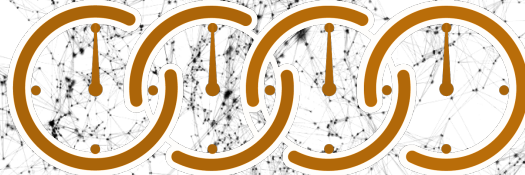




Dynamics

Part 1: diffusion

Analysis of complex interconnected data



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

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

change on structure

- **Cascading graphs**

- evolving graphs that trace propagation without a given underlying structure

structure as change

- **Dynamic Graphs**

- graphs that naturally change through time, nodes and edges are added/removed

structure is changing

- **Streaming Graphs**

- Dynamic graphs that are too large to be considered at once

substructure is changing

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, rumours, or gossip

Exposed, **believed**, **credulity**

FAKE
NEWS

Oldest and youngest

are more susceptible to
“fake news”: 41% of
consumers ages 18-34
and 44% ages 65+ admit
to falling for it.



"Old and young US adults most susceptible to fake news,"
YouGov, June 13, 2018

#DidYouKnow

the
news
literacy
project

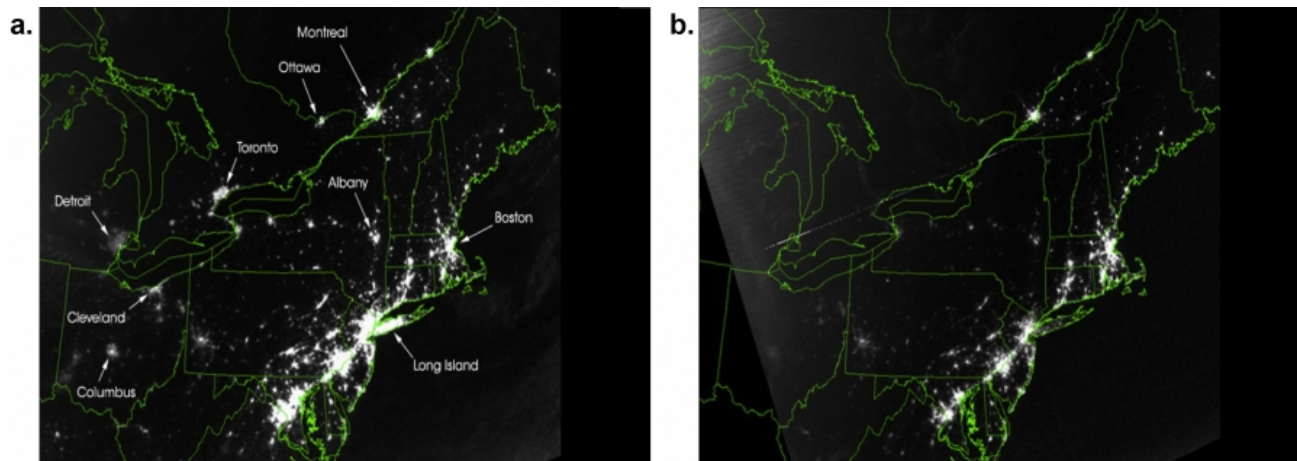


Diffusion Processes as flows

traffic (transport nets), population mobility, electricity
cascading failure as a contagious behaviour

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





Modelling Epidemics as Spreads

Infectious diseases spread when people come into close contact

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

Close contact can be modelled 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?

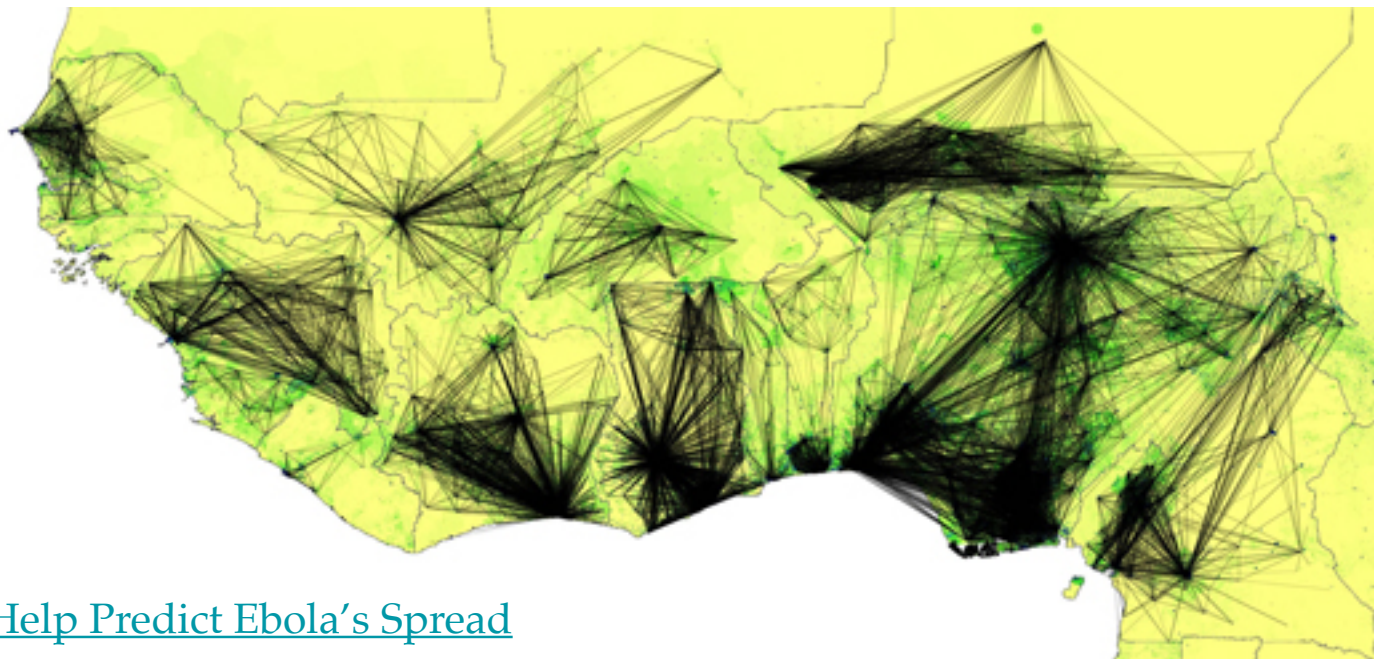
Contact Graphs Data Sources

- 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.

