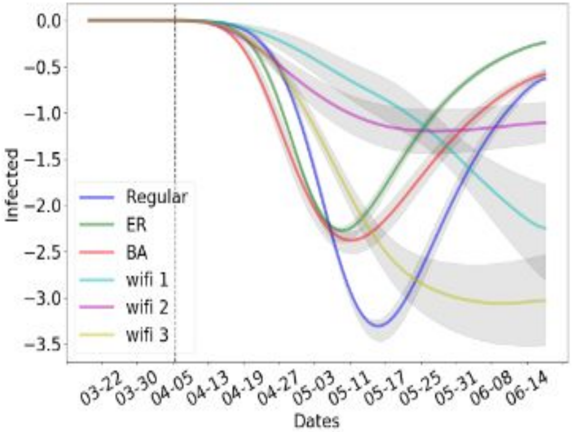
(a) ER (b) Wifi 2

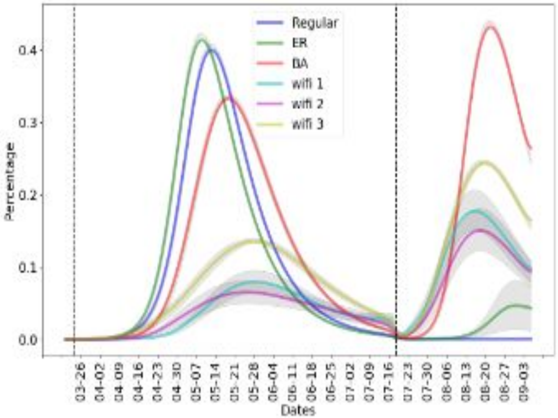
Quarantining delays the peak of infection on the ER graph whereas the peak on the real world graphs are lowered but not delayed significantly.

Contact Graph Epidemic Modelling of COVID-19 example



The ER graph significantly underestimates the effect of wearing masks in terms of the total decrease in the final attack rate





ER graph significantly underestimates the second peak after reopening public places, i.e. allowing back hubs.

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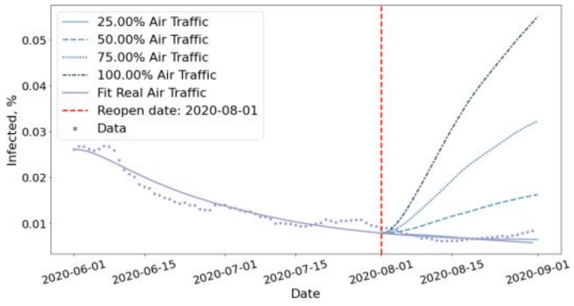
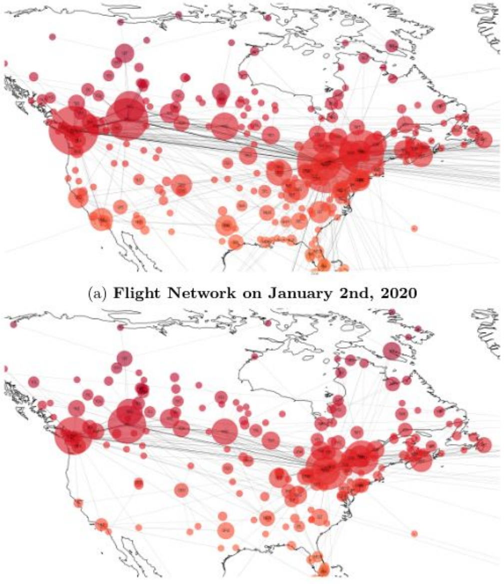
Incorporating Dynamic Flight Network in SEIR to Model Mobility between Populations

- Early detection of outbreaks due to imported pre-symptomatic and asymptomatic cases
- More accurate estimation of the reproduction number
- Evaluation of the impact of travel restrictions and the implications of lifting these measures

