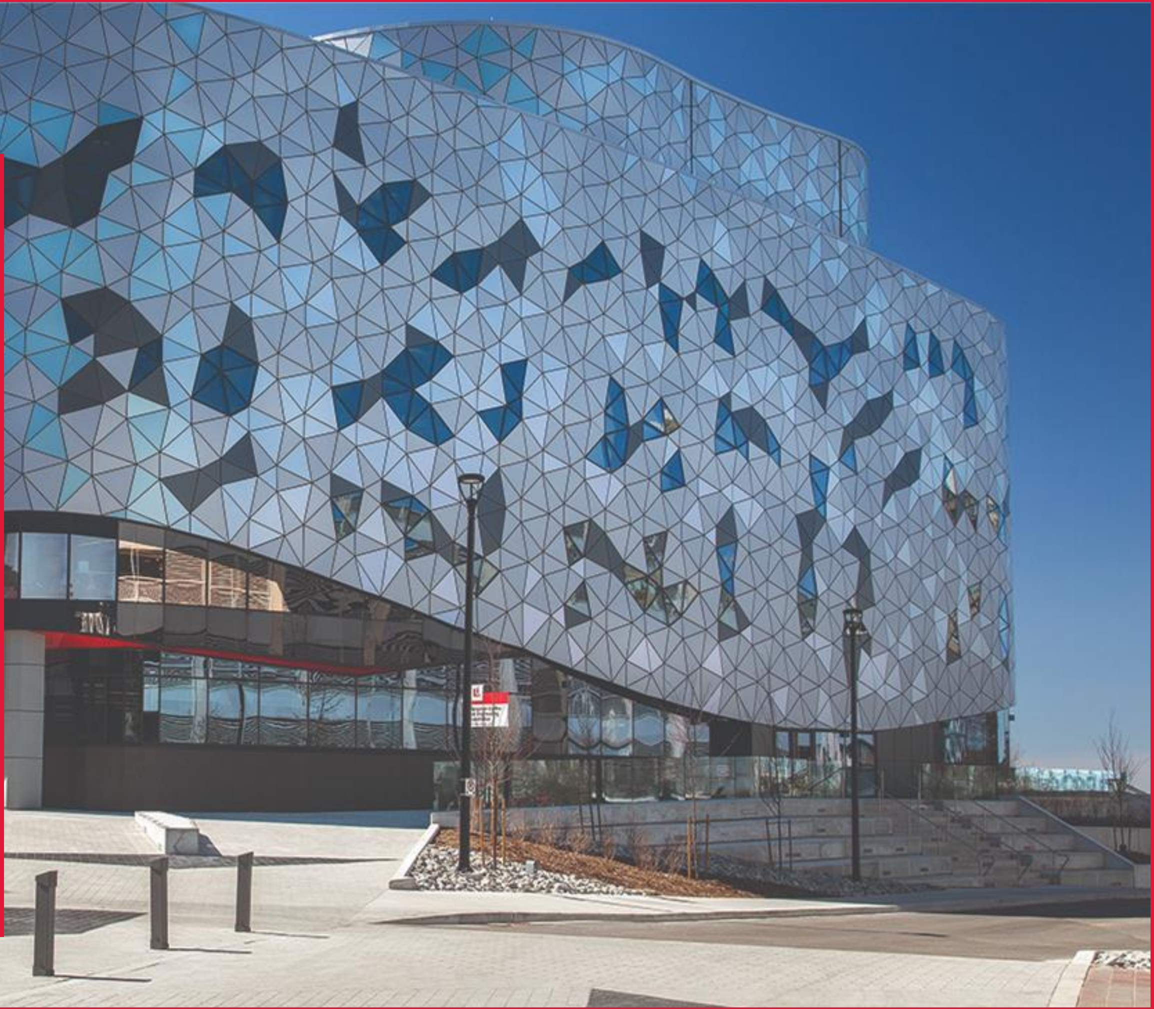
Mobility-based Models of Epidemic Spreading

Tilemachos Pechlivanoglou, Jing Li, Jialin Sun, Gian Alix, Nina Yanin, Farzaneh Heidari, Manos Papagelis

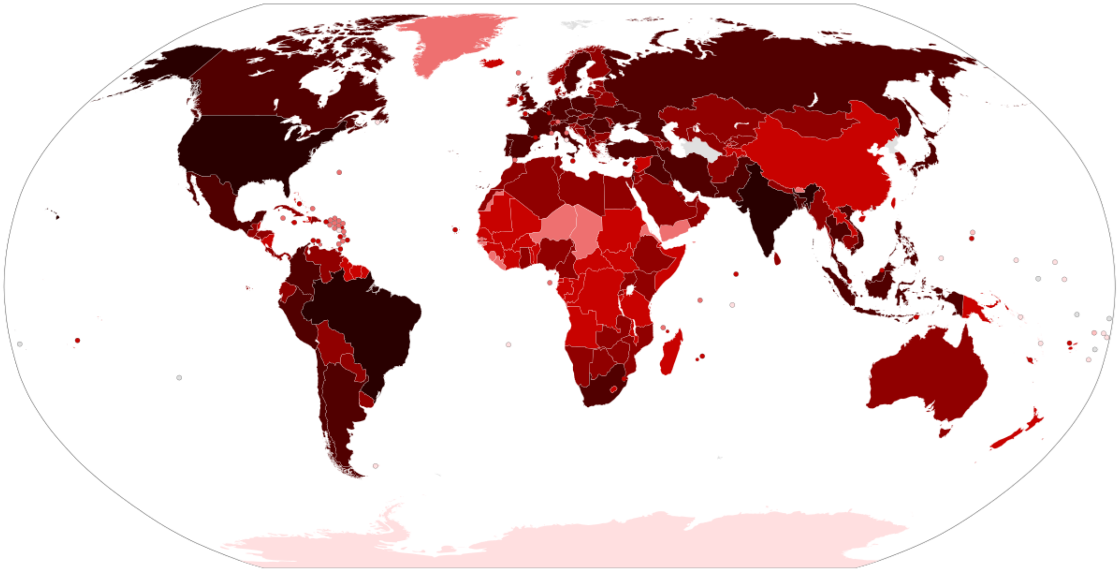
Presenter: Manos Papagelis

YorkU LAMPS Lab Invited Talk, Nov 2021



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

 Wikipedia, COVID-19 data collection from multiple national health agencies

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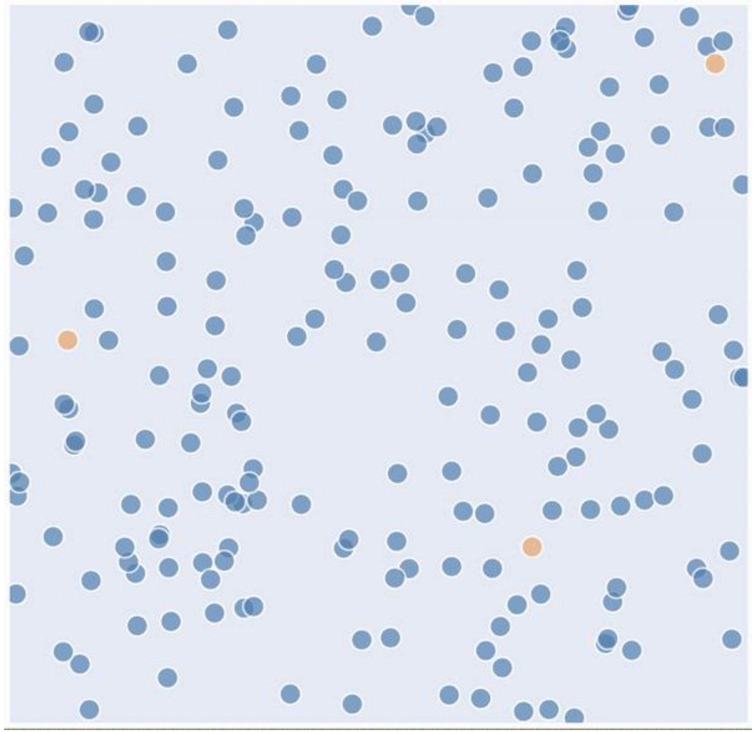
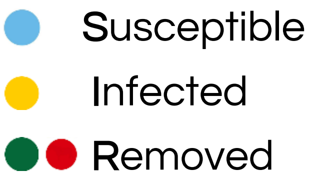
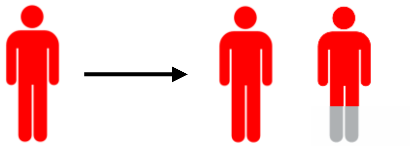
Mechanism of infectious disease spreading



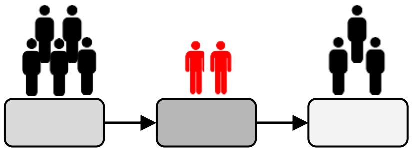


 Source: Matt Crooks, towards data science

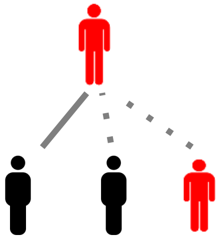
Revisiting epidemic concepts



reproductive number



compartmental models
(population-based)



offline contact tracing

Basic reproductive number (R_0)

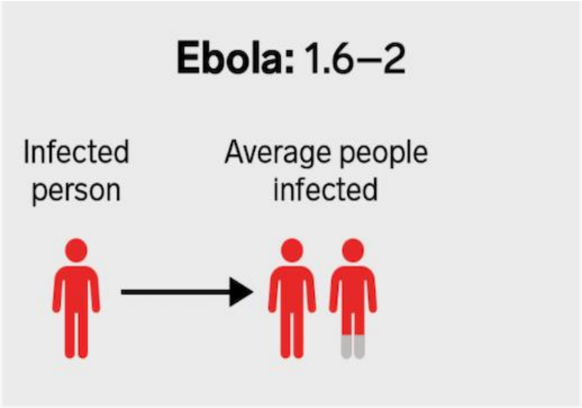
The **expected** number of people that an individual infects

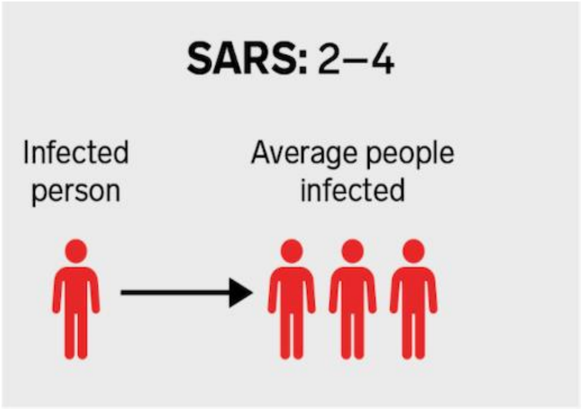
$R_0 < 1$ infection dies out

$R_0 > 1$ infection persists

$$R_0 = p \times k$$

p: transmission probability k: number of contacts





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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

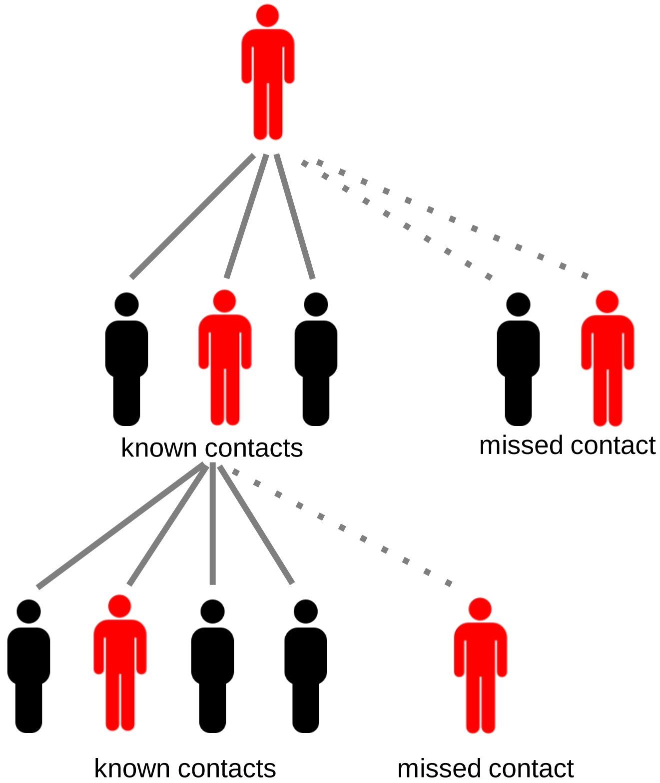
more realistic epidemic models need to

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

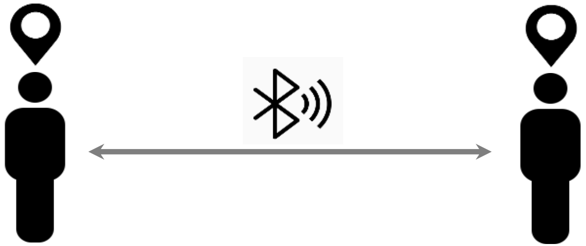
monitor **actual contacts** of individuals

Offline contact tracing (through interviews)

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



Digital contact tracing



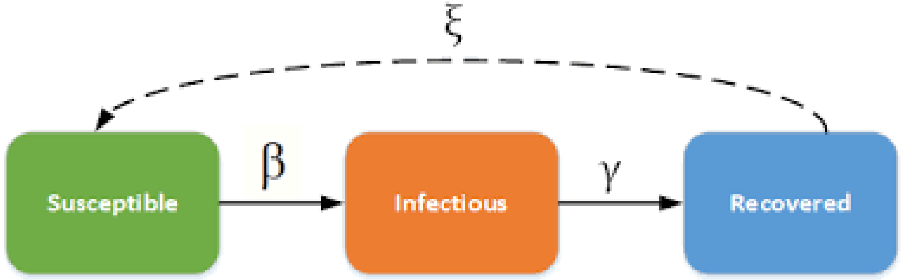
Enabled by mobile apps, geolocation devices, etc.