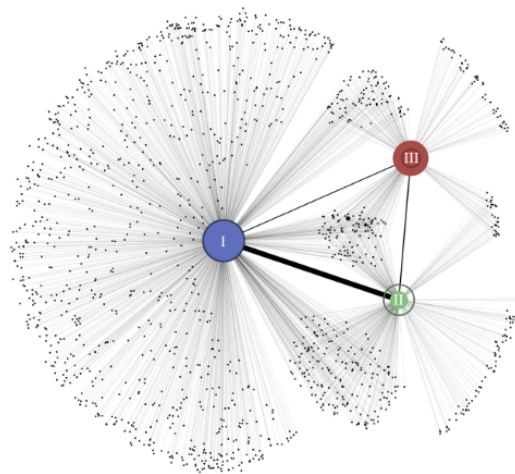
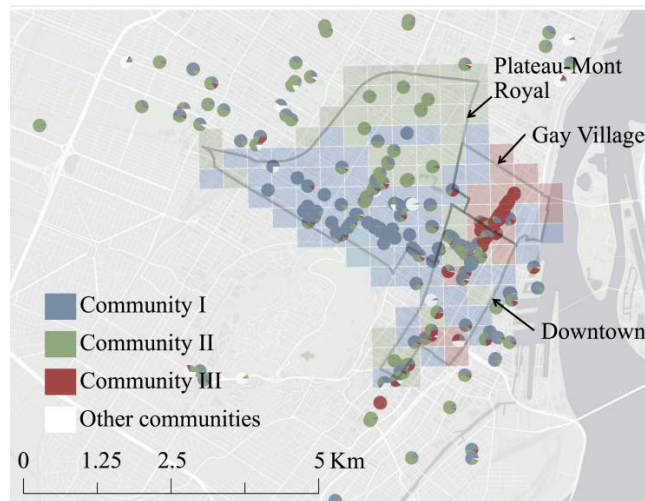


[Cell-Phone Data Might Help Predict Ebola's Spread](#)

Contact Graphs from Wifi providers: example

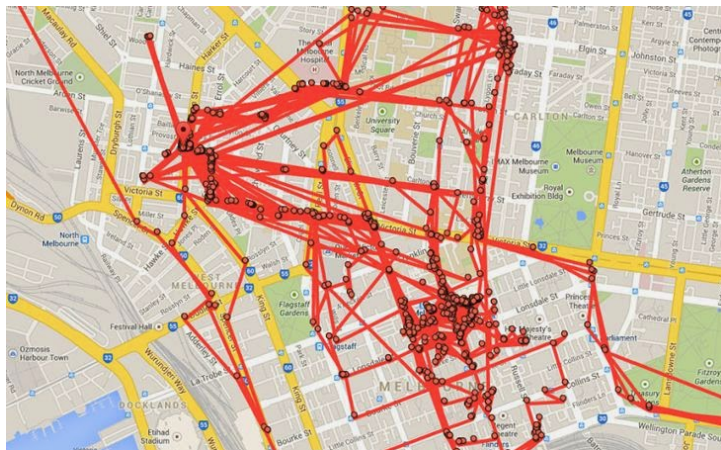
edges are formed between nodes (mobile phones) that are connected to the same public wifi hub at the same time

Île Sans Fil (ISF) 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



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”

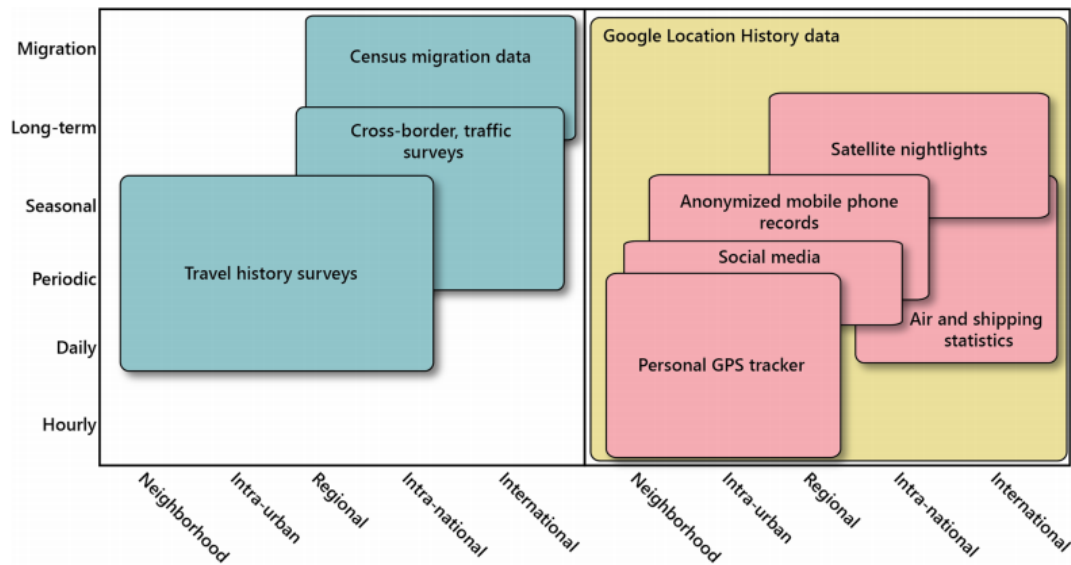


Fig. 1 The information niche that Google Location History occupies. Adapted from [9]; left includes traditional mobility data, right includes mobility data available with more recent technologies. Google Location History data (yellow) record location points similarly to GPS trackers, while spanning timescales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

