HYPERGRAPHS: THEORY, APPLICATIONS AND CHALLENGES
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A Design-Methodology for Epidemic Dynamics via Time-Varying Hypergraphs

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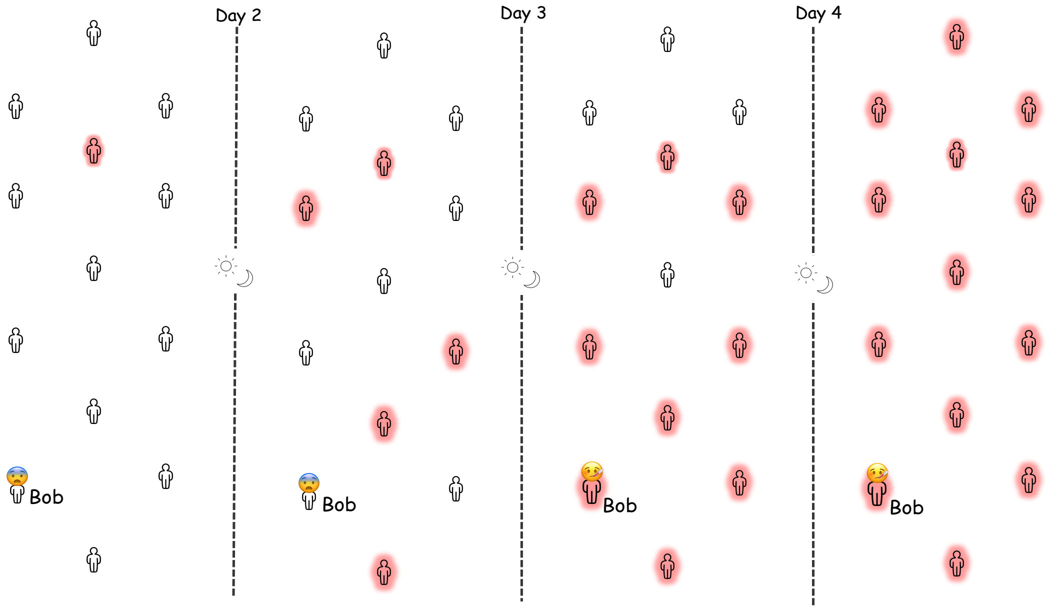
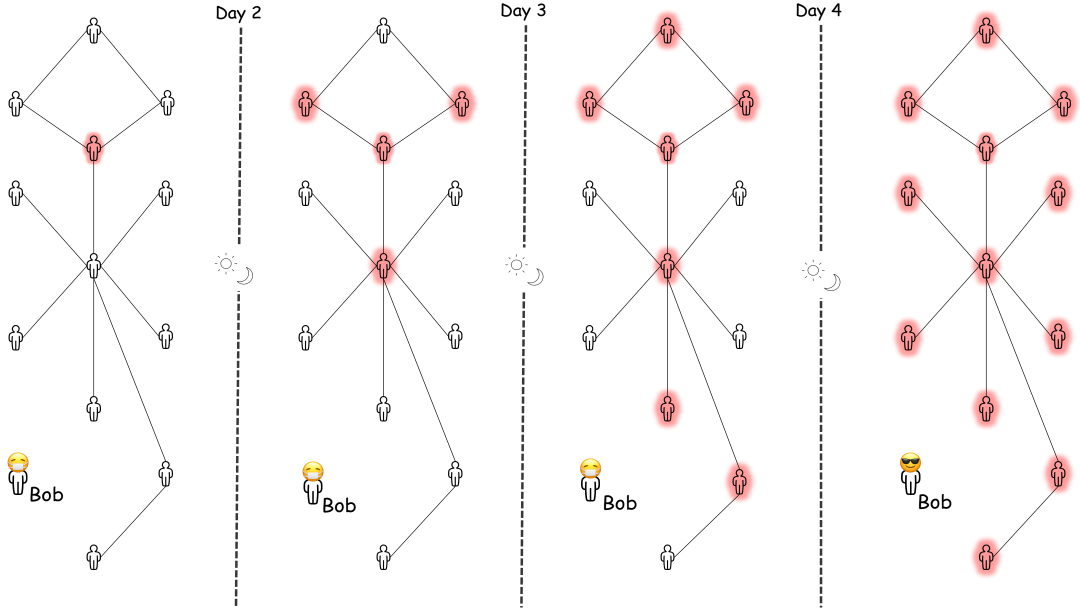
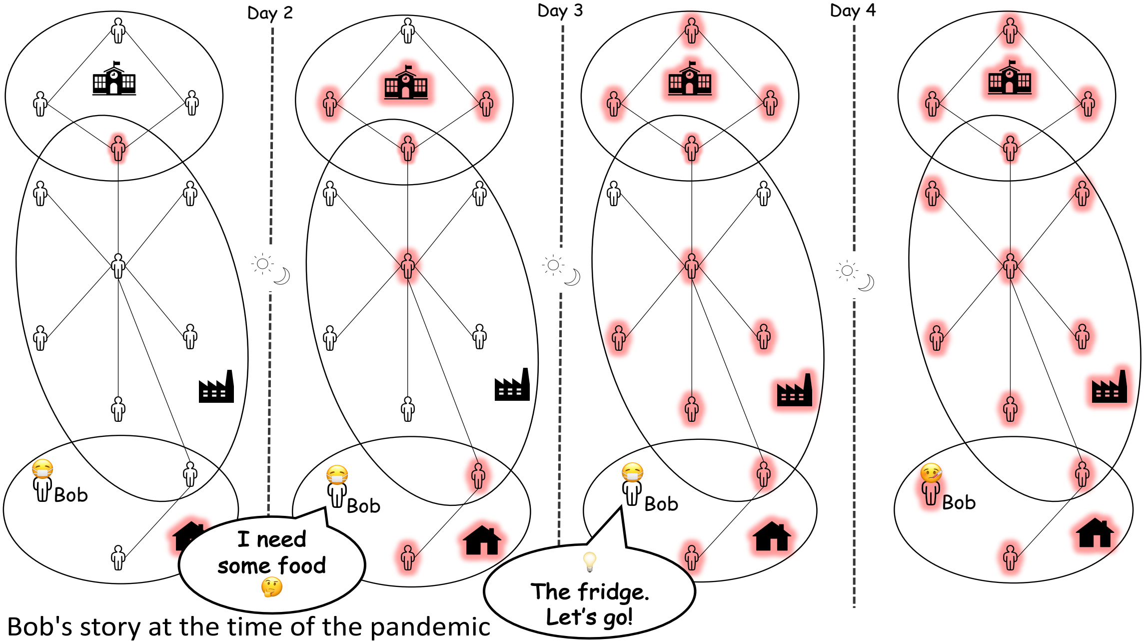