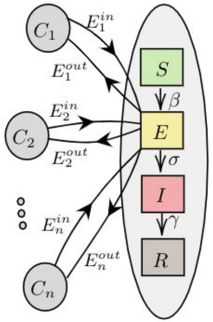




(a) **Flight Network on January 2nd, 2020**

(b) **Flight Network on April 2nd, 2020**

Figure 1: **Flight network before and after imposing travel restrictions**



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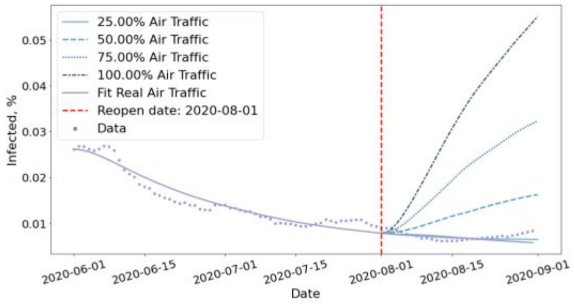

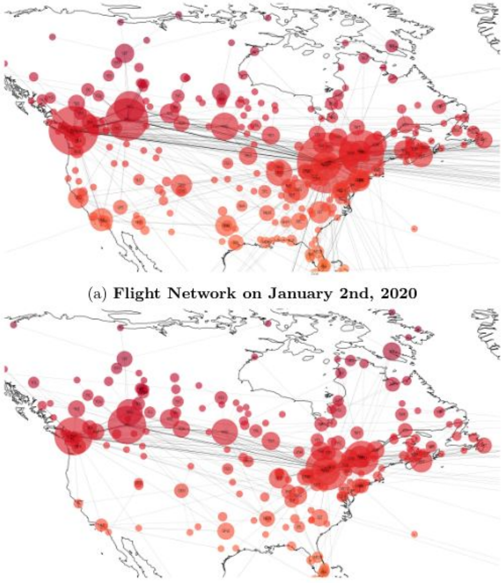

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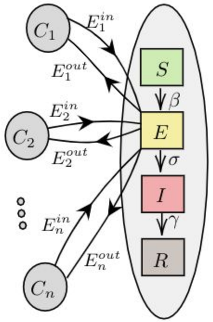

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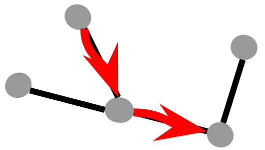
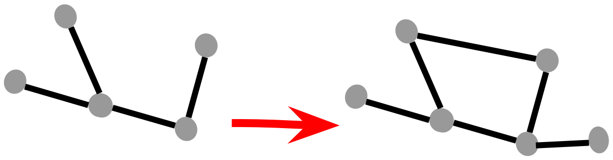
Common Types of Temporal Information

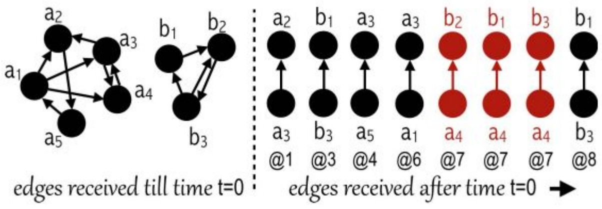
- Diffusion Processes
  - Graph structure provides the routes for dynamic processes
  - An entity propagates/spreads over the graph



- Dynamic Graphs
  - Graph evolves over time
  - Structure is changing, as interactions/edges often happen at a specific time
    - Some edges are more dynamic than others: email exchanges, v.s. followership

- Streaming edges
  - Graphs received over time and can not be kept fully

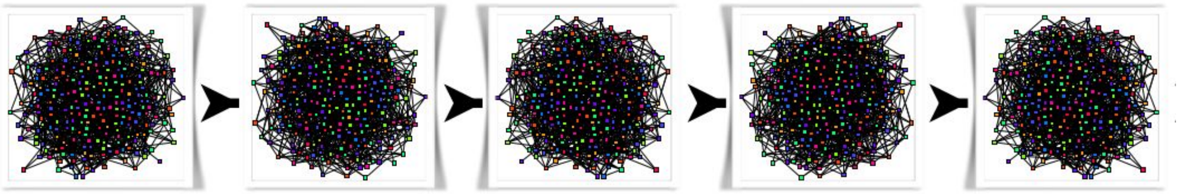




[SEDANSPOT: Detecting Anomalies in Edge Streams]()