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

Contact Graphs from rfid: example

Hospital Acquired Infections are costly and common

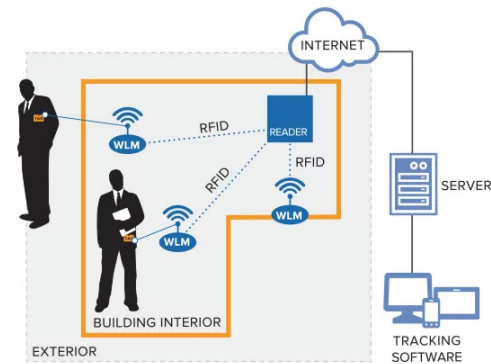
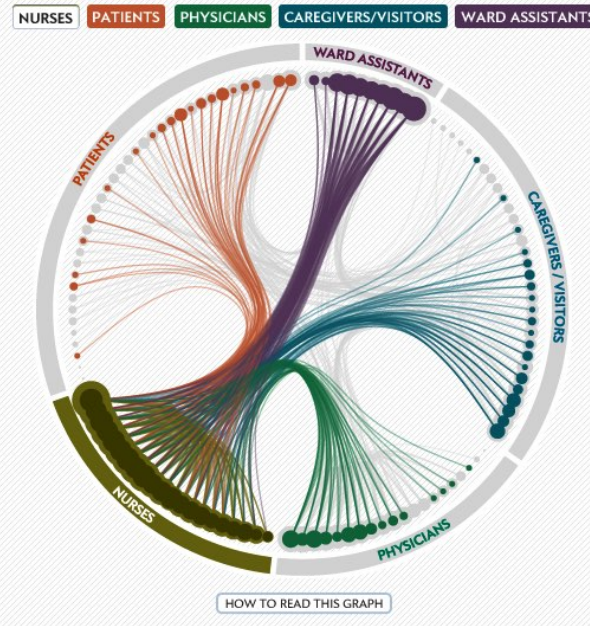
	Cases	Deaths
US	1.7M	200K
Canada	99K	8K

Click the labels on the right to filter the data displayed

Hospitals shouldn't make you sicker. But plenty of people acquire illnesses while hospitalized—in some countries, such so-called nosocomial infections afflict more than 10 percent of patients.

To investigate transmission pathways, European researchers of the SocioPatterns collaboration fitted 119 people in a ward of the Bambino Gesù Children's Hospital with radio-frequency identification (RFID) badges. The tags registered face-to-face interactions—and the potential spreading of airborne pathogens.

Nurses interacted with the widest variety of individuals across the ward—patients, doctors, other nurses, and so on. The study indicates that nurses should take priority in strategies for preventing or controlling hospital outbreaks.



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

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

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.

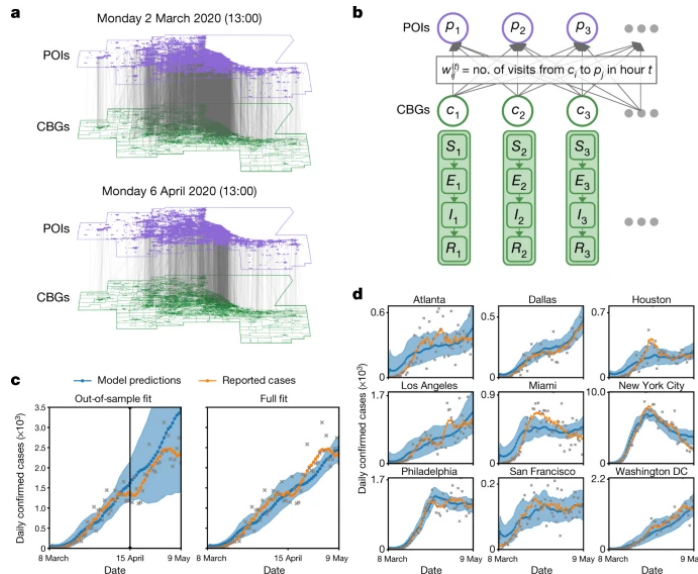
- Data sources:

- 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](#)
- Data Brokers
 - [Mobility network models of COVID-19 explain inequities and inform reopening](#)

See the covid infected flights in and out of Canada: <https://youtu.be/FJOumlNAg0I>

Mobility Graphs from Data Brokers: example

- SafeGraph: data broker for POI data
- A “point of interest” refers to any building, monument, landmark, or physical space – other than a private residence – that people may want to visit



These networks map the hourly movements of 98 million people from census block groups (CBGs), which are geographical units that typically contain 600–3,000 people, to specific points of interest (POIs)

<https://www.safegraph.com/data-examples>

Article | [Published: 10 November 2020](#)

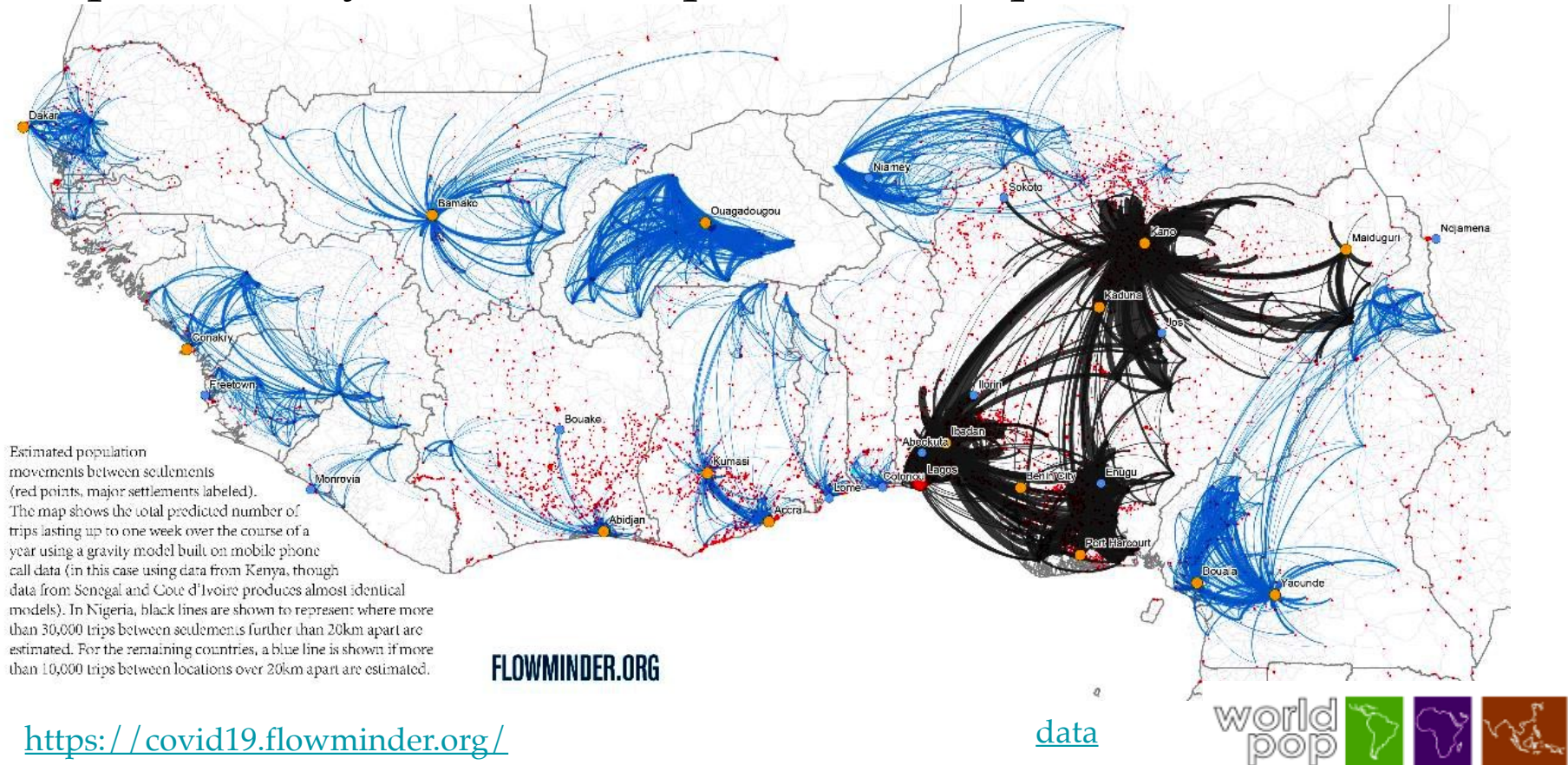
Mobility network models of COVID-19 explain inequities and inform reopening