Bob's story at the time of the pandemic



Bob's story at the time of the pandemic



Bob's story at the time of the pandemic

The potion pot of epidemic modeling

- Mathematical modeling
  - Compartmental models (SIS, SIR, . . .)
- Human mobility patterns
- Human behavior
- Contagious patterns
- Pathogen properties
  - Contagiousness
  - Length of infectious period
  - Ability to persist on surfaces and environments
  - Severity

The ingredients of our ‘potion’

- Agent-based modeling
- Contagious pathways
  - Human-to-human
  - Human-to-environment
  - Environment-to-human
- Epidemic models on time-varying networks

The ideas behind our contribution

We propose an innovative modeling approach to study and analyze the **propagation** of an epidemic over a set of autonomous **individuals** (agents) modeling the contagious patterns using **many-to-many** relationships by exploiting **hypergraphs**.

Outline

1. Epidemic Dynamics via Time-Varying Hypergraphs
2. Experiments and Results
3. Evaluating Non-Pharmaceutical Interventions (ongoing research..)
4. Conclusion

Exploiting hypergraphs in epidemiological analysis

In 2016, Bodó et al. highlighted two *key* properties of a real model of an epidemic outbreak.

- *Community structure built-up from smaller units.* This idea is translated into practice using different contagion probabilities according to the place.
- *Infection pressure.* The probability that a susceptible individual becomes infected in a unit is not proportional to the number of infected individuals.

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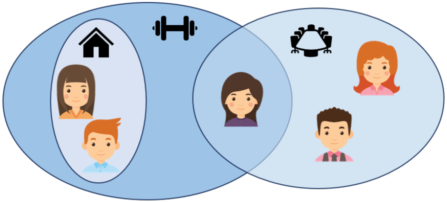
Time-Varying Hypergraphs (TVHs)

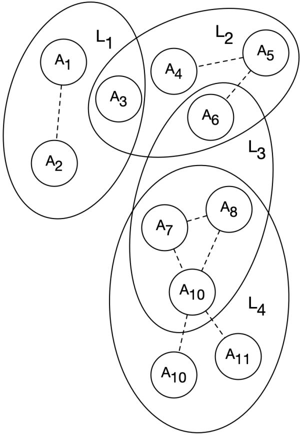


A TVH for an **epidemic diffusion** is a hypergraph $\mathcal{H} = (V, E, \mathcal{T}, \rho)$, where

- V is the set of n vertices (*people*);
- E is the set of m hyperedges (*locations*);
- $\mathcal{T}$ is the lifetime of the system;
- $\rho : V \times E \times \mathcal{T} \rightarrow \{0, ct_{v,\ell}\}$ is a function mapping whether a given vertex v has visited the location e in a given time span t. The value $ct_{v,\ell}$ is the last check-in time of v in ℓ.

Building a TVH and epidemic model parameters

- A **check-in** specifies when an individual has visited a location.
  - Φ: time-span of the data sampling.
- **Indirect contacts** (oval shapes): touching furniture, eating contaminated food, airborne.
  - Δ: time interval within which an *indirect contact* may occur.
- **Direct interactions** (dotted lines): sneezing, whispering, shaking hands.
  - δ: time interval within which an *direct contact* may occur.



