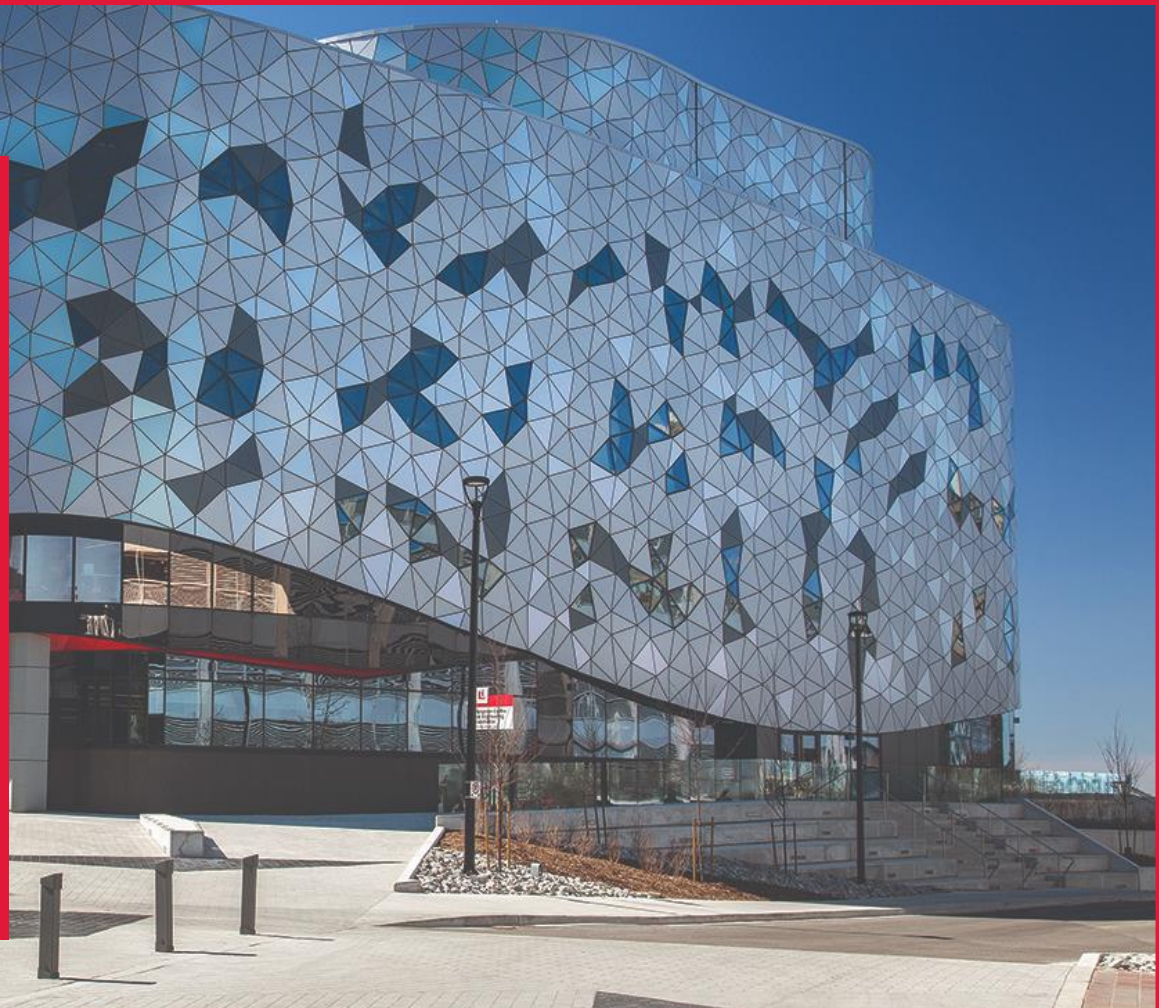


Epidemic Spreading in Trajectory Networks

Tilemachos Pechlivanoglou, Jing Li,
Jialing Sun, Farzaneh Heidari,
Manos Papagelis

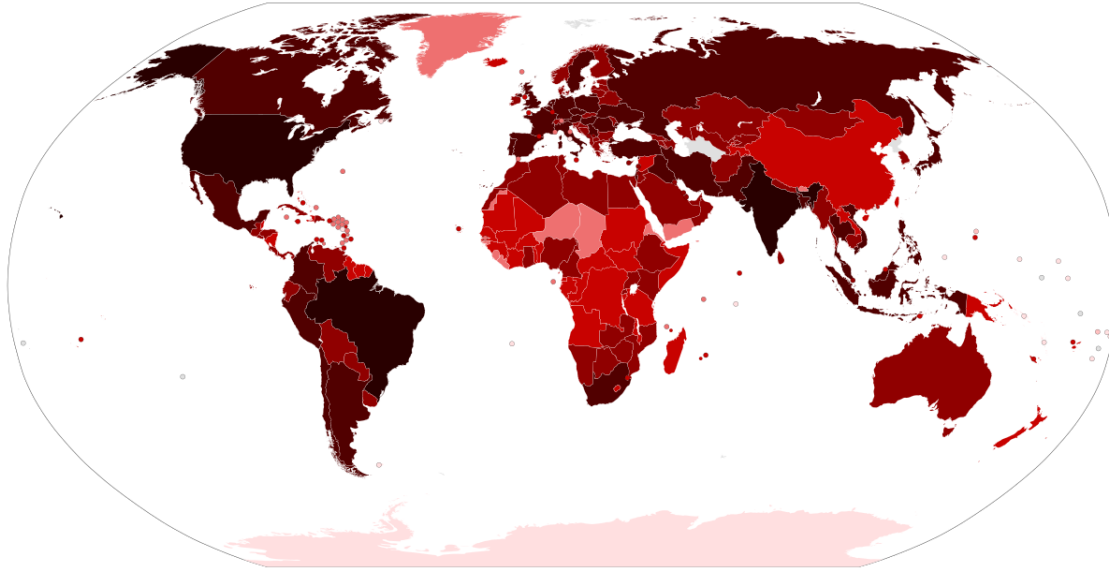
Presenter: Manos Papagelis

YORK 



Background and Motivation

Covid-19 (a global pandemic)

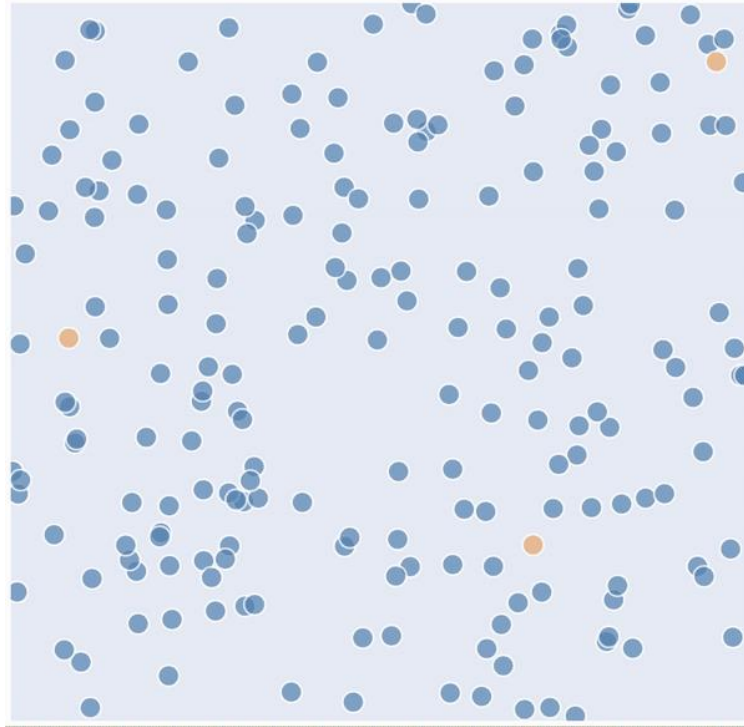


containment measures
physical **distancing**
business, social life **lockdown**

side effects
economic downturn
psychological well-being
...