[Serina Chang](#), [Emma Pierson](#), [Pang Wei Koh](#), [Jaline Gerardin](#), [Beth Redbird](#), [David Grusky](#) & [Jure Leskovec](#) 

[Nature](#) **589**, 82–87 (2021) | [Cite this article](#)

602k Accesses | 468 Citations | 11362 Altmetric | [Metrics](#)

Population Dynamics from phones: example

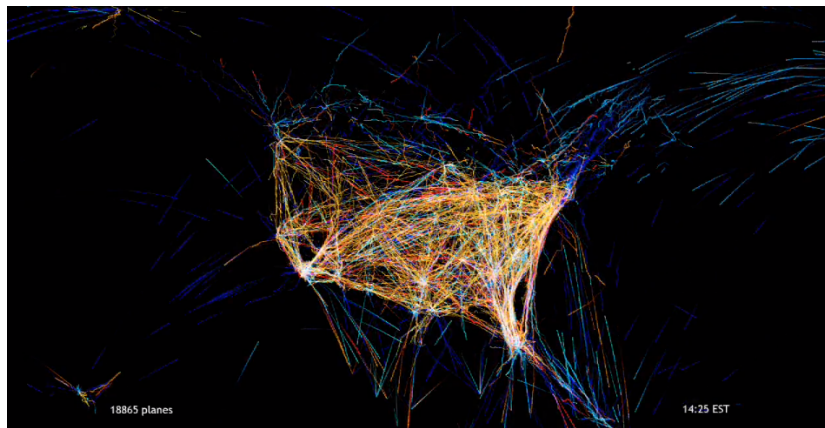


Population Dynamics from flights: example

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

GLEAM maps each geographic location into the nodes of a network. Transport between these nodes, representing the links, are provided by global transportation data, like airline schedules. GLEAM estimates the epidemic parameters using a network-based approach.

First successful real time pandemic forecast based on network science



North American Flight
Patterns: [https://
vimeo.com/5368967](https://vimeo.com/5368967)

captures the worldwide spread of the pandemic

Outline

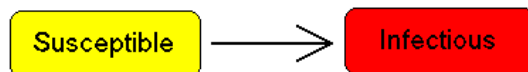
- Graphs and Time
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Compartmental Models of the spread of infection

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

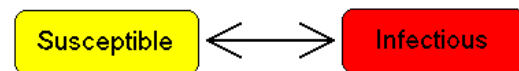
The SI model



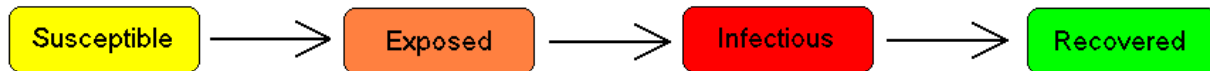
The SIR model



The SIS model



The SEIR model



Many more models

from [Wiki](#)

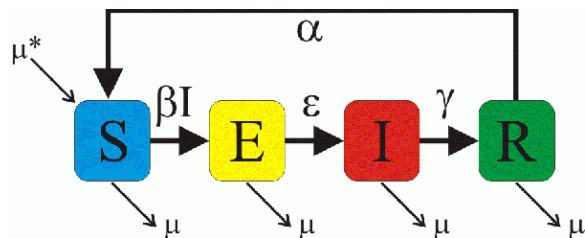
Compartmental Models: traditional models

- 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

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

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

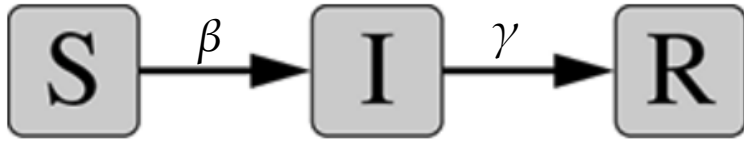
$$\frac{dR(t)}{dt} = \gamma I(t) - \alpha R(t) - \mu R(t)$$



differential equations
Solve (analytically or
numerically), or simulate

[source](#)

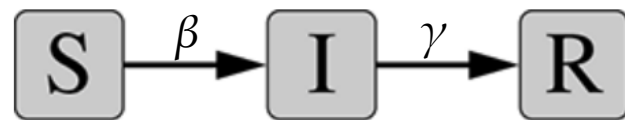
SIR model: compartments



What are S, I, R?