Modelling Dynamic Graphs

Sequence of graphs:



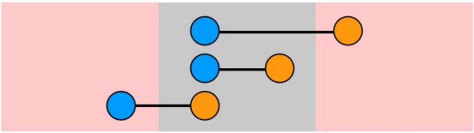
$G_{t=1}$ G_2 G_3 G_4 G_5

time-stamped interactions: $e = (i, j, t)$

Consider edge persistence

edges have durations $e = (i, j, t_s, \Delta t)$

edge in G_t if



$t-1$ t $t+1$

From Clauset’s slides

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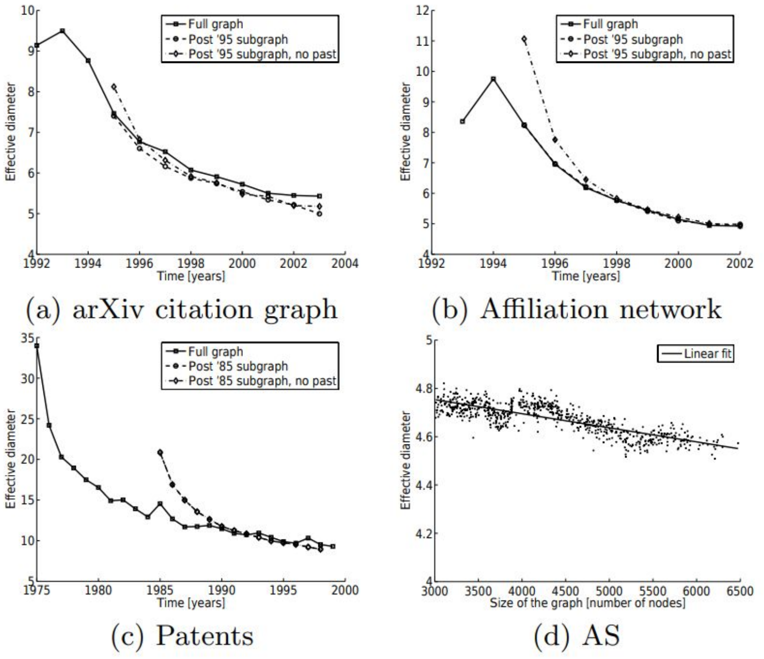
Dynamic network analysis: Patten example

We can define and study patterns in dynamic graphs

E.g. diameter over time

[Graphs over Time: Densification Laws, Shrinking Diameters, and Possible Explanations."]()



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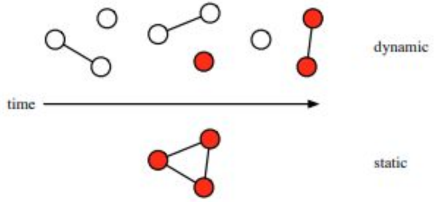
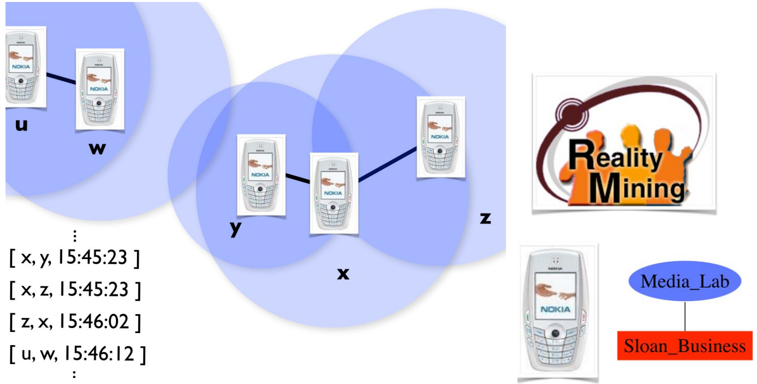
Dynamic network analysis: Measures example

