# Microscopic Modelling of Spatiotemporal Epidemic Dynamics

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SpatialEpi '22 - Workshop

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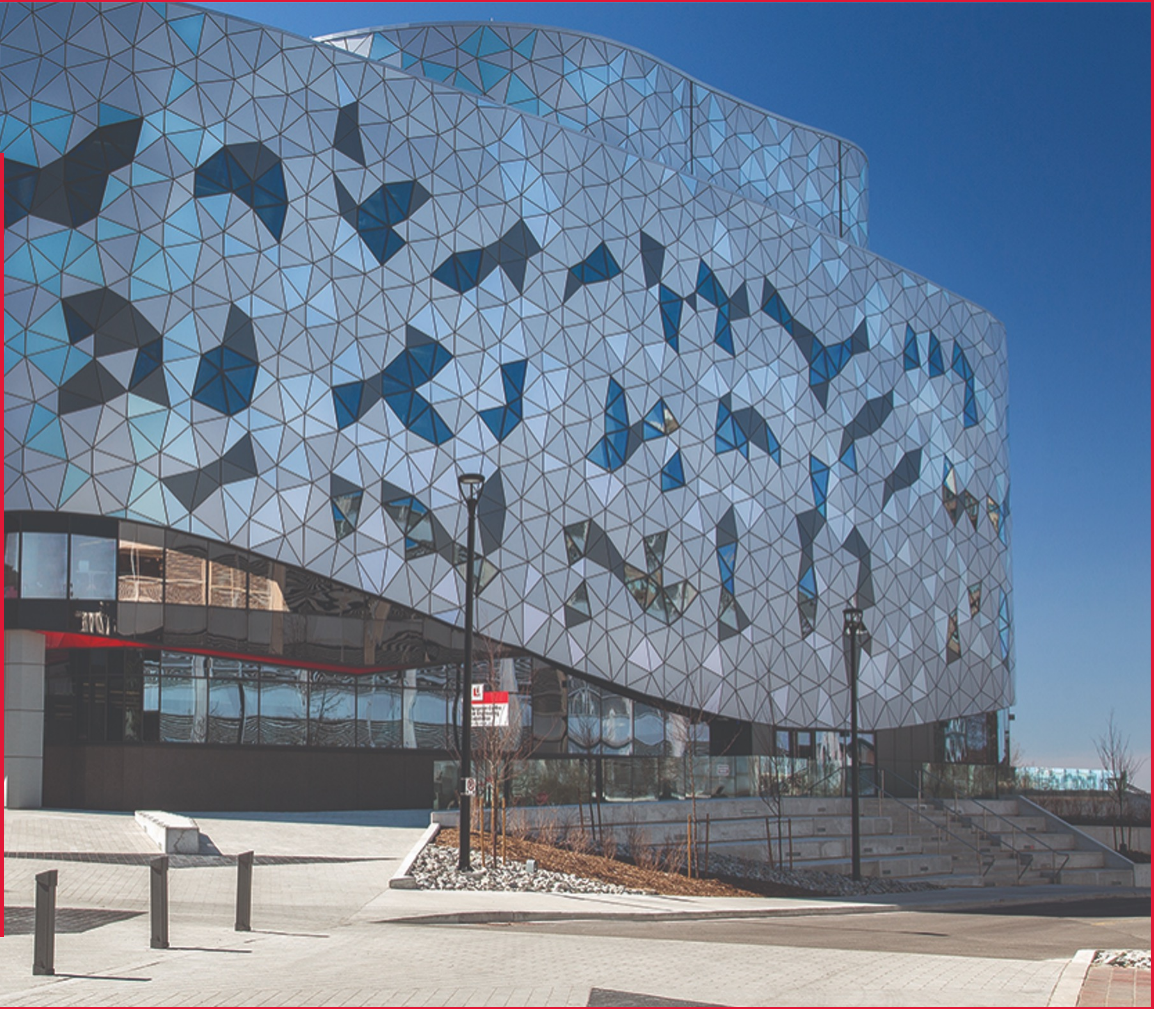
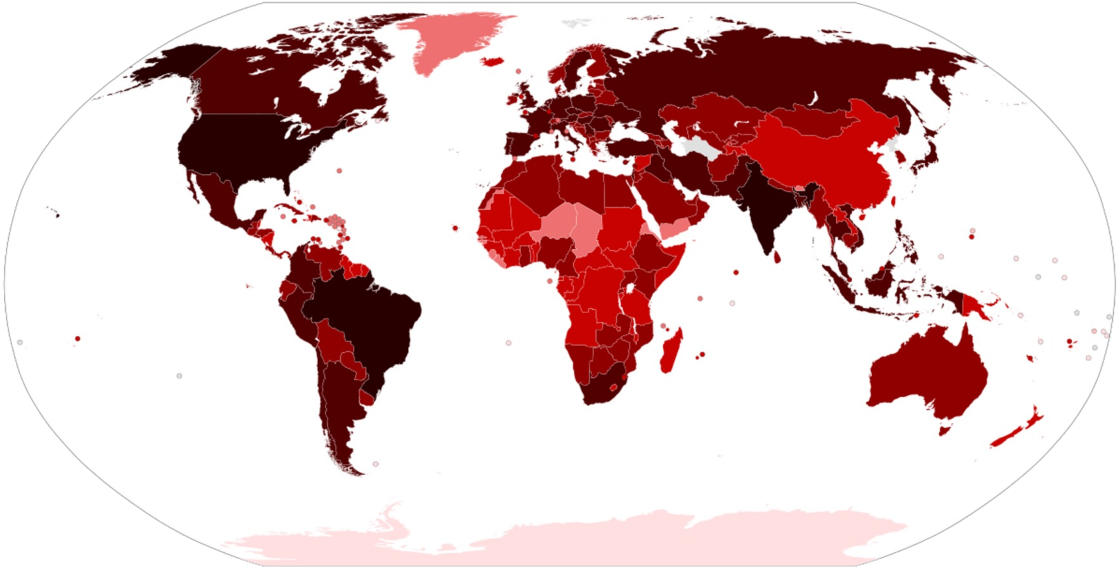


# Background and Motivation

# COVID-19 (a global pandemic)



**containment measures**

physical distancing

business, social life lockdown

**side effects**

economic downturn

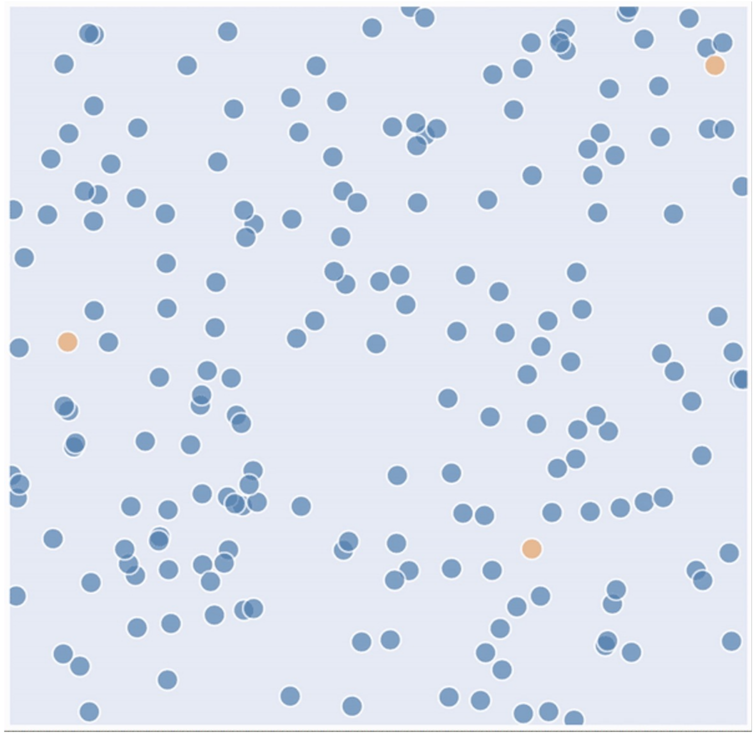
psychological well-being

...

need for more moderate contact-reduction policies

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

# Mechanism of infectious disease spreading



Susceptible

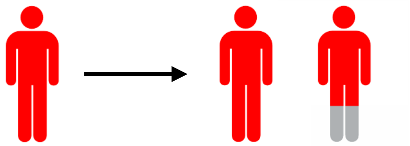
Infected

Removed

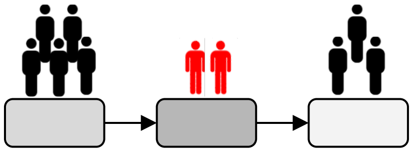


Source: Matt Crooks, towards data science

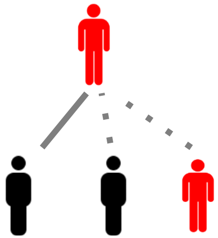
# Revisiting epidemic concepts



**reproductive number**



compartmental models
(population-based)



**offline contact tracing**

# Basic reproductive number ($R_0$)

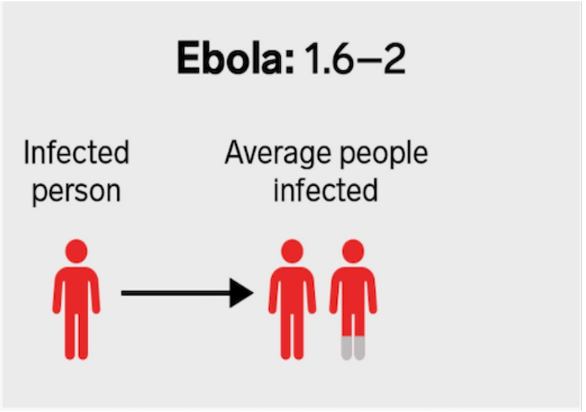
The **expected** number of people that an individual infects