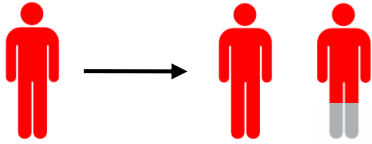
need for more **moderate** contact-reduction policies

Mechanism of infectious disease spreading

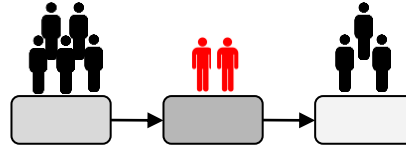


- Susceptible
- Infected
- Removed

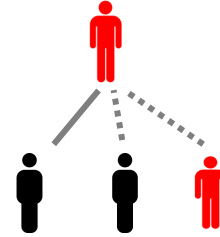
Revisiting epidemic concepts



reproductive number



**compartmental models
(population-based)**



offline contact tracing

Basic reproductive number (R_0)

The **expected** number of people that an individual infects

$R_0 < 1$ infection **dies out**

$R_0 > 1$ infection **persists**

$$R_0 = p \times k$$

p : transmission probability k : number of contacts

Ebola: 1.6–2

Infected person

Average people infected



SARS: 2–4

Infected person

Average people infected



Beyond R0

(unrealistic) assumptions of R0

homogeneous population: all individuals are equally susceptible

full population mixing: all individuals are equally likely to come into contact with each other

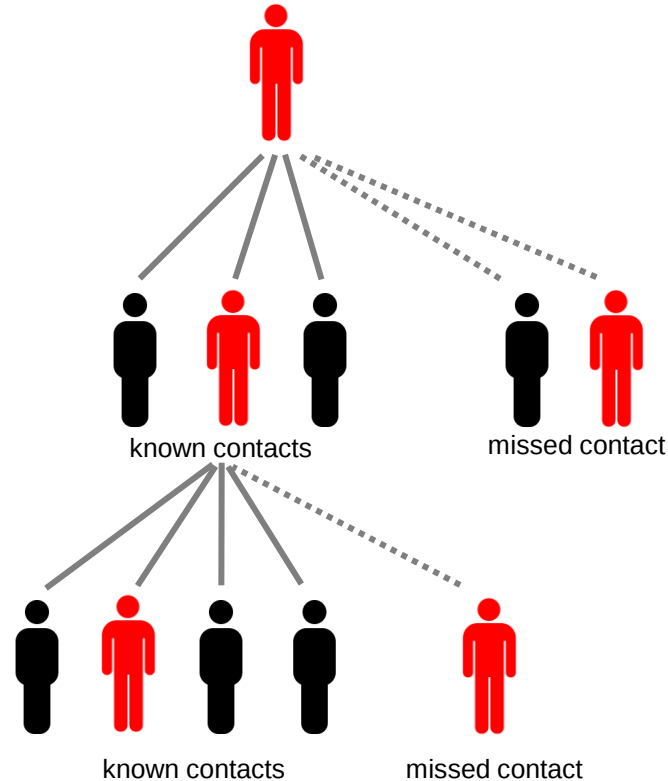
more realistic epidemic models need to

integrate **heterogeneity** of individuals, e.g., different contact patterns

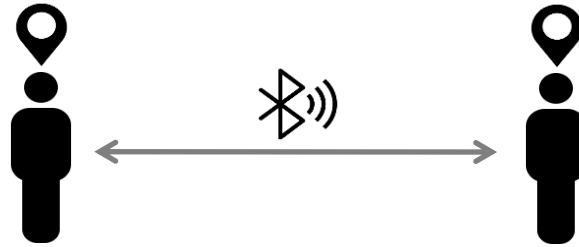
monitor **actual contacts** of individuals

Offline contact tracing (through interviews)

- ✗ time-consuming
- ✗ resource-intensive
- ✗ lack of **accuracy**



Digital contact tracing

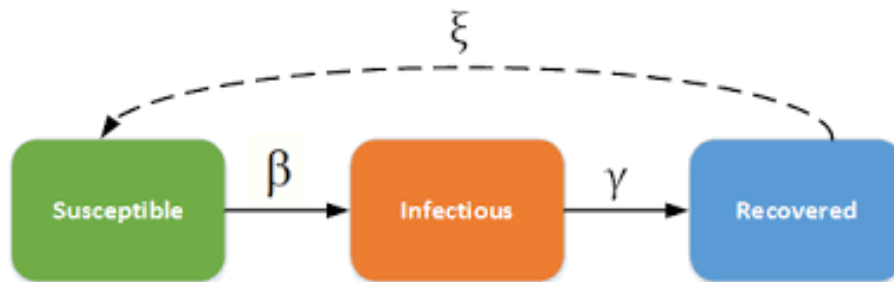


Enabled by mobile apps, geolocation devices, etc.

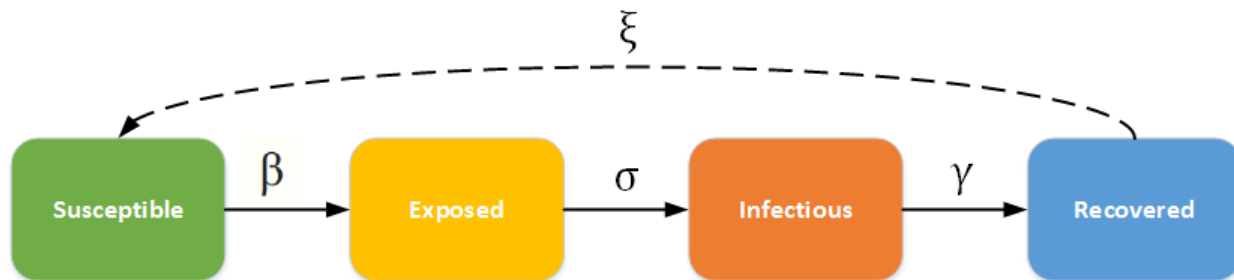
- ✓ addresses limitations of traditional contact tracing
- ✗ privacy concern