✔ addresses limitations of traditional contact tracing

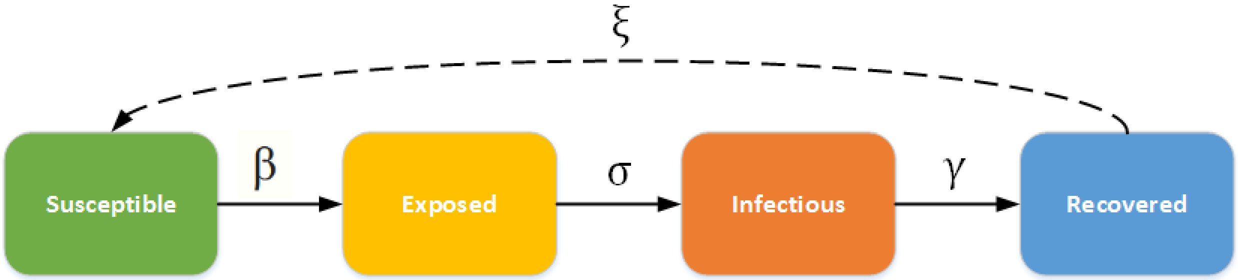
✖ privacy concern

Compartmental models

SIR

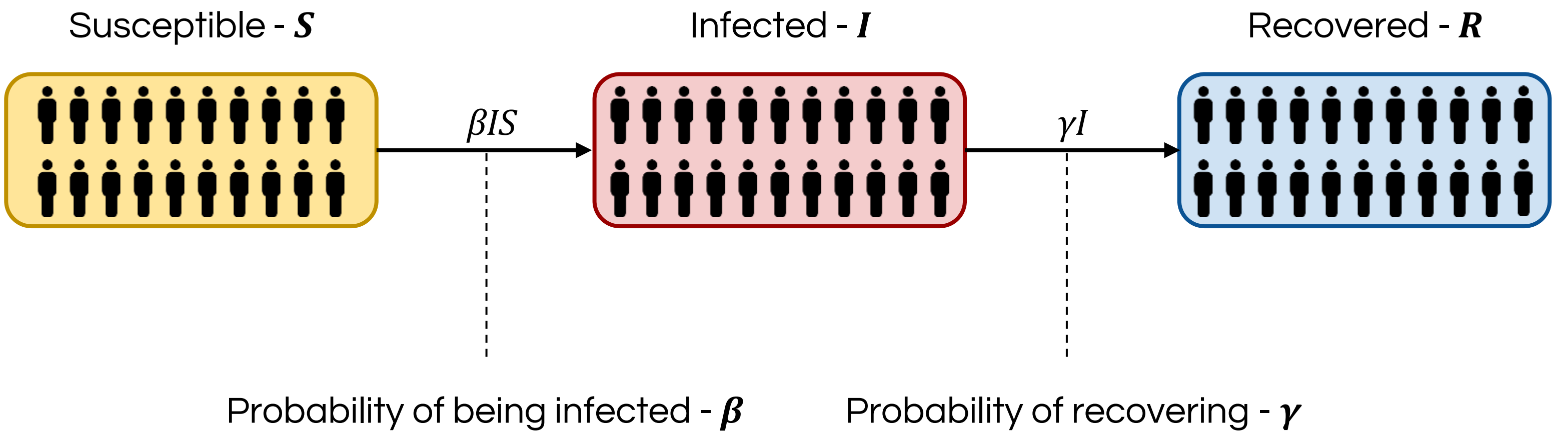


SEIR

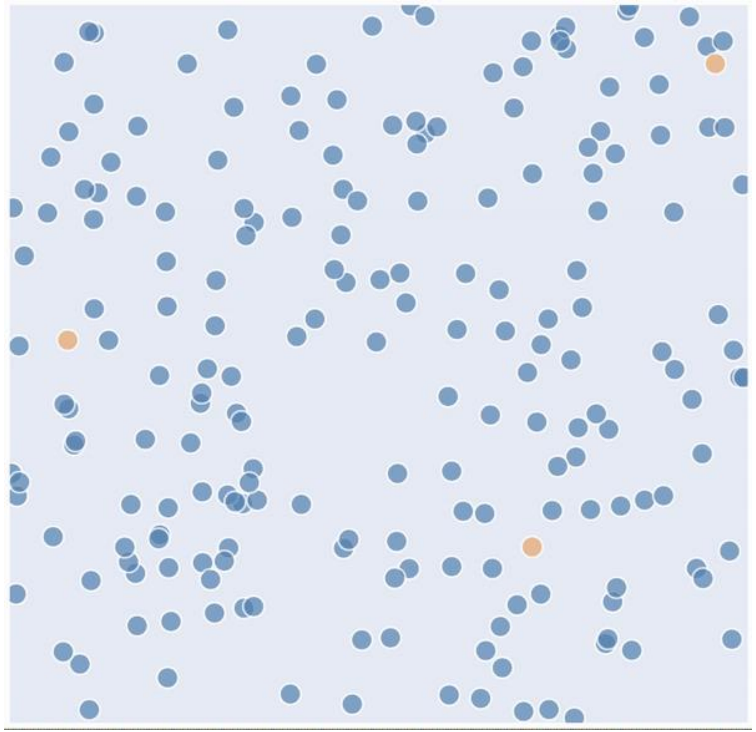


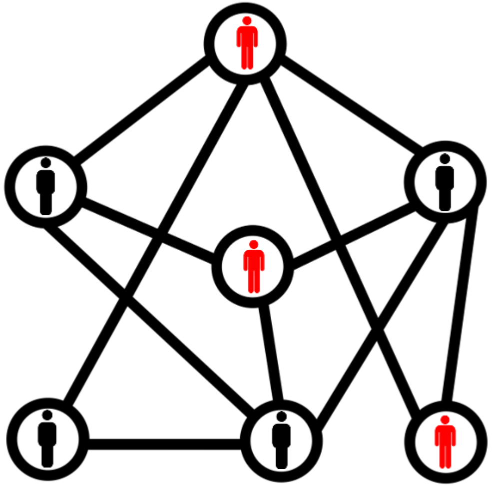
SIR model

Time t =



Individual-based models

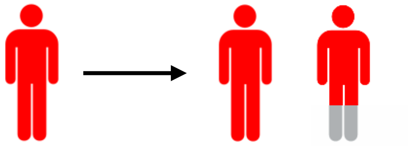




mobility network / contact network

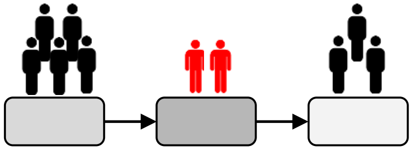
nodes: individuals
edges: social interaction
contagion: stochastic infection due to spatial proximity

Motivation



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

Today's Overview

- Epidemic Spreading in Trajectory Networks
- Microscopic Modeling of Spatiotemporal Epidemic Dynamics

They offer two complementary approaches

Epidemic Spreading in Trajectory Networks

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

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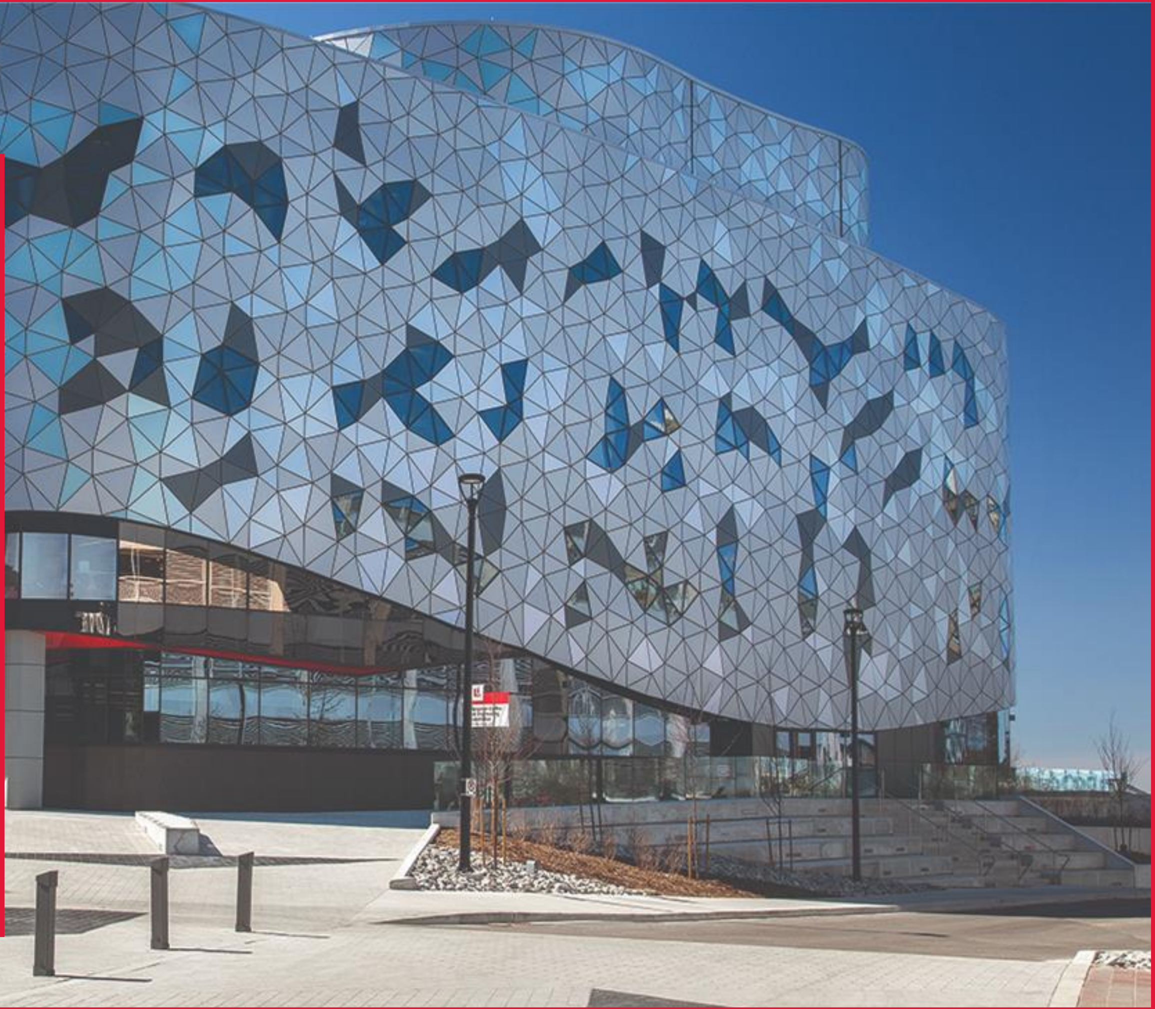
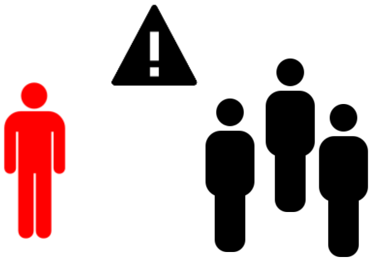


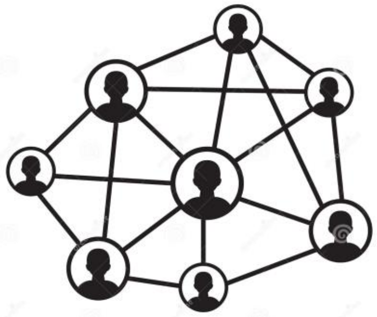
Research Questions

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



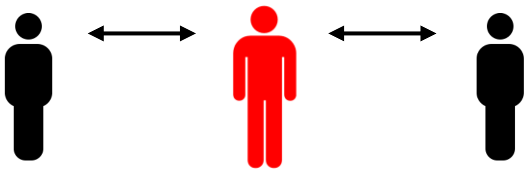
model **relative risk** of individuals as a factor of **their contacts** over time

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

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Problem Statement

The Problem

Input

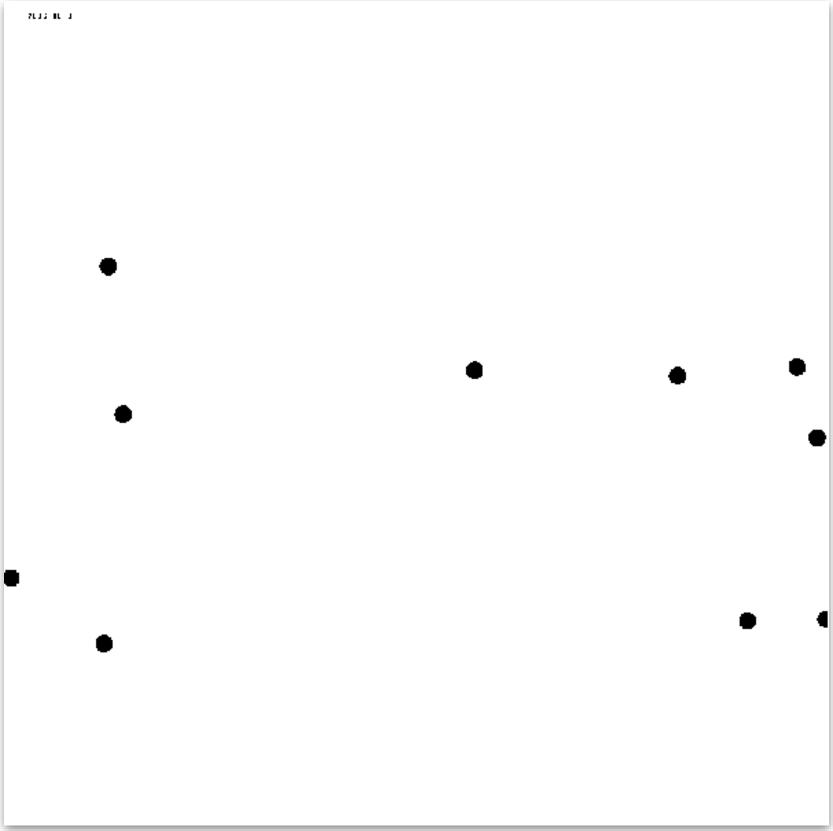
- Historical data of individual trips (trajectories)

Output

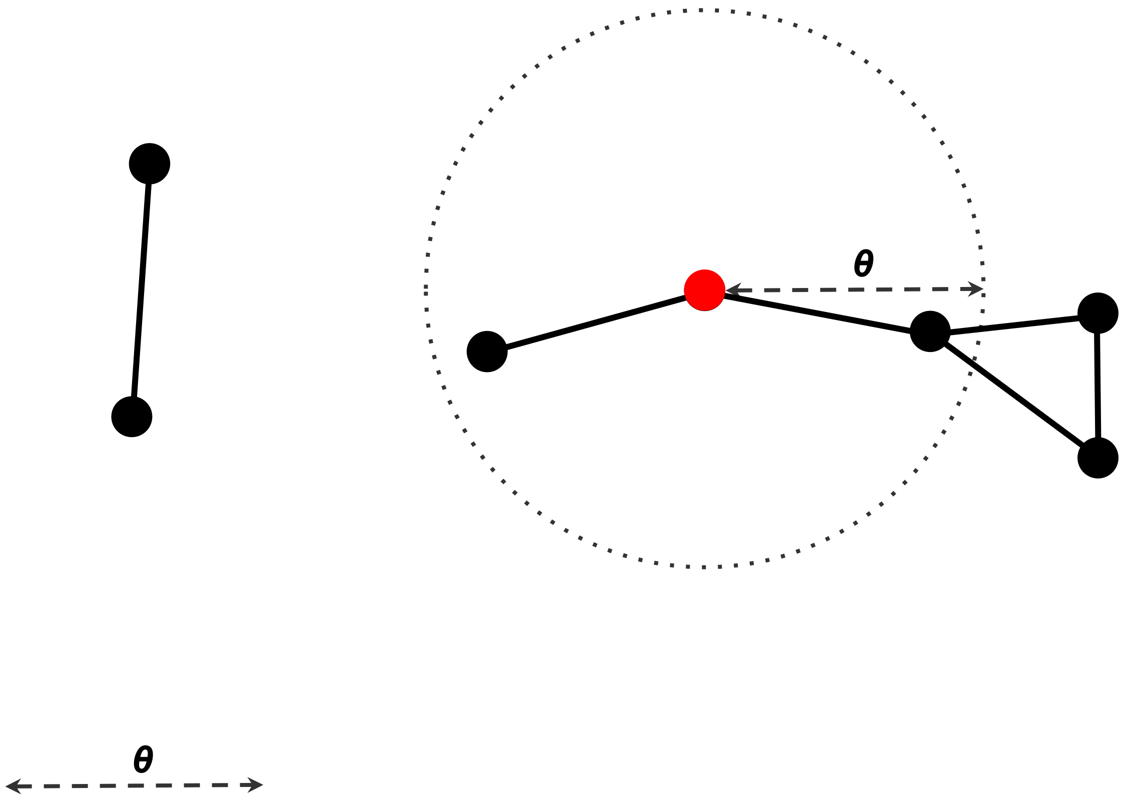
- Assess the relative risk of infection of individuals
- Assess the size of a disease outbreaks due to specific individuals
- Assess the impact of targeted non-pharmaceutical intervention strategies
- Provide support to health policy-making

Methodology

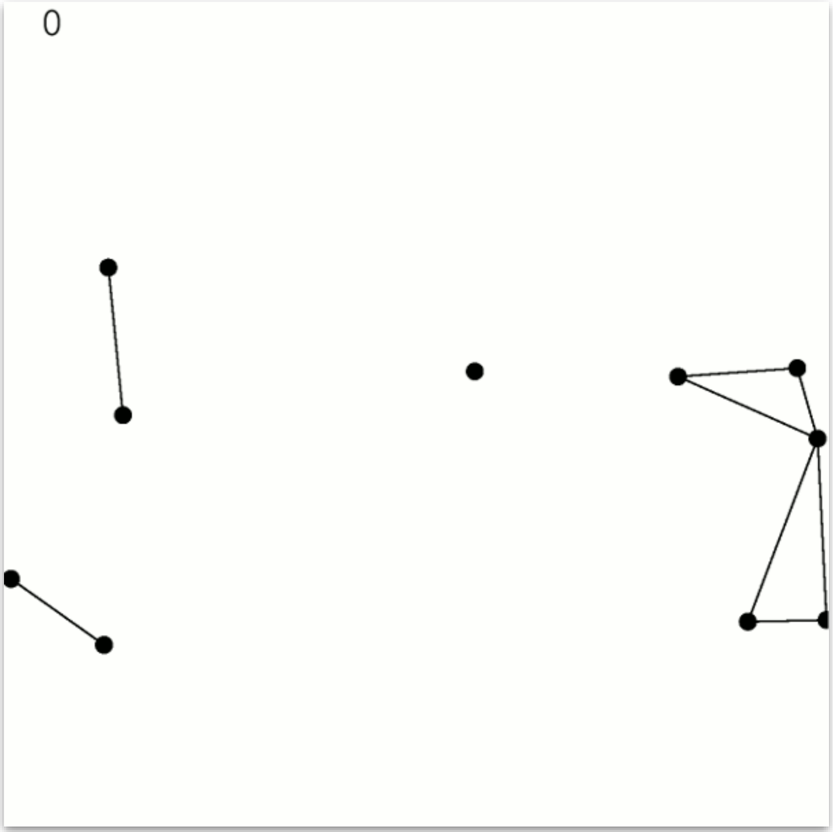
Trajectories of individuals



Proximity network



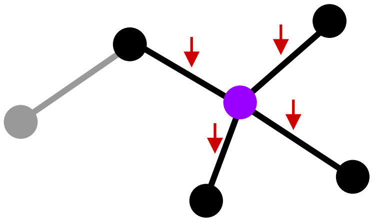
Trajectory network



Modeling risk of infection

Three (3) methods for measuring risk of infection

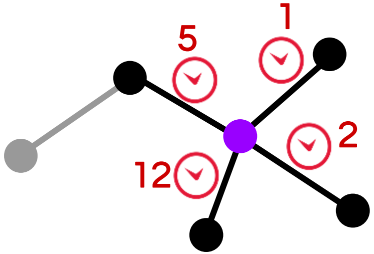
$1+1+1+1 = 4$



(1) # of contacts (node degree)