Time interval *i*		
Agent	Location	Time
A_1	L_1	08:00:00
A_2	L_1	08:00:49
A_3	L_1	08:30:00
A_3	L_2	09:00:00
A_4	L_2	09:30:00
A_5	L_2	09:30:40
A_6	L_2	09:30:45
A_6	L_3	10:00:00
A_7	L_3	09:00:00
A_8	L_3	09:00:10
A_9	L_3	09:00:15
A_7	L_4	09:30:00
A_8	L_4	09:40:00
A_9	L_4	10:00:00
A_{10}	L_4	10:00:10
A_{11}	L_4	10:00:20

Our design methodology

Suppose we want to analyze the spreading of an epidemic over a population of agents through a compartmental model, such as SIS.

1. Given a set of check-ins, build a TVH from it.
2. Define model parameters regulating the contagion:
   - the probabilities of a *direct* and an *indirect* contagion;
   - the probabilities of a spontaneous recovery;
   - the infection pressure of indirect propagation.
3. For each time interval in $|\mathcal{T}|$, simulate the epidemic spreading over a population of agents according to a **diffusion algorithm**.

Our design methodology

- Γ_t and N_t define the neighborhood functions of an agent $a \in V$ in a given simulation time t. Specifically,

  $$\Gamma_t(a) = \{\ell \in E : \omega(a, \ell, t) = 1\}$$

  is the set of locations visited by a during the interval t.
- $\mathrm{N}_t(a)$ is the set of neighbors of a during the simulation time t, which corresponds to the agents that visited at least one of the locations visited by a. Formally,

  $$\mathrm{N}_t(a) = \bigcup_{\ell \in \Gamma_t(a)} V_t(\ell),$$

  where $V_t(\ell)$ denotes the set of agents that visited the location ℓ during the interval t.

Our design methodology

- $\Upsilon(a, \ell)$ is a time function which provides the last check-in time of the agent a in the venue ℓ. In other words, it returns the weight of a in ℓ in the hypergraph $\mathcal{H}$.
- $\mathrm{T}_t(a)$ and $\mathrm{T}_t(\ell)$ denote the infection state of an agent or a location at a given time t, respectively.
- $\mathrm{X}_t(a, b)$ is a direct contact function. Given two agents a and b, it returns 1 if they have a direct contact in the time span t, 0 otherwise. Formally,

$$\mathrm{X}_t(a, b) = \begin{cases} 1, & \text{if} \quad \exists \ell \in \Gamma_t(a) \cap \Gamma_t(b) \text{ AND } |\Upsilon(a, \ell) - \Upsilon(b, \ell)| < \delta \\ 0, & \text{otherwise.} \end{cases}$$

Our diffusion algorithm on TVHs

Each iteration of the diffusion algorithm consists of three contagion phases:

1. *Agent-to-Environment* $\rightarrow$ Infection of environment by agents;
    - Evaluated on the number of infected agents that have visited a non-contaminated location.
2. *Agent-to-Agent* $\rightarrow$ Direct propagation to agents;
    - Evaluated on number of infected neighbors for each non-infected agent.
3. *Environment-to-Agent* $\rightarrow$ Indirect propagation to agents;
    - Evaluated on number of infected locations visited for each non-infected agent.

(1) *Agent-to-Environment*

For all non contaminated locations, (i.e., $\ell \in E : T(\ell) = 0$), we compute the number of infected agents that have visited that location:

$$I^e(\ell) = \sum_{a \in V(\ell)} \mathrm{T}(a).$$

This value is then used to update the contagiousness level of ℓ as expressed by the following:

$$\mathrm{T}(\ell) = \begin{cases} 1, & \text{infected according to the value } f^e(I^e(\ell)) \\ 0, & \text{not infected,} \end{cases}$$

where $f^e()$ is a non-linear function:

$$f^e(x) = \begin{cases} x, & \text{if } \; 0 \leq x \leq c \\ c, & \text{if } \; x > c, \end{cases}$$

where c is a constant value given as parameter.

(2) *Agent-to-Agent*

For all non infected agents (i.e., $a \in V : T(a) = 0$), the total number of infected neighbors is computed. Formally,

$$I^d(a) = \sum_{b \in \mathrm{N}(a)} \mathrm{T}(b)\mathrm{X}(a, b).$$

This value is then used to update the infection state of a, as

$$\mathrm{T}(a) = \begin{cases} 1, & \text{infected according to the value } I^d(a) \\ 0, & \text{not infected.} \end{cases}$$

(3) *Environment-to-Agent.*

For all non infected agents, (i.e., $a \in V : T(a) = 0$), we compute the number of infected locations visited. Formally,

$$I^i(a) = \sum_{\ell \in \Gamma(a)} \mathrm{T}(\ell).$$

This value is then used to update the infection state of a, as

$$\mathrm{T}(a) = \begin{cases} 1, & \text{infected according to the value } I^i(a) \\ 0, & \text{not infected.} \end{cases}$$

Diffusion Algorithm Parameters

Parameter	Description
β_d	Probability that an agent a_i is infected by another agent a_j via a direct-contact in *Agent-to-Agent*
β_i	Probability that an agent a is infected via an indirect-contact due to a location ℓ in *Environment-to-Agent*
β_e	Probability that a location ℓ is infected by an agent in *Agent-to-Environment*
γ_a	Probability that an agent a spontaneously recovers
γ_e	Probability that a location ℓ is sanitized
c	Number of contact in *Agent-to-Environment*