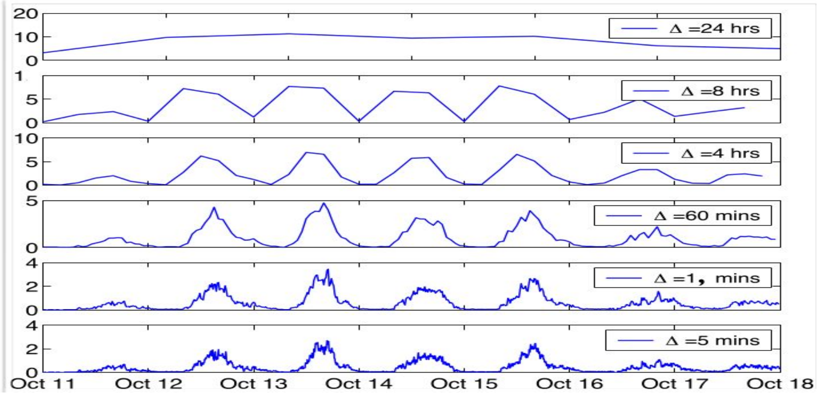
We can define measure on dynamic graphs



E.g. compute mean degree over time

time-varying physical proximity of 115 individuals over the course of one month in the MIT Reality Mining study





[Persistence and periodicity in a dynamic proximity network]

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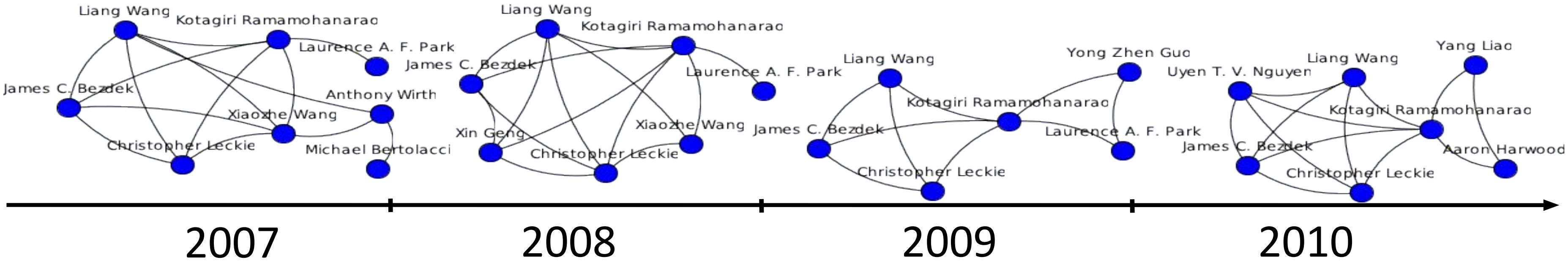
Dynamic network analysis: Modules examples

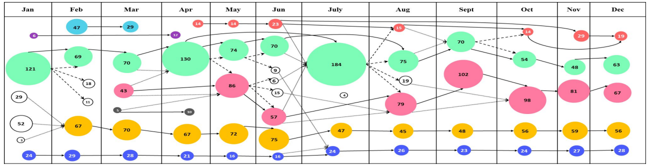
We can find persistent or evolving communities over time

E.g. Communities have fluctuating members in DBLP co-authorship network

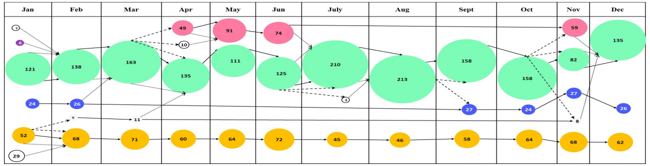


Dynamic network analysis: Modules examples

- Independent Community Mining
  - Detect communities at each snapshot without considering temporal information
  - Suitable for networks with highly dynamic community structures
  - Communities are tracked and matched based on their similarity