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

$5+1+2+12 = 20$

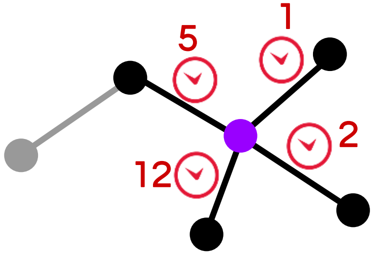


(2) total contact time

- ✔ 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

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Modeling epidemic spreading

Simulating disease spreading on a trajectory network

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

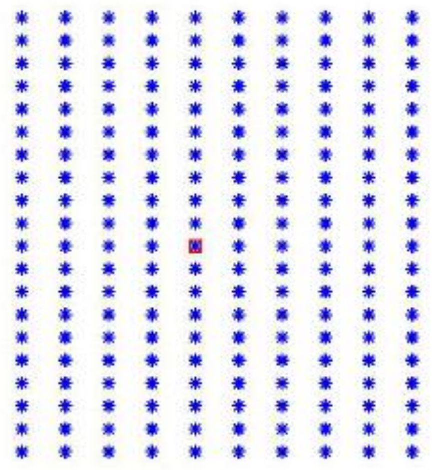
Each node (person) has a $p_{u,v}$ chance to infect their neighbors

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

where

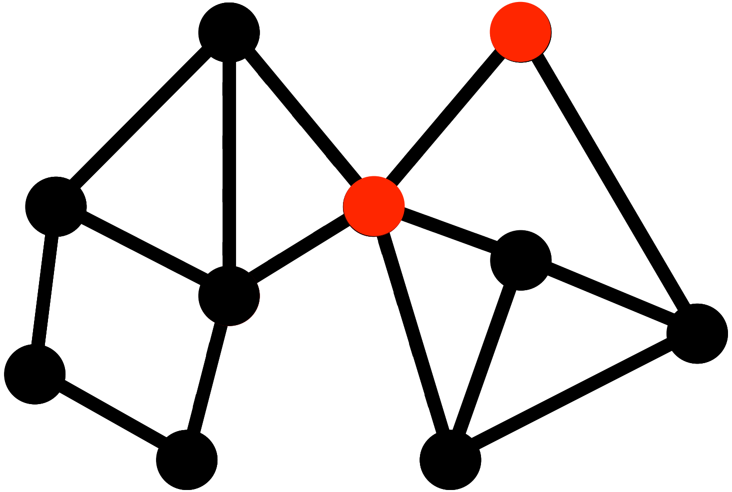
$\boldsymbol{\beta}$: transmission probability

k: duration (in timesteps)



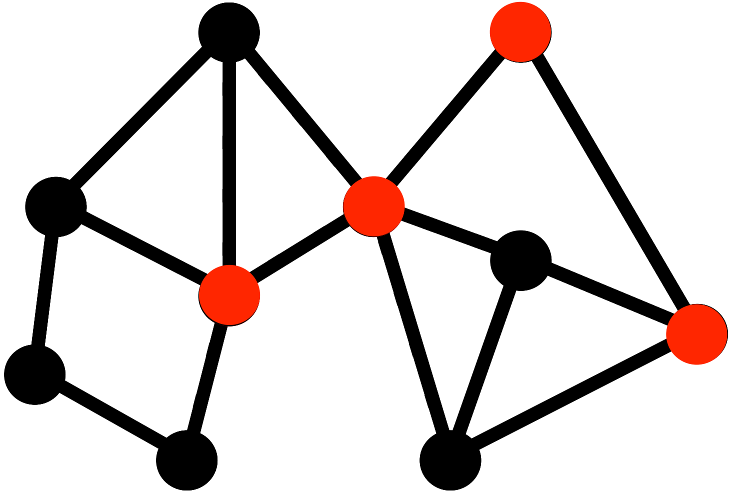
Disease spreading

Timestamp: 1



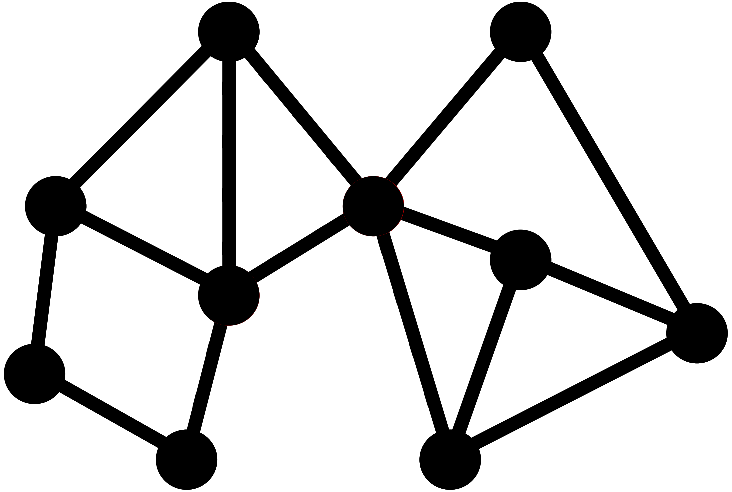
Disease spreading

Timestamp: 2



Targeted network interventions

Intervention policy 1 (centralized): node immunization

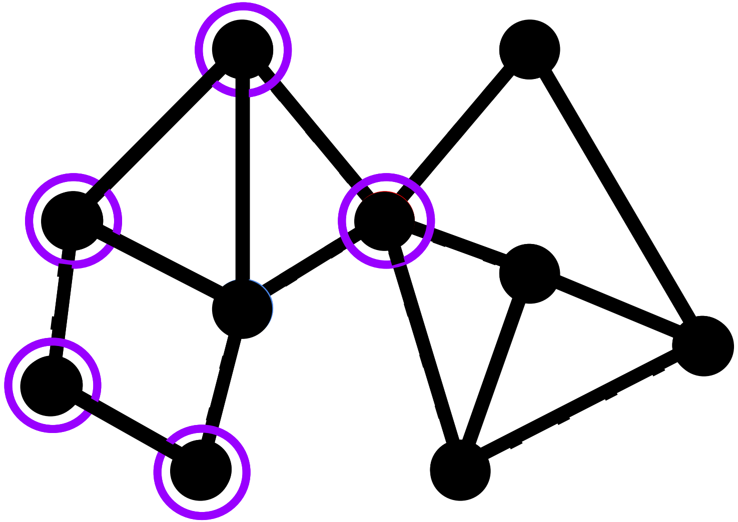


Given a “snapshot” of the network at time t

Find “hotspots” highest-risk nodes

Remove those highest-risk nodes

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

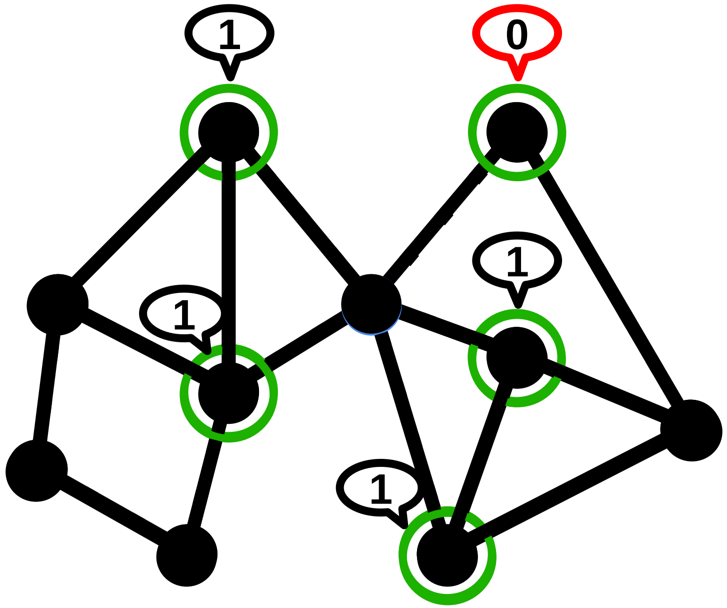


Select the x% highest risk one
and remove the edge

For every node, rank
of their neighbors by risk

Repeat for all nodes

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



For every node, pick top % of their neighbors
by common contacts (triangles in common)

Experimental results

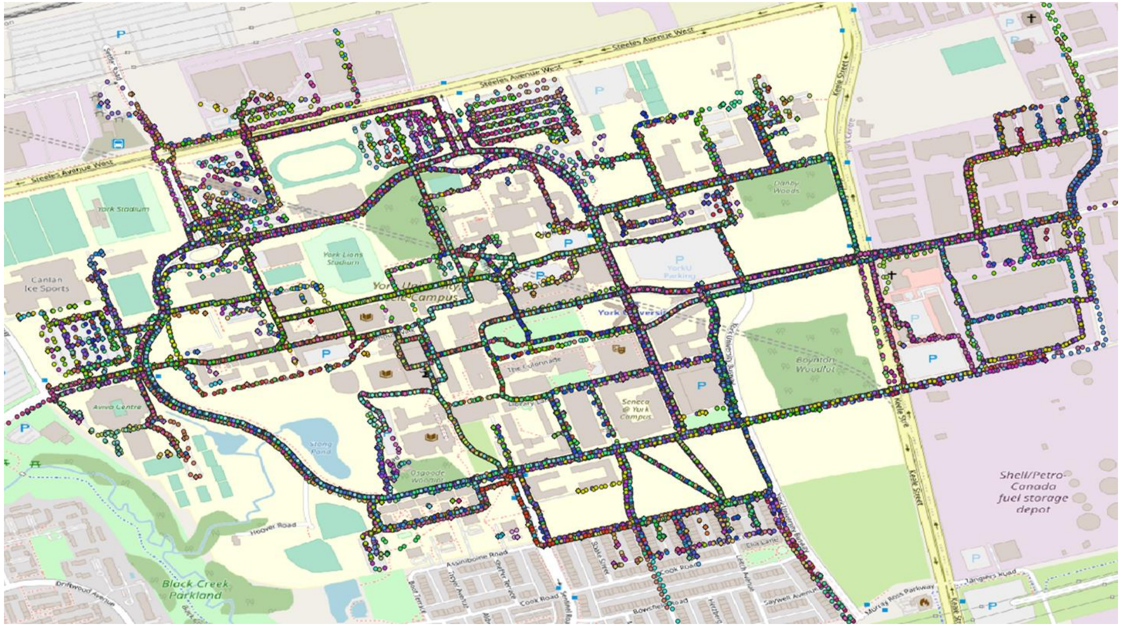
Pedestrian simulation data

map: YorkU campus map
(from OpenStreetMap)

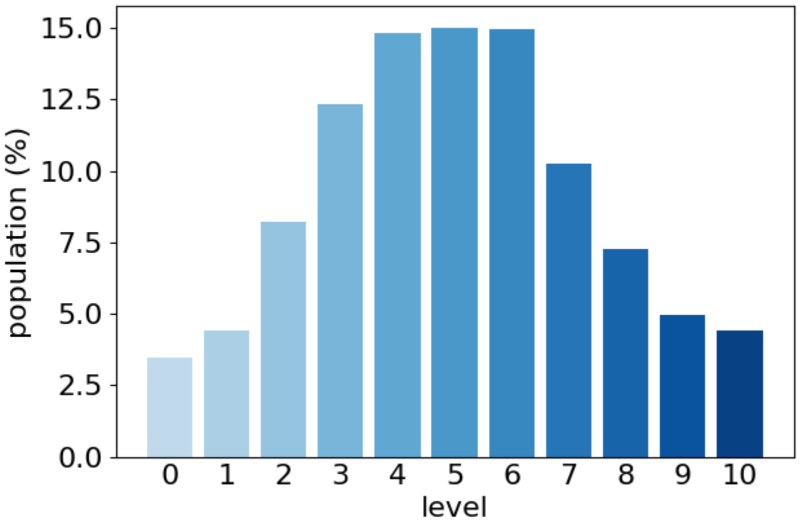
trips: random individual trips based on **daily activity patterns** (with SUMO)

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

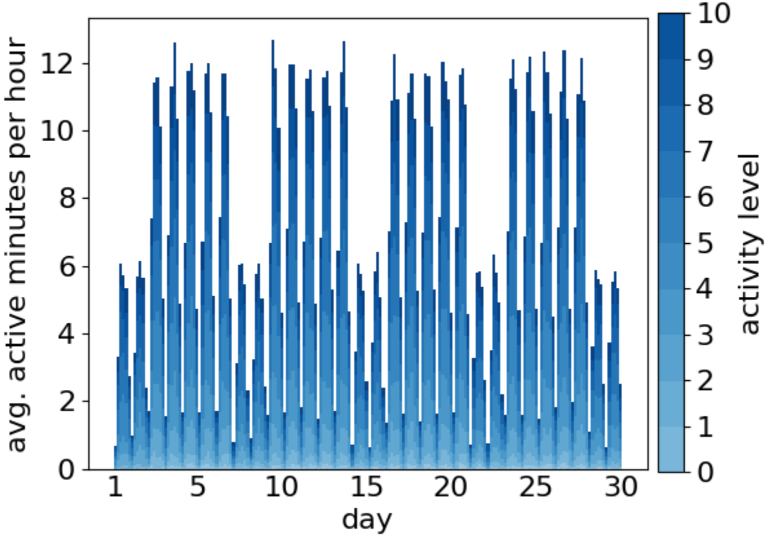
mobility network: spatiotemporal network (**10k** nodes, ~**56M** edges)



Modeling real-world activity patterns



distribution of activity levels

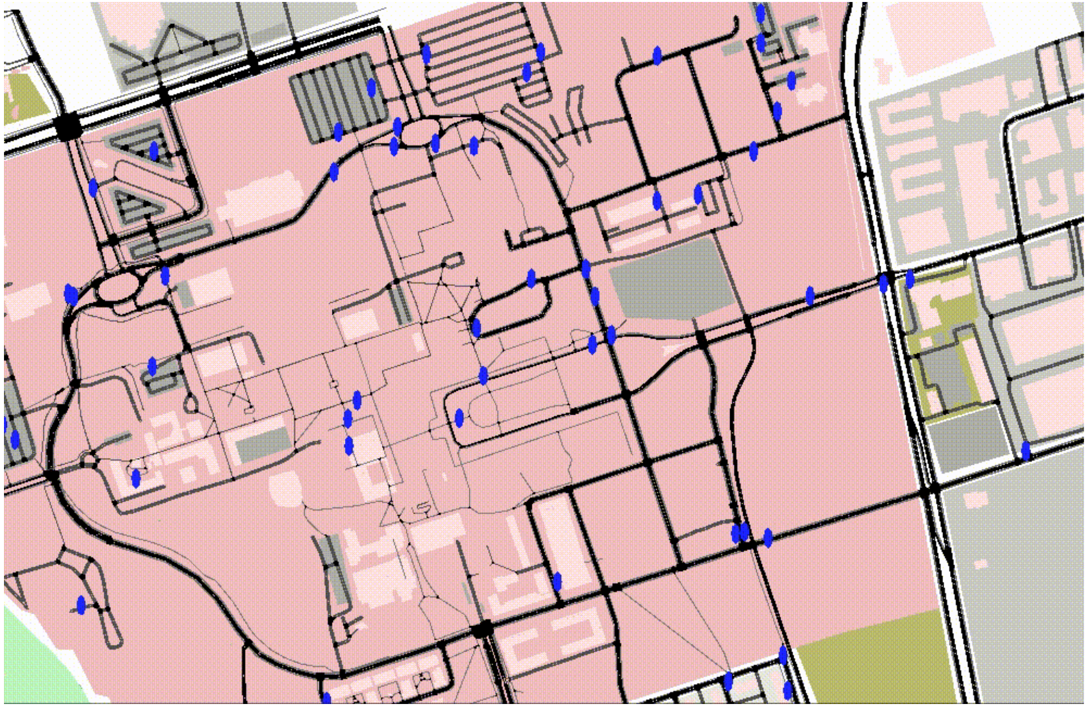


hourly activity

Synthetic Data Generator

Simulation of Urban MObility (SUMO)