Compartmental models

SIR

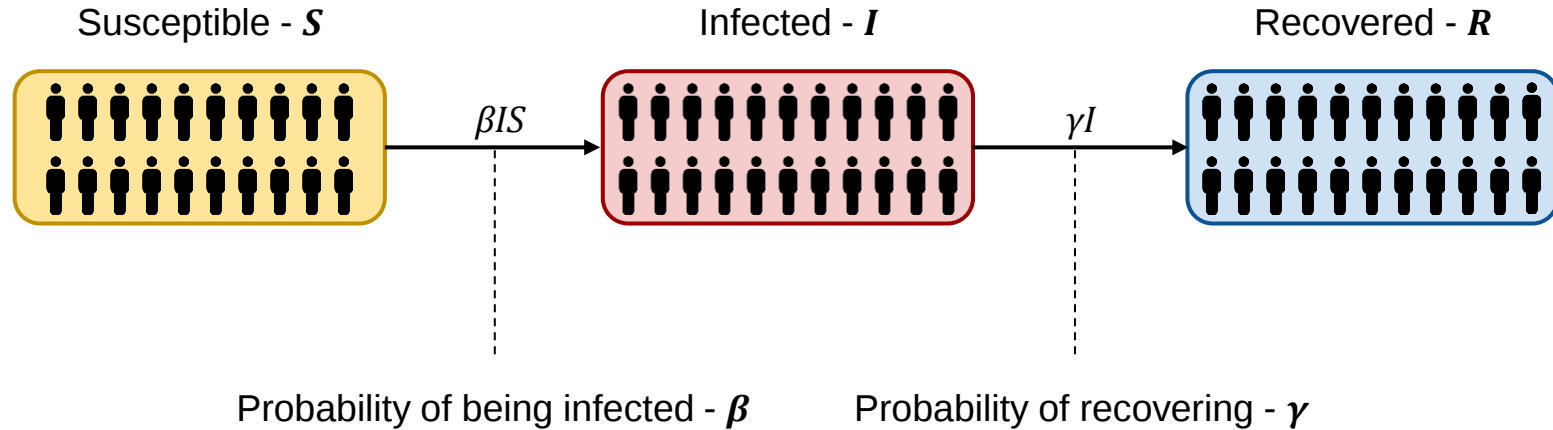


SEIR

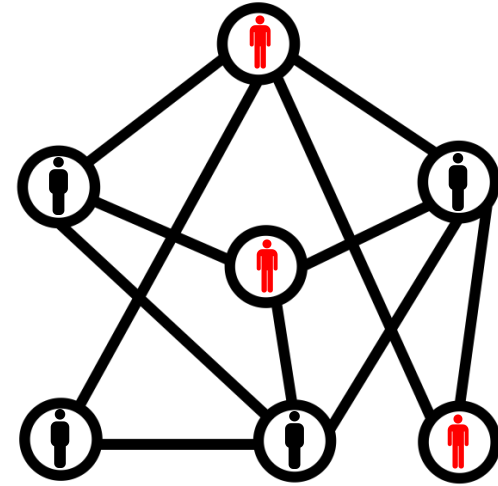
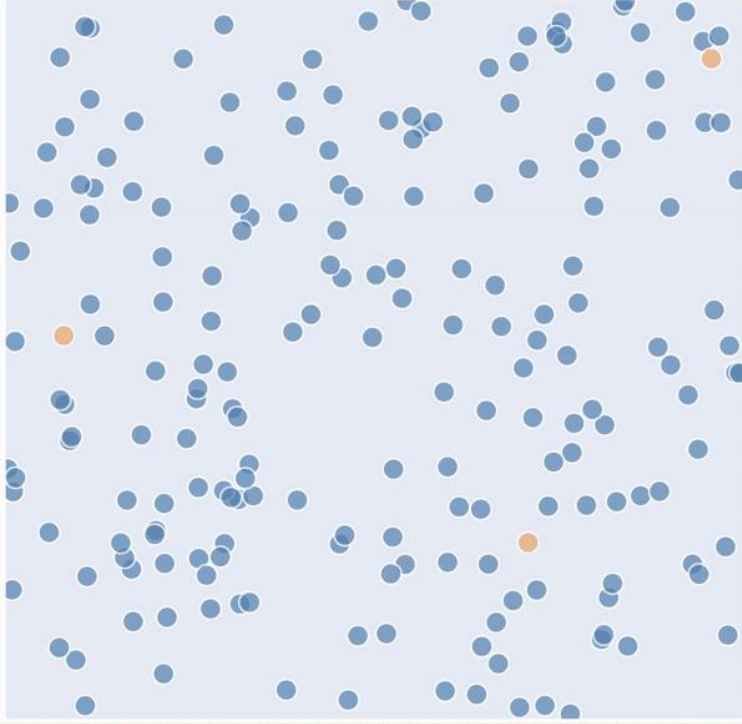


SIR model

Time $t = 0$



Individual-based models



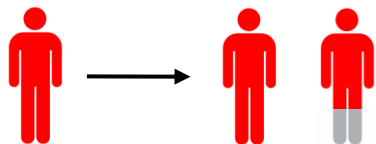
mobility network / contact network

nodes: individuals

edges: social interaction

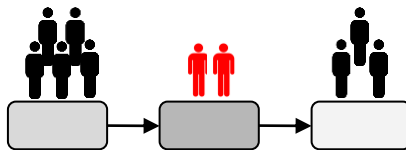
contagion: stochastic infection due to spatial proximity

Models comparison



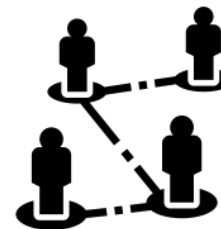
reproductive number

- ✓ very simple
- ✗ assumes full mixing
- ✗ ignores **heterogeneity** of individuals



compartmental

- ✓ learning transition probabilities (as a group)
- ✗ ignores **heterogeneity** of individuals



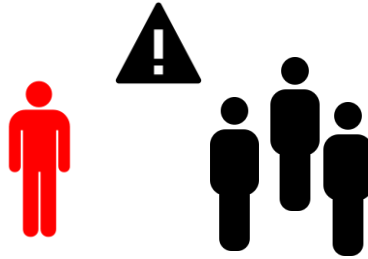
individual-based

- ✓ best reflection of real life
- ✓ monitor individual transition between compartments
- ✗ requires extensive, very detailed data

focus of this research

Research Questions

RQ1: How to take (mobility) heterogeneity into account?



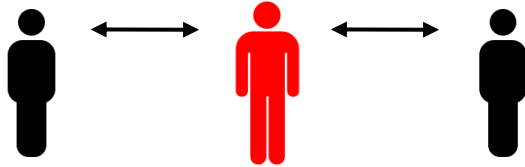
model **relative risk** of individuals as a factor of
their contacts over time

RQ2: How to model epidemic spreading?



model epidemic spreading as **cascading** process
in **dynamic spatiotemporal networks**

RQ3: How to contain an epidemic?



design **targeted network interventions** that aim at containing/controlling the contagious process

Problem Statement

The Problem

Input

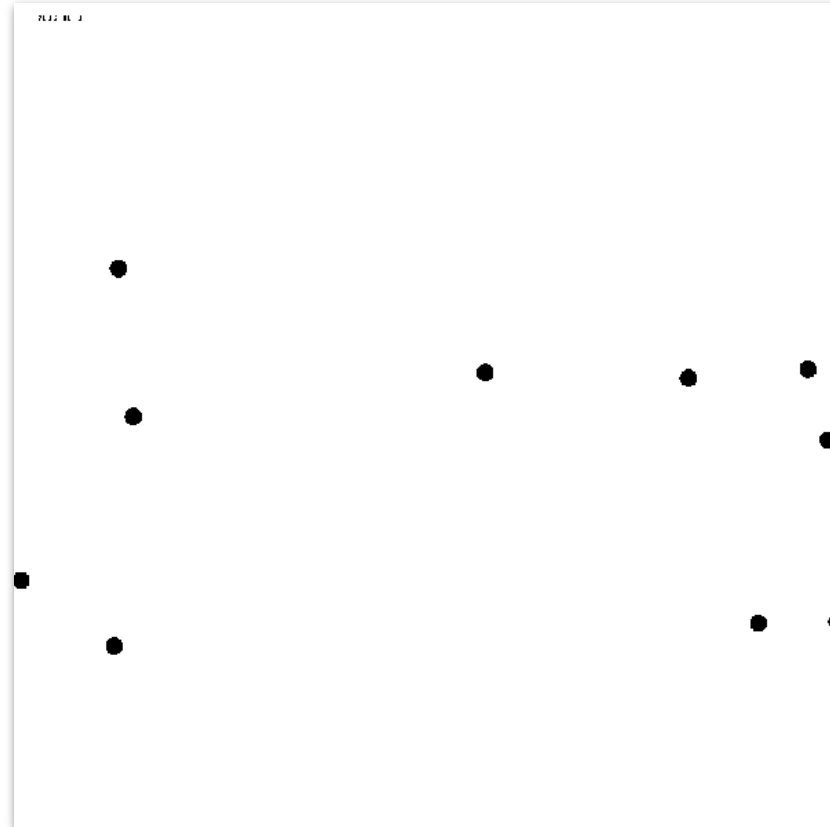
- Historical data **of individual trips** (trajectories)

Output

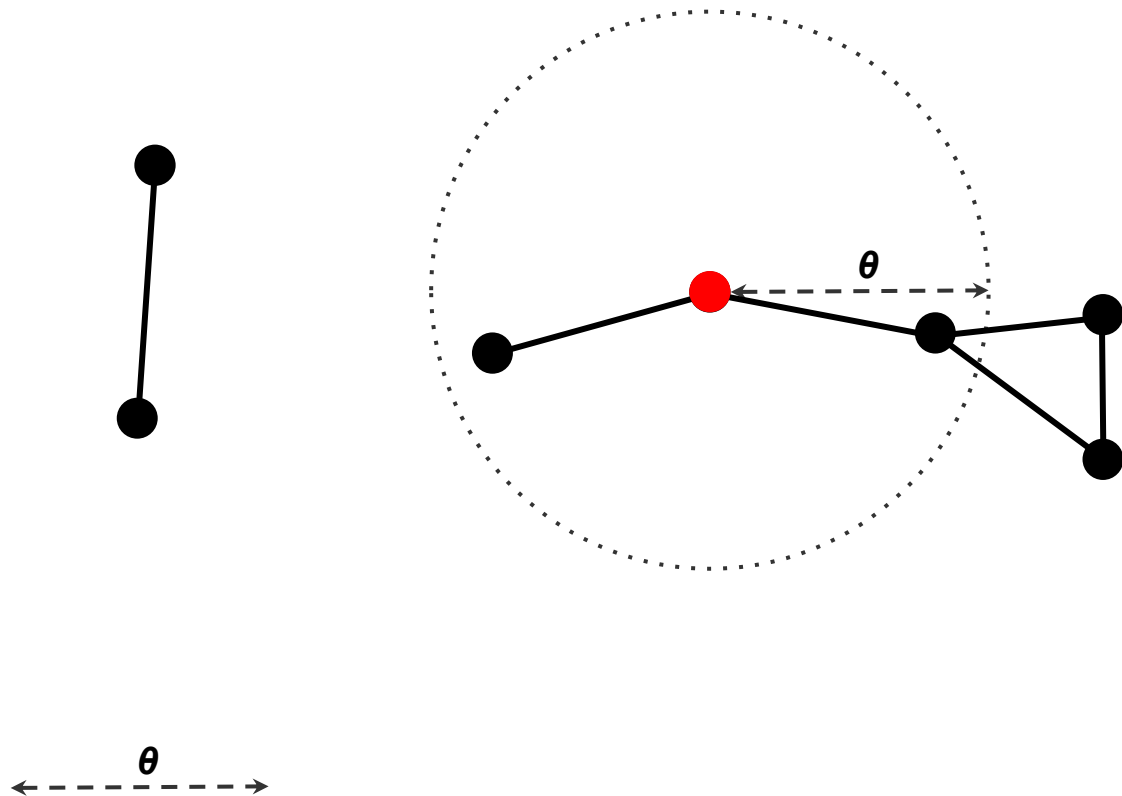
- Assess the **relative risk of infection of individuals**
- Assess the **size of a disease outbreaks** due to specific individuals
- Assess the **impact of targeted non-pharmaceutical intervention strategies**
- Provide **support to health policy-making**