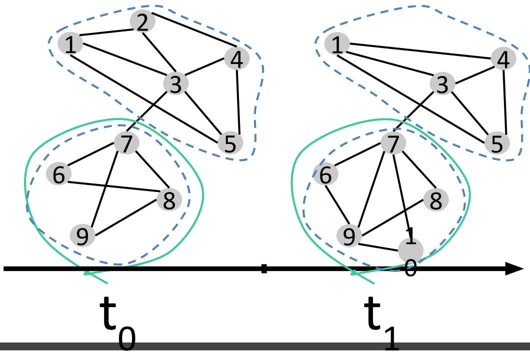


- Incremental Community Mining
  - Use the temporal information directly to detect communities
  - Suitable for networks with community structures that are more stable over time



$$cost = \alpha SC(G_i, C_i) + (1-\alpha) TC(C_{i-1}, C_i)$$

- *SC*: snapshot cost *TC*: temporal cost



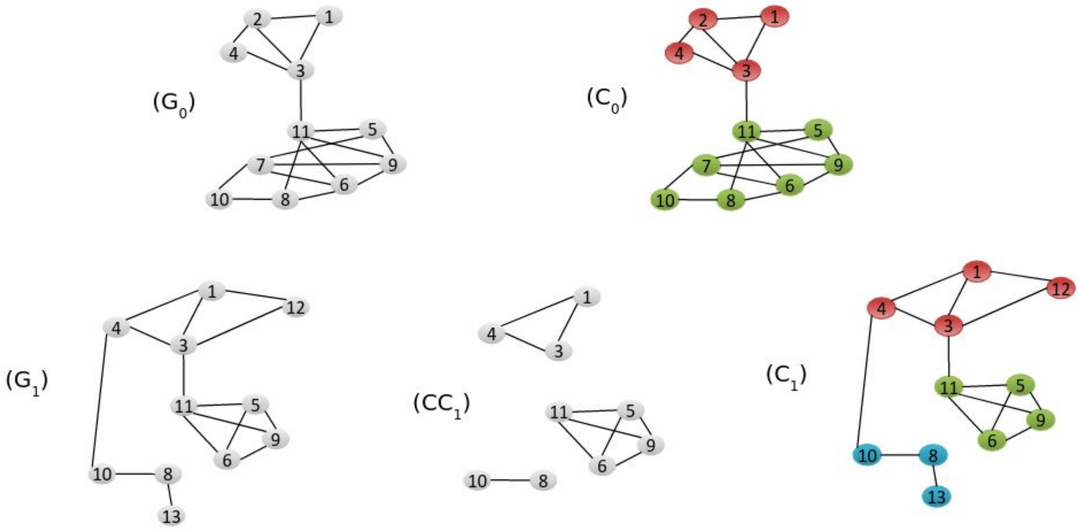
the snapshot cost SC() measures the quality of the detected communities
the temporal cost TC() measures how similar the current communities are with the previous detected communities

Dynamic network analysis, incremental example

The community structure is updated as new data arrives

group the nodes based on the communities detected at previous snapshot and current graph structure
i.e. only consider edges in the same module and find connect components