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



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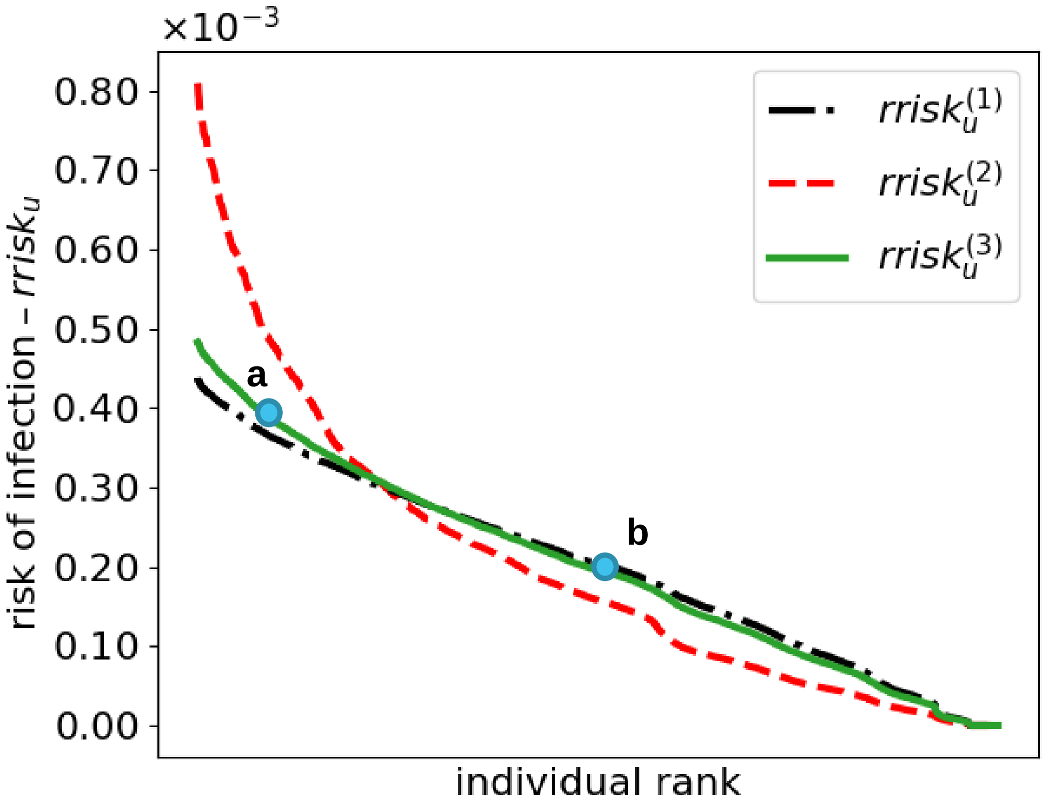
Distribution of relative risks of individuals



rrisk$_u^{(3)}$ **more smooth**

a **3x higher risk** than **b**

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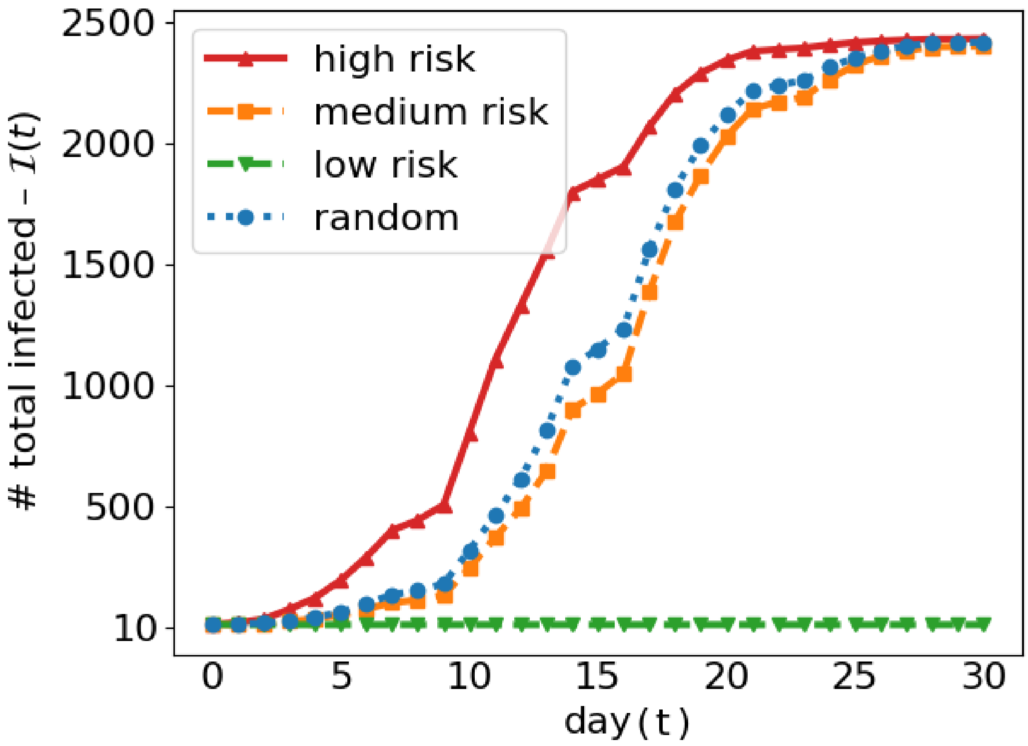
Outbreaks due to “seed” nodes belonging to different risk groups



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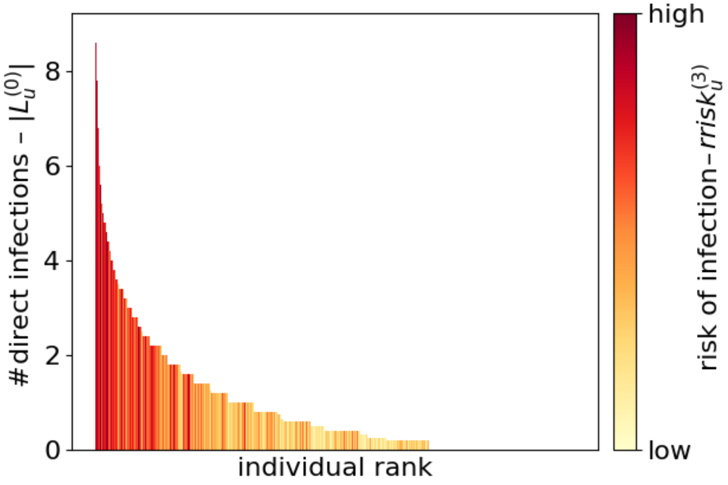
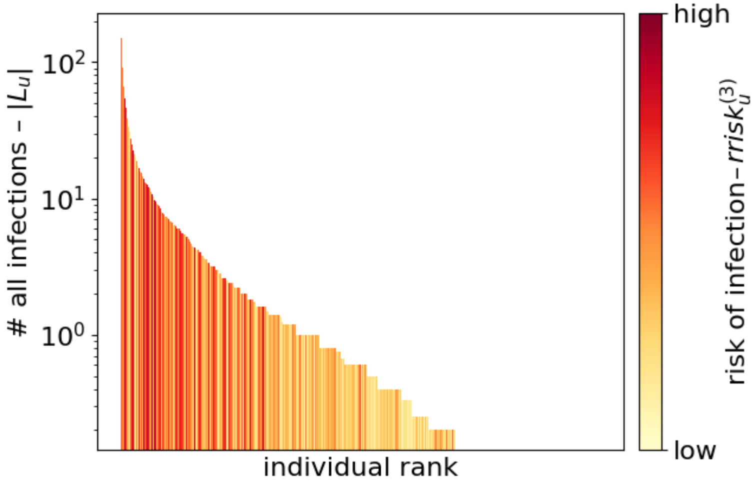
Direct vs secondary infections

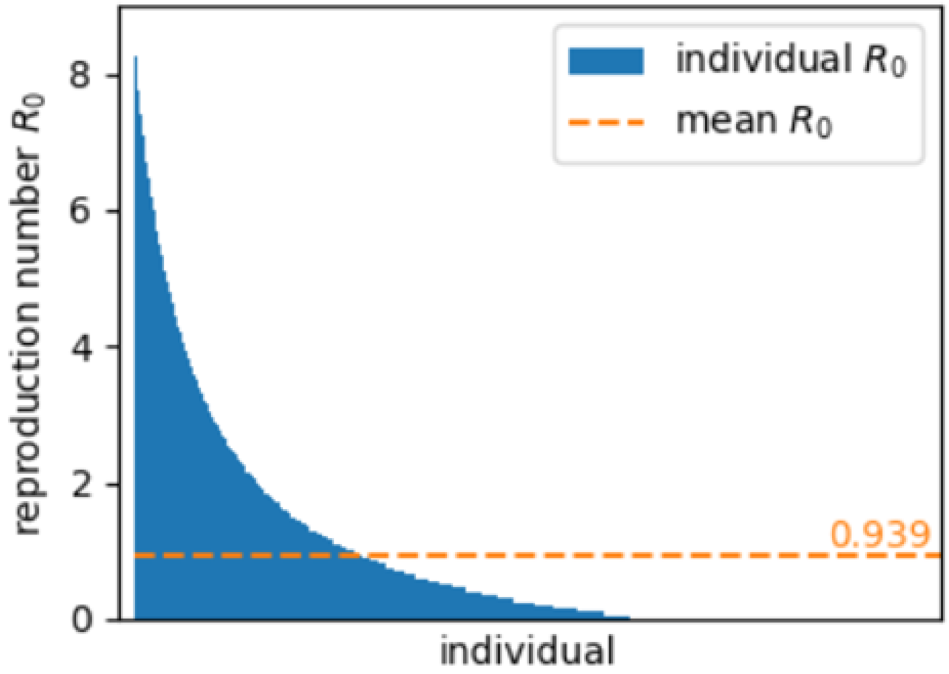


direct infections



indirect, secondary infections

R_0 distribution of individuals



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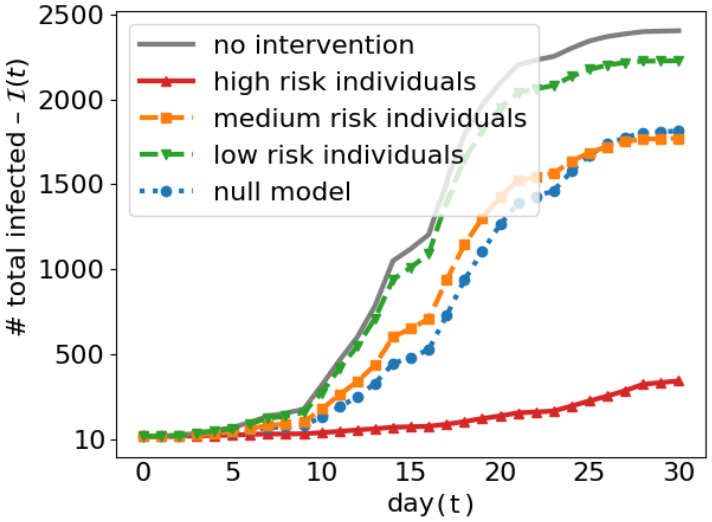
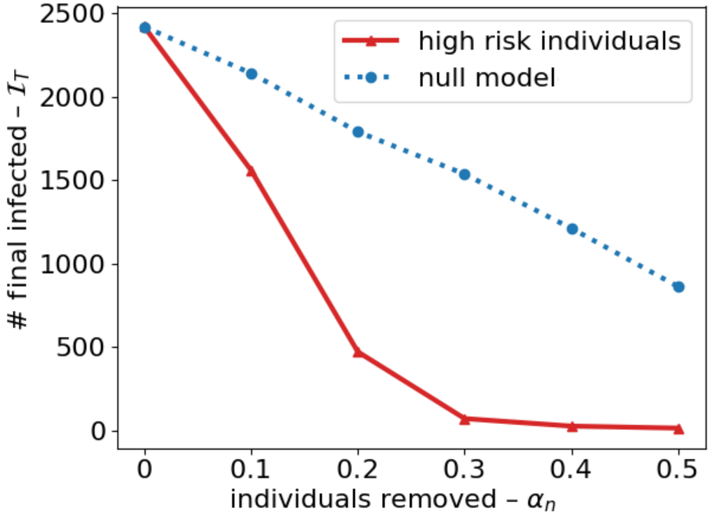
Intervention 1 vs null model (same # of random edges removed)

node immunization



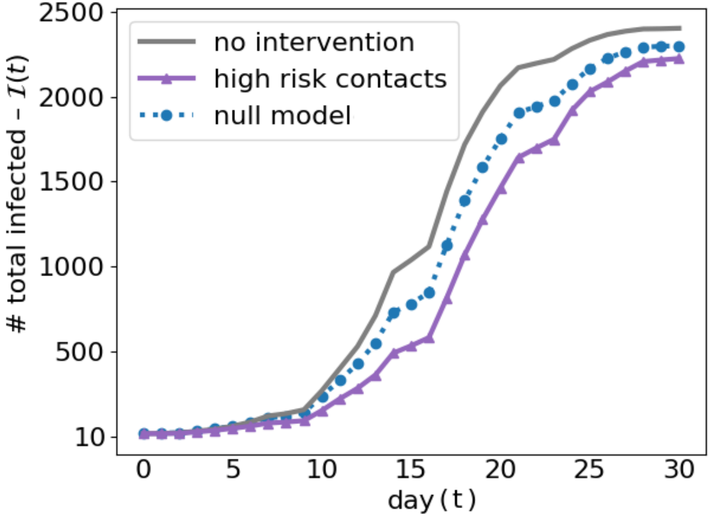
SEIR progress ($\boldsymbol{\alpha}$ = 20%)



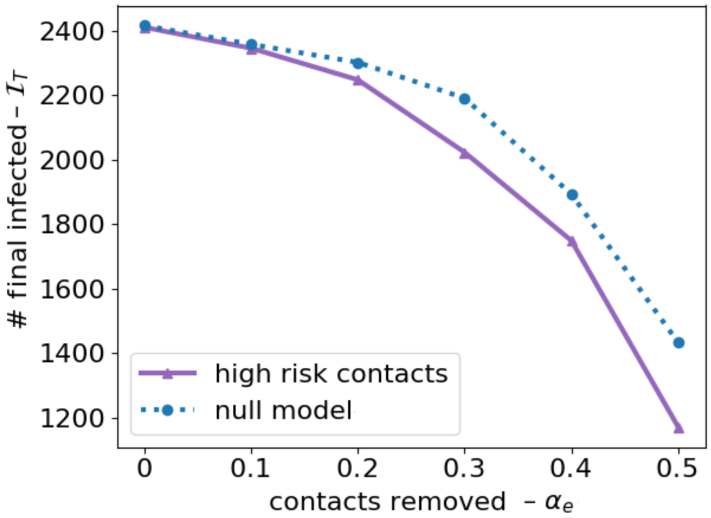
infections for varying $\boldsymbol{\alpha}$

Intervention 2A vs null model

avoiding high-risk contacts



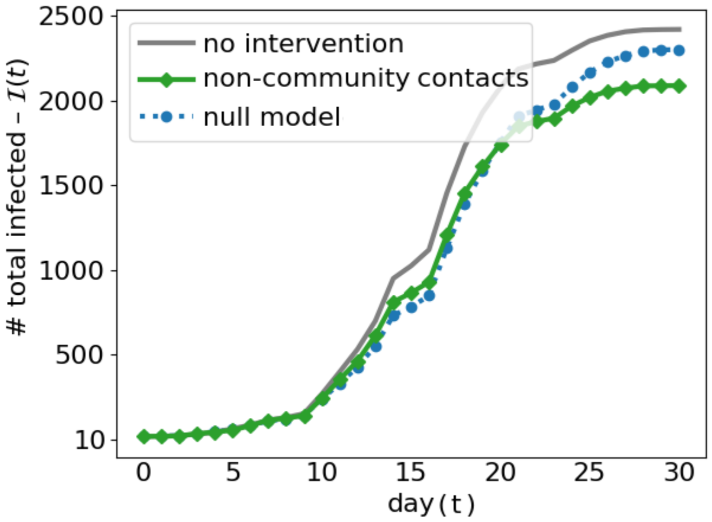
SEIR progress (**α** = 20%)



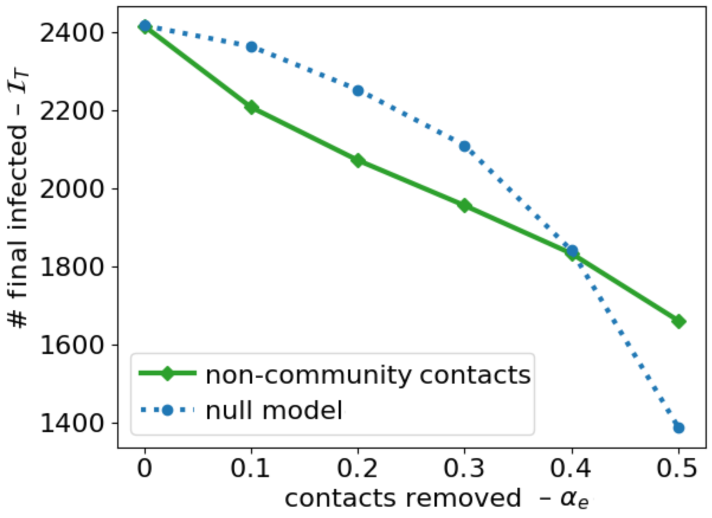
infections for varying **α**

Intervention 2B vs null model

maintaining a “social bubble”

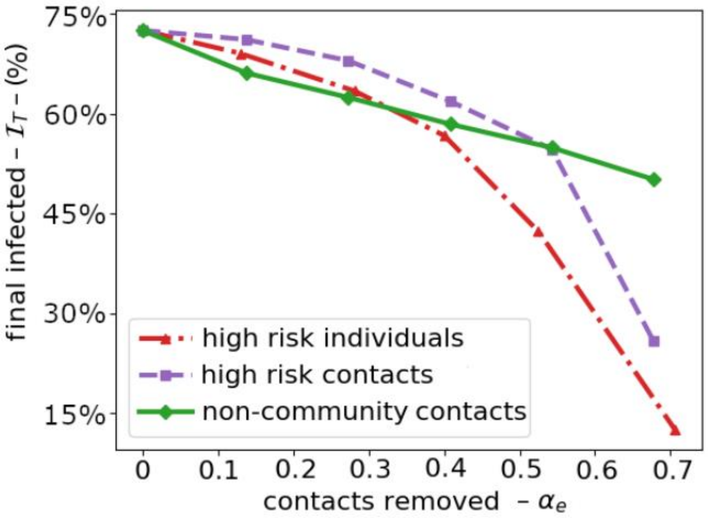


SEIR progress ($\boldsymbol{\alpha}$ = 20%)