Diffusion Algorithm

r ▷ a random number generator $\in [0, 1]$.

for $t \in \mathcal{T}$ **do**

  $\mathcal{H} \leftarrow \xi(t)$

  for $\ell \in E$ **do** ▷ Agent-to-Environment.

    if $\mathrm{T}_t(\ell) == 0$ **then**

      if $r_{next} < 1 - e^{-\beta_e f^e(I^e(\ell))}$ **then**

        $\mathrm{T}_{t+1}(\ell) = 1$

    else if $r_{next} < 1 - e^{-\gamma_e}$ **then**

      $\mathrm{T}_{t+1}(\ell) = 0$

  for $a \in V$ **do** ▷ Agent-to-Agent.

    if $\mathrm{T}_t(a) == 0$ **then**

      if $r_{next} < 1 - e^{-\beta_d I^d(\ell)}$ **then**

        $\mathrm{T}_{t+1}(a) = 1$

  for $a \in V$ **do** ▷ Environment-to-Agent.

    if $\mathrm{T}_t(a) == 0$ **then**

      if $r_{next} < 1 - e^{-\beta_i I^i(\ell)}$ **then**

        $\mathrm{T}_{t+1}(a) = 1$

    else if $r_{next} < 1 - e^{-\gamma_a}$ **then**

      $\mathrm{T}_{t+1}(a) = 0$

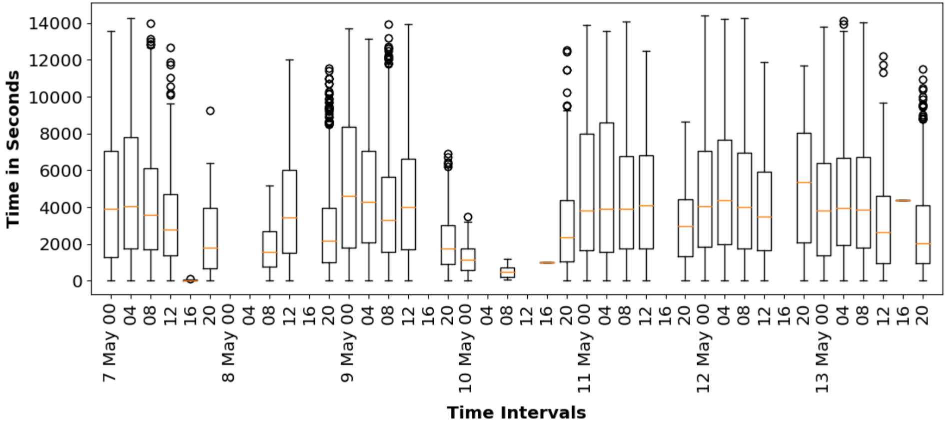
Outline

The Foursquare Data set

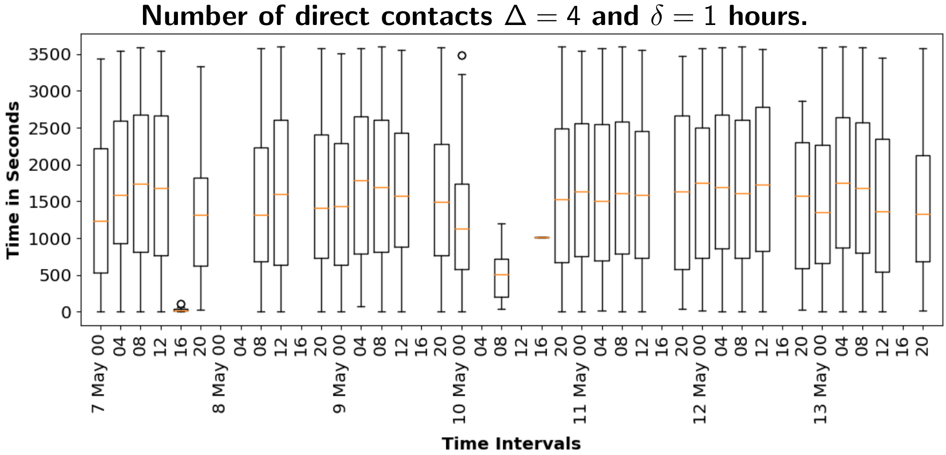
- Foursquare social network data [YANG2015+].
- Tokyo, from 12 April 2012 to 16 February 2013.
- $573,703$ check-ins, $2,293$ users, $61,858$ locations.
- Most crowded month: May, 2012.