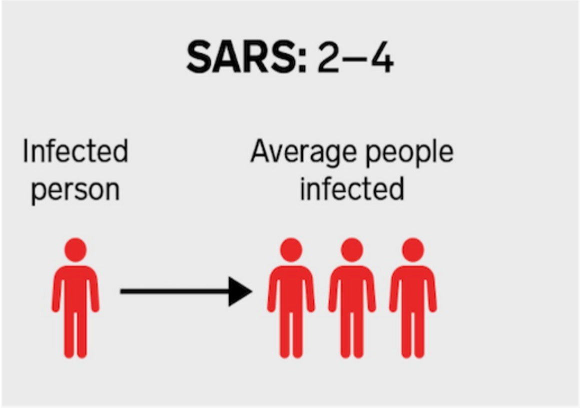
$R_0 < 1$ infection dies out

$R_0 > 1$ infection persists

$$R_0 = p \times k$$

$p$: transmission probability $k$: number of contacts



# 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

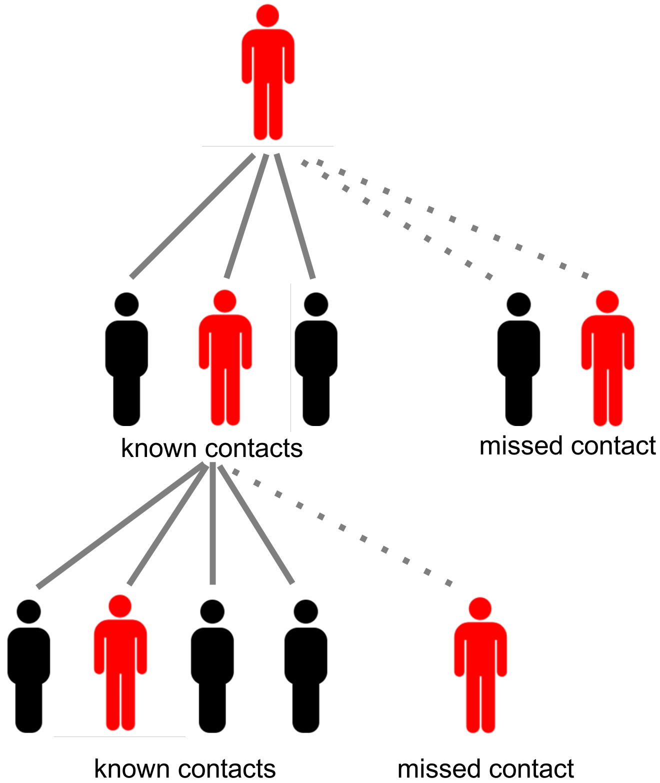
## more realistic epidemic models need to

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

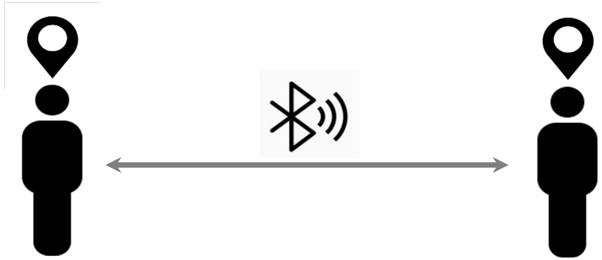
monitor actual contacts of individuals

# Offline contact tracing (through interviews)

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



# Digital contact tracing



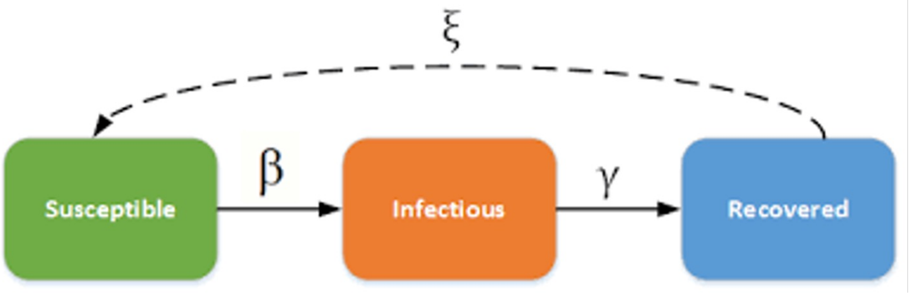
Enabled by mobile apps, geolocation devices, etc.

✓ addresses limitations of traditional contact tracing

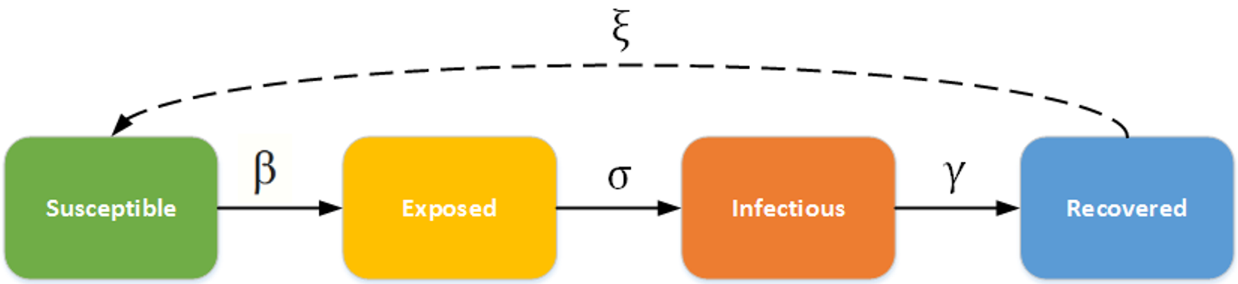
✗ privacy concern

# Compartmental models

SIR

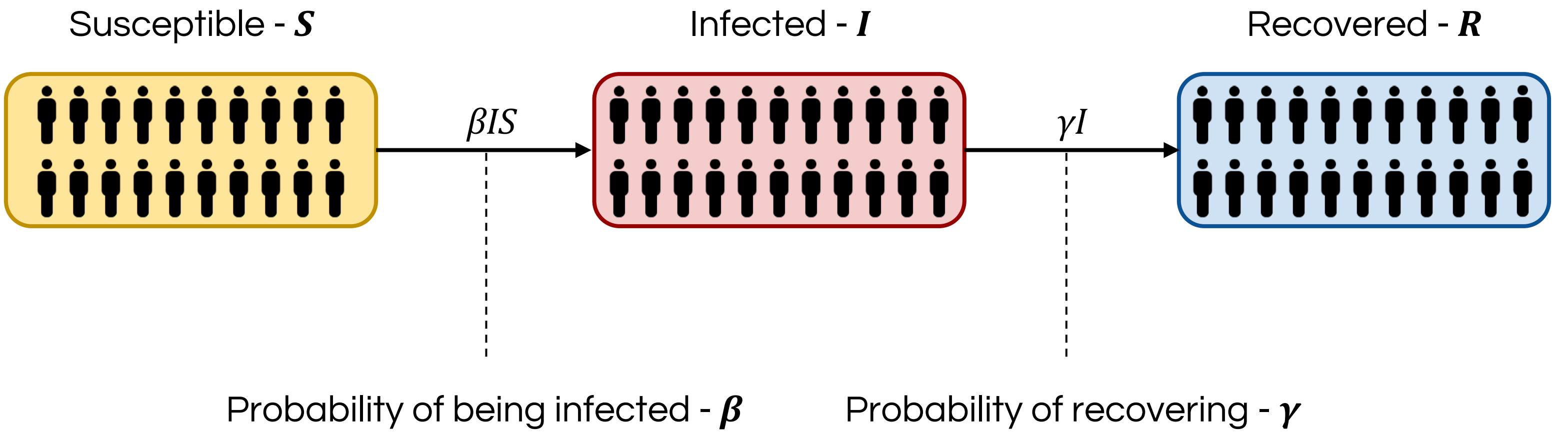



SEIR

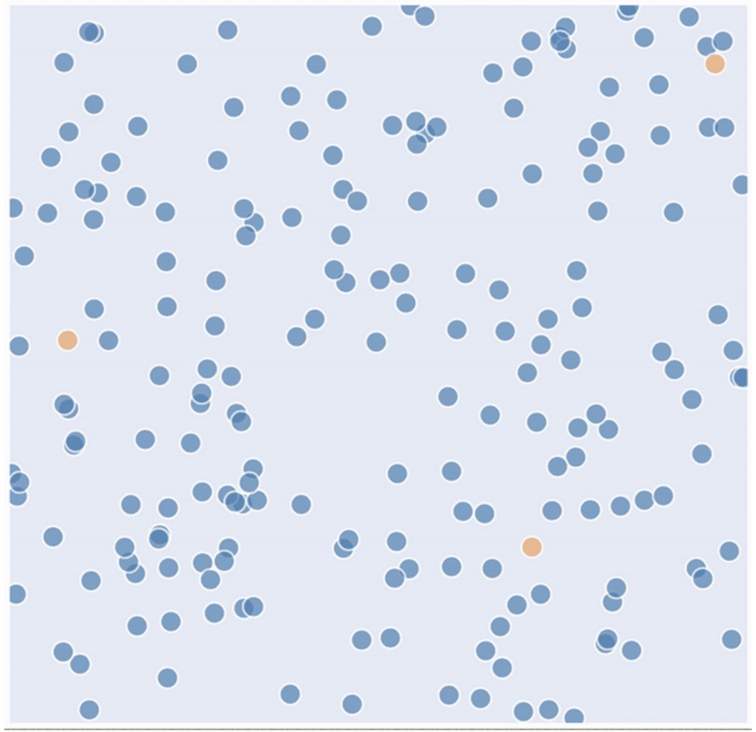


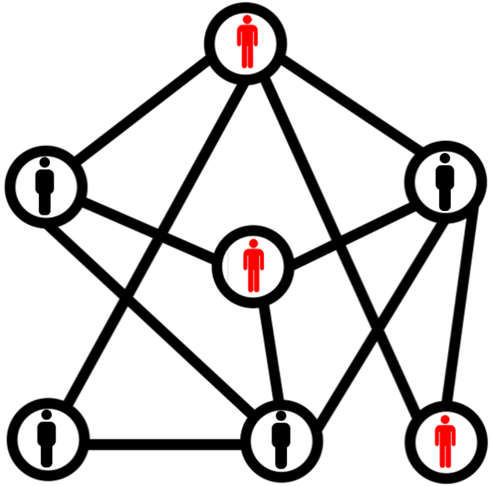
# SIR model

Time $t$ =



# Individual-based models

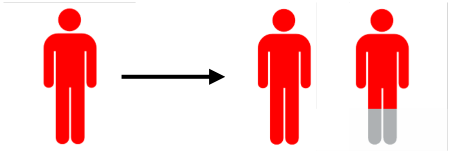




mobility network / contact network

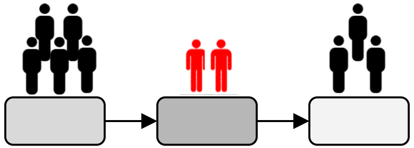
**nodes**: individuals
**edges**: social interaction
**contagion**: stochastic infection due to spatial proximity