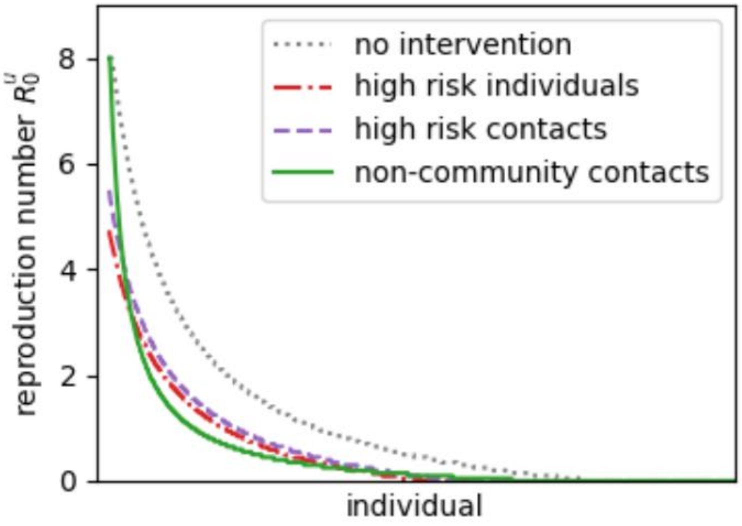


infections for varying $\boldsymbol{\alpha}$

Comparison of interventions



comparison of infected counts



comparison of R_0 distributions

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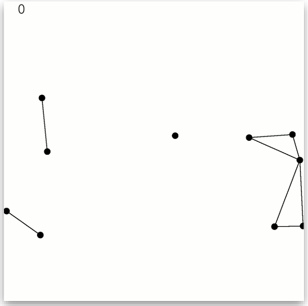
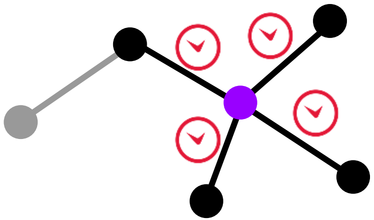
Takeaway

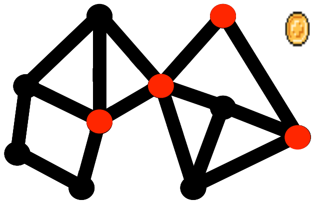
agent-based



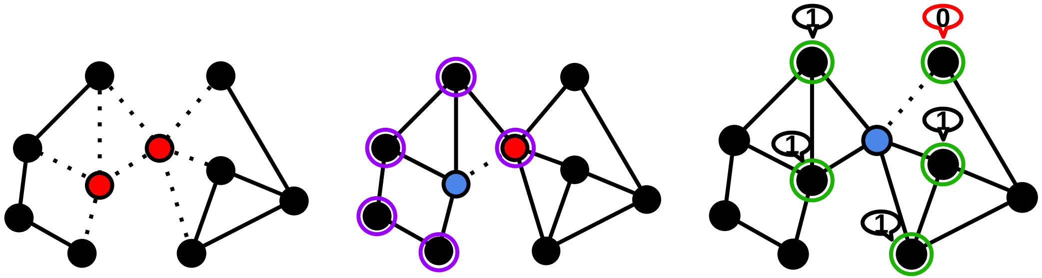
mobility network



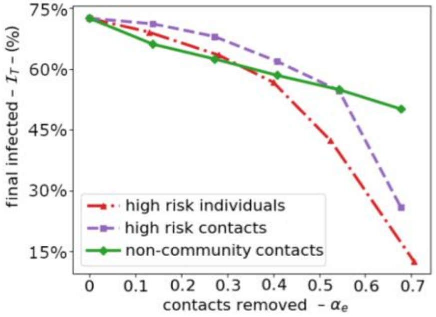
infection risk



stochastic propagation



targeted intervention policies



support policy-making

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Microscopic Modeling of Spatiotemporal Epidemic Dynamics

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Presenter: Manos Papagelis

November 2021

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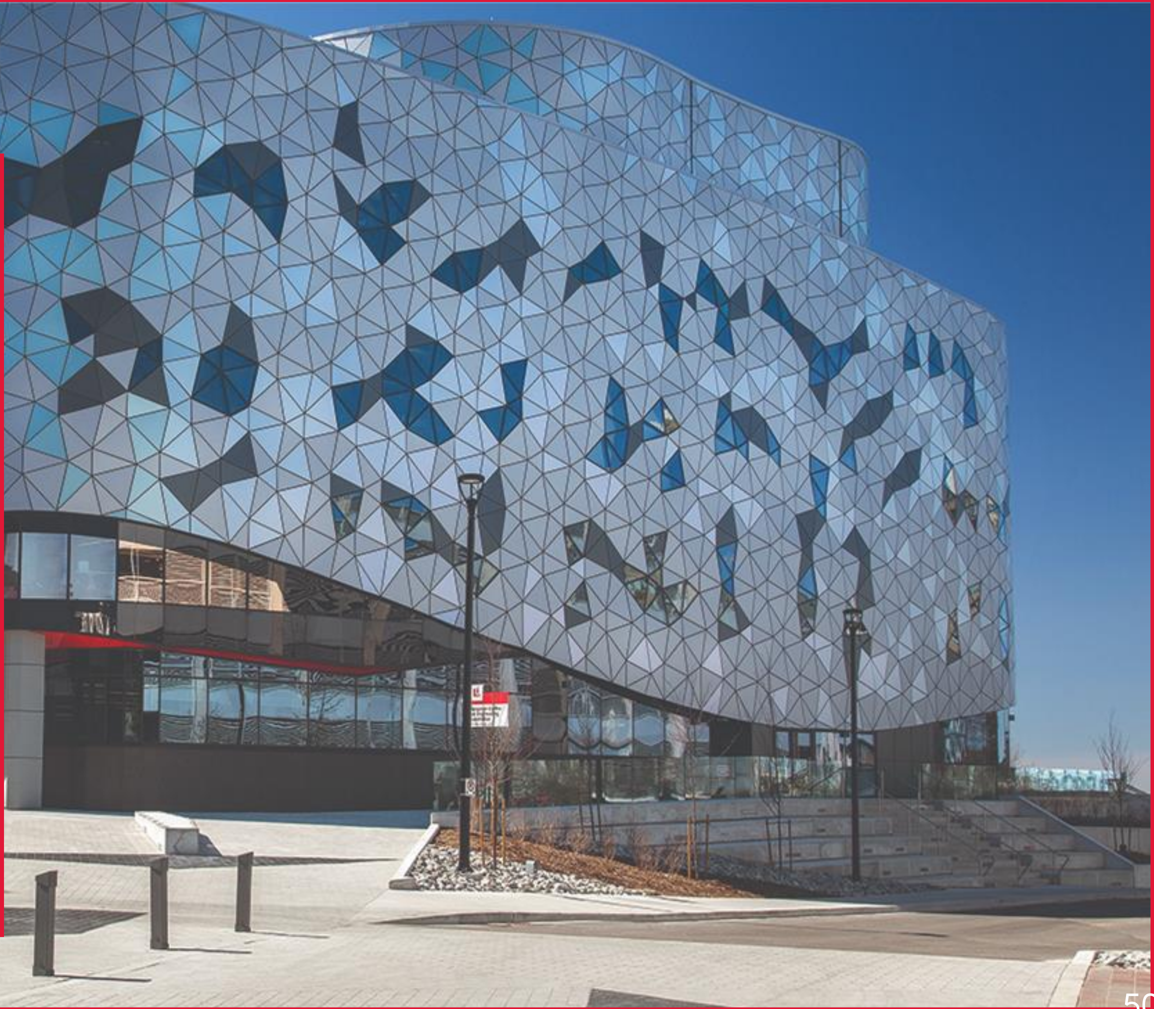


Problem Statement

The Problem

Input

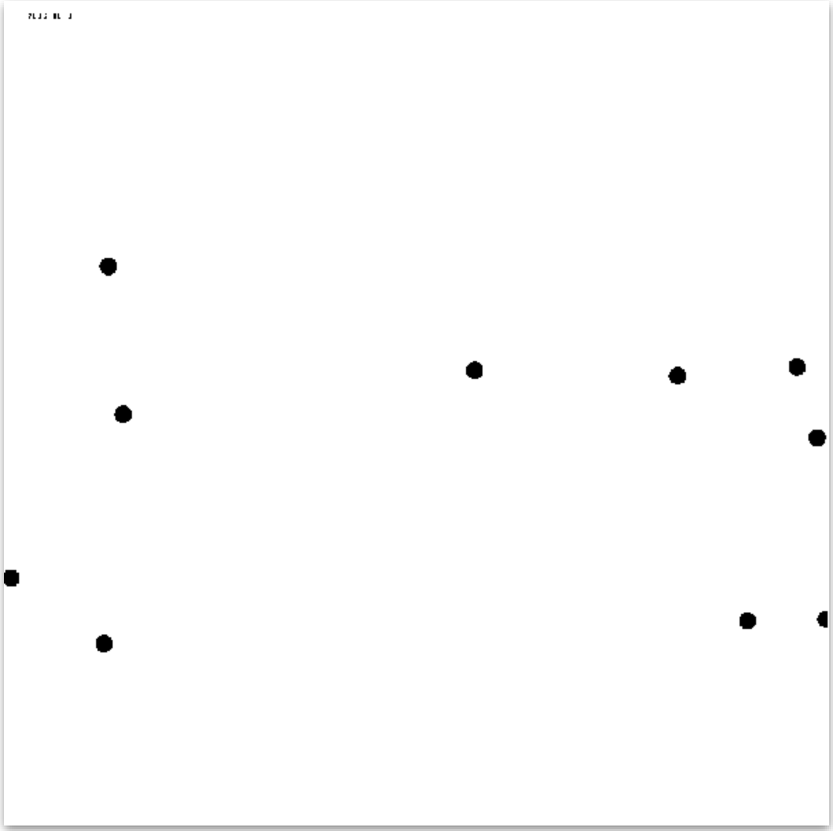
- Historical data of individual trips (trajectories)

Output

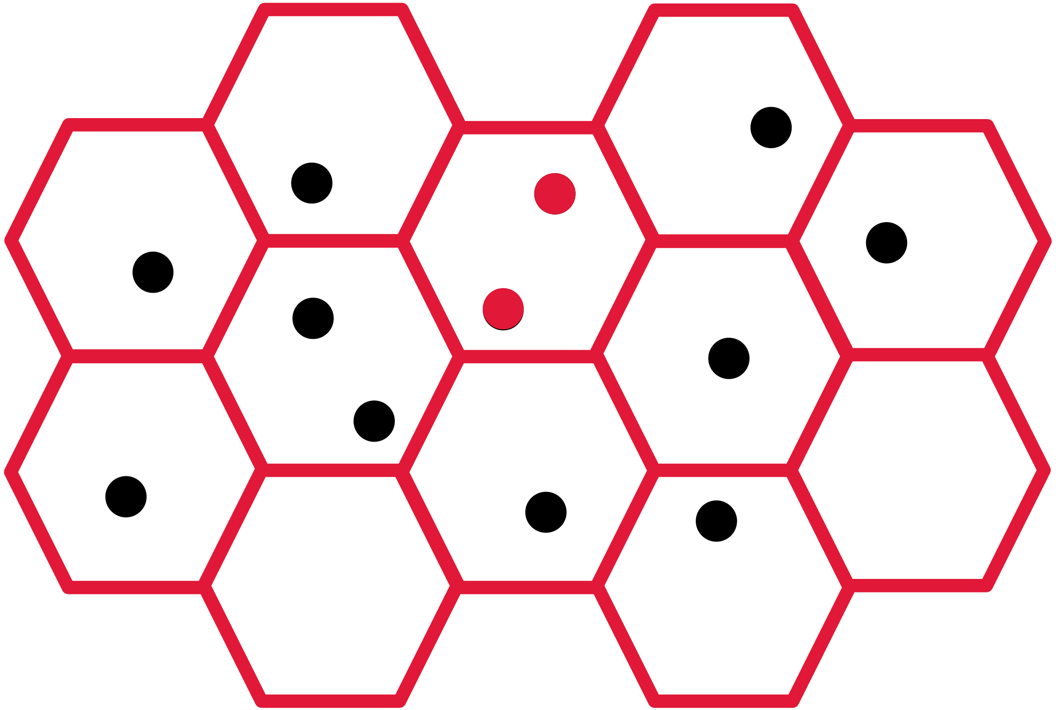
- Assess the relative risk of infection of individuals
- Assess the relative risk of infection of geographic areas and points-of-interest (POIs)
- Assess the risk of infection of a (pedestrian) trip in an urban environment
- Recommend alternative trips that mitigate the risk of infection
- Assess the impact of targeted non-pharmaceutical intervention strategies
- Provide support to health policy-making

Methodology

Trajectories of individuals



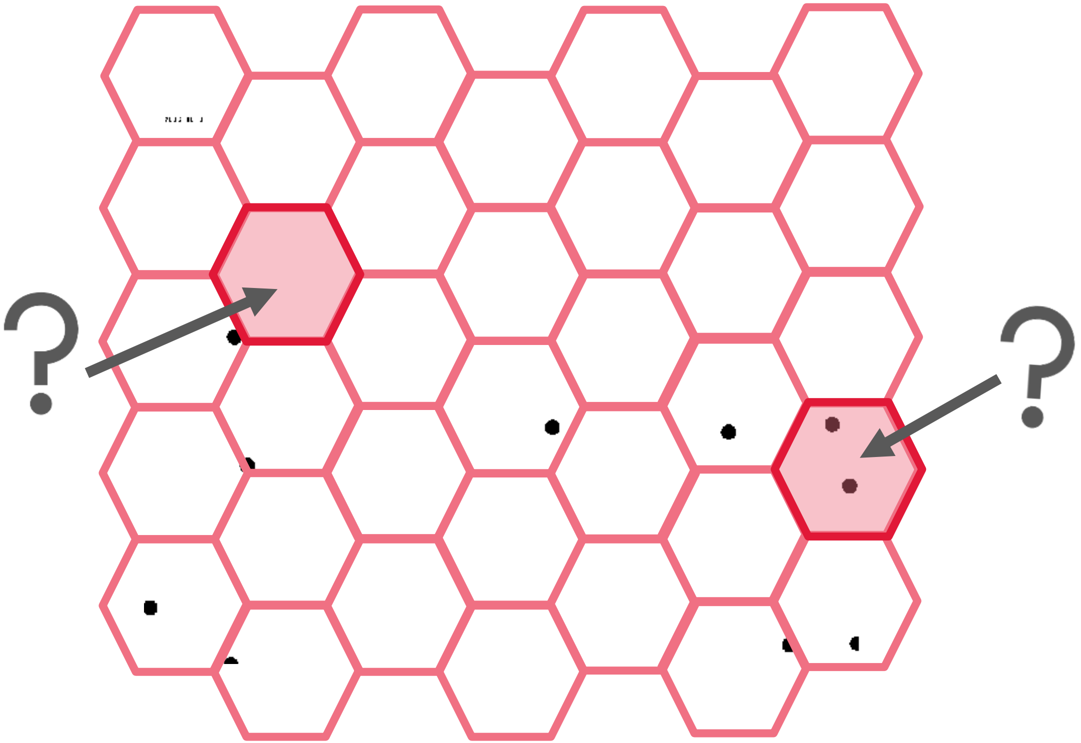
Geographic area tessellation



We define **blocks** by applying plane tessellation using a hexagonal grid (**honeycomb**)

Block risk of infection

Block infection risk (1/2)



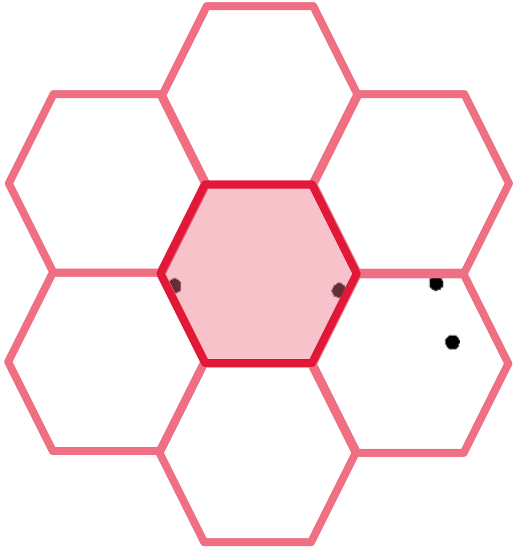
What is the risk of infection of a **block**?

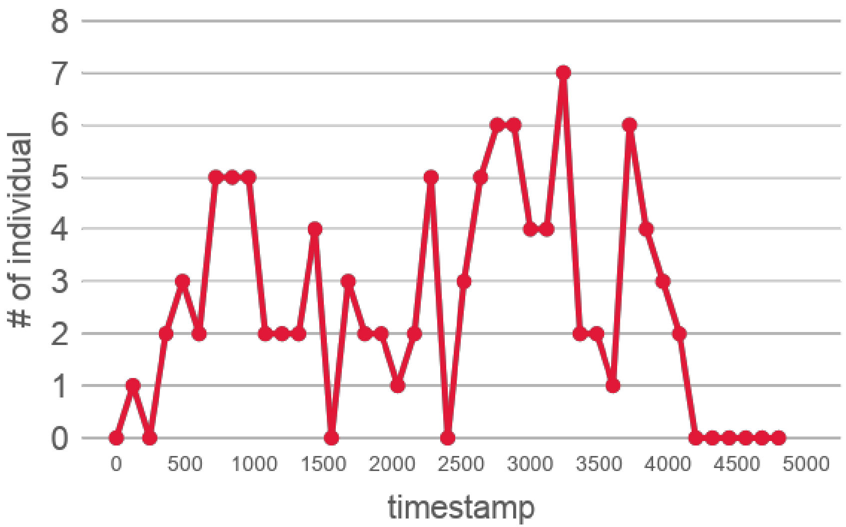
How they compare to each other?