SIR model: rate of infection



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

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)

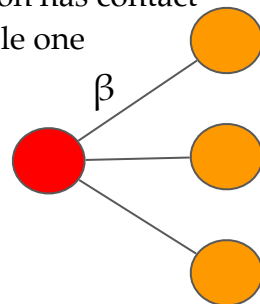
$dS/dt = ?$

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

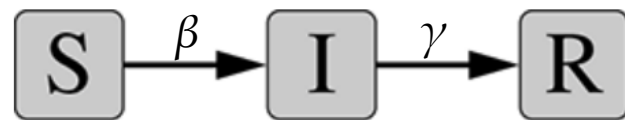
How many susceptible people an infected person meets? $\beta S/n$

Overall average rate of new infections is? $\beta SI/n$

disease is transmitted when
an infected person has contact
with a susceptible one



SIR model: dynamics



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

Overall average rate of new infections is? $\beta SI/n$

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

reformulating in terms of population ratios

$$\frac{ds}{dt} = -\beta si$$

$$s + i + r = 1, \quad s = \frac{S}{n}, \quad i = \frac{I}{n}, \quad r = \frac{R}{n}$$

other rate of changes, derived similarly

$$\frac{di}{dt} = \beta si - \gamma i$$

$$\frac{dr}{dt} = \gamma i$$

$$\frac{1}{s} \frac{ds}{dt} = -\frac{\beta}{\gamma} \frac{dr}{dt} \rightarrow s = s_0 e^{-\beta r / \gamma}$$

we integrate both sides
with respect to t to get

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

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

SIR model: epidemic curves

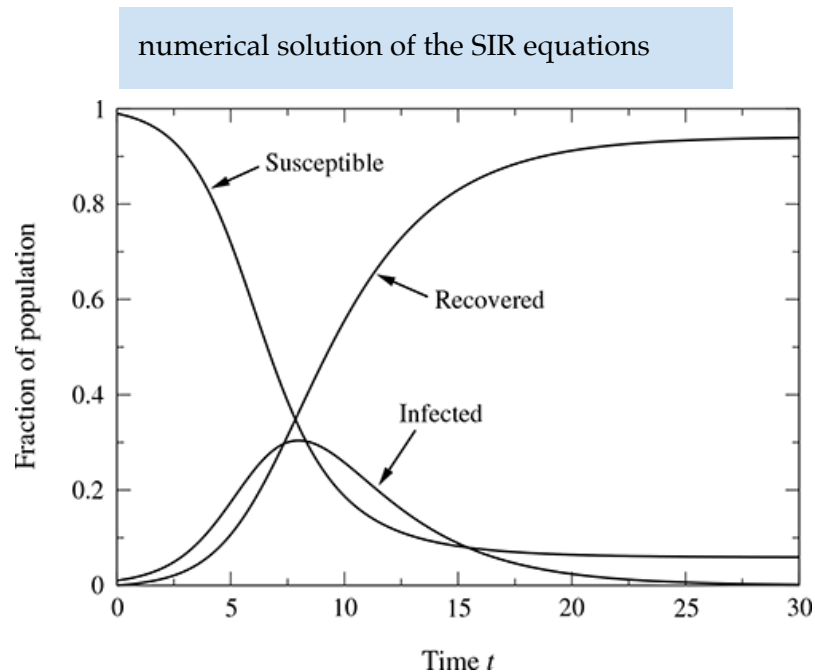


$$s + i + r = 1, \quad s = \frac{S}{n}, \quad i = \frac{I}{n}, \quad r = \frac{R}{n}$$

$$\frac{ds}{dt} = -\beta si$$

$$\frac{di}{dt} = \beta si - \gamma i$$

$$\frac{dr}{dt} = \gamma i$$

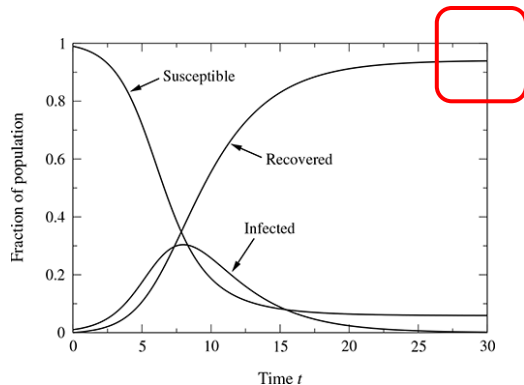


Time evolution of the SIR mode

$\beta=1$, $\gamma=0.4$, $s_0=0.99$, $i_0=0.01$, and $r_0=0$

From Newman's book

SIR model: epidemic threshold



What does asymptotic value of r represent? $\frac{dr}{dt} = 0$

total number of individuals who ever catch the disease
total outbreak size, final attack rate

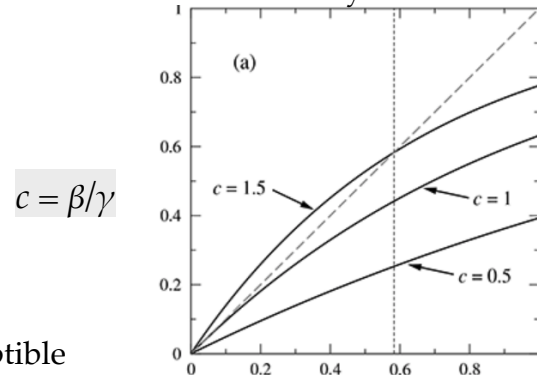
$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\beta r/\gamma}) = 0 \Rightarrow r = 1 - e^{-\beta r/\gamma}$$

When do we have outbreak? $\beta/\gamma > 1 \Rightarrow \beta > \gamma$

epidemic threshold ($\beta=\gamma$)

We have no epidemic at all for $\beta \leq \gamma$: “infected individuals recover faster than susceptible individuals become infected, so the disease cannot get a foothold in the population”

$y = 1 - e^{-cx}$ & $y = x$
 intersect only when $c > 1$



SIR model: relation to ER graphs

The size of the giant component in ER graphs has the same formula as the total outbreak size of the SIR model