# Models comparison



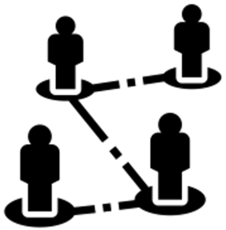
**reproductive number**

✔ 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



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# Problem Statement

# The Problem

## Input

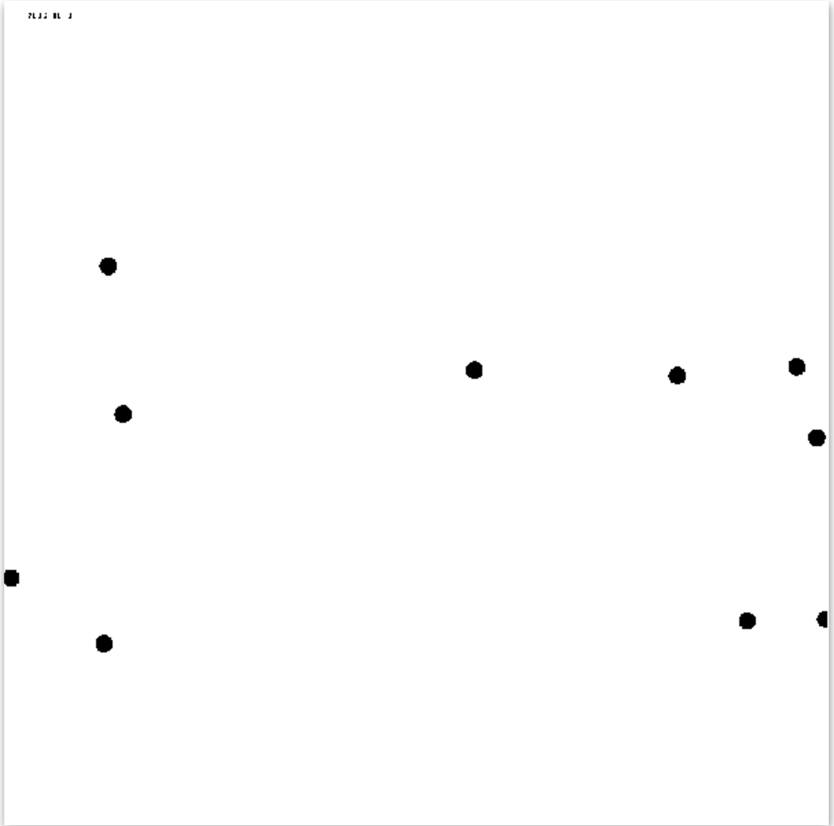
- Historical data of individual trips (trajectories)

## Output

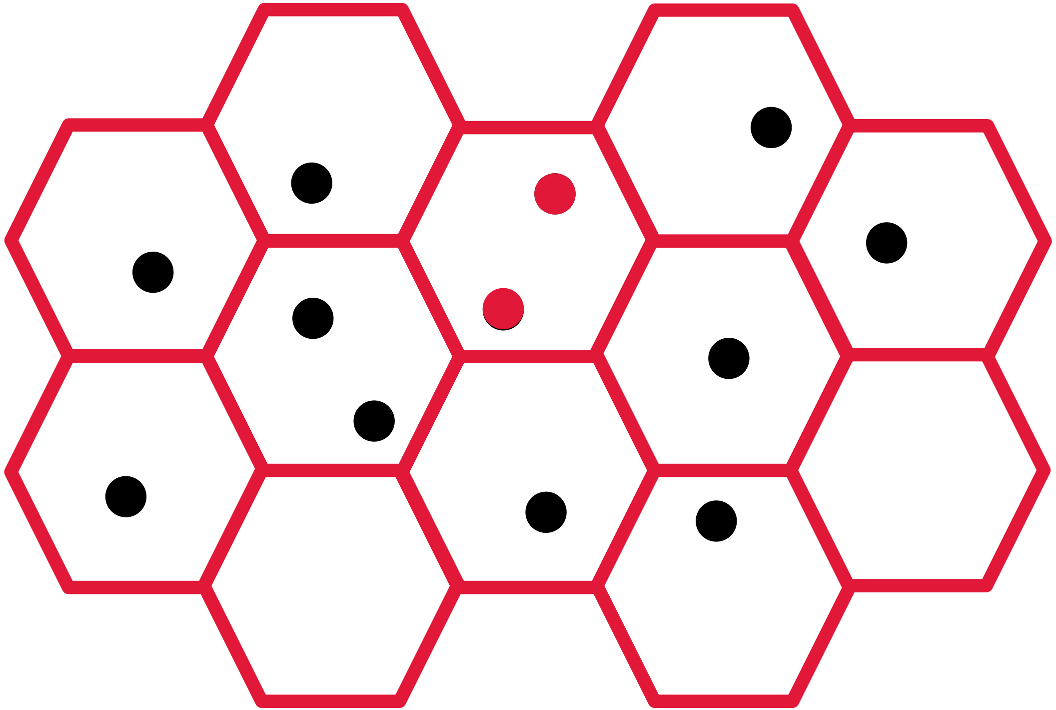
- Assess the relative risk of infection of individuals
- Assess the relative risk of infection of geographic areas and points-of-interest (POIs)
- Assess the risk of infection of a (pedestrian) trip in an urban environment
- Recommend alternative trips/safe POIs that mitigate the risk of infection
-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

# Methodology

# Trajectories of individuals



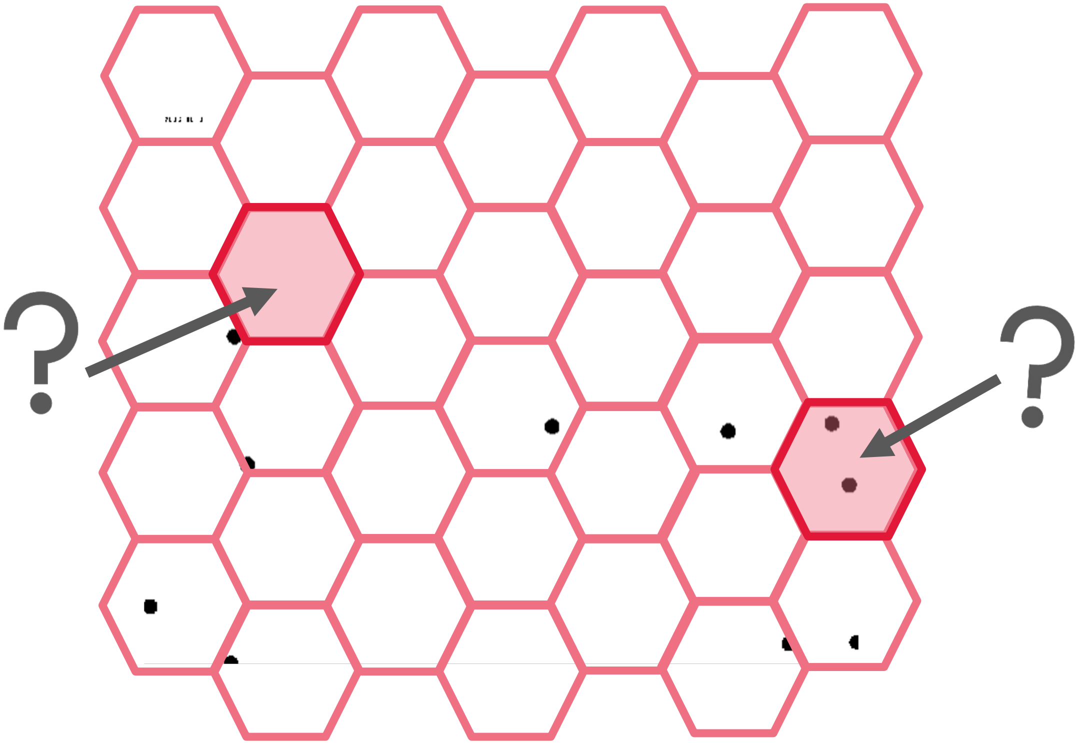
# Geographic area tessellation



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

# Block risk of infection

# Block infection risk (1/2)



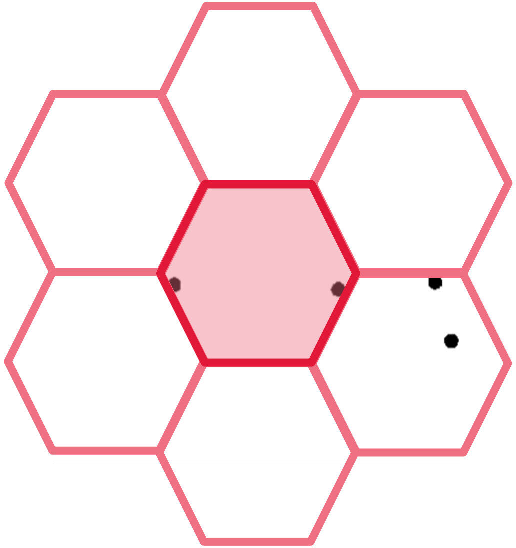
What is the risk of infection of a **block**?

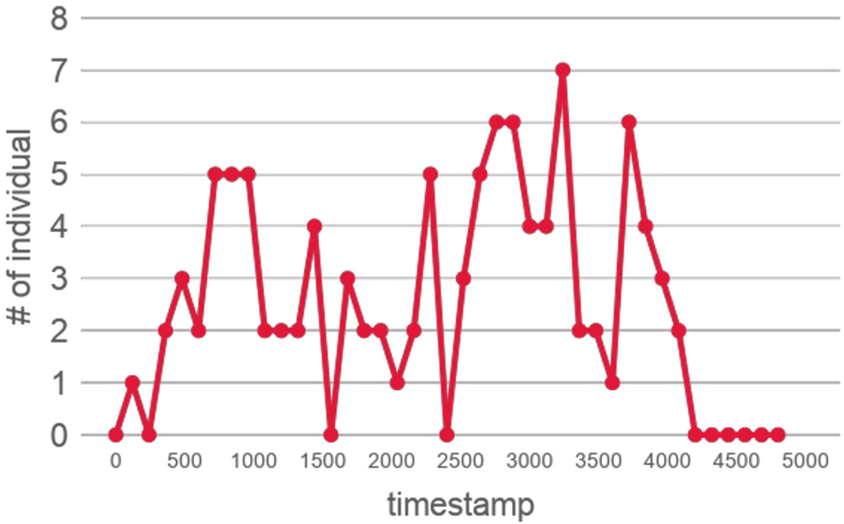
How they compare to each other?

# 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



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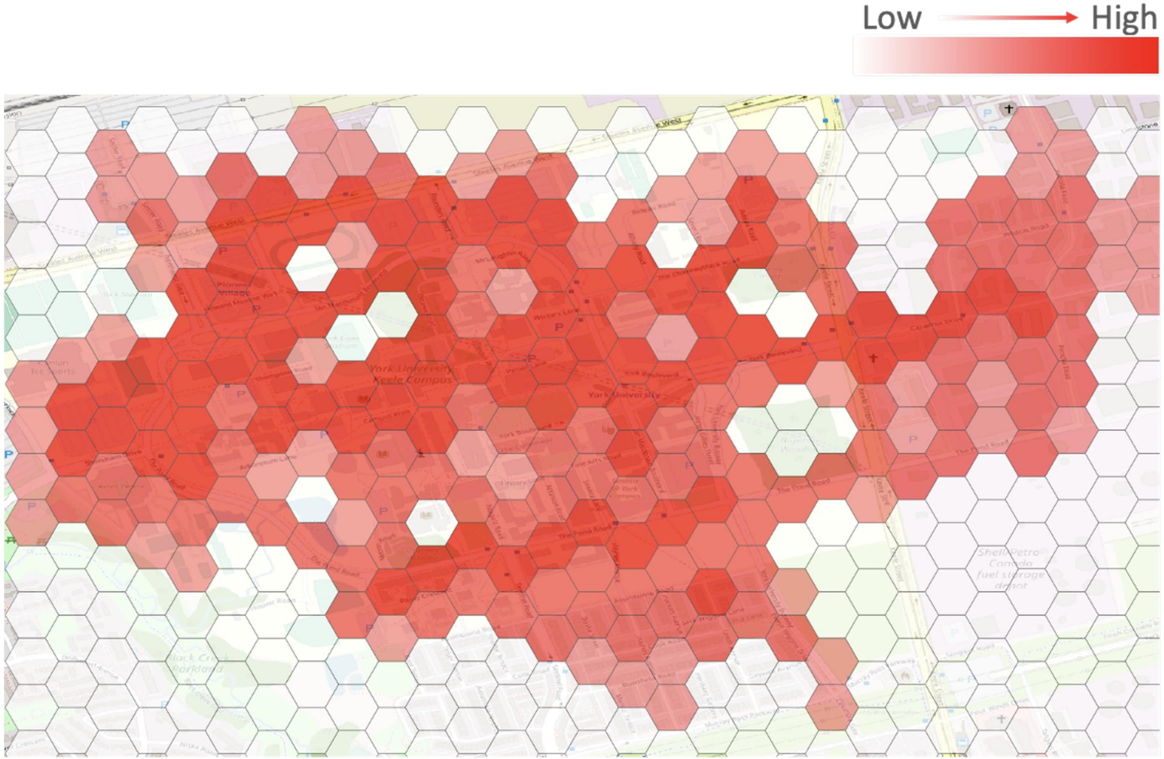
# Risk map example (overlay of a geographic area)