Block infection risk (2/2)

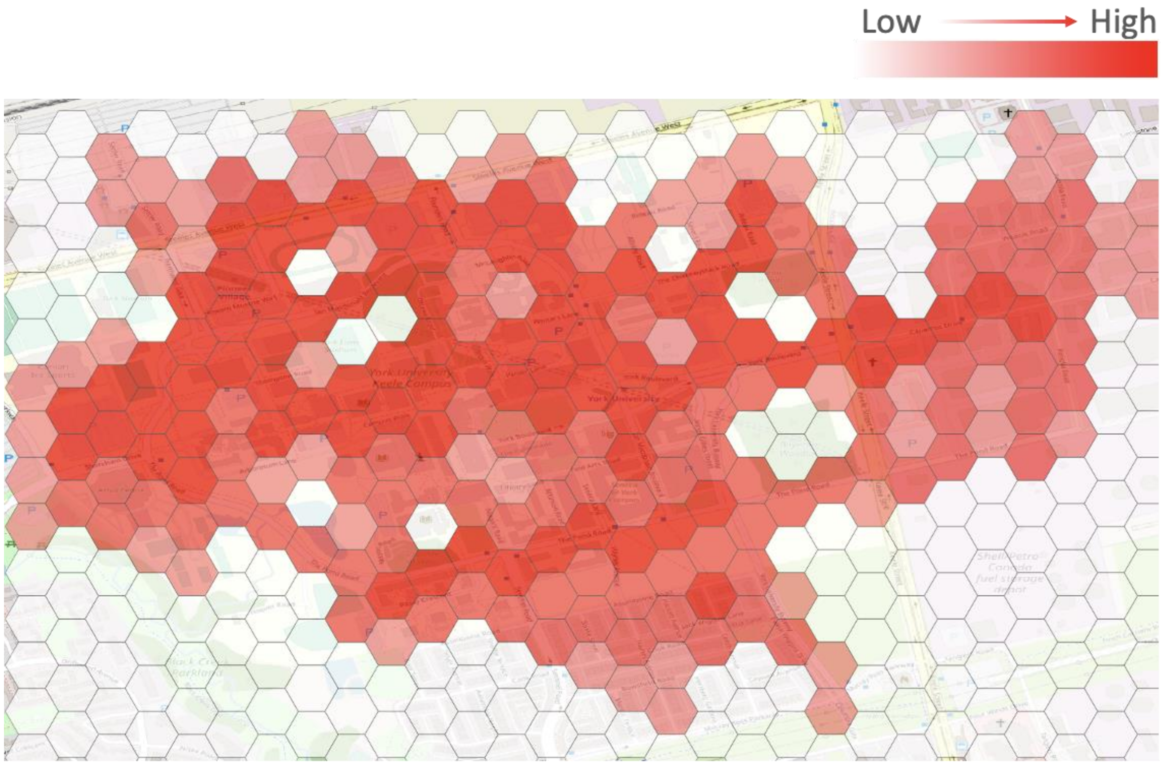
the risk brisk(b, t) of a block b at time t is a function of the #pairs of individuals in b at t

the risk $brisk_b$ is the average risk of a block over an observation period



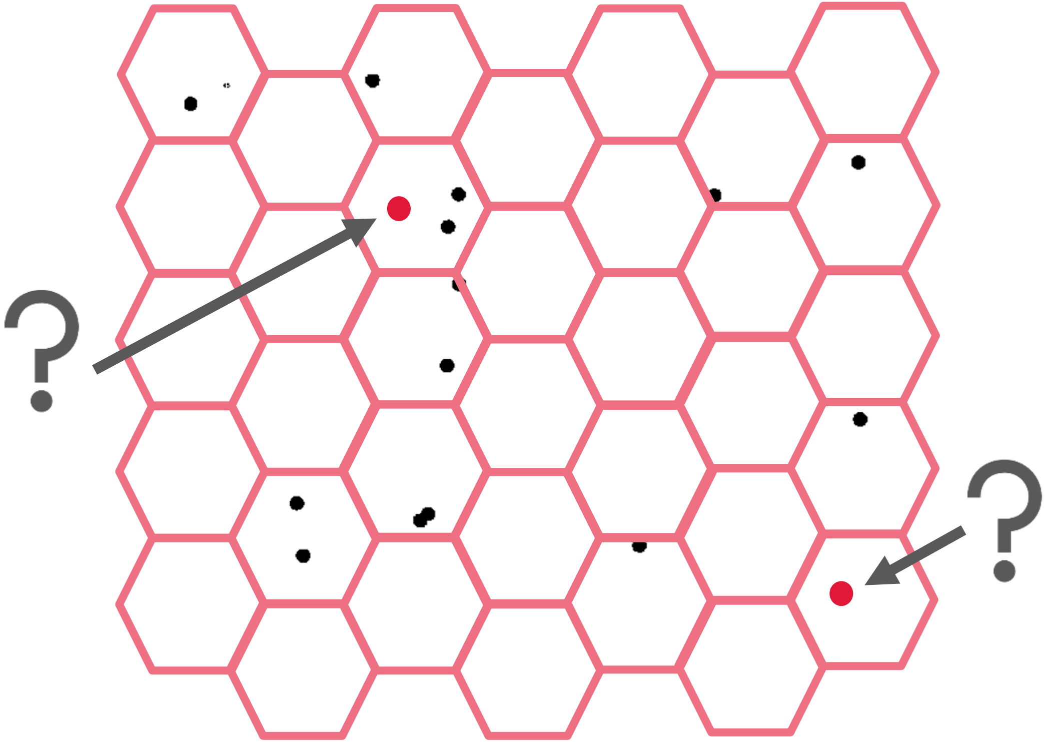


Risk map example (overlay of a geographic area)



Individual risk of infection

Individual infection risk (1/2)

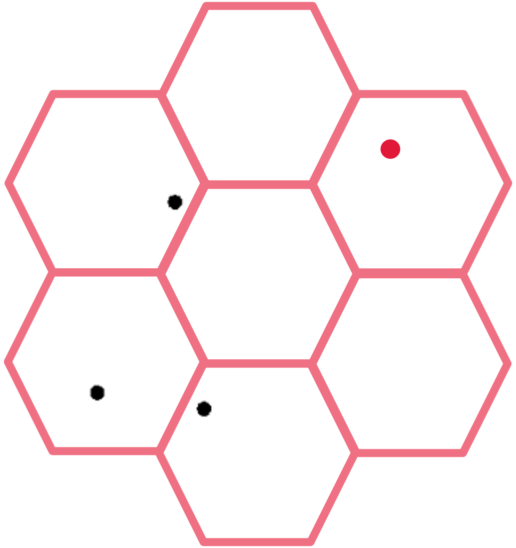


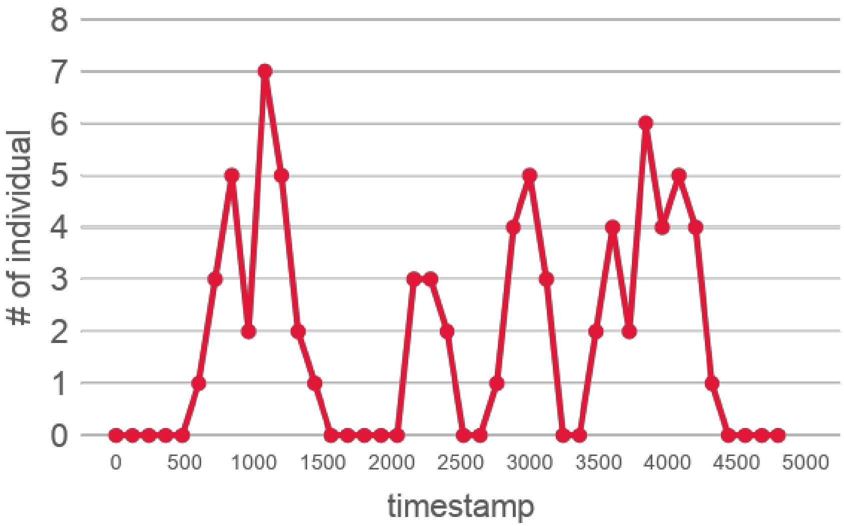
What is the risk of infection of an **individual**?

How they compare to each other?

Individual infection risk (2/2)

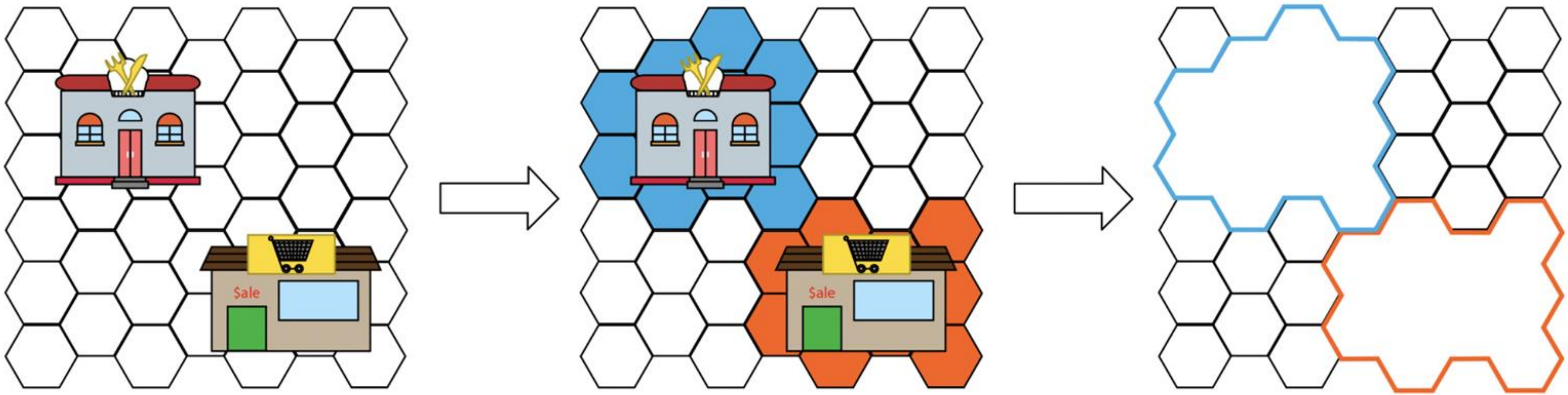
the risk risk$_u$ of an individual is a function of the risks brisk$_b$ of all blocks traversed