Methodology

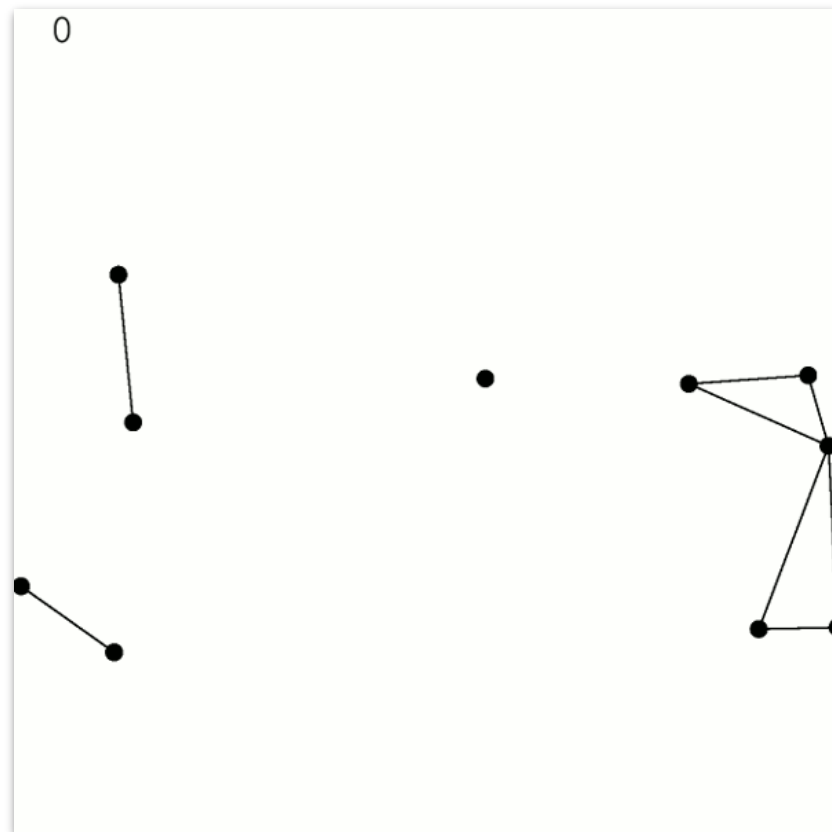
Trajectories of individuals



Proximity network



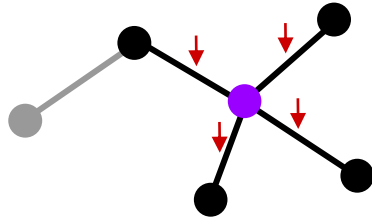
Trajectory network



Modeling risk of infection

Three (3) methods for measuring risk of infection

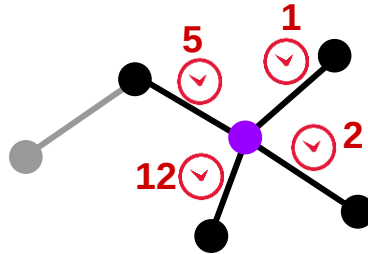
$$1+1+1+1 = 4$$



(1) # of contacts
(node degree)

- ✓ intuitive
- ✗ doesn't consider time spent in contact

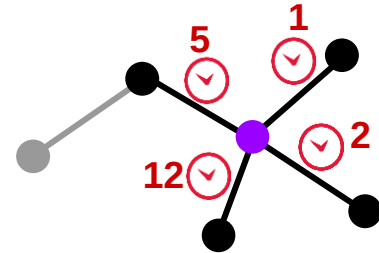
$$5+1+2+12 = 20$$



(2) total contact time

- ✓ considers contact time
- ✗ long contacts skew result

$$\beta = 0.1$$
$$4 - 0.9^5 - 0.9^1 - 0.9^2 - 0.9^{12} \cong 1.4$$



(3) sum of contact times
in geometric function

- ✓ considers contact time
- ✓ very long contacts don't count as much

Modeling epidemic spreading

Simulating disease spreading on a trajectory network

we employ **a stochastic agent-based SEIR network model**

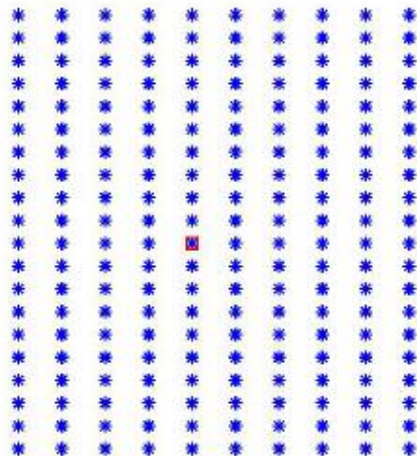
Each node (person) has a $p_{u,v}$ chance to infect their neighbors

$$p_{u,v} = 1 - (1 - \beta)^k$$

where

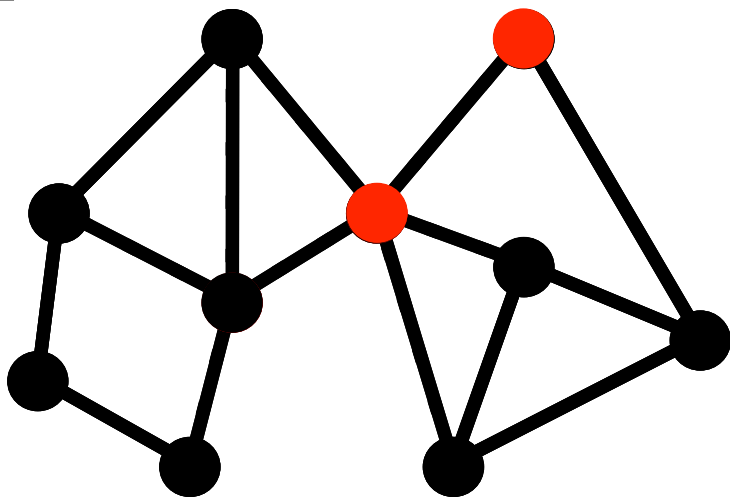
β : transmission probability

k : duration (in timesteps)