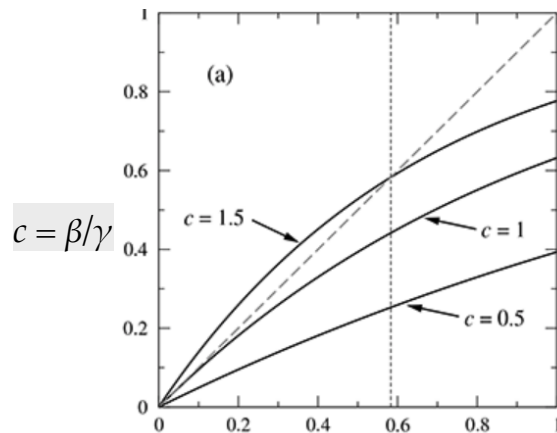
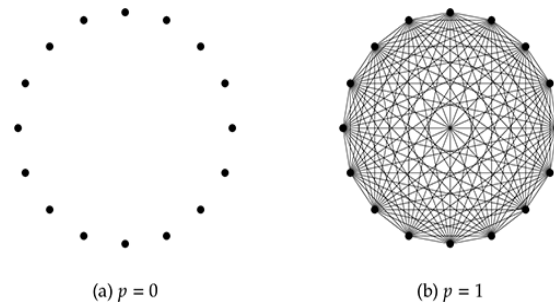
fraction of nodes that are in the giant component

$$S = 1 - e^{-cS}$$

fraction of nodes that are infected

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

We see a giant component in ER graphs when average degree is greater than one
(NG/N is finite; NG grows in proportion to N)



SIR model: recovery time

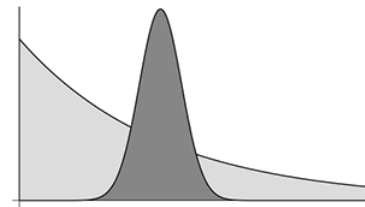
probability that the individual is still infected after a total time τ is given by

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

probability of recovering in any time interval $\delta\tau$

probability the individual remains infected for time τ and then recovers in the interval between τ and $\tau+d\tau$

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



“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: recovery time

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

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

probability of recovering in any time interval $\delta\tau$

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

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”

$$R_0 = \beta\gamma \int_0^{\infty} \tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma} \quad R_0=1 \Rightarrow \text{epidemic threshold } (\beta=\gamma)$$

Diffusion on Graphs: Quick recap

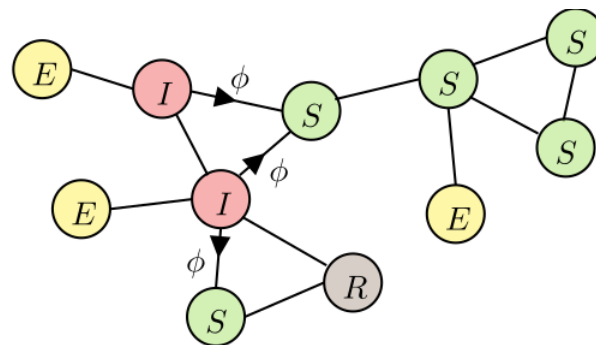
- An entity that spreads/flows over the graph: disease, meme & news (social media), etc.
- Epidemic modelling with contact graphs & between population dynamics
- Classic compartment based models
 - Differential equations of compartment size changes (S, I, E, R)
 - Total outbreak size (asymptotic value 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
 - Assumes full mixing (= ER contact graph)
 - Everyone in I component can infect anyone if S component



Epidemic models on networks

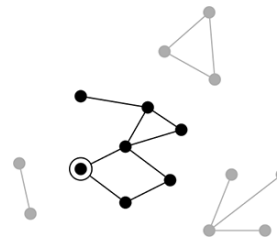
SIR can be generalized to the network case considering transmission rate for edges

Instead of full mixing that assumes anyone could contact/infect anyone, we model the infection routes and **infected nodes spread the disease to their susceptible neighbours**



Would we always have an outbreak?

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



An outbreak starting with a single infected individual (circled) will eventually affect all those in the same component of the network, but leave other components untouched.

Epidemic models on networks: Attack Size

SIR model, **transmission probability**

$$\phi = 1 - e^{-\beta\tau}$$

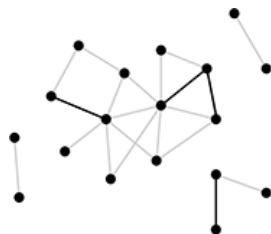
the amount of time for which the infected individual remains infected
the probability that the disease is not transmitted

If we assume τ to be constant, then ϕ is the same for all edges

Consider selecting a fraction of ϕ edges uniformly at random \Leftarrow This is called bond percolation

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

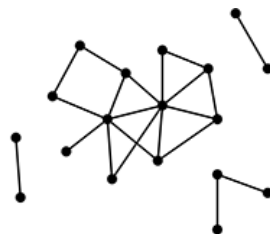
As ϕ increases, S also increases and hence both the probability and the size of an epidemic increase with ϕ



(a) $\phi = 0.2$



(b) $\phi = 0.5$



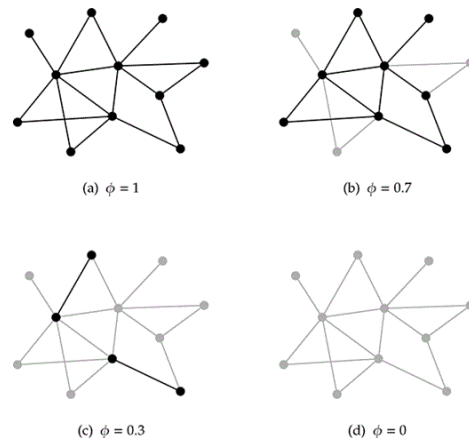
(c) $\phi = 1$

percolation transition \Rightarrow
epidemic threshold

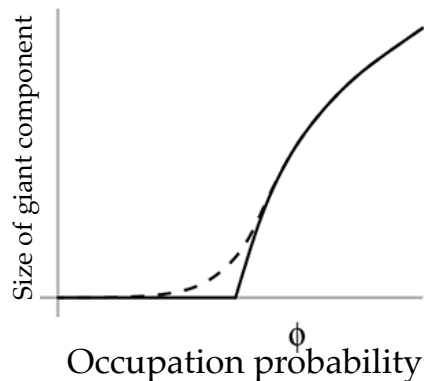
Final attack size? count the nodes in the appropriate connected component

Percolation

- Percolation process:
 - Site percolation: nodes are randomly removed from a network
 - E.g. failure of routers on the Internet, vaccinated individuals
 - Bond percolation: edges are randomly removed from a network
 - E.g. physical distancing
- Percolation phase transition: a giant percolating cluster forms



The phase transition at which the giant cluster appears is only sharp in an infinite system (solid line). In a finite-sized system it gets rounded off (dashed line).