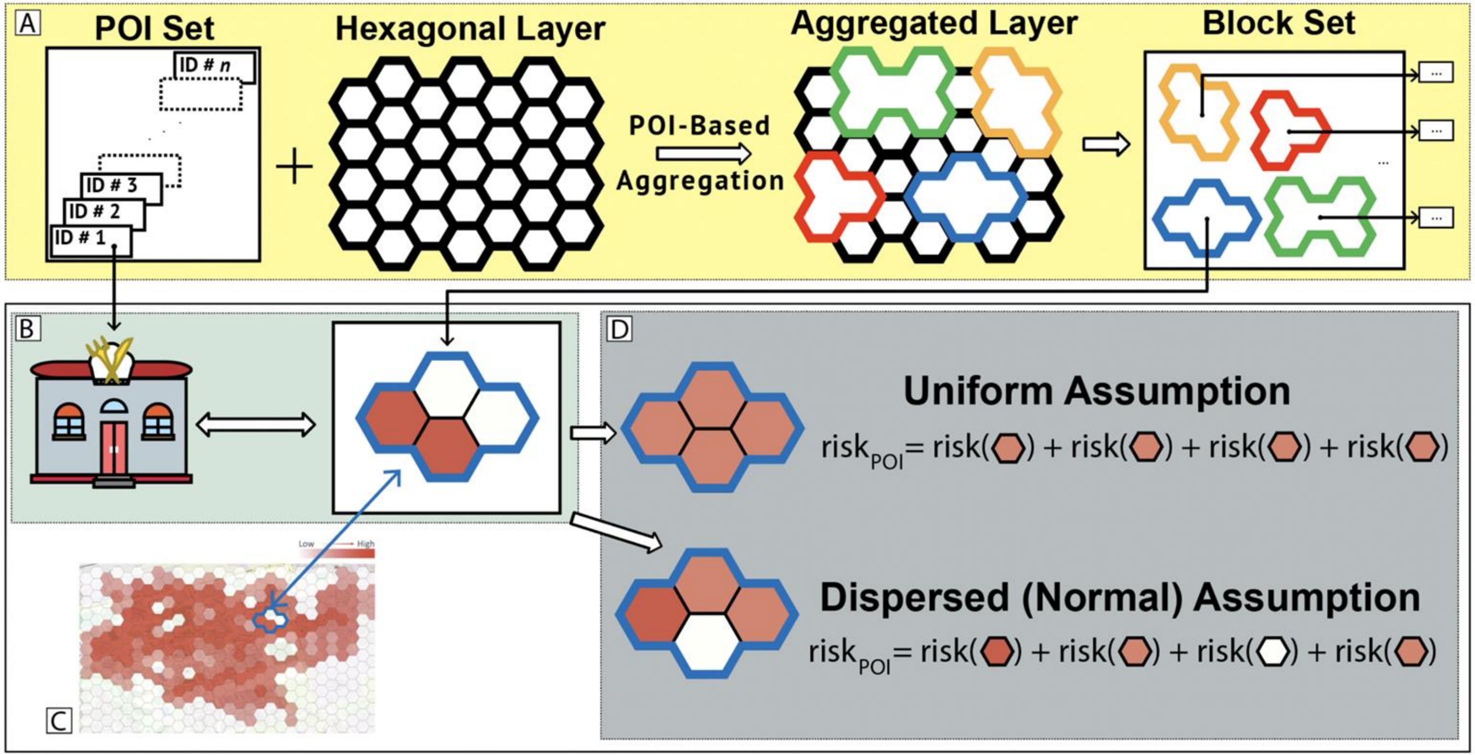


Point-of-interest (POI) risk of infection

Multi-block: POI-based hierarchical block aggregation



Point-of-interest (POI) risk of infection

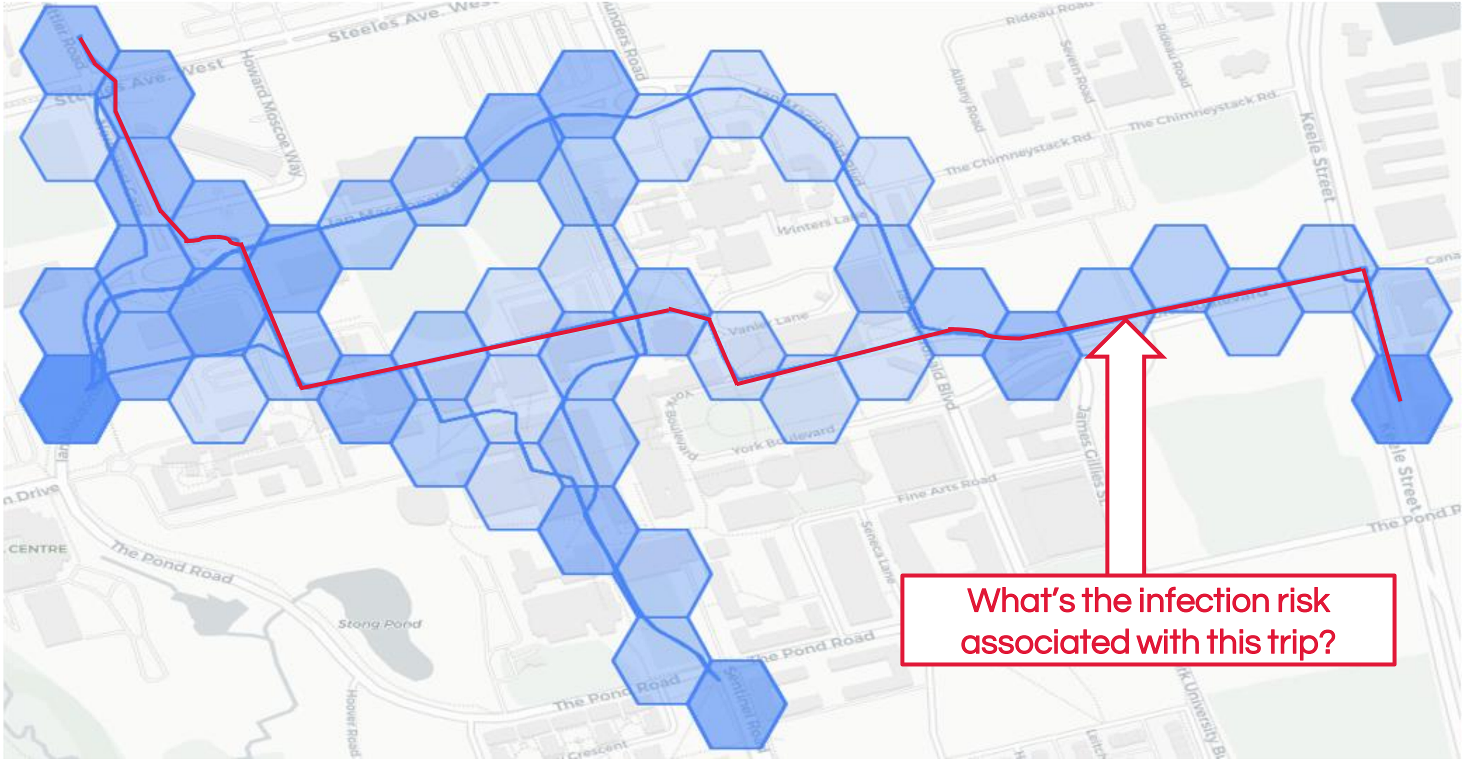


YORK U

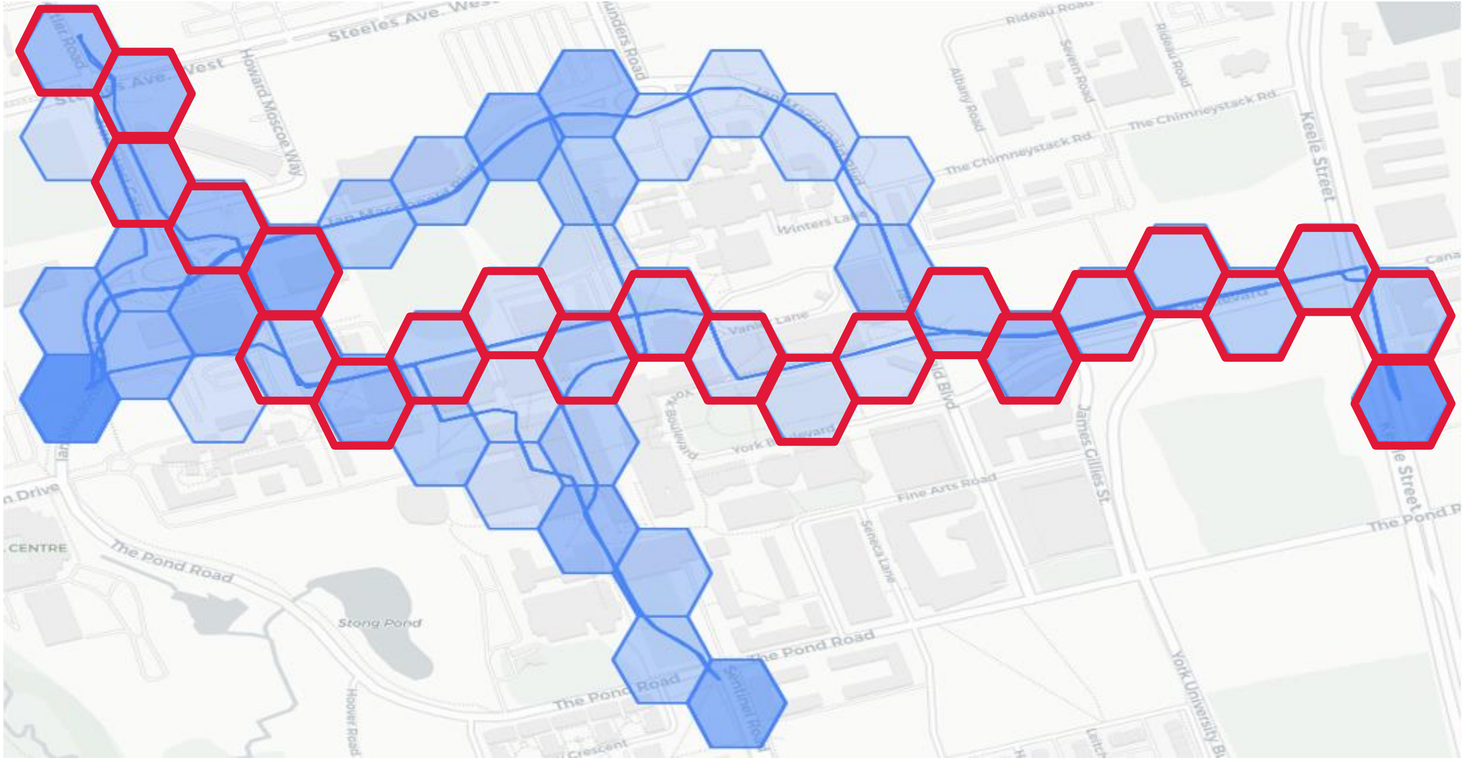
Pedestrian trip risk of infection

Blocks and trips

Pedestrian trip risk of infection (1/3)



Pedestrian trip risk of infection (2/3)



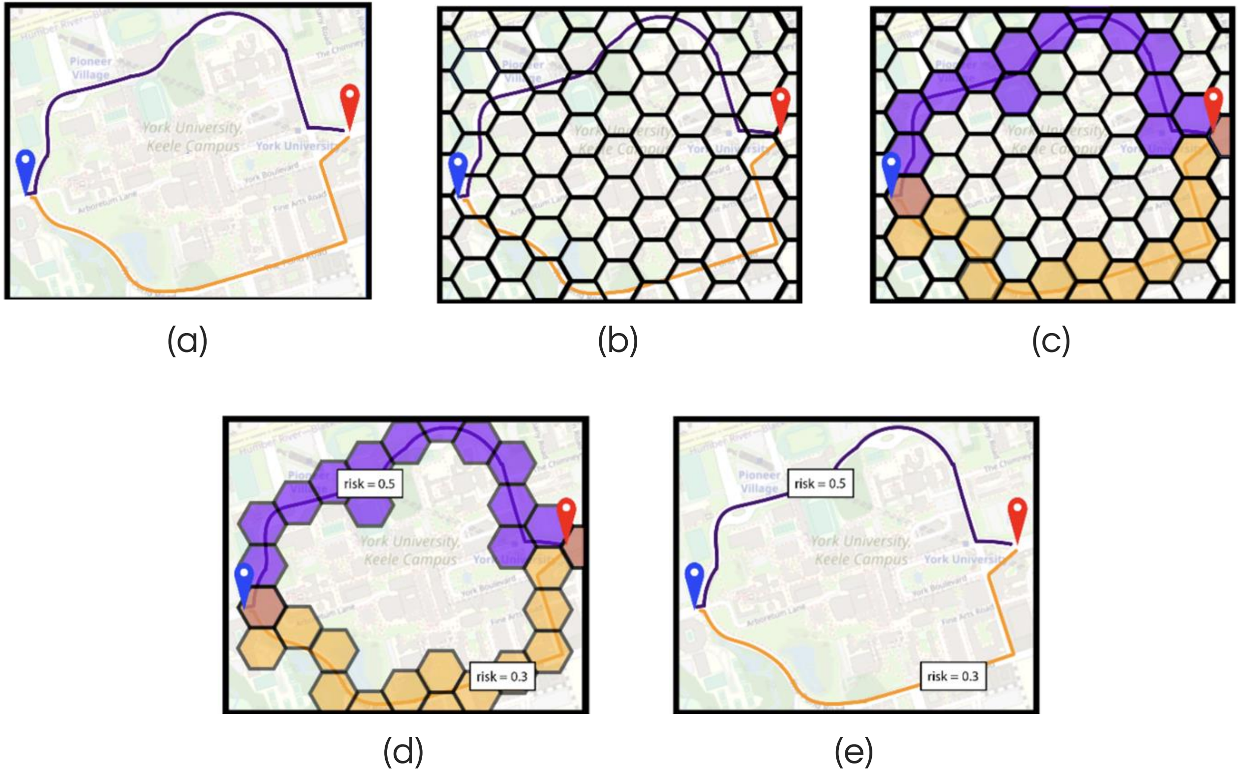
YORK U

Pedestrian trip risk of infection (3/3)

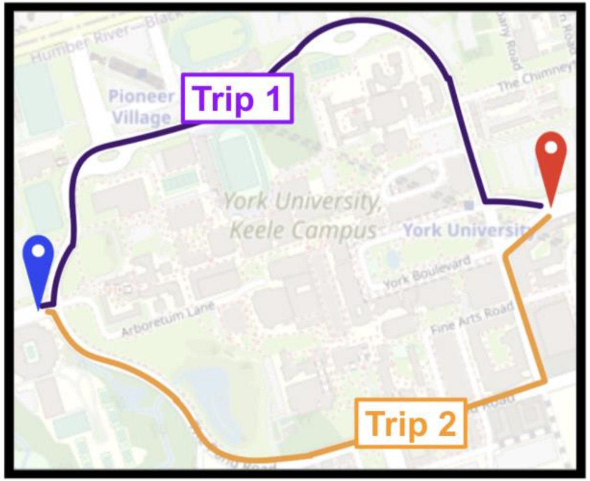
risk of trip at time *n* = risk( ) + risk( ) + risk( ) + ··· + risk( )

Pedestrian trip recommendation

Pedestrian trip recommendation



Pedestrian trip recommendation model



distance
travel time
infection risk

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Risk-based trip/POI recommendation

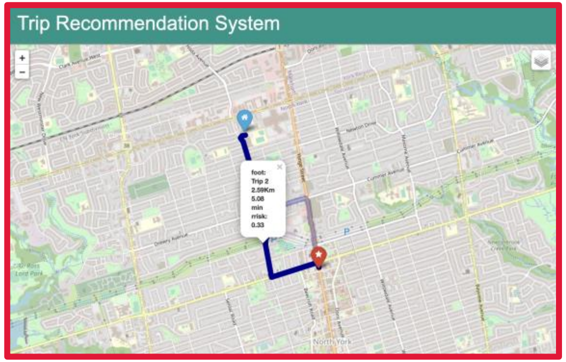
Input: Query

Output: Recommended Trips/POIs

Origin-destination trip recommendation

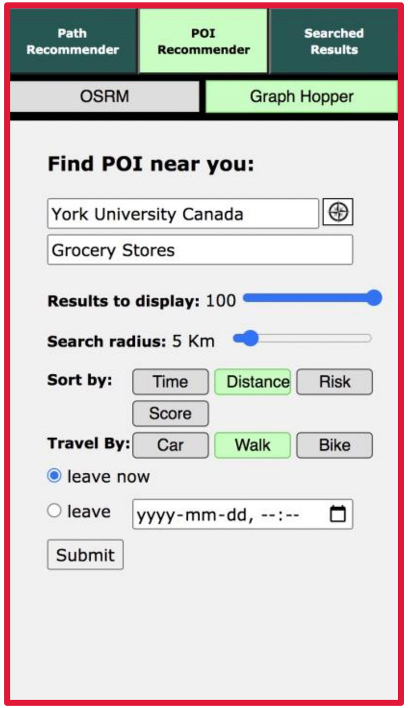
Input: Query (origin, destination , time)

Output: risk-based trip recommendation

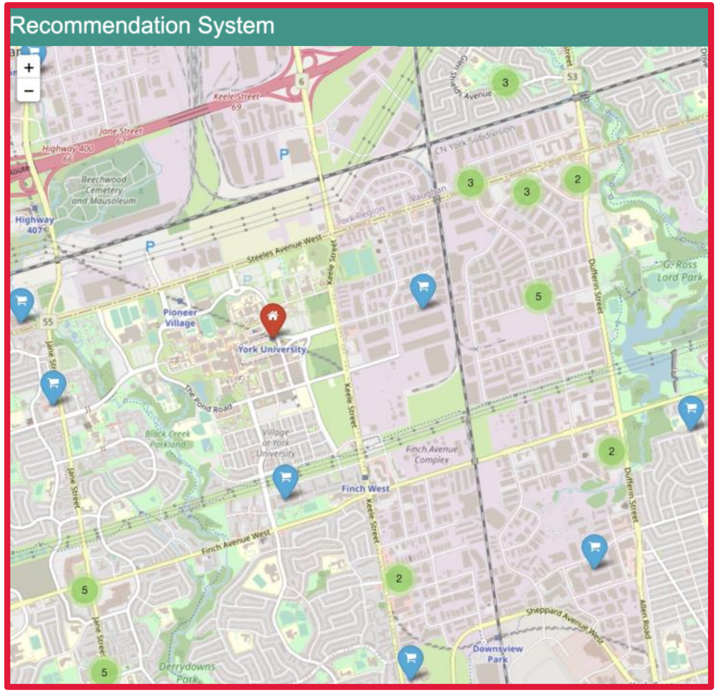


POI recommendation example

Input: Query (POI type, radius, time)



Output: risk-based POI recommendation



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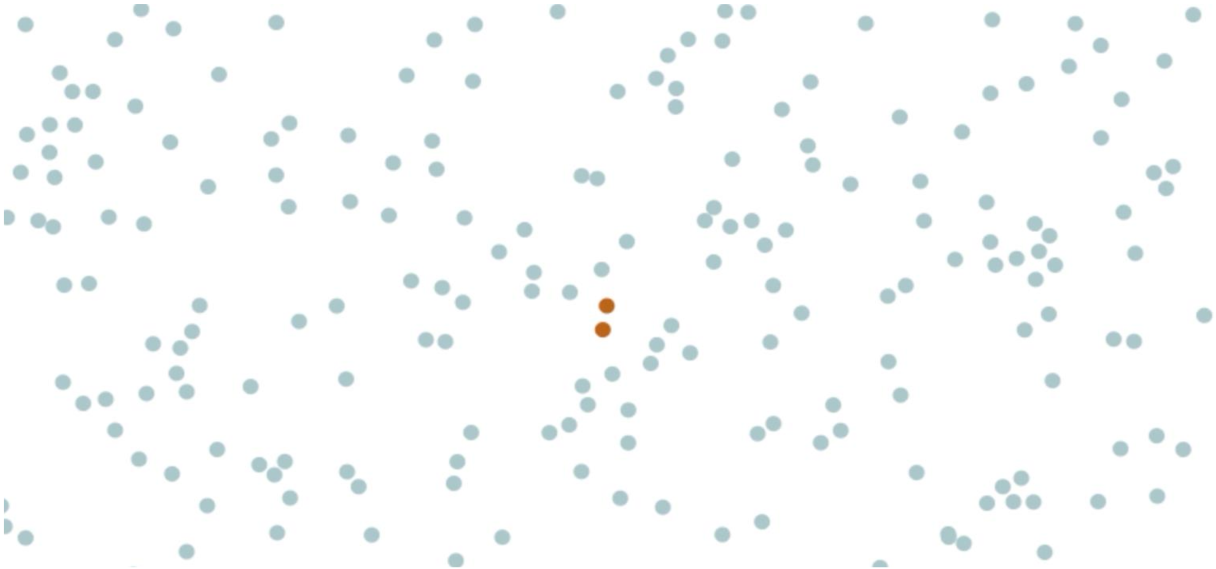
Modeling epidemic spreading

Infectious disease spreading

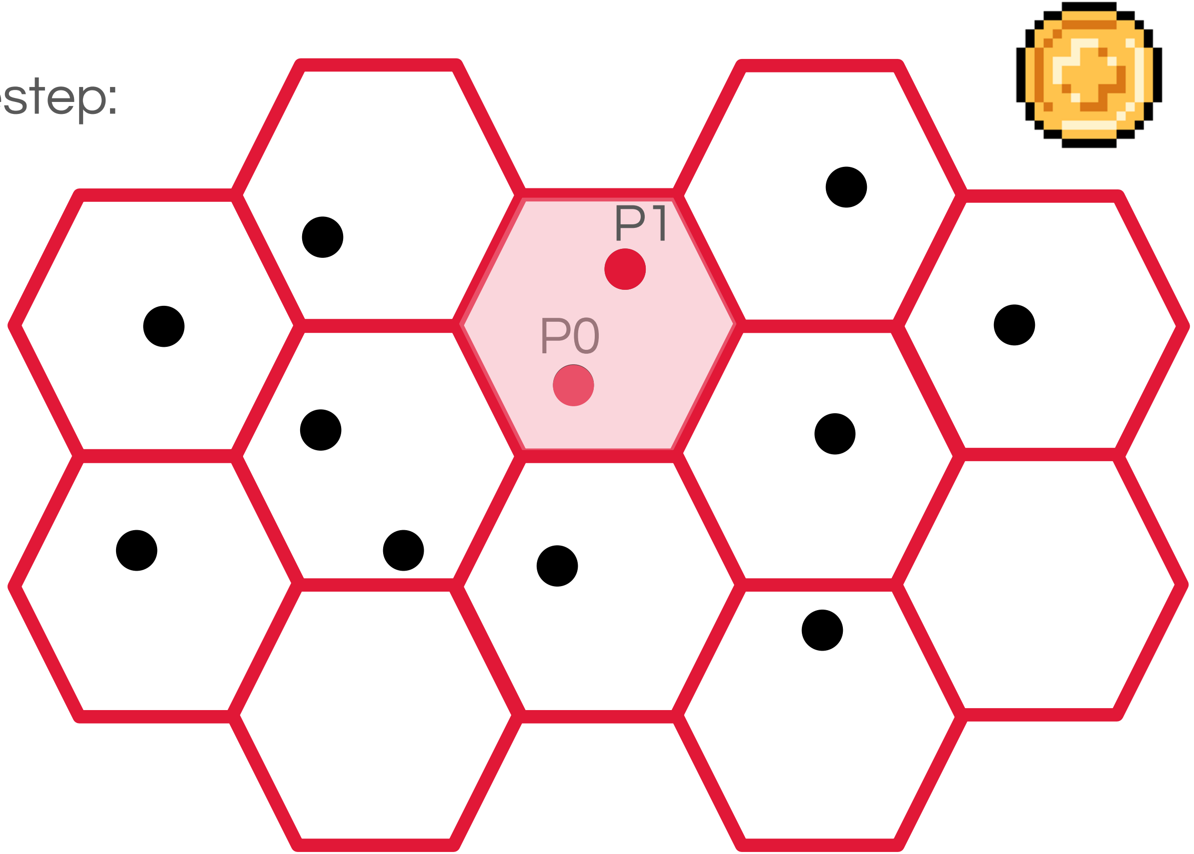


assumptions

- SIR model: Susceptible, Infectious and Recovered
- seed nodes: some people are infected at time 0