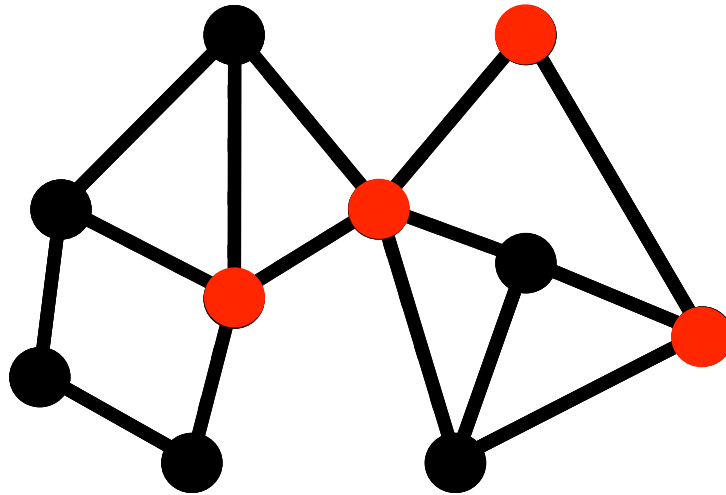
Disease spreading

Timestamp: 1



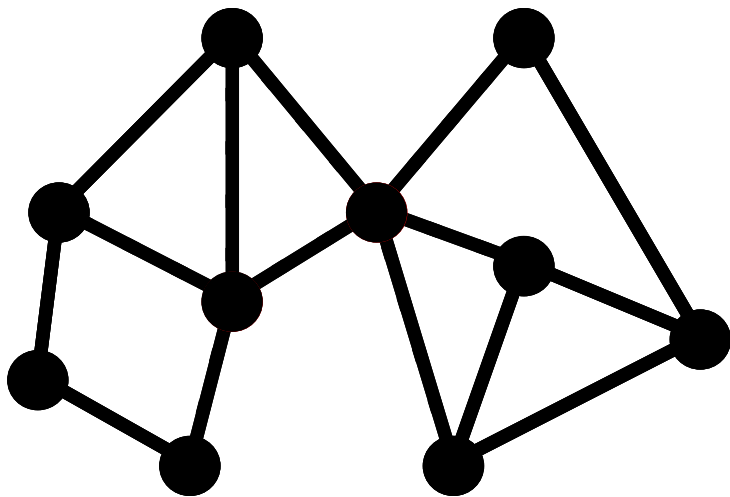
Disease spreading

Timestamp: 2



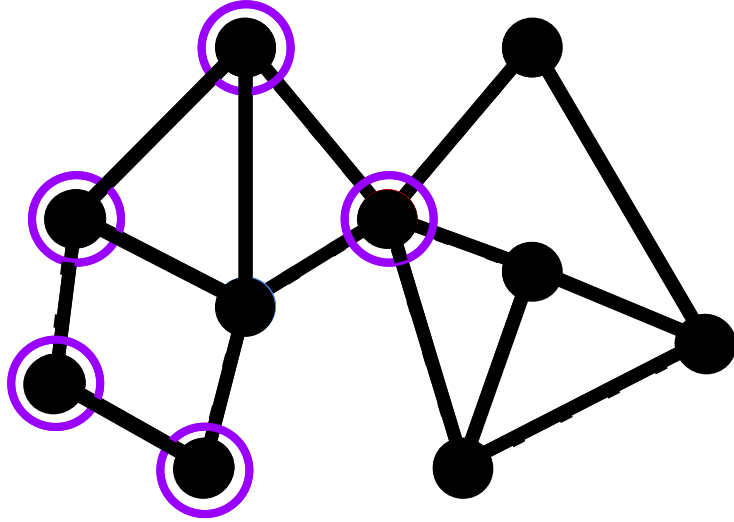
Targeted network interventions

Intervention policy 1 (centralized): node immunization



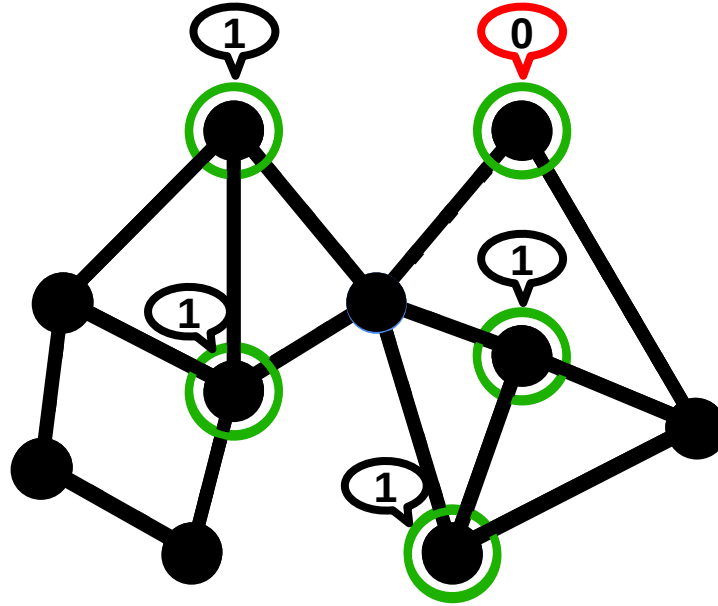
Find the node of
highest degree
and immunize it

Intervention policy 2A (individual): avoiding high-risk contacts



Select only high-risk nodes
and remove them by risk

Intervention policy 2B (individual): maintaining a “social bubble”



For every node, keep only the $\alpha\%$ neighbors
by **common contacts** (triangles common)

Experimental results

Pedestrian simulation data

map: YorkU campus map
(from OpenStreetMap)

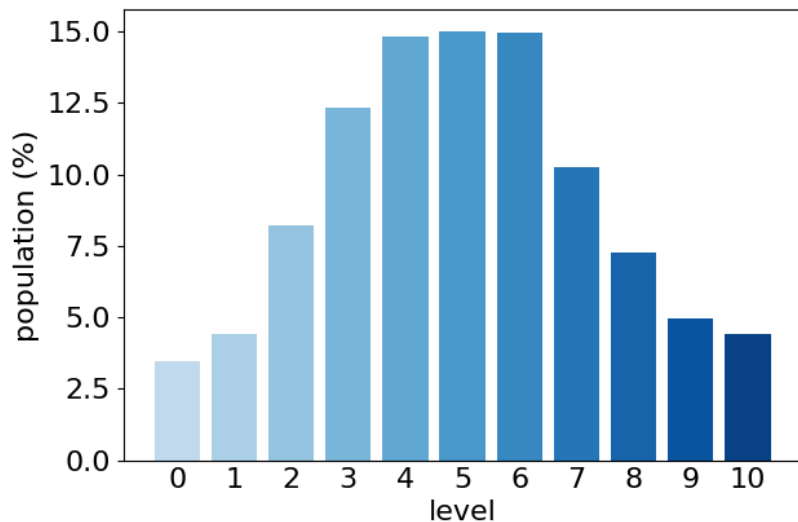
trips: random individual trips based
on **daily activity patterns** (with
SUMO)

granularity level: min-by-min
movement of 10k pedestrians over
30 days (with SUMO)

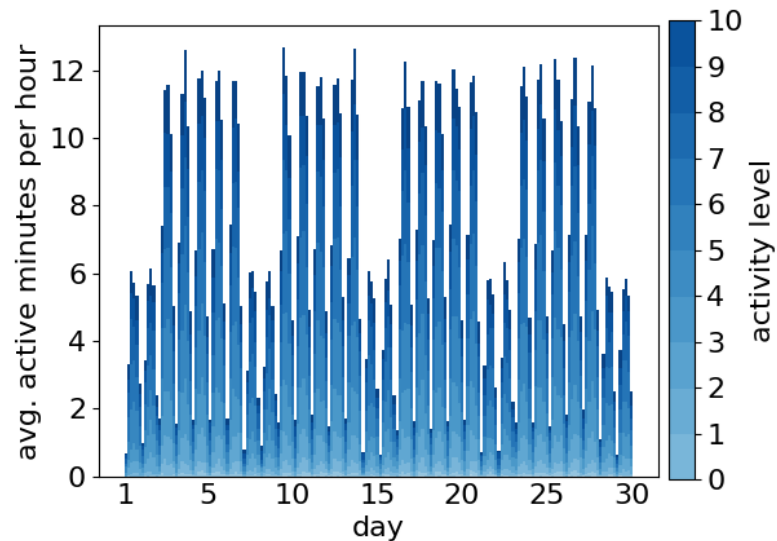
mobility network: spatiotemporal
network (**10k** nodes, **~56M** edges)