Can be used to study
Network Resilience

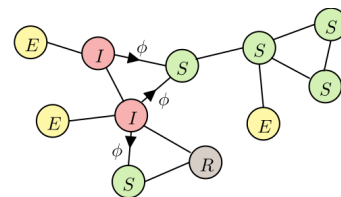
Epidemic SIR model on networks: eigenvalues of adjacency matrix

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

$$\frac{\beta}{\gamma} = \frac{1}{\lambda^*}$$

An individual's probability of infection at early times is proportional to **eigenvector centrality**: higher \Rightarrow infected sooner

We can measure the long-time behaviour, about the overall total number of individuals infected by the disease and the above, however for the temporal evolution of the disease outbreak we need to run simulation



Network Modelling & Simulation

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



Graph Model

$$\frac{ds_i}{dt} = -\beta s_i \sum_j A_{ij} x_j$$

$$\frac{dx_i}{dt} = \beta s_i \sum_j A_{ij} x_j - \gamma x_i$$

$$\frac{dr_i}{dt} = \gamma x_i$$

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

Original Model

$$\frac{ds}{dt} = -\beta s x$$

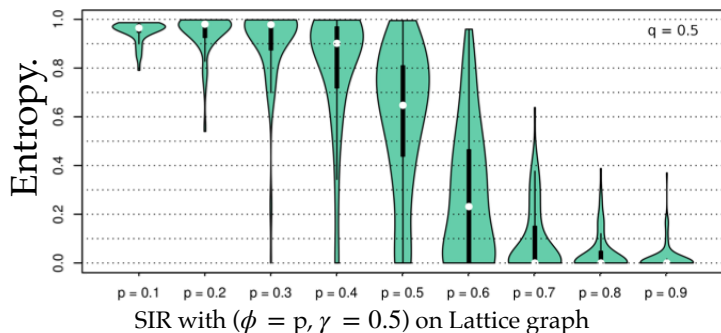
$$\frac{dx}{dt} = \beta s x - \gamma x$$

$$\frac{dr}{dt} = \gamma x$$

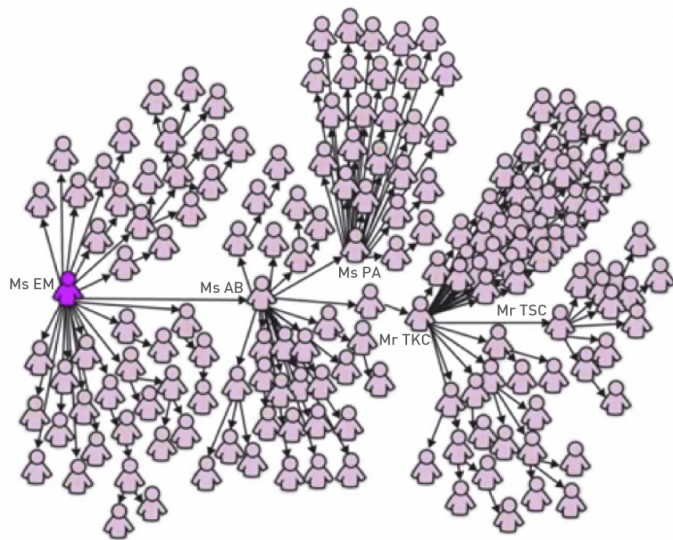
Epidemic models on networks: Contact Tracing

Network structure and **patient zero** are both important

We can also infer the source probability distributions, and measure the entropy
low entropy => high detectability



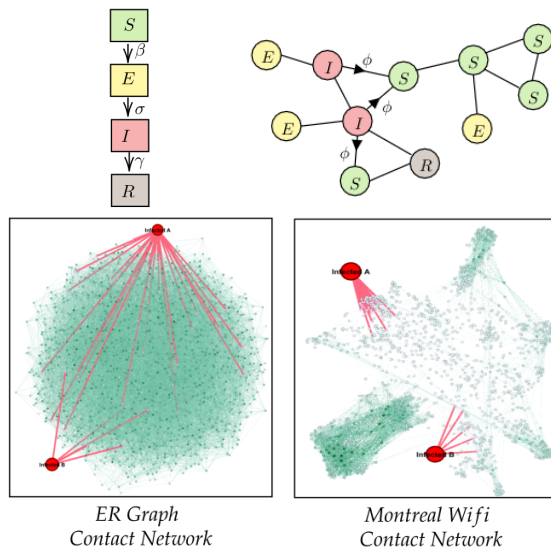
[See here: Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations](#)



One-hundred-and-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.

Contact Graph Epidemic Modelling of COVID-19 example

for Transmission and Intervention Strategies



structure of the contact networks significantly changes the epidemic curves, effectiveness of different NPIs, and outcomes of re-opening strategies

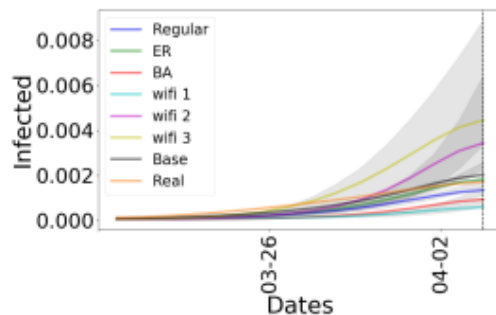
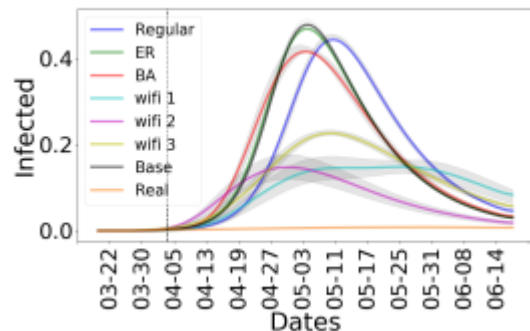
Leung A, Ding X, Huang S, Rabbany R. Contact Graph Epidemic Modelling of COVID-19 for Transmission and Intervention Strategies. arXiv preprint arXiv:2010.03081. 2020 Oct 6.