The Foursquare Data set

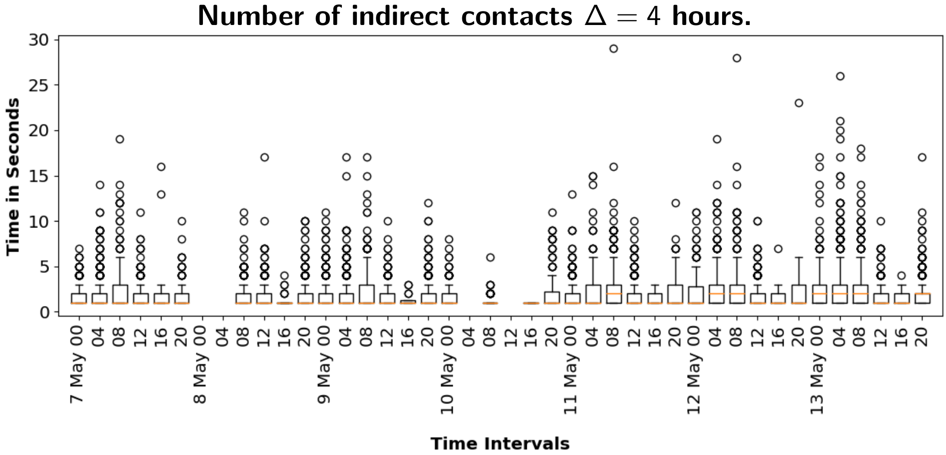
Time difference distribution of check-ins within the same place in 7 days and $\Delta = 4$ hours.



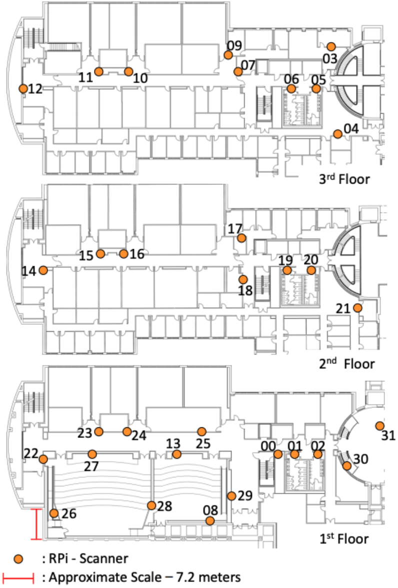
The Foursquare Data set



The Foursquare Data set

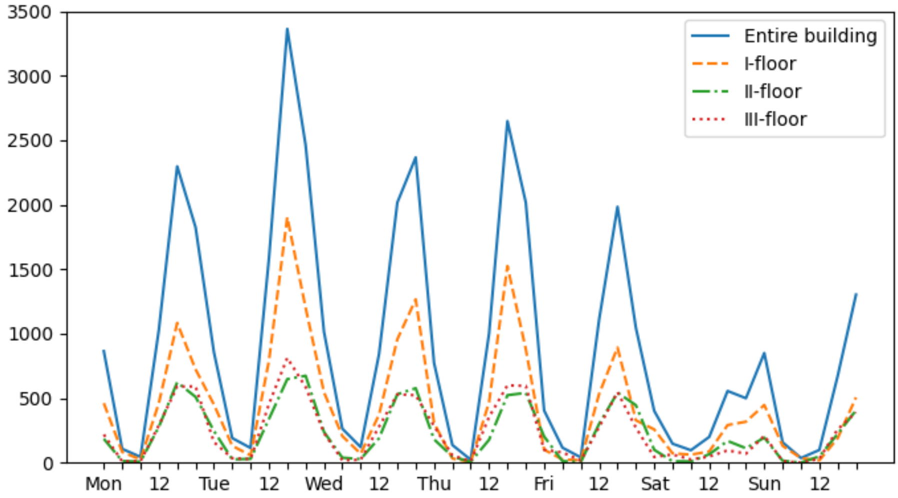


The BLEBeacon Data set

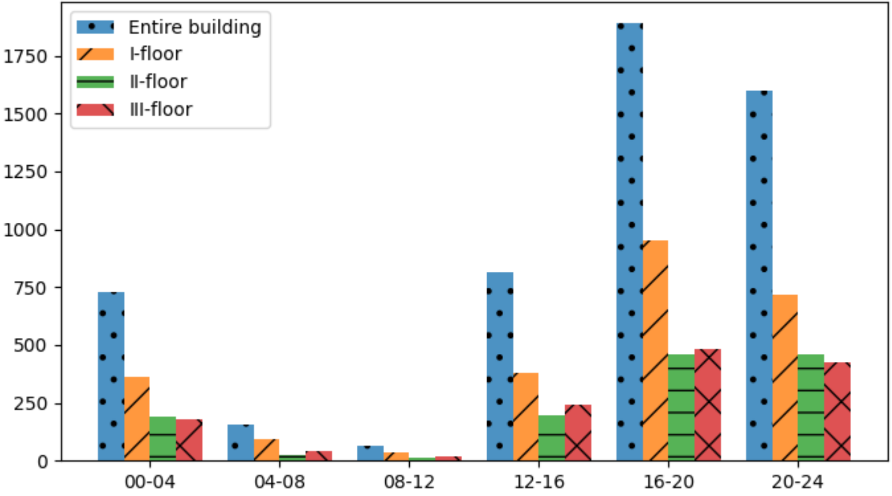


- BLEBeacon data [Sikeridis2018+].
- A collection of Bluetooth Low Energy (BLE) advertisement packets/traces generated from BLE beacons carried by people following their daily routine inside a university building.
- From 15 September 2016 to 17 October 2016.
- 46 users, 32 locations.

