Interdisciplinary Behavioral Model (IBM) for Controlling Infectious Diseases

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Motivation

Challenges

- Lockdown across the world due to SARS-CoV-2 manifest the need of **robust** and **dynamic** models, to guide decision making.
- Accounting for **individual behaviour** through an epidemic outbreak by using **large scale models**.
- Capturing **spread of the disease** through **individuals daily activities**.
- **Assess the impact** that a certain policy has on **different segments of the population**.
- Difficulty of finding **disaggregated data** to **validate** the model.

Research gaps

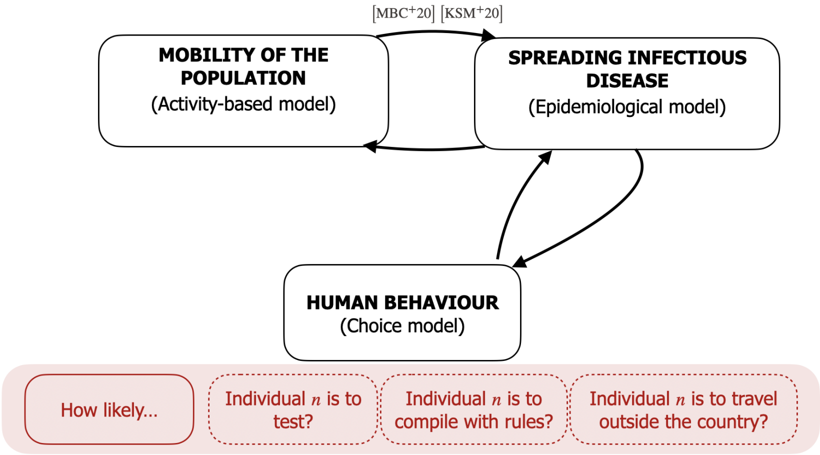
Limitations

- Lack of disaggregated data leads to adding aggregated parameters inside the agent-based models, [TYK+20].
- Agent-based models in order to define more **targeted** and less disruptive **interventions**, [SACB20].
- A methodology to know which variables and **latent states** are meaningful inside an epidemiological model to explain **human behavior**, [CPK+21].
- Make the **latent states** that define the spreading **socio-economic dependent**, since the impact of COVID-19 on **travel behavior** is **different** in the various **segments of the population**, [MBCV20, XLH+23].

Outline of this talk

1. Added value of using disaggregate models for modelling SARS-CoV-2 spreading.
2. Description of the preliminary considerations and presentation of a model that allows modeling human behavior for controlling infectious diseases.
3. Potential of these models to study SARS-CoV-2 policy decision making.

IBM: Cycle to understand