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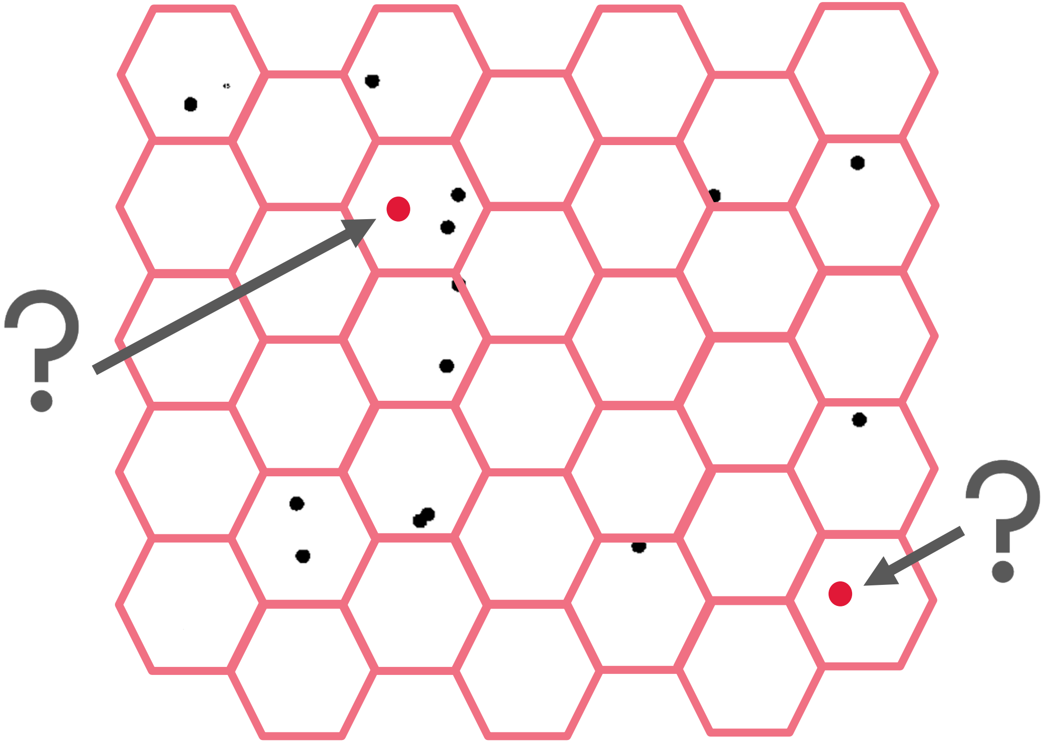
# Individual risk of infection

# Individual infection risk (1/2)

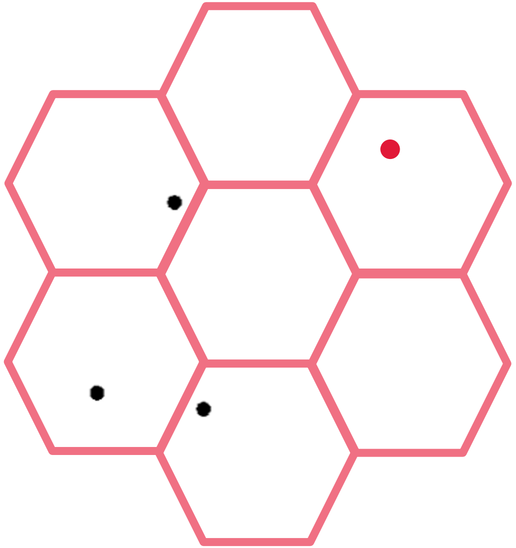


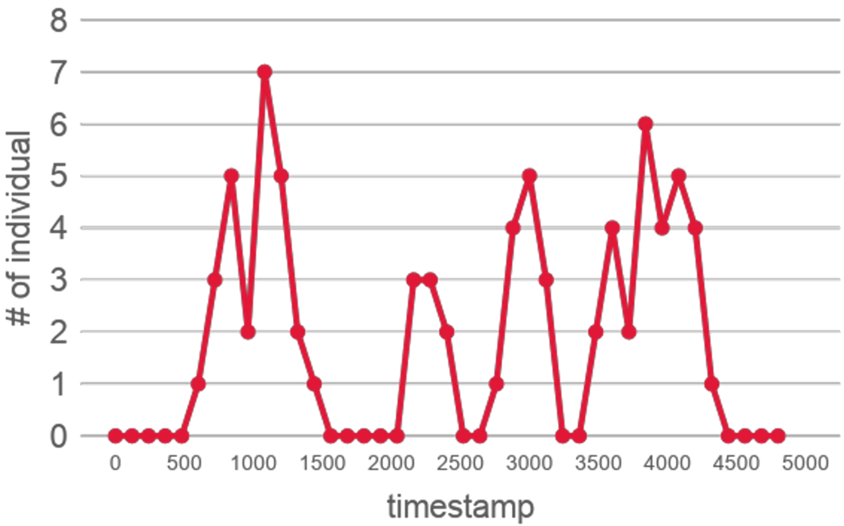
What is the risk of infection of an **individual**?

How they compare to each other?

# Individual infection risk (2/2)

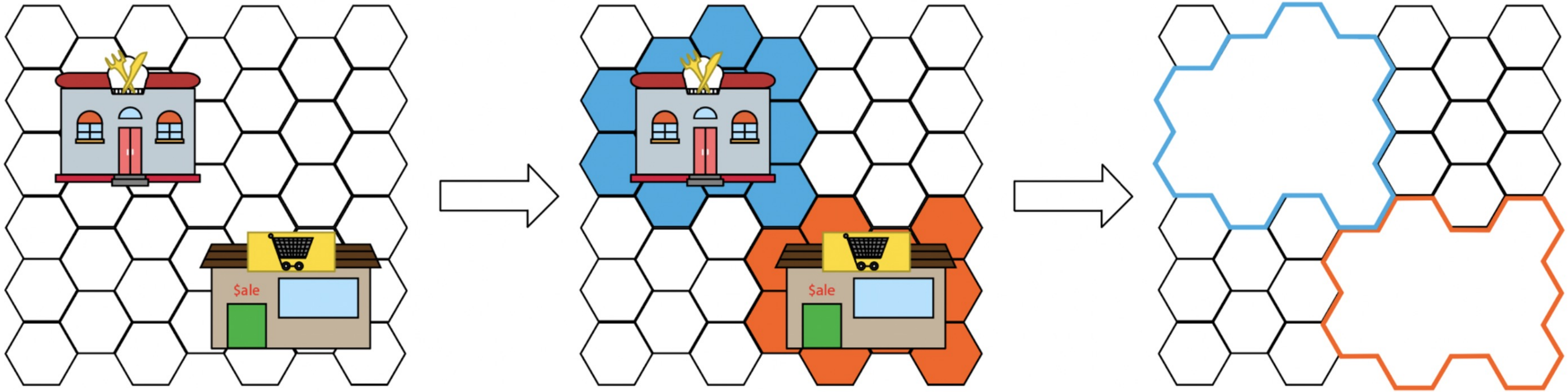
the risk $risk_u$ of an individual is a function of the risks $brisk_b$ of all blocks traversed