The BLEBeacon Data set: Weekly check-ins



The BLEBeacon Data set: Daily check-ins



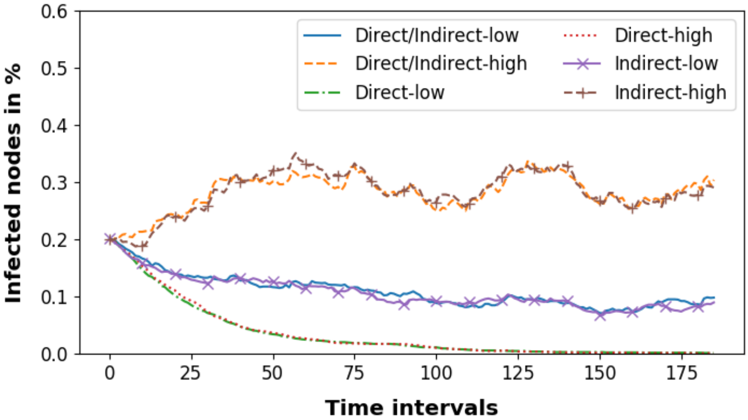
Experiments

- We experimented the SIS model on the contact-network built upon the Foursquare and BLEBeacon data sets.
- Experimental scenarios:
  1. **Direct** *vs* **Indirect**, testing the model expressiveness in distinguishing direct and indirect contagion pathways.
  2. **Time proprieties of contacts**, effect of time varying intervals length when direct or indirect contacts happen.

Direct vs Indirect Contagions Settings: Foursquare

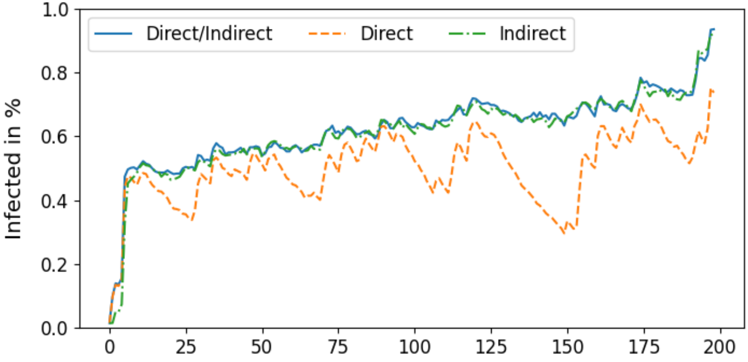
- **Goal**. Testing the model expressiveness in distinguishing direct and indirect contagion pathways;
- $\Delta = 4$ hours, $\delta = 1$ minutes;
- 80% of the agents *susceptible*, the remaining 20% to *infected*;
- Two parameters configurations has been investigated:
  - *Low*: $\beta_d = 0.2$, $\beta_i = 0.1$, $\beta_e = 0.06$, $\gamma_e = 0.06$, $\gamma_a = 0.1$, and $c = 5$;
  - *High*: $\beta_d = 0.8$, $\beta_i = 0.4$, $\beta_e = 0.26$, $\gamma_e = 0.06$, $\gamma_a = 0.1$, and $c = 5$
  - Fixed β_d
    - $\beta_i = \frac{\beta_d}{2}$;
    - $\beta_e = \frac{\beta_d}{4}$.

Direct vs Indirect Contagions: Foursquare



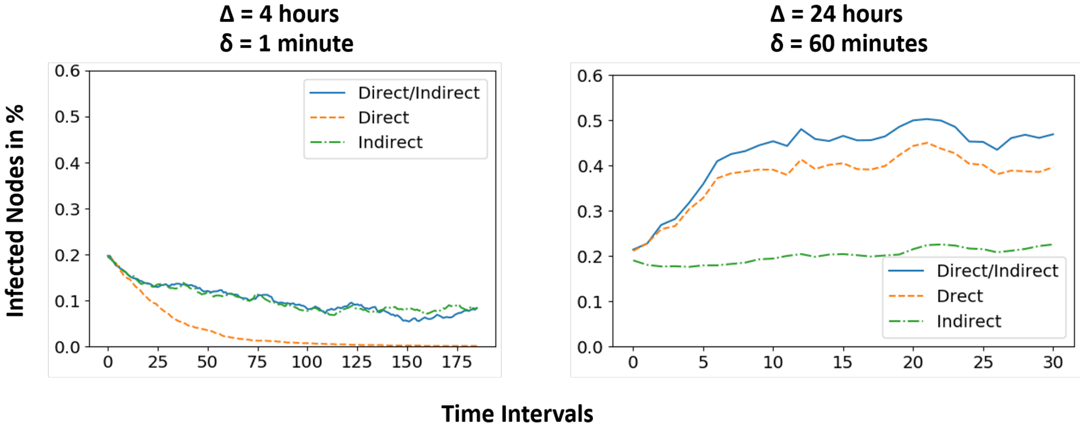
Indirect contacts are crucial in spreading the epidemic.
They should be investigated when studying epidemic diffusion processes.