Modeling real-world activity patterns



distribution of activity levels

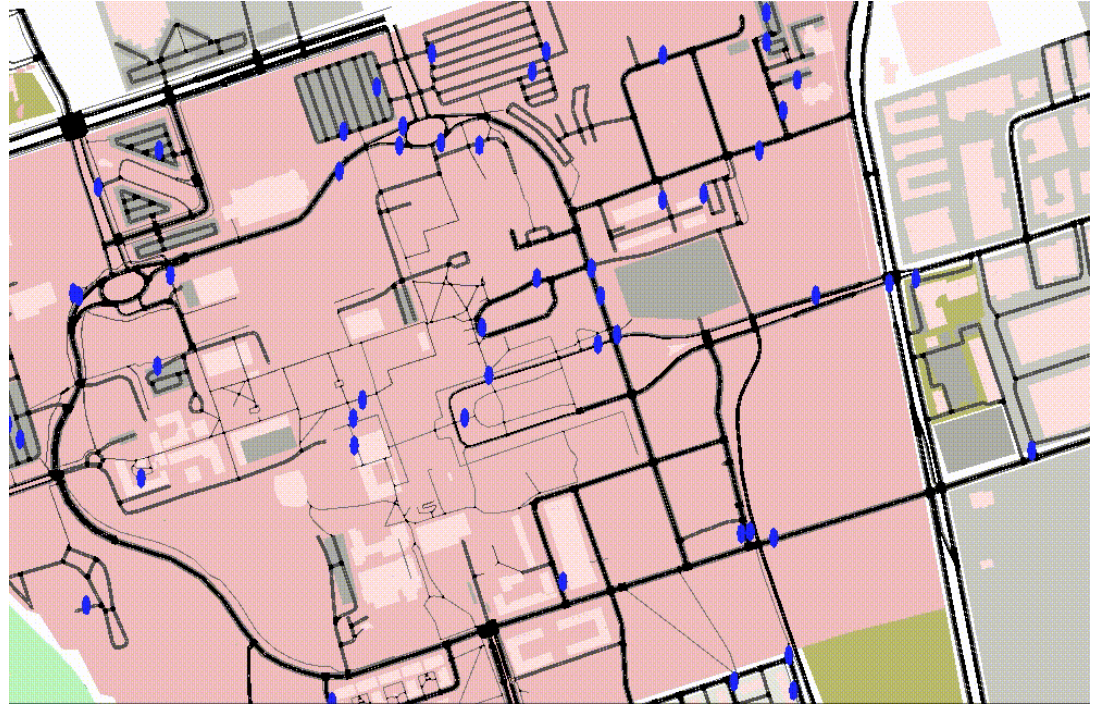


hourly activity

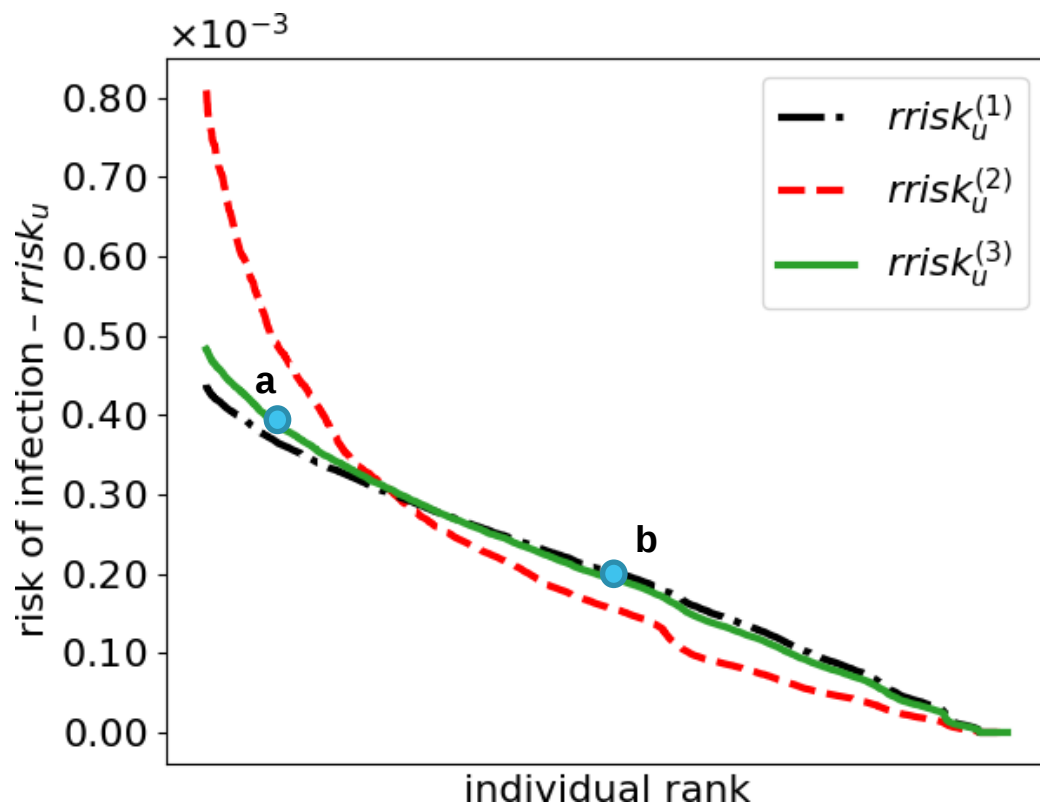
Synthetic Data Generator

Simulation of Urban Mobility (SUMO)

- designed for traffic/ pedestrian flow prediction
- supports real map analysis



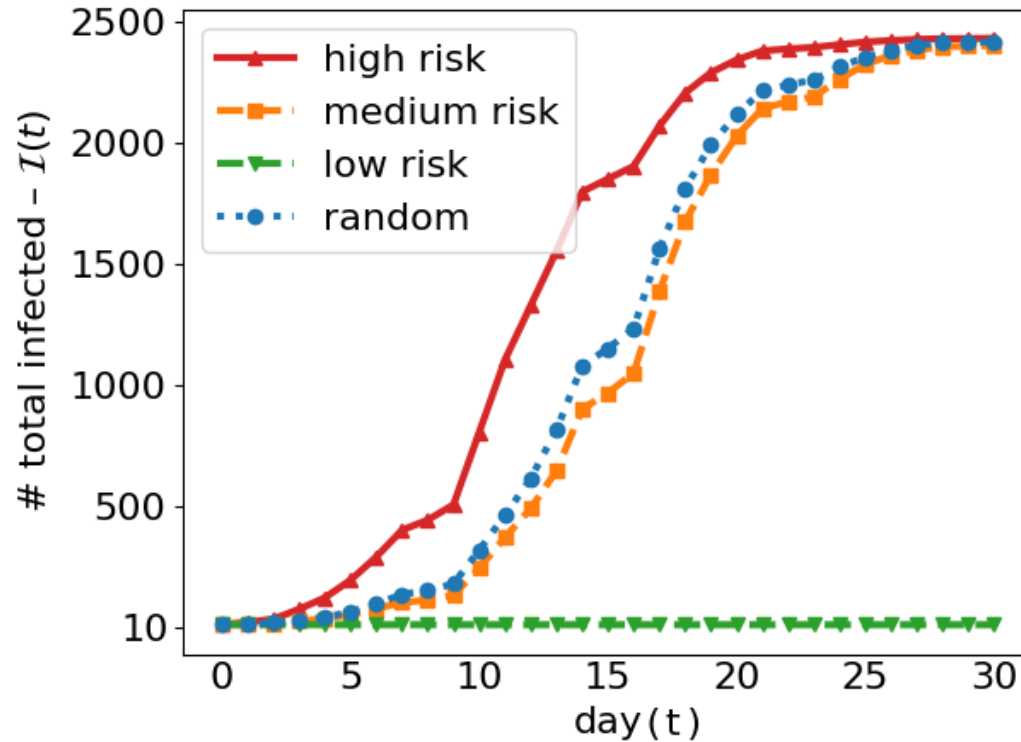
Distribution of relative risks of individuals