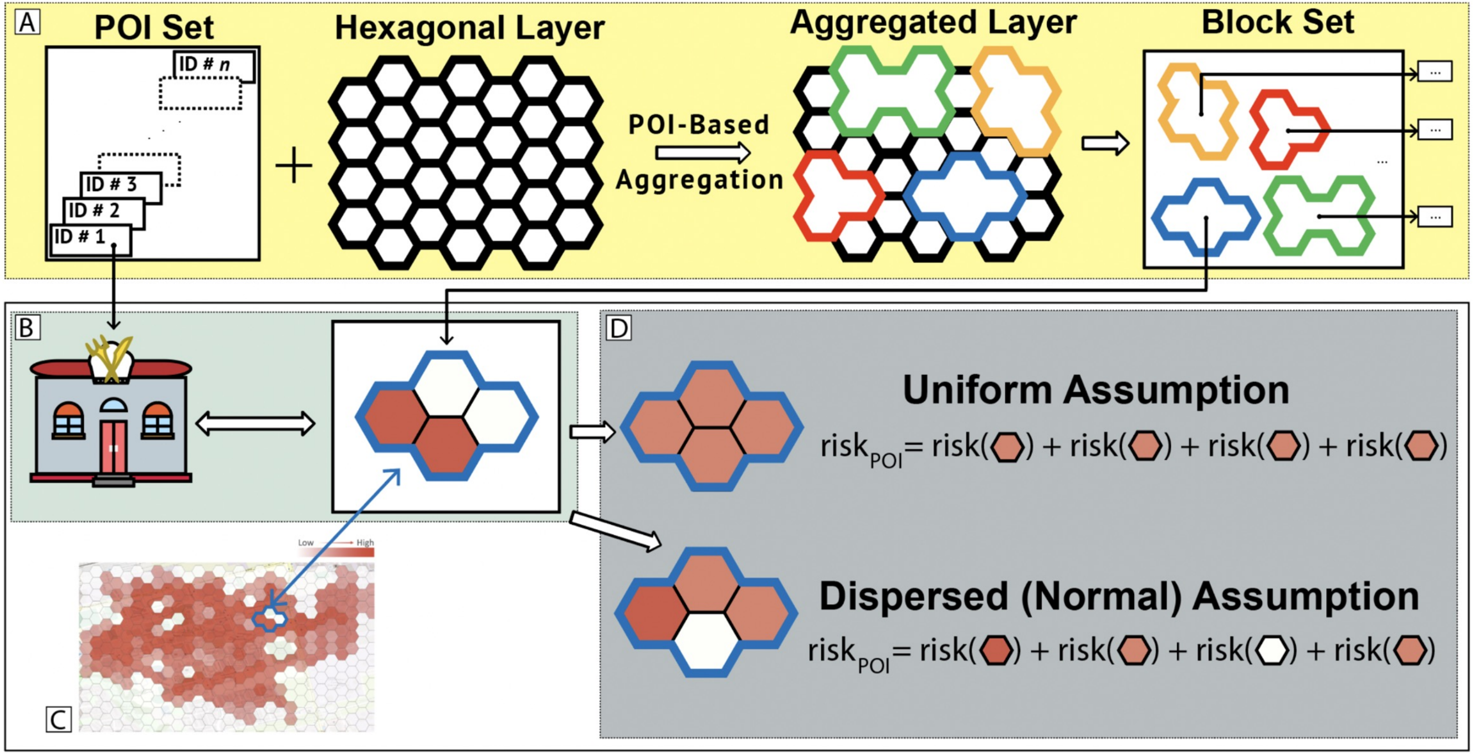


# Point-of-interest (POI) risk of infection

# Multi-block: POI-based hierarchical block aggregation

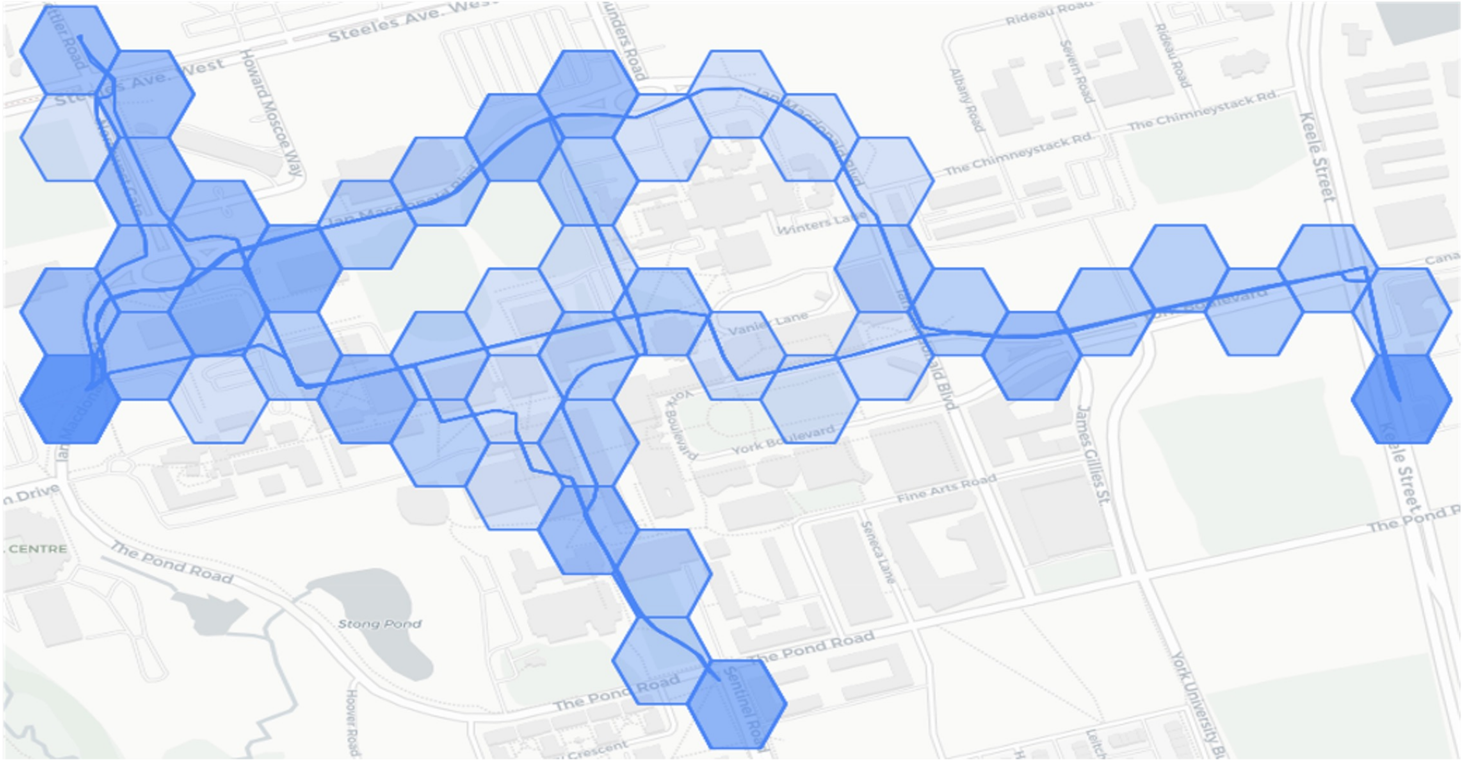


# Point-of-interest (POI) risk of infection

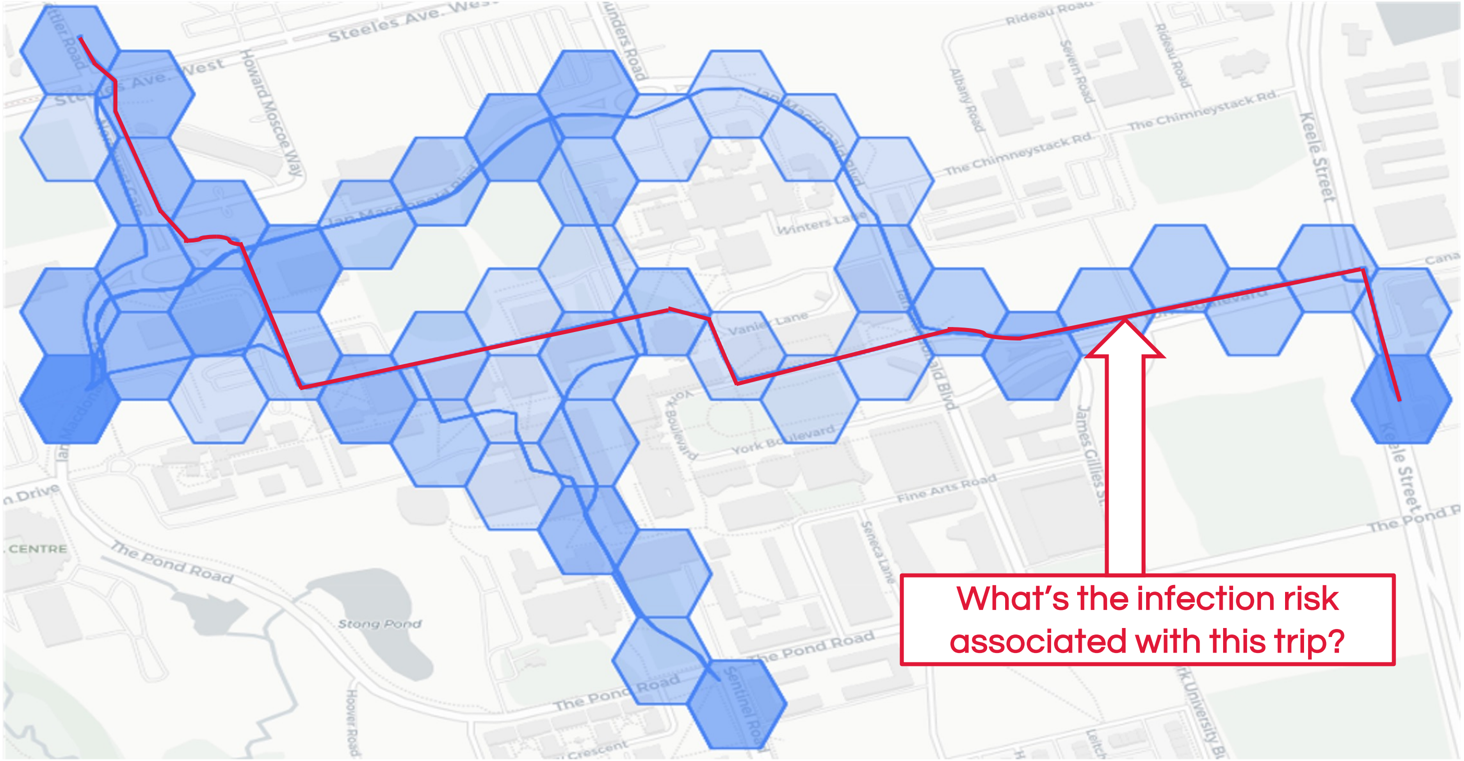


# Pedestrian trip risk of infection

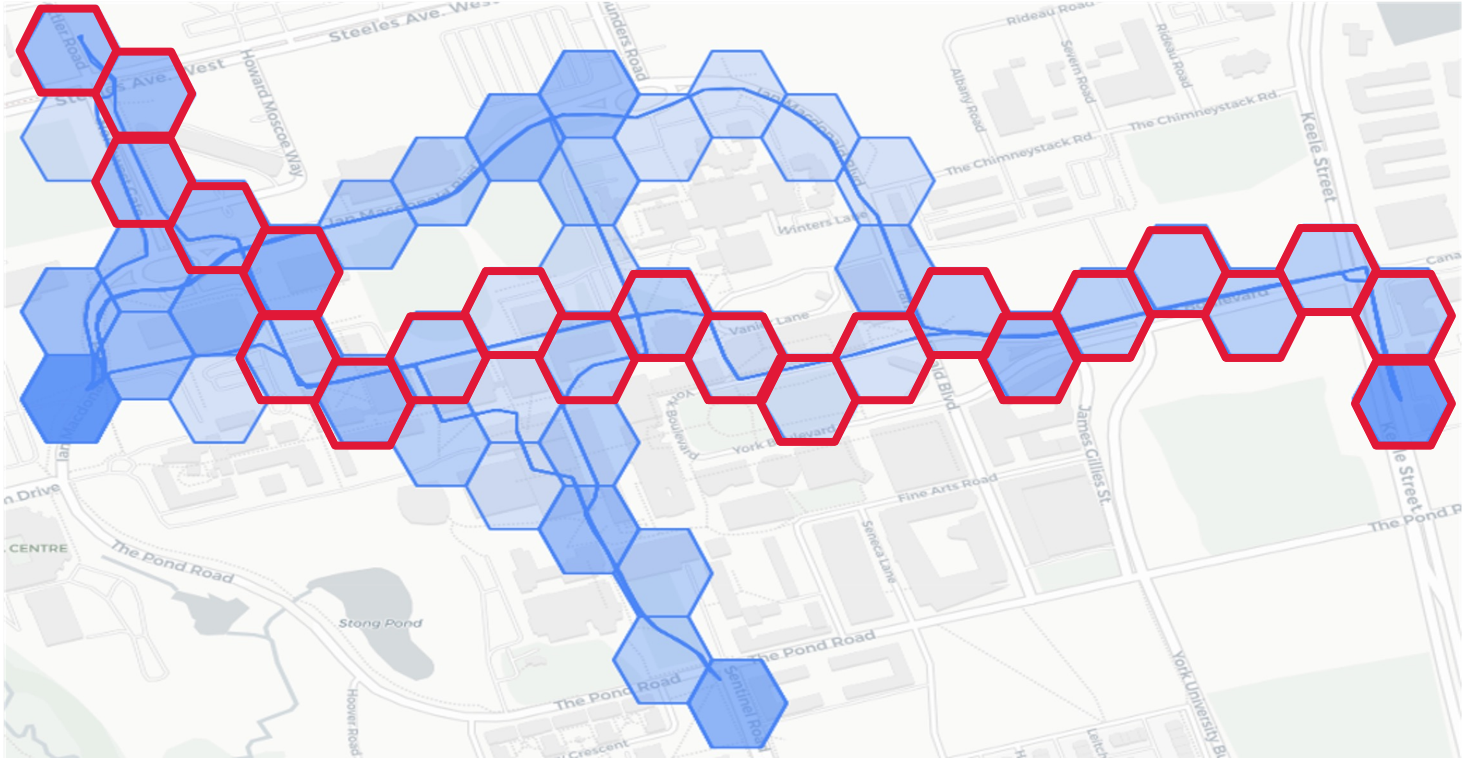
# Blocks and trips



# Pedestrian trip risk of infection (1/3)



# Pedestrian trip risk of infection (2/3)

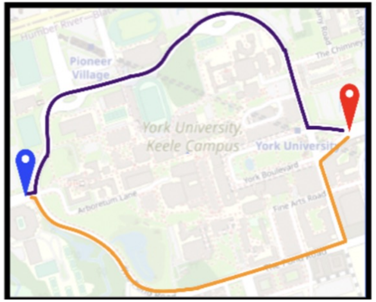


# Pedestrian trip risk of infection (3/3)

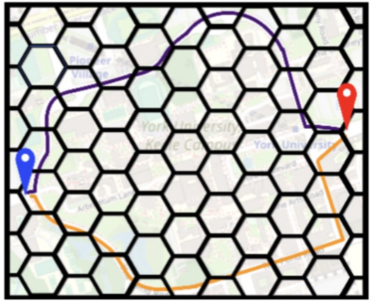
**risk of trip at time *n* = risk( ) + risk( ) + risk( ) + ··· + risk( )**

# Pedestrian trip recommendation

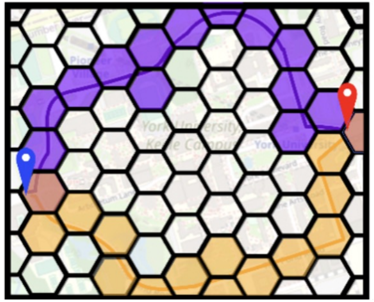
# Pedestrian trip recommendation



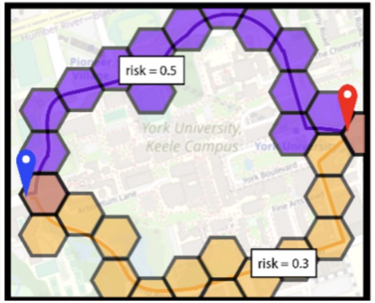

(a)



