Mobility-based Models of Epidemic Spreading

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Presenter: Manos Papagelis
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

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

Susceptible → Infectious → Recovered

SEIR

Susceptible → Exposed → Infectious → Recovered

\[ \xi \]
SIR model

Susceptible - $S$

Infected - $I$

Recovered - $R$

Probability of being infected - $\beta$

Probability of recovering - $\gamma$

Time $t = 0\, 1\, 2\, 3\, 4\, 5\, 6\, 7\, 8$
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
- X assumes full mixing
- X ignores heterogeneity of individuals

**compartmental**
- ✔ learning transition probabilities (as a group)
- X ignores heterogeneity of individuals

**individual-based**
- ✔ best reflection of real life
- ✔ monitor individual transition between compartments
- X 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

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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
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. **# of contacts** (node degree)
   
   $1+1+1+1 = 4$

   - ✔ intuitive
   - ❌ doesn’t consider time spent in contact

2. **Total contact time**
   
   $5+1+2+12 = 20$

   - ✔ considers contact time
   - ❌ long contacts skew result

3. **Sum of contact times in geometric function**
   
   $\beta = 0.1$
   
   $4-0.9^5-0.9^1-0.9^2-0.9^{12} \approx 1.4$

   - ✔ 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
- $\beta$: 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 the list of the $a\%$ highest risk nodes.
Intervention policy 2A (individual): avoiding high-risk contacts

For every node, rank each of their neighbors by risk.
Repeat for all nodes.
Select the a% highest-risk one and remove the common edge.
Intervention policy 2B (individual): maintaining a “social bubble”

For every node, rank each of their neighbors by common contacts (triangles in common). Remove the edges to the a% with the least common contacts.

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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

\[ r \text{risk}_u(3) \text{ more smooth} \]

\[ a \text{ 3x higher risk than } b \]
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 $\alpha$
Intervention 2A vs null model

avoiding high-risk contacts

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

Infections for varying $\alpha$
Intervention 2B vs null model

maintaining a “social bubble”

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

infections for varying $\alpha$
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
Microscopic Modeling of Spatiotemporal Epidemic Dynamics

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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
What is the risk of infection of a block?

How they compare to each other?
Block infection risk (2/2)

the risk $\text{brisk}(b, t)$ of a block $b$ at time $t$ is a function of the number of pairs of individuals in $b$ at $t$. The risk $\text{brisk}_b$ 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 $\text{risk}_u$ of an individual is a function of the risks $\text{brisk}_b$ 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

**Uniform Assumption**
\[
risk_{\text{POI}} = risk(\bigcirc) + risk(\bigcirc) + risk(\bigcirc) + risk(\bigcirc)
\]

**Dispersed (Normal) Assumption**
\[
risk_{\text{POI}} = risk(\bigcirc) + risk(\bigcirc) + risk(\bigcirc) + risk(\bigcirc)
\]
Pedestrian trip risk of infection
Blocks and trips
Pedestrian trip risk of infection (1/3)

What’s the infection risk associated with this trip?
Pedestrian trip risk of infection (2/3)
Pedestrian trip risk of infection (3/3)

\[
\text{risk of trip at time } n = \text{risk( ) } \oplus \text{risk( ) } \oplus \text{risk( ) } \oplus \cdots \oplus \text{risk( ) }
\]
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
Modeling epidemic spreading
Infectious disease spreading

assumptions

• **SI classification**: 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

Diagram showing spread of disease with nodes labeled P0, P1, P2, and P4.
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
Q2 Effect of POI visitor distribution, occupancy and initial infected seed size on direct infections

![Graph showing the effect of POI visitor distribution, occupancy and initial infected seed size on direct infections.](image)
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


Thank you!

Questions?