Direct vs Indirect Contagions: BLEBeacon



- 1 randomly infected at time $t = 0$.
- $\beta_d = 0.56$, $\beta_i = 0.29$, $\beta_e = 0.29$, $\gamma_e = 0.017$, $\gamma_a = 0.034$, and $c = 5$.

Contacts time analysis: Foursquare



First and last of the 16 configurations in the paper.

Changing the direct and indirect contagious contact-time dramatically shift the epidemic spreading pathways.

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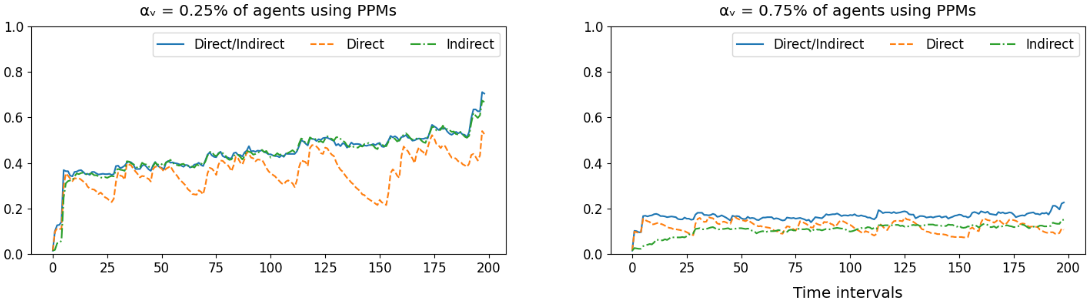
Non-Pharmaceutical Interventions (ongoing research..)

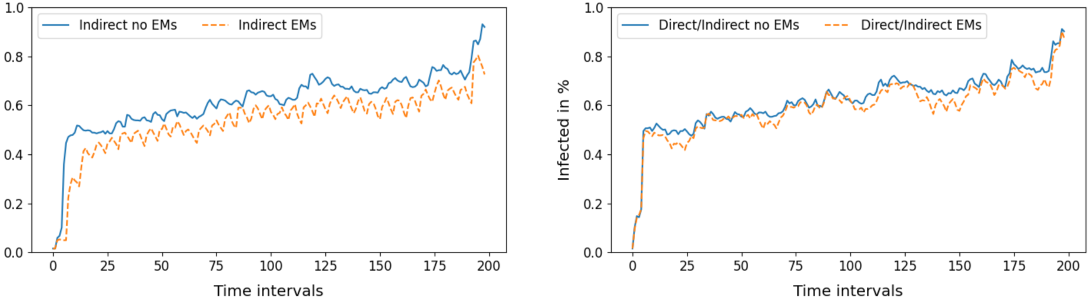
- *WHO World Health Organization. 2019. Non-pharmaceutical public health measures for mitigating the risk and impact of epidemic and pandemic influenza.*
  1. Personal protective measures (PPMs).
  2. Environmental measures (EMs).
  3. Social distancing measures (SDMs):
     - Isolation;
     - Quarantine;
     - Avoiding crowding;
     - Contact Tracing.
- Experiments on NPIs

NPIs - PPMs



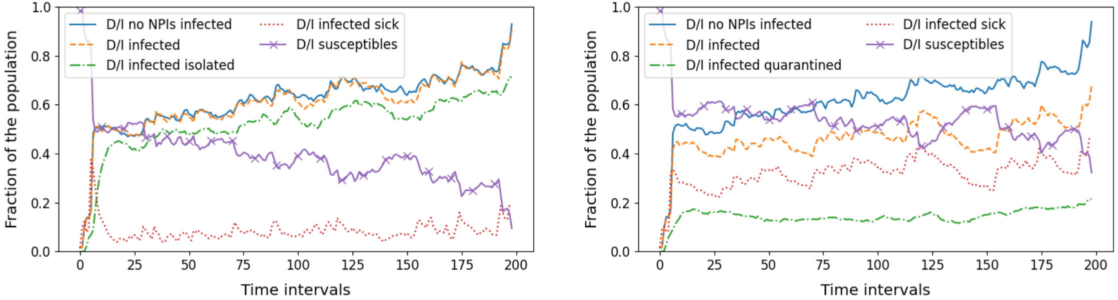
- The transmission probabilities for both direct/indirect are reduced.
- Varying the $\alpha\%$ of agents that adopt the PPM.