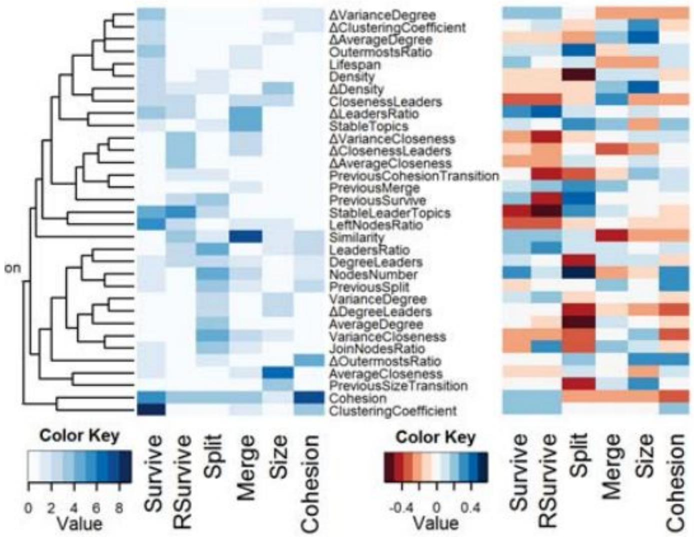
Expand these cores for find new modules



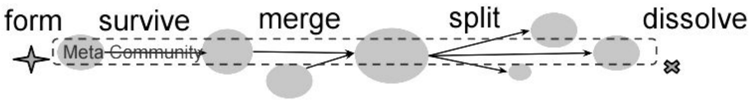
Incremental Local Community Identification in Dynamic Social Networks

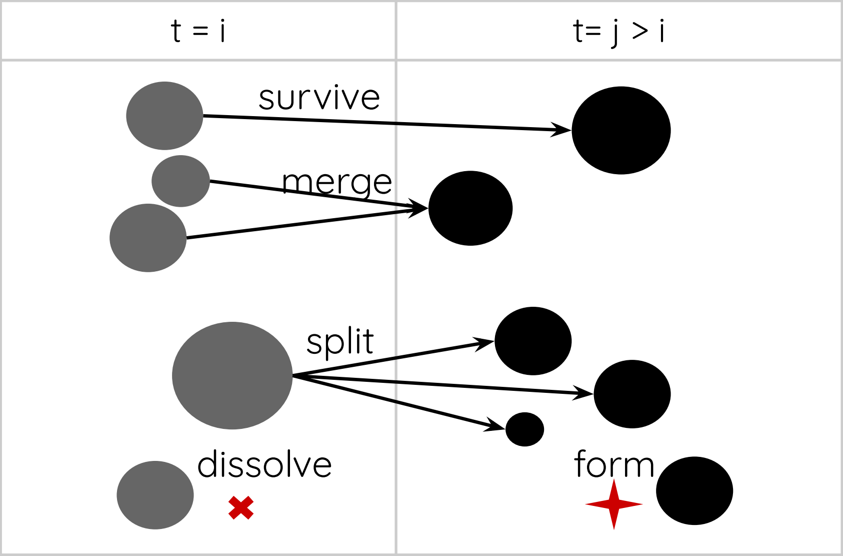
Dynamic network analysis, prediction example

We can predict what happens to a community



[Community evolution prediction in dynamic social networks]()