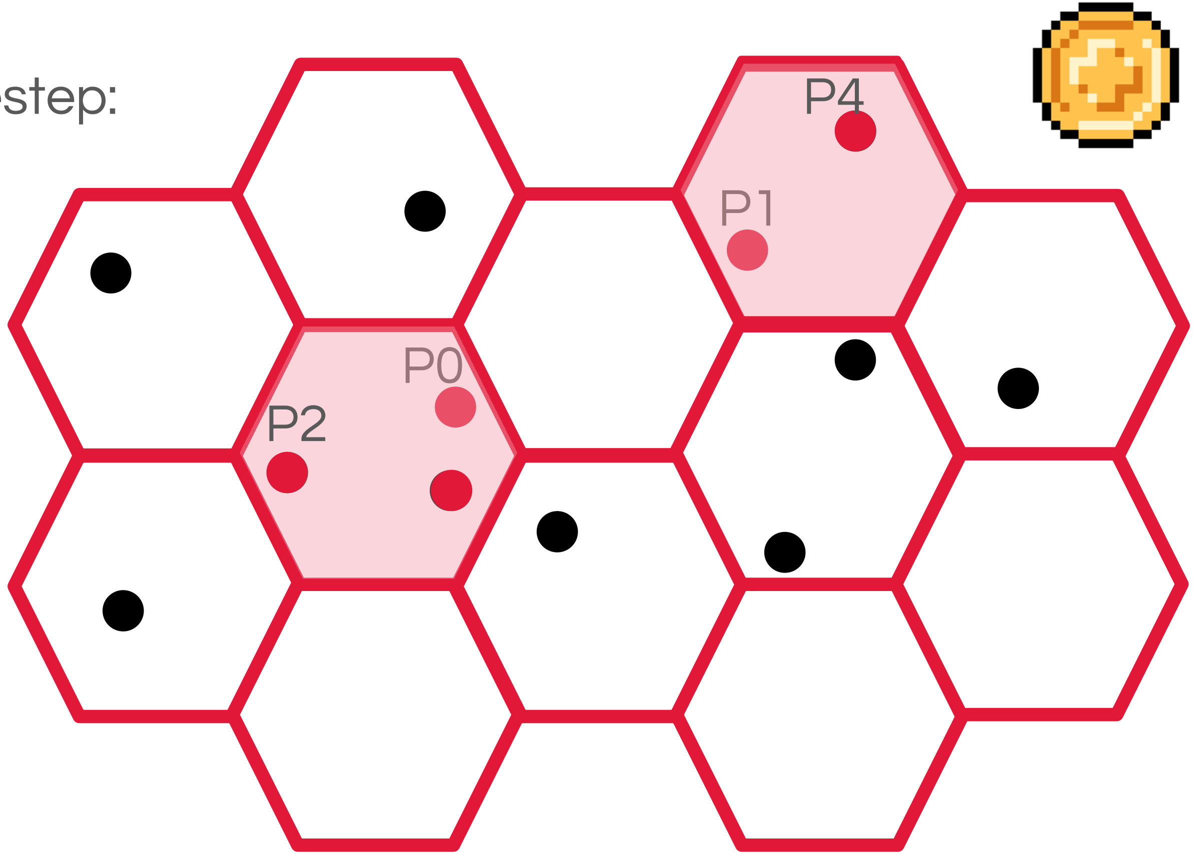
Stochastic modeling of infectious disease spreading (1/2)

Timestep:
1



Stochastic modeling of infectious disease spreading (2/2)

Timestep:
2



Experimental results

Experimental Scenarios

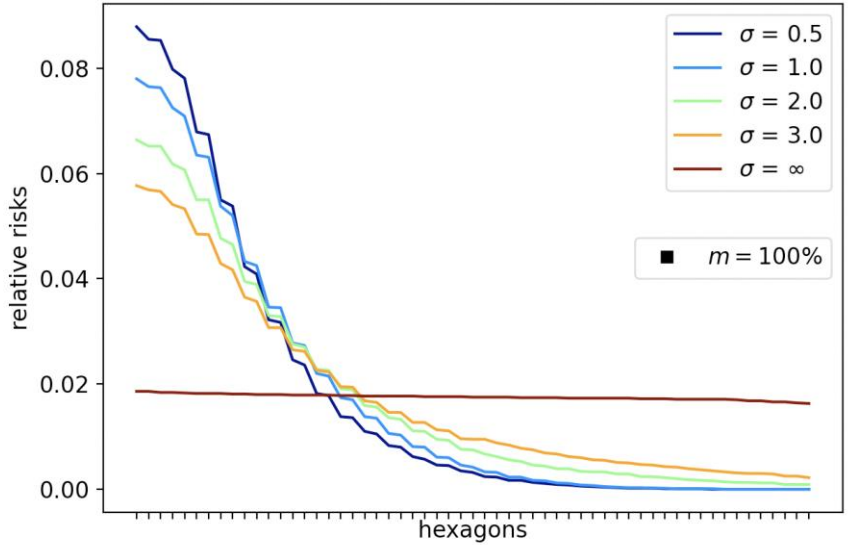
Q1 Effect of POI visitor distribution on risk

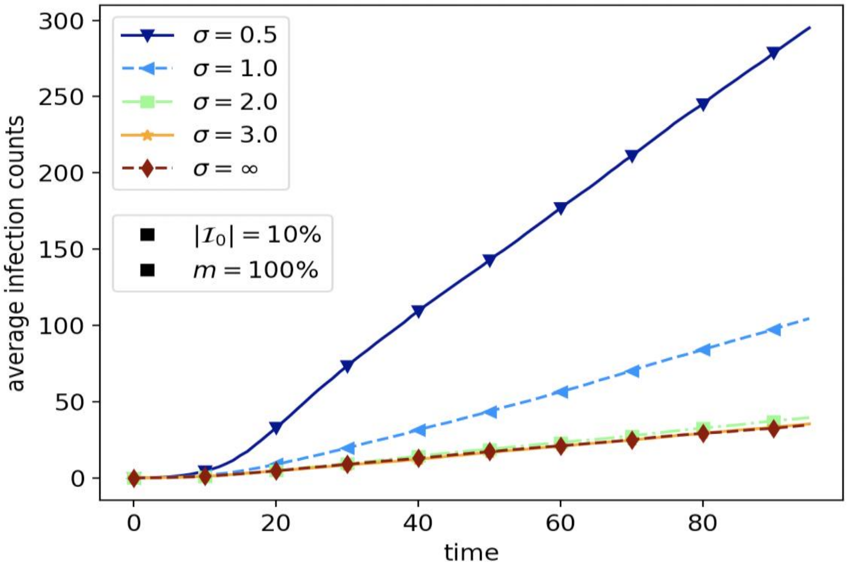
Q2 Effect of POI visitor distribution, occupancy and initial infected seed size on direct infections

Q3 Impact of targeted and non-targeted intervention strategies

Q4 Impact of recommendation policy

Q1 Effect of POI visitor distribution on risk





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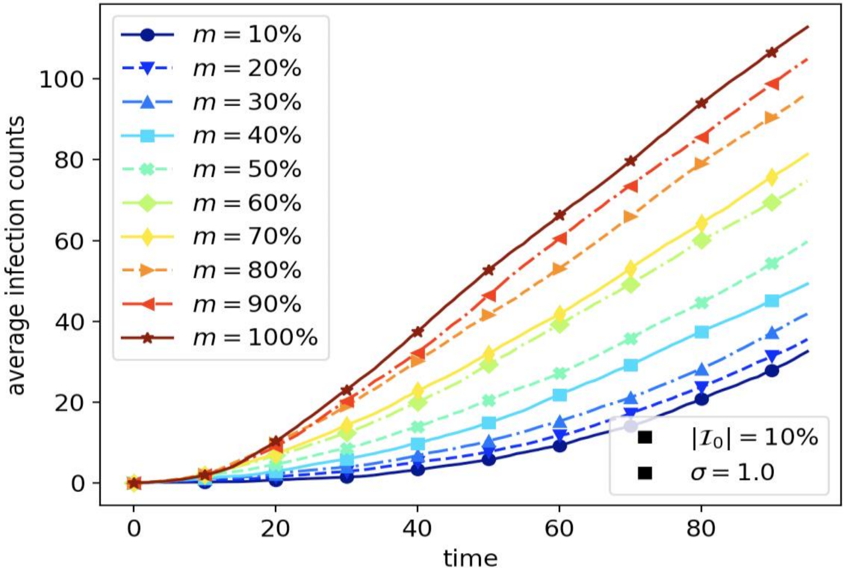
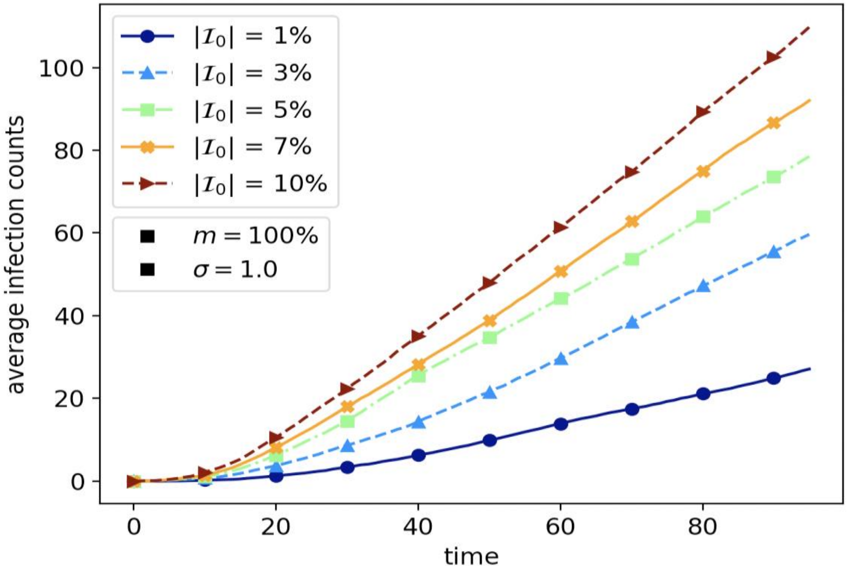
Q2 Effect of POI visitor distribution, occupancy and initial infected seed size on direct infections





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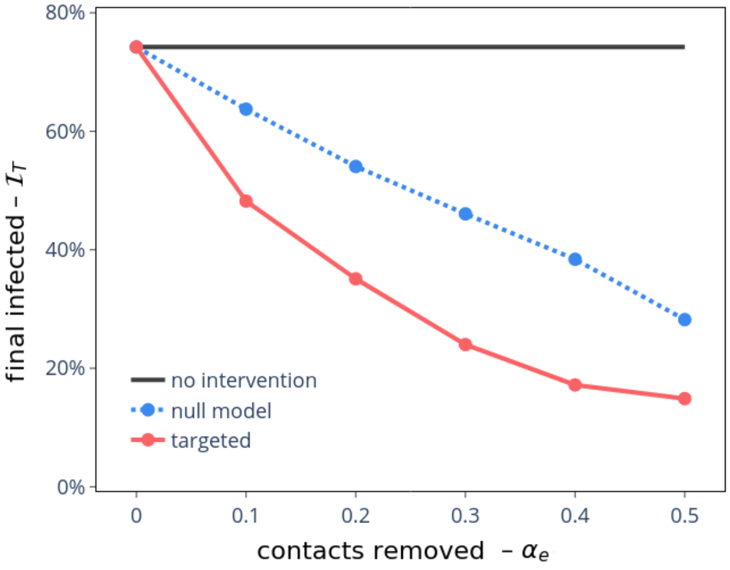
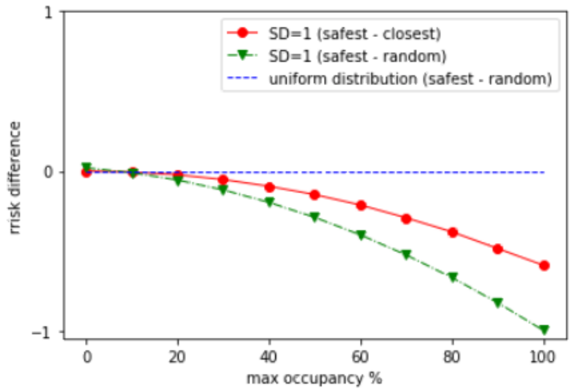
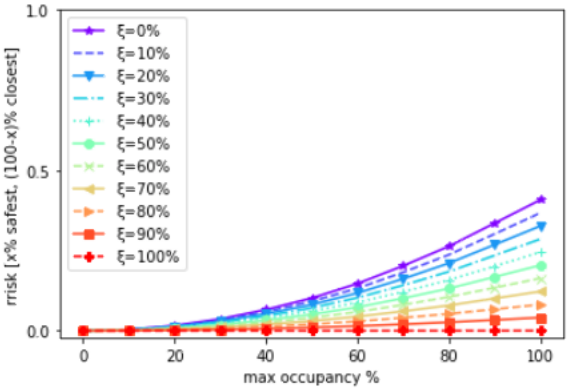
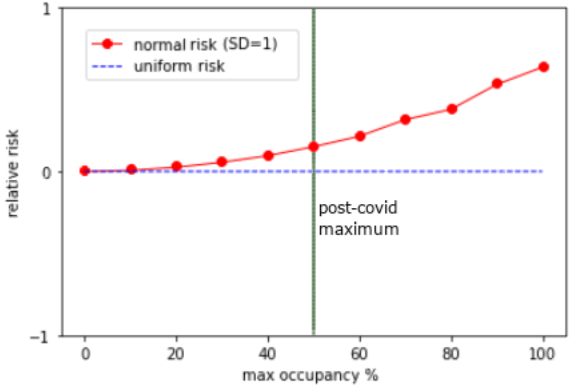
Q3 Impact of targeted and non-targeted intervention strategies



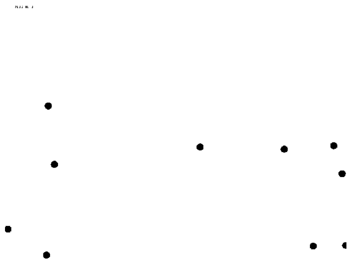
Q4 Impact of recommendation policy



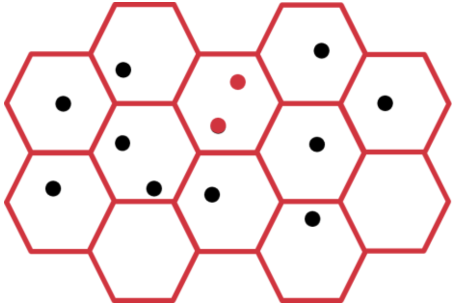




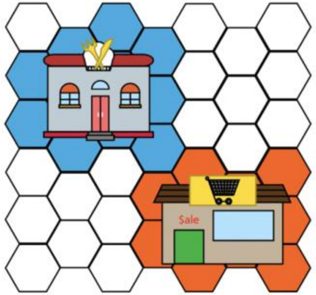
Takeaway



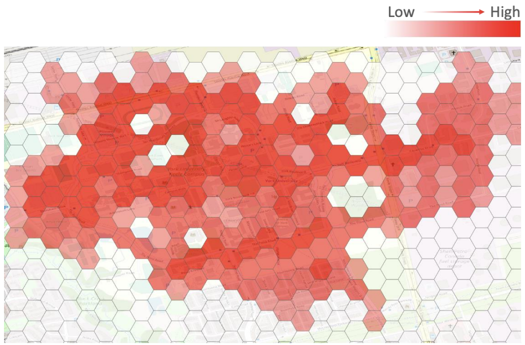
trajectories



microscopic modeling



hierarchical modeling



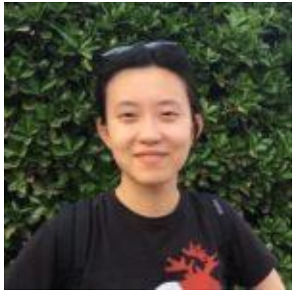
risk maps

risk of trips

trip recommendations

Credits

Tilemachos Pechlivanoglou



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Gian Alix

Jialin Sun

Nina Yanin

Farzaneh Heidari

Epidemic Spreading in Trajectory Networks. T. Pechlivanoglou, J. Li, J. Sun, F. Heidari, M. Papagelis. **Big Data Research** (BDR, Vol. 27, 100275, pp 1-15, 2022).

Microscopic Modeling of Spatiotemporal Epidemic Dynamics. T. Pechlivanoglou, G. Alix, N. Yanin, J. Li, F. Heidari, M. Papagelis. **Submitted.**

Thank you!

Questions?