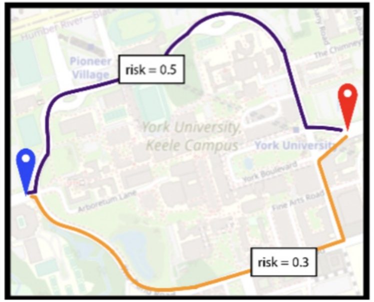
(b)



(c)

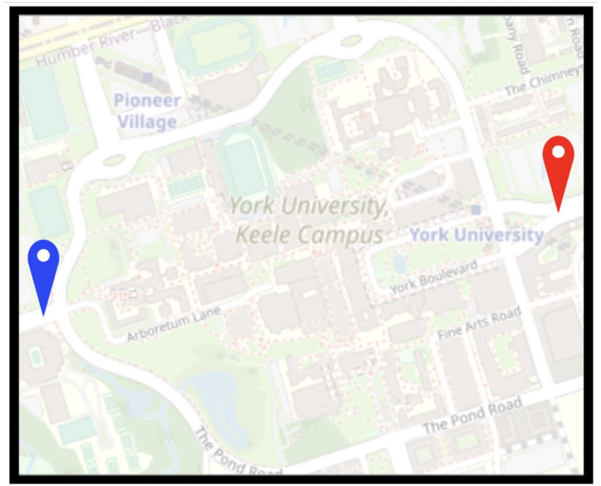


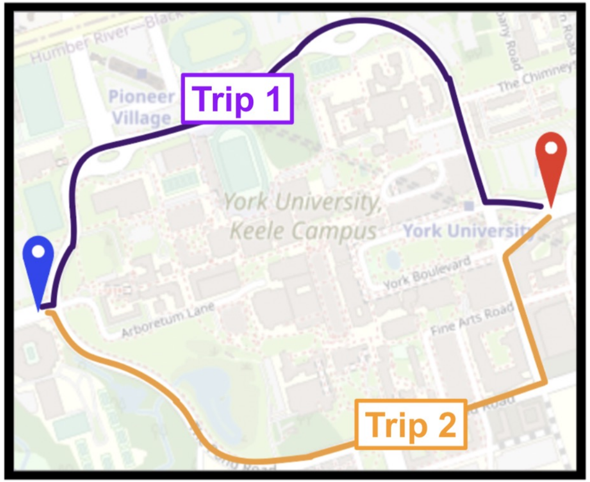

(d)




(e)

# Pedestrian trip recommendation model




distance
travel time
infection risk

# Risk-based trip/POI recommendation

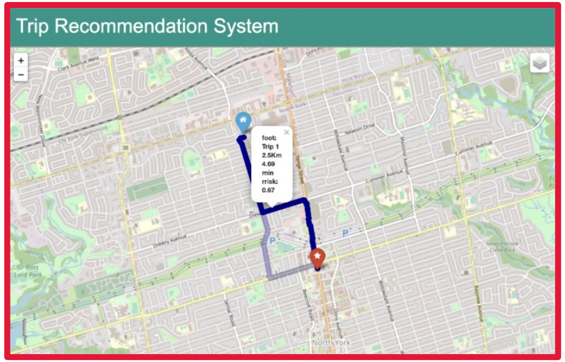

Input: Query

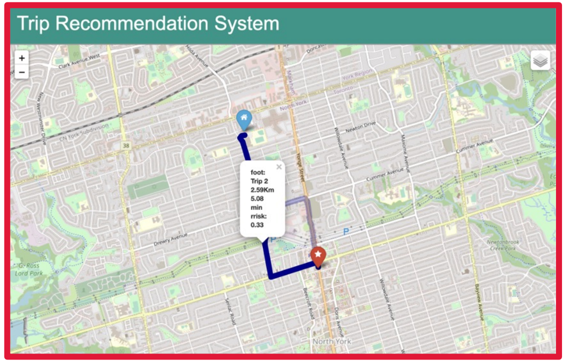
Output: Recommended Trips/POIs

# Origin-destination trip recommendation

**Input:** Query (origin, destination , time)

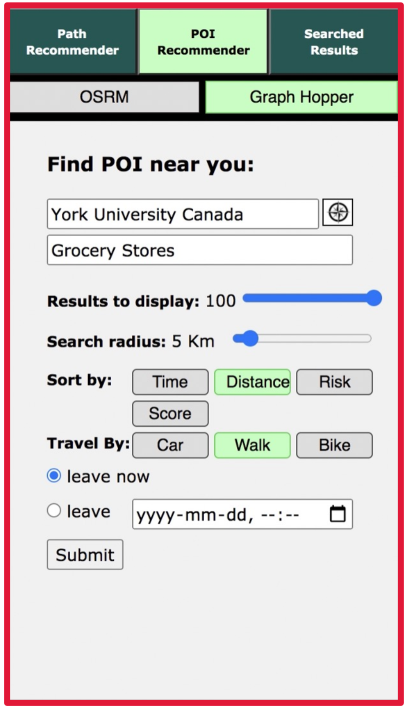

**Output:** risk-based trip recommendation



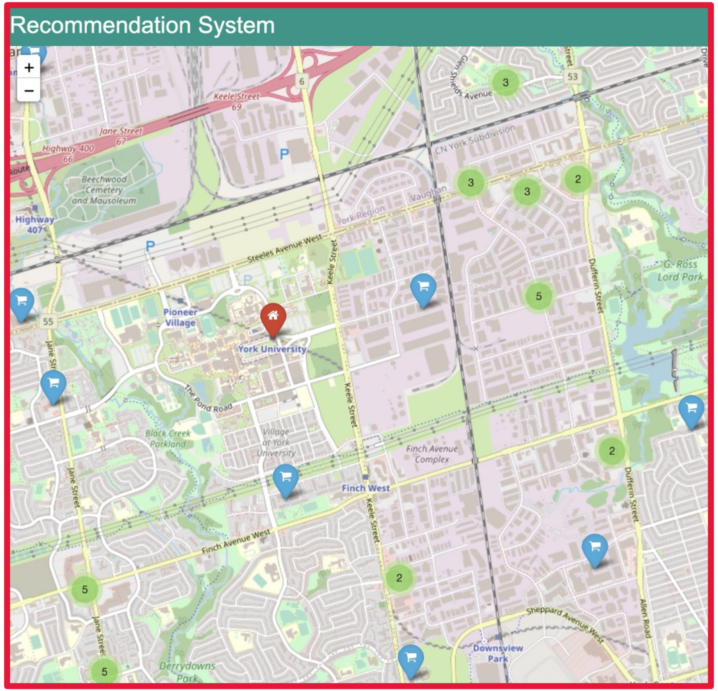



# POI recommendation example

Input: Query (POI type, radius, time)




Output: risk-based POI recommendation



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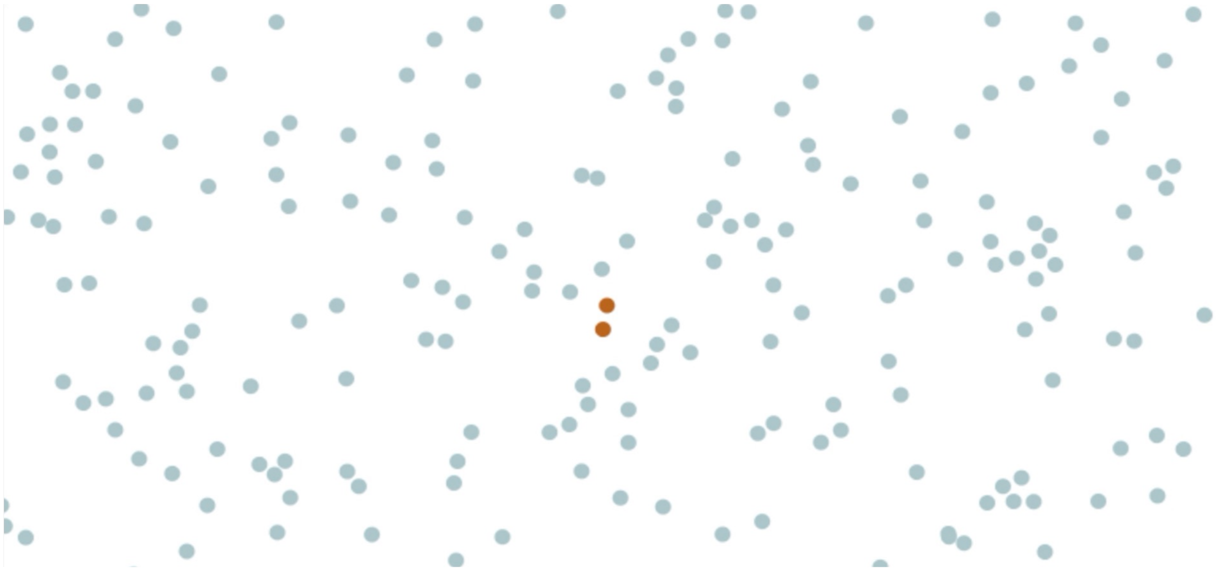
# Modeling epidemic spreading