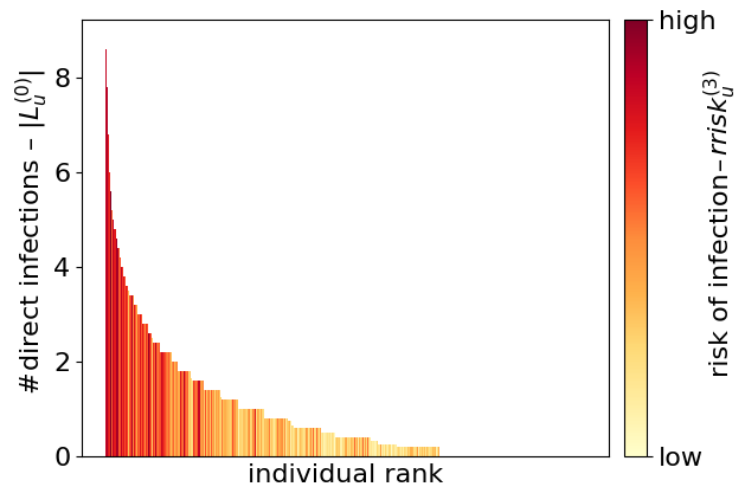
$rrisk_u^{(3)}$ more smooth

a 3x higher risk than b

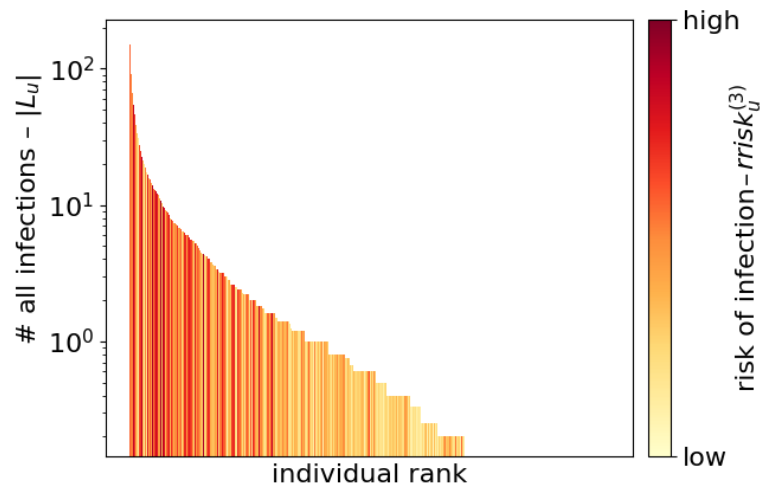
Outbreaks due to “seed” nodes belonging to different risk groups



Direct vs secondary infections

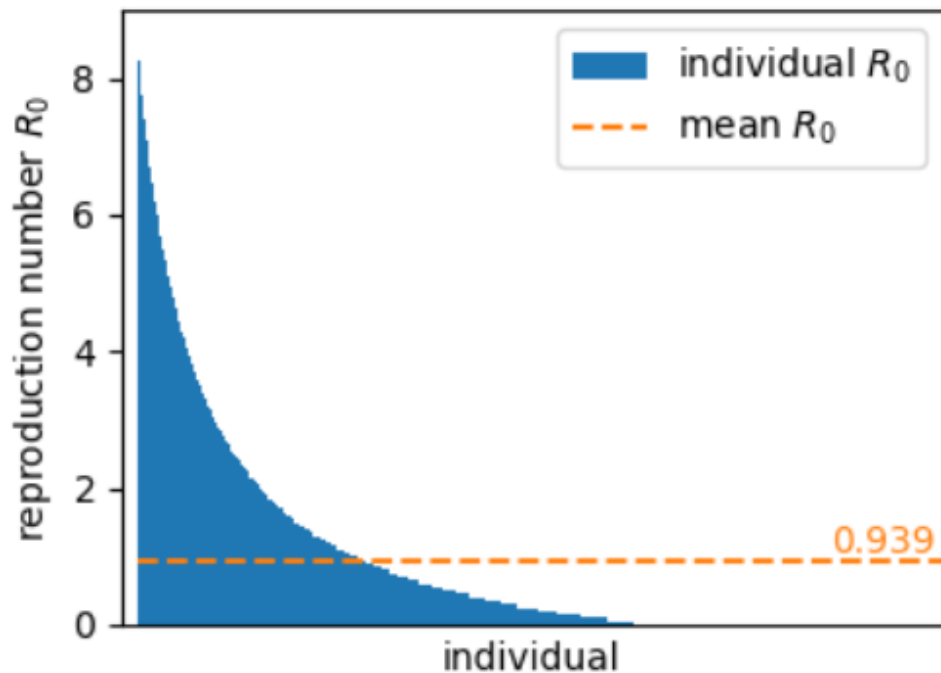


direct infections



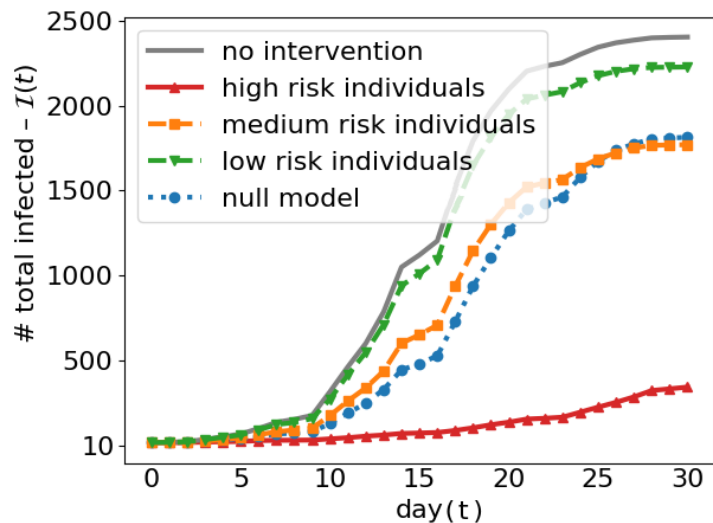
indirect, secondary infections

R_0 distribution of individuals

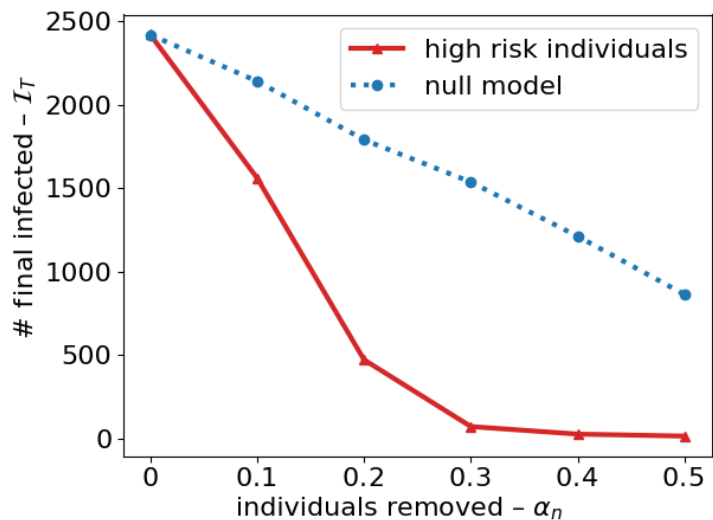


Intervention 1 vs null model (same # of random edges removed)

node immunization



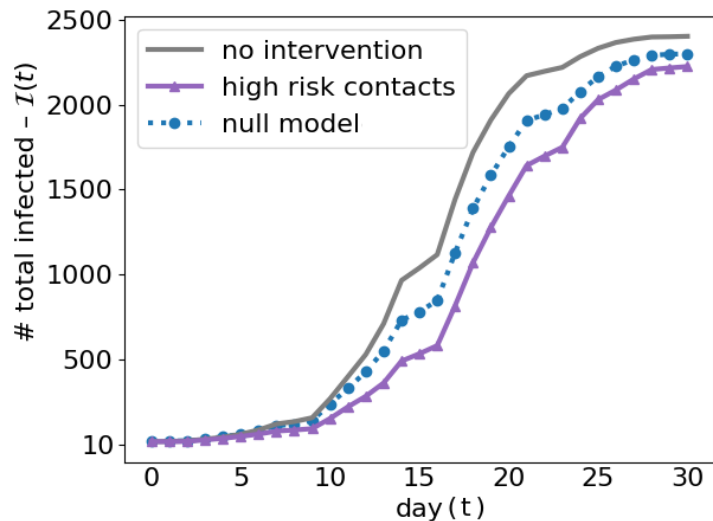
SEIR progress ($\alpha = 20\%$)