NPIs - EMs



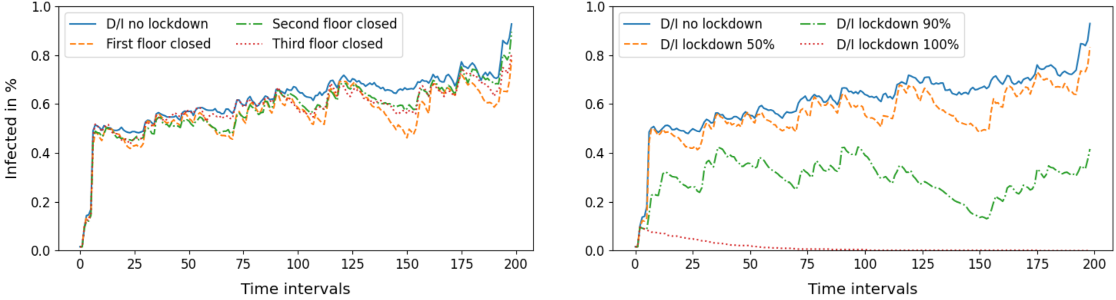
- Each location is cleaned (the infection is removed) at the end of the most crowded intervals: 12:00-16:00 — 16:00-20:00 — 20:00-24:00.

NPIs - SDMs: Isolation and quarantine



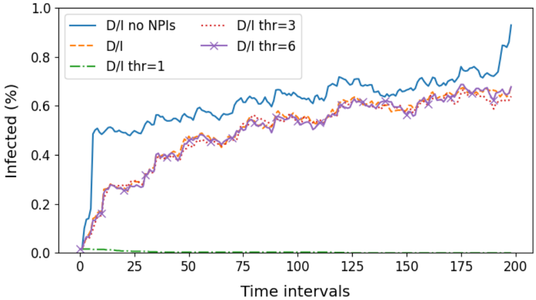
- **Isolation** (left): at the beginning of each step, an agents put itself in isolation with a probability $\beta_{isolation}$, proportional to the number of the infected meets, if it is infected.
- **Quarantine** (right): at the beginning of each step, an agent put itself in quarantine with probabilities $\beta_{q-direct}$, proportional to the number of the infected meets, and $\beta_{i-direct}$, proportional to the number of the infected location visited.

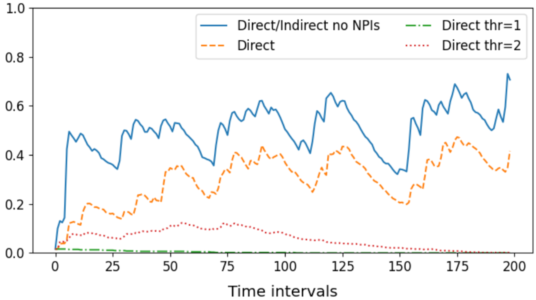
NPIs - SDMs: Location closure (lockdown)



- **By type** (left): all location of a certain type is closed.
- **Most crowded** (right): a % of the most crowded location is closed.

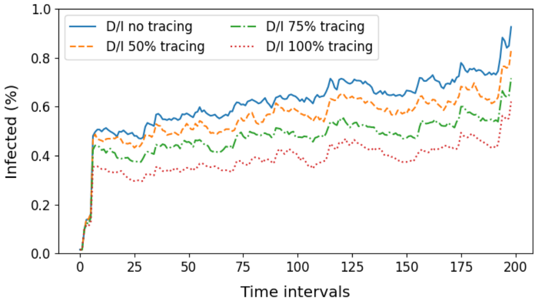
NPIs - SDMs: Avoiding crowding

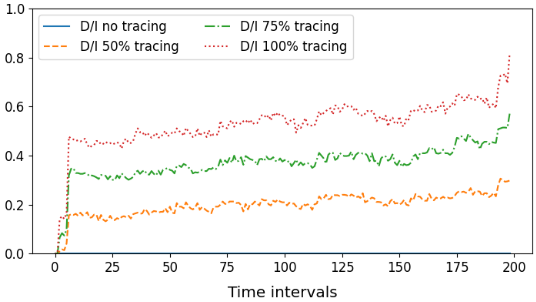




- For each day the building capacity is reduced of 50%.
- **Special Number (thr)**: only a limited number of agents $(1 - 3 - 6)$ are allowed to stay in a location together.

NPIs - SDMs: Contact tracing





- **Quarantine approach**: at the beginning of each step, an agent put itself in quarantine with probability $\beta_{tracing}$, proportional to the number of the infected reported by a tracing application.
- Only a α% of the agents use the tracing application.
- Percentage of quarantined individuals on the right.

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Conclusion

- We formally defined the **Time Varying Hypergraphs** for modeling contact-networks.
- We provided a design-methodology for **enhancing the accuracy** in epidemiological study combining:
  - Agent-based Modeling and Hypergraphs.
- We showed how hypergraphs allow us to **distinguish** different contagious pathways among the contact-network: *direct* and *indirect*.
- We experimented the SIS model on Foursquare users-mobility data, revealing:

1. the **importance of indirect** propagation in epidemic contact-network;
2. the **consequence of modeling contact-time** in epidemic simulation for both direct and indirect contacts.

What's next

- Study epidemic control strategies (NPIs, ongoing research).
- Analyze immunization and quarantine techniques on agents or environment:
  - by developing dedicated immunization strategies for hypergraphs.
- Testing our methodology on other classical epidemic models.
- Experiments on more real-world datasets.
  - Unfortunately, now we should find data about human mobility patterns during the *COVID-19* pandemic, generated by pandemic control applications already adopted in many countries.

Time for questions

Thank You

For Your Attention!

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