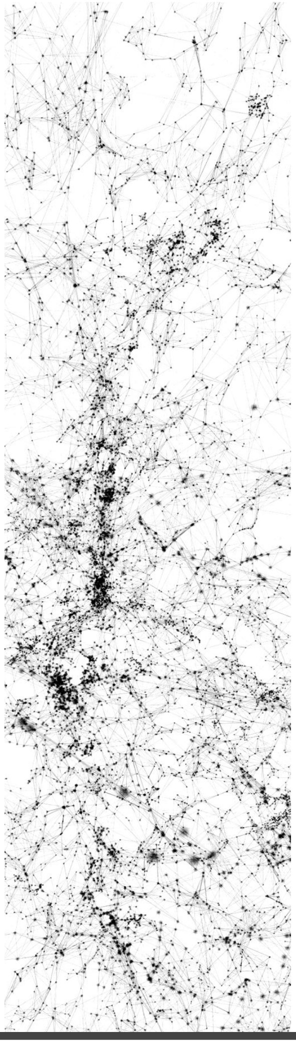




events that characterize the evolution of communities

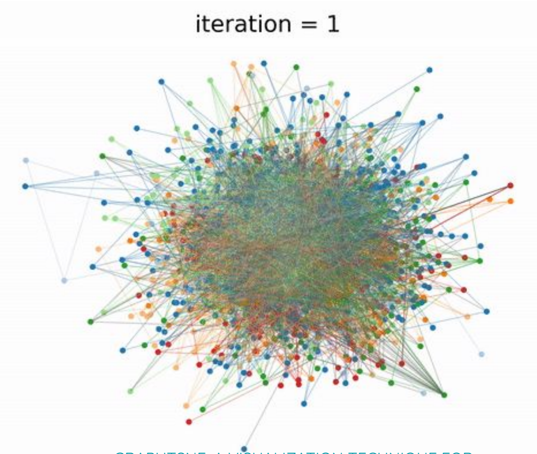
Common tasks in network science

- Pattern & Anomaly Detection
- Modelling of Structure, Evolution, & Dynamics
- Measurements of Ranking & Similarity
- Clustering & Community Detection
- Prediction of Missing Link & Attributes
- Summarization, Visualization, & Layouts
- Temporal analysis of Evolution & Diffusion



What tasks are unsupervised in Network Science?

- Community Detention
  - a.k.a. clustering nodes, finding modules
  - If semi-supervised or supervised, it becomes attribute prediction or classification
- **Anomaly Detection**
  - A.k.a. outlier detection
  - Goes hands in hands with pattern detection
- Summarization
  - How to compress the graph
- Visualization
  - How to plot the graph
- Alignment
  - How to align two given graphs

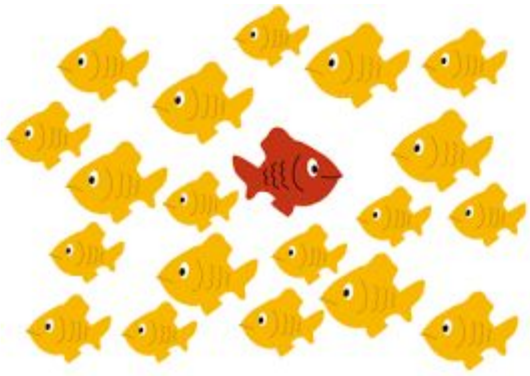


[GRAPHTSNE: A VISUALIZATION TECHNIQUE FOR GRAPH-STRUCTURED DATA]

What is an anomaly?

"An outlier is an observation that differs so much from other observations as to arouse suspicion that it was generated by a different mechanism."

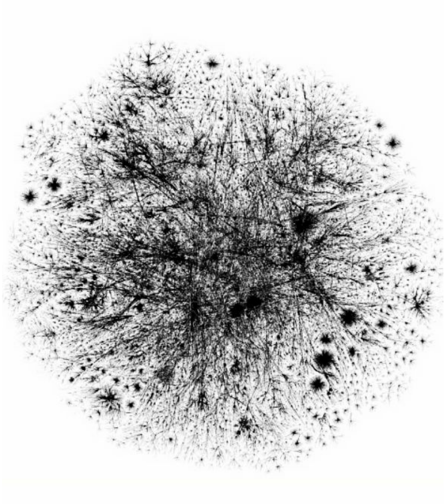
Hawkins' Definition of Outlier, 1980

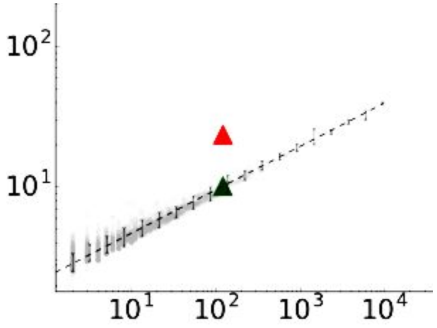


Slides based on:
Akoglu L, Tong H, Koutra D. Graph based anomaly detection and description: a survey. Data mining and knowledge discovery. 2015 May 1;29(3):626-88.

General Graph Anomaly Detection Problem

Given a graph, find the graph objects (nodes/edges/substructures) that differ significantly from the majority of the reference objects in the graph.





More on this later