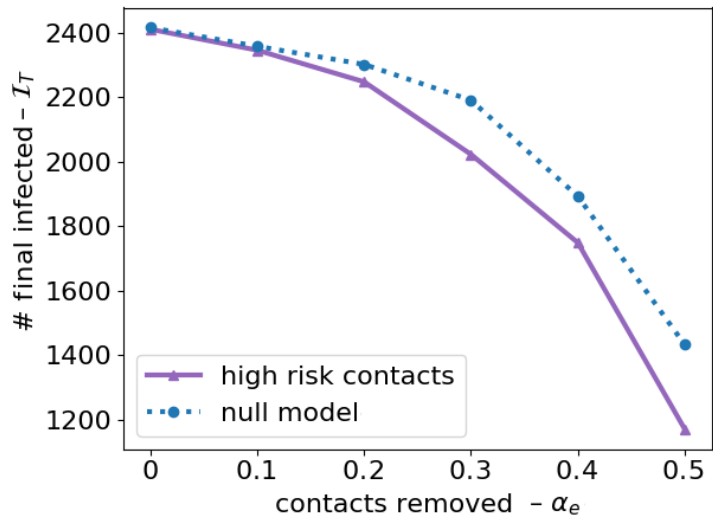
infections for varying α

Intervention 2A vs null model

avoiding high-risk contacts



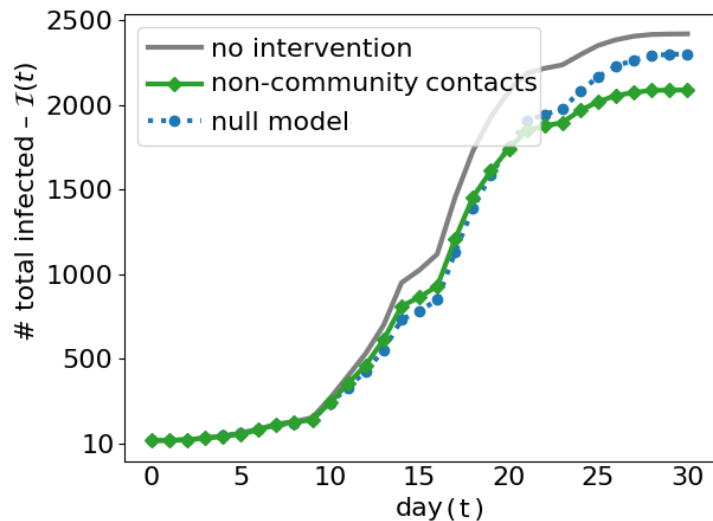
SEIR progress ($\alpha = 20\%$)



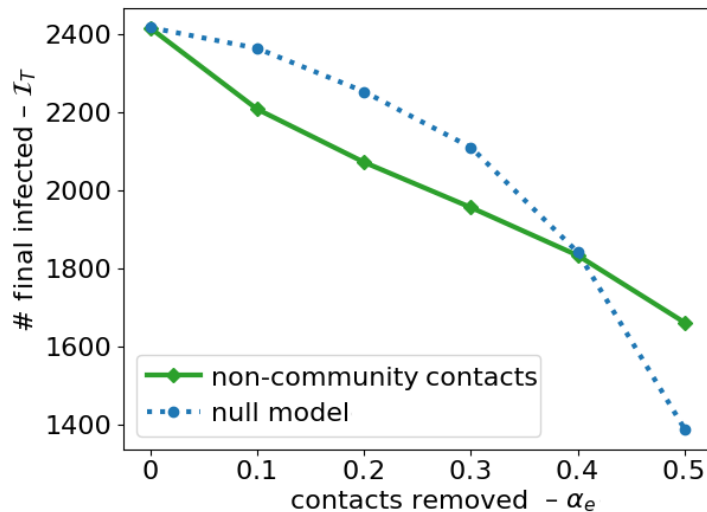
infections for varying α

Intervention 2B vs null model

maintaining a “social bubble”

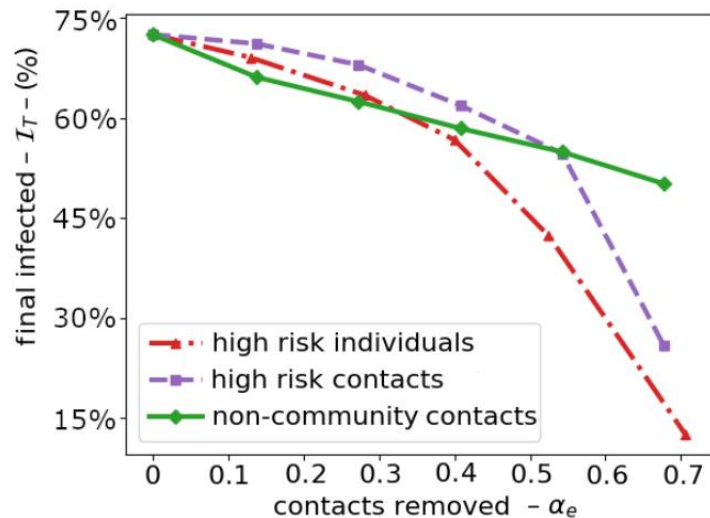


SEIR progress ($\alpha = 20\%$)

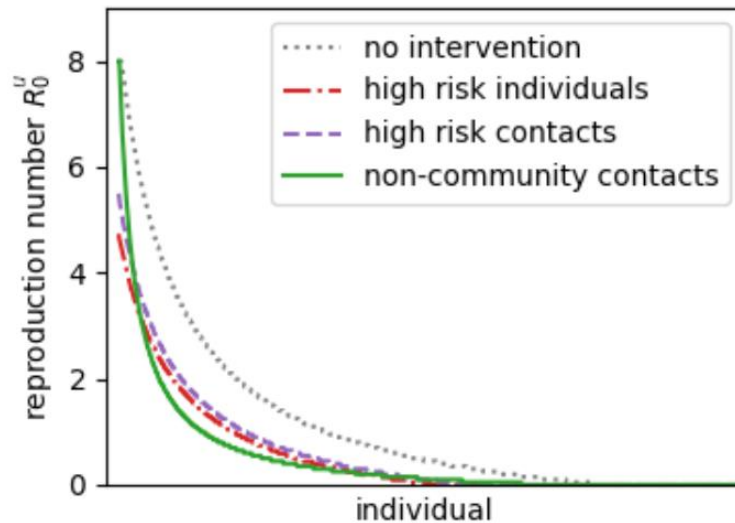


infections for varying α

Comparison of interventions



comparison of infected counts

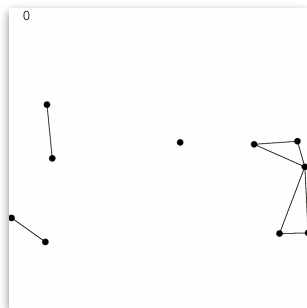


comparison of R_0 distributions

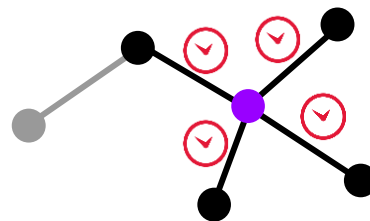
Takeaway



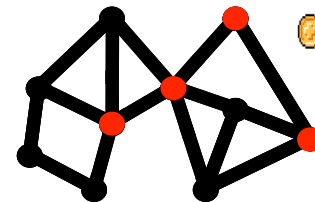
agent-based



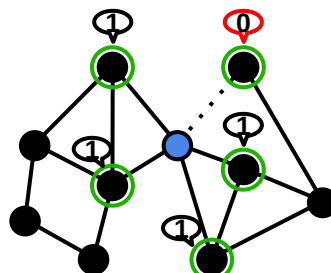
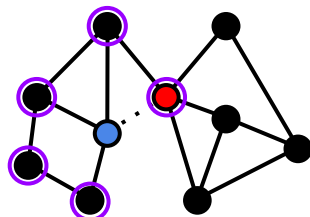
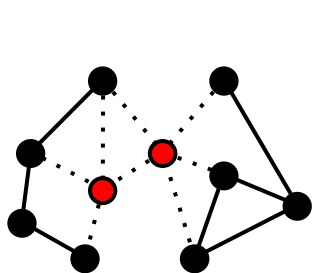
mobility network



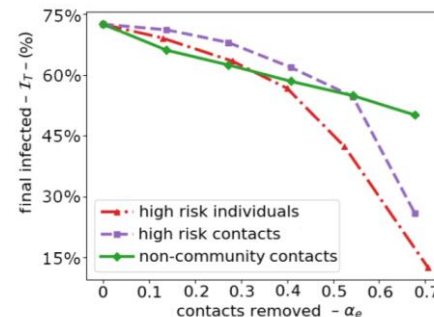
infection risk



stochastic propagation



targeted intervention policies



support policy-making

Credits



Tilemachos Pechlivanoglou



Jing Li



Jialin Sun



Farzaneh Heidari

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T. Pechlivanoglou, J. Li, J. Sun, F. Heidari, M. Papagelis.

Big Data Research (BDR, Vol. 27, 100275, pp 1-15, 2022).

Thank you!

Questions?