# Infectious disease spreading

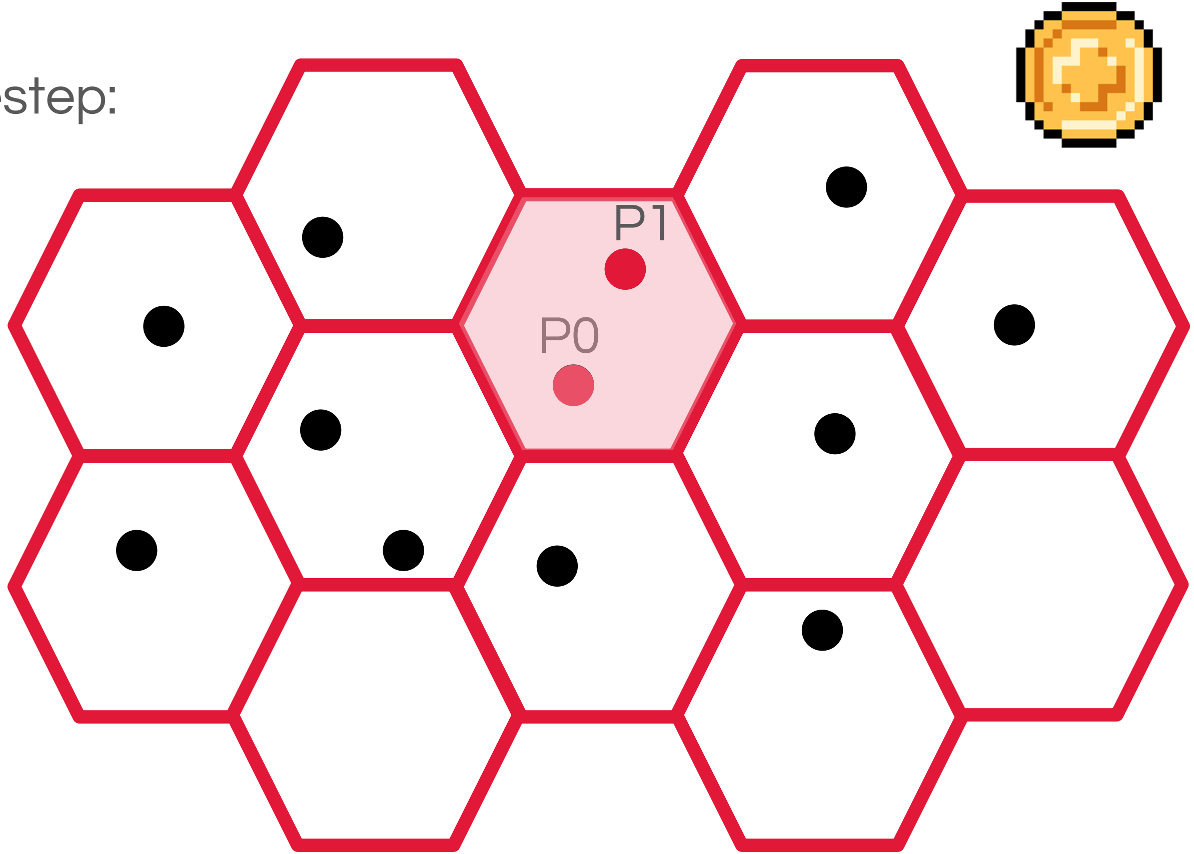


assumptions

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

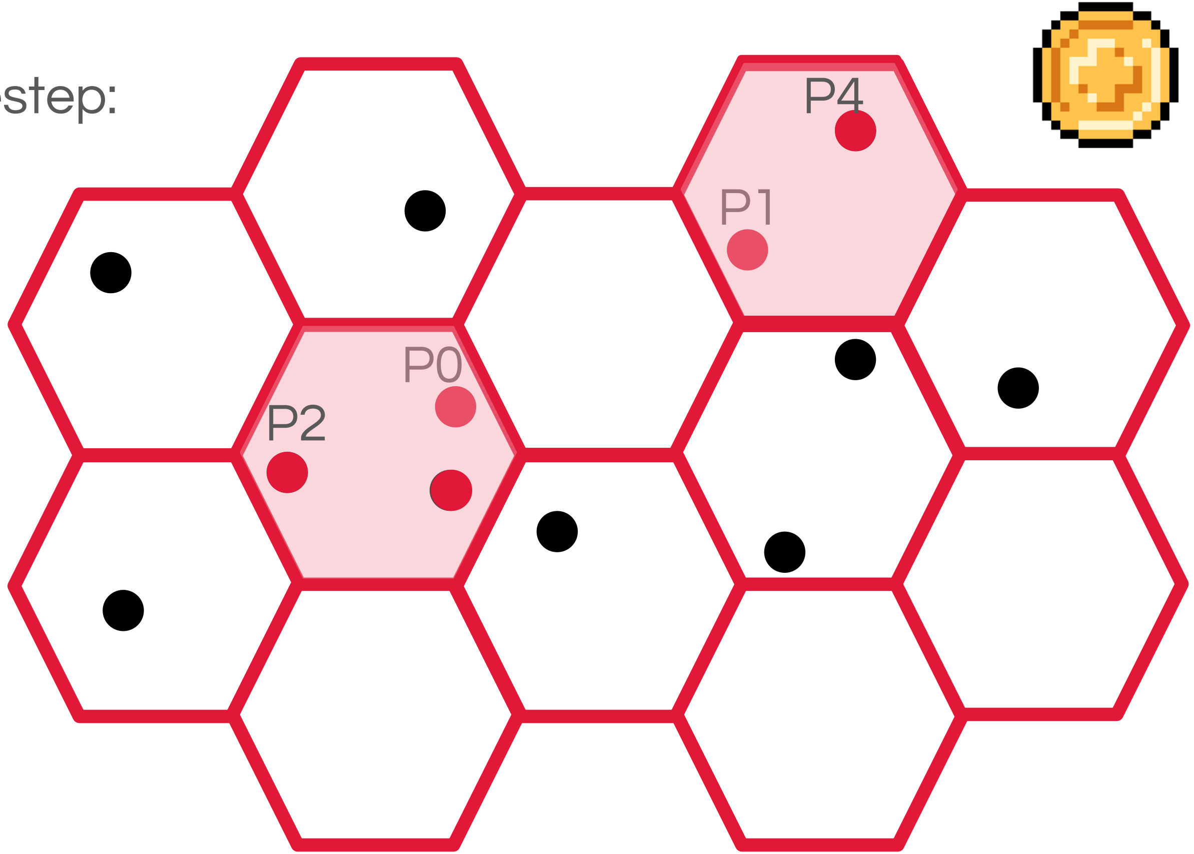
# Stochastic modeling of infectious disease spreading (1/2)

Timestep:
1



# Stochastic modeling of infectious disease spreading (2/2)

Timestep:
2



# Targeted interventions

# Targeted intervention

- Assume individuals are provided the risk of every trip they plan to make
- Cancel $\alpha$ most risky trips → less trips
- Eliminating a fraction of $\alpha_e$ overall contacts

Baseline: **Null Model**

- Eliminating the same fraction of $\alpha_e$ overall contacts
- Contacts are chosen uniformly at random

# Experimental results

# Experimental Scenarios

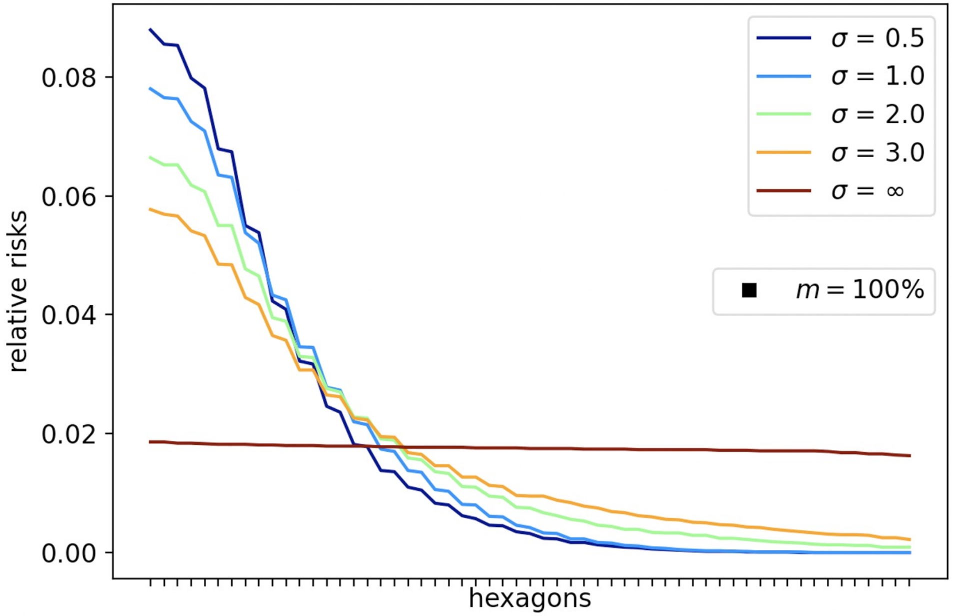
Q1 Effect of POI visitor distribution on risk