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

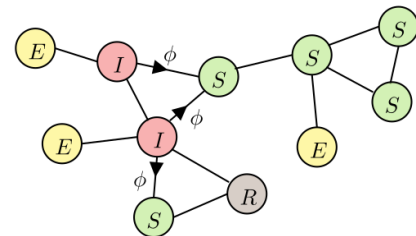
Table 1: Timeline of Canada COVID-19 selected NPI events based on (Vogel 2020; Trevor Lawson 2020)

Read more [here](#) & [here](#)

Contact Graph Epidemic Modelling of COVID-19 example

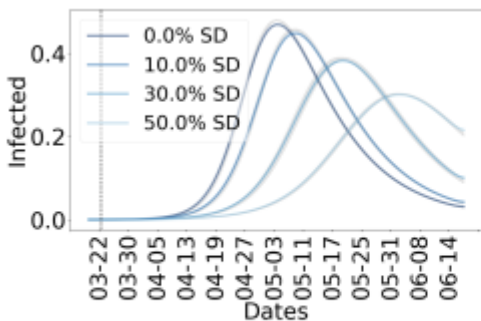


CGEM closely approximates the base **SEIR** model when the contact network is assumed to be Erdős-Reñyi graph.

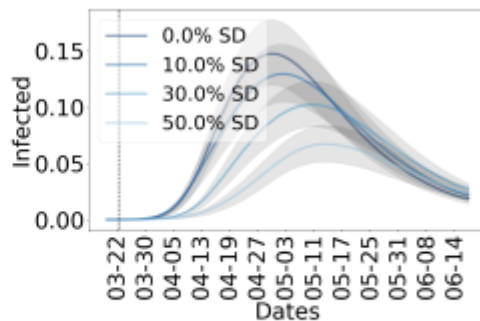


Assuming an Erdős-Reñyi graph as the contact network overestimates the impact of COVID-19 by more than a factor of 3 when compared with more realistic structures.

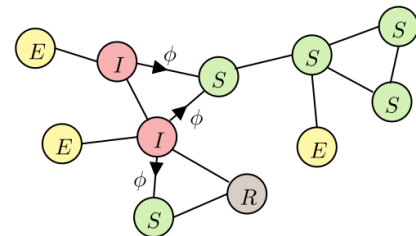
Contact Graph Epidemic Modelling of COVID-19 example



(a) ER



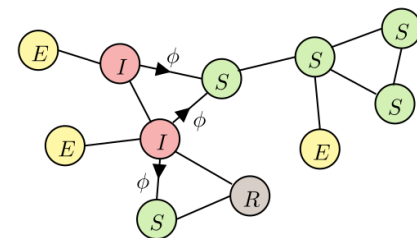
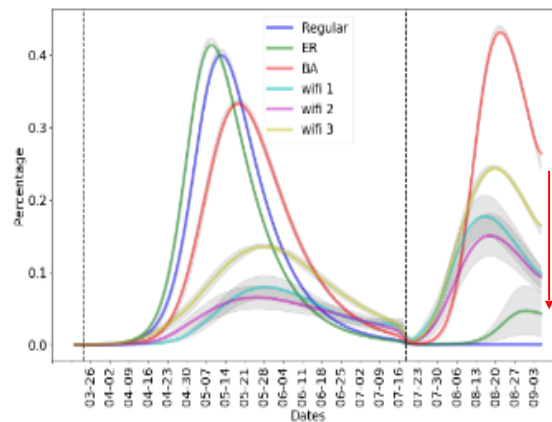
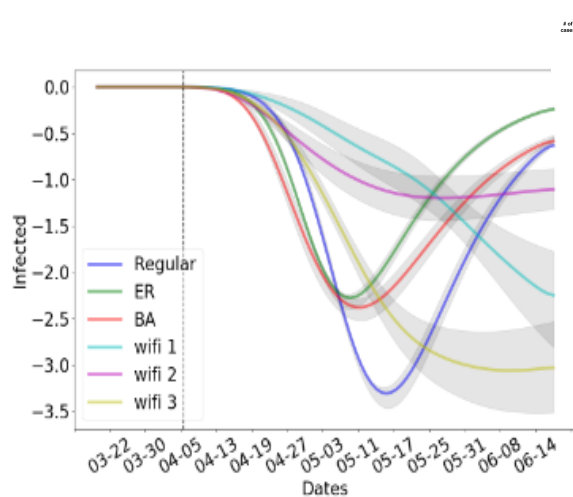
(b) Wifi 2



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

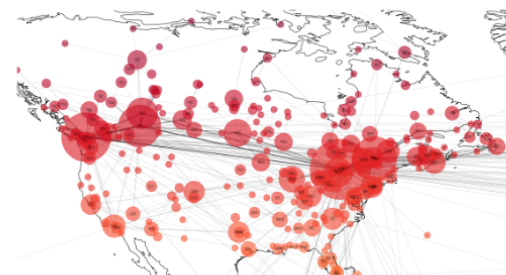
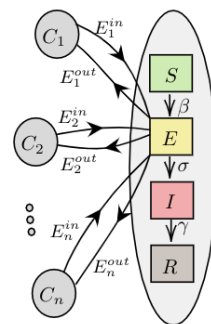
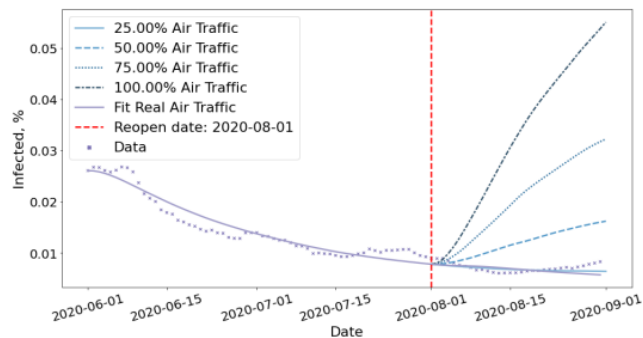
The ER graph significantly underestimates the effect of wearing masks in terms of the total decrease in the final attack rate



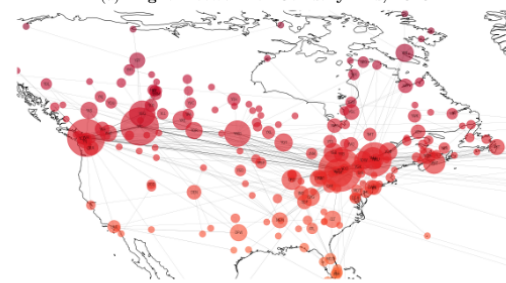
ER graph significantly underestimates the second peak after reopening public places, i.e. allowing back hubs.

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

Ding X, Huang S, Leung A, Rabbany R. Incorporating Dynamic Flight Network in SEIR to Model Mobility between Populations. Applied Network Science 6 (1), 2021