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 of blocks

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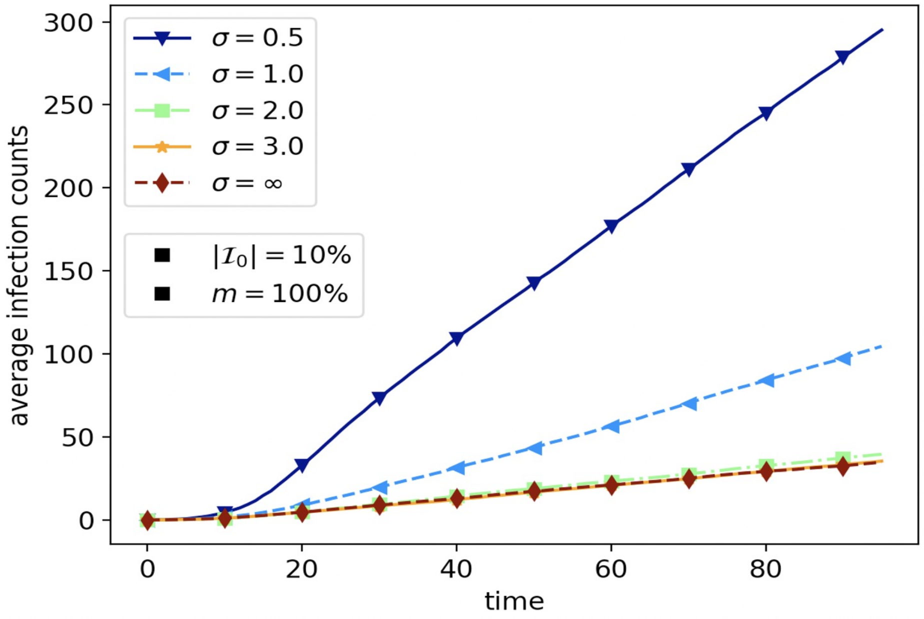
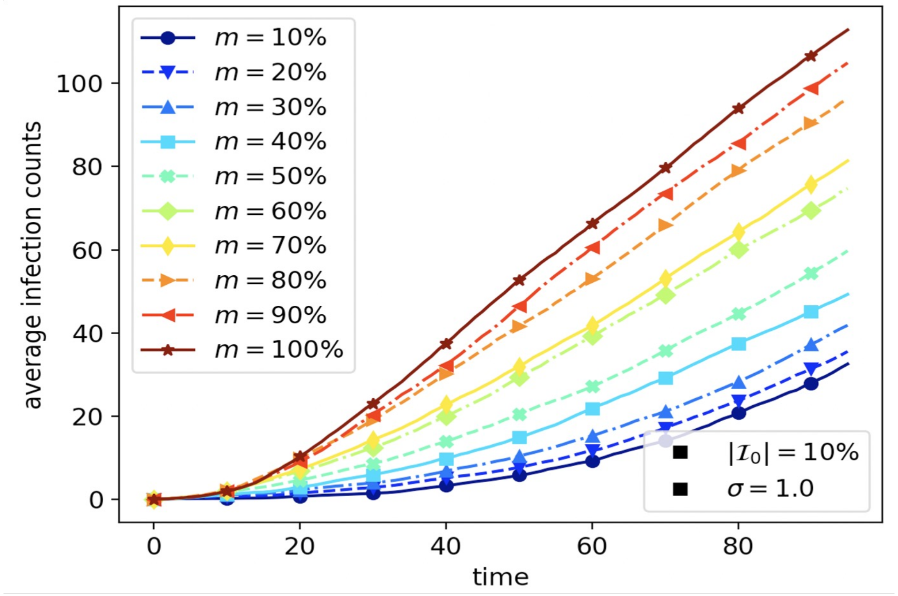
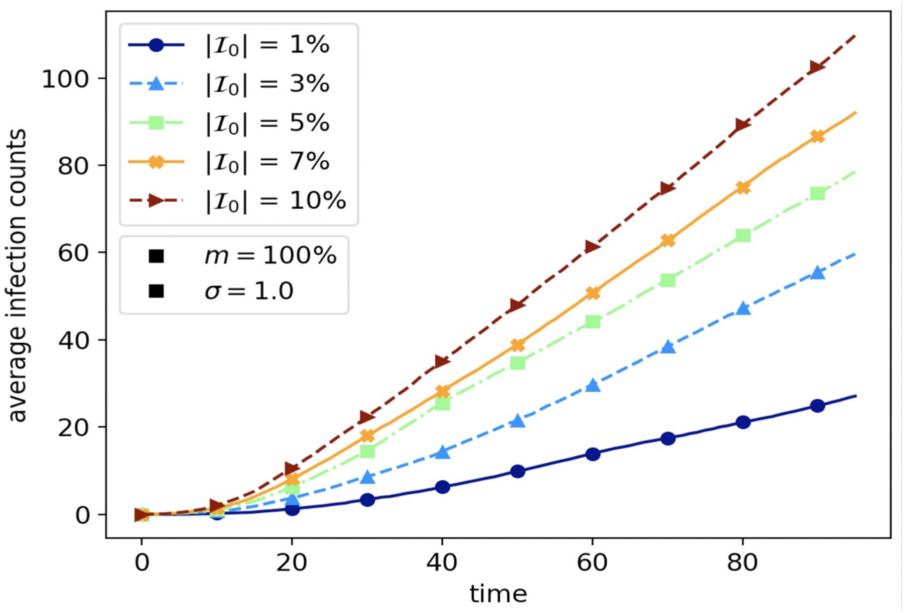
# Q2a Effect of POI visitor distribution on direct infections



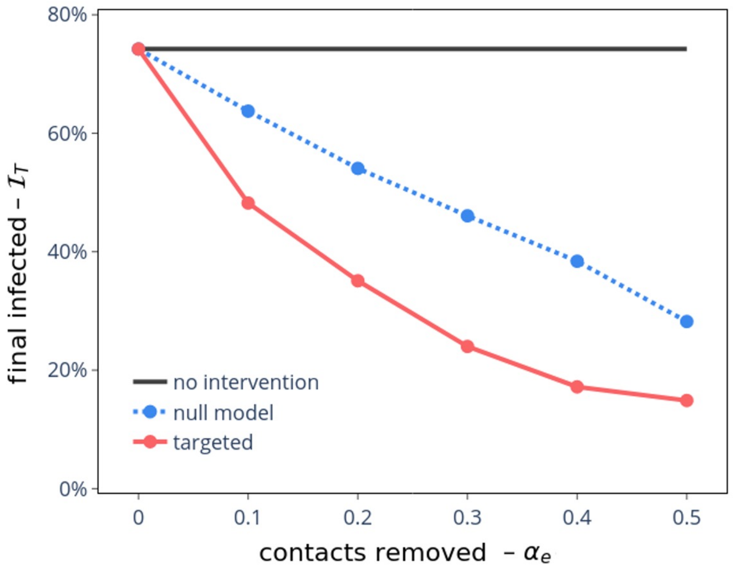
# Q2b Effect of POI maximum occupancy on direct infections



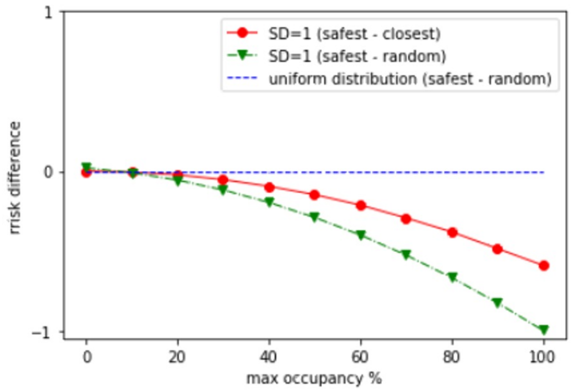
# Q2c Effect of initial infected seed size on direct infections

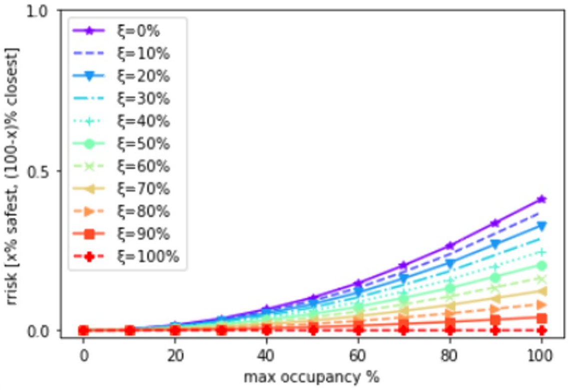


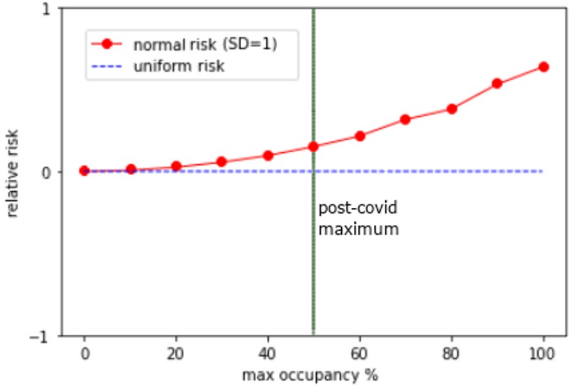
# Q3 Impact of targeted and non-targeted intervention strategies



# Q4 Impact of recommendation policy

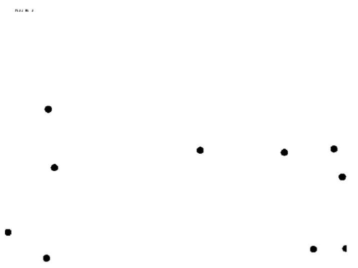


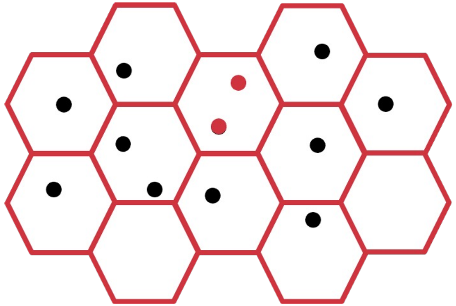



# Conclusions

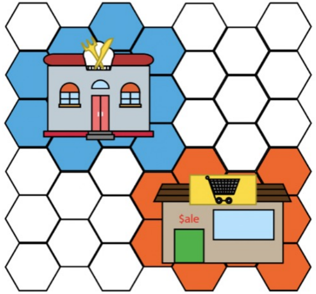
# Takeaway



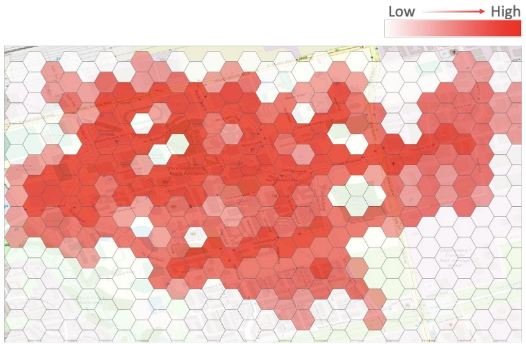
trajectories



microscopic modeling

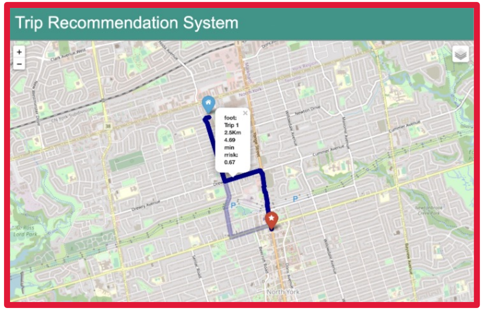


hierarchical modeling




risk maps

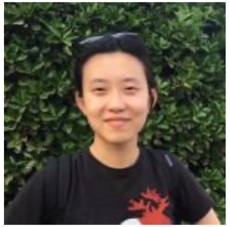
risk of trips




trip/POIs recommendations

# Credits – Epidemics Team @ the YorkU Data Mining Lab

Tilemachos Pechlivanoglou



Jing Li

Gian Alix

Jialin Sun

Nina Yanin

Farzaneh Heidari

Manos Papagelis

**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).

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# Thank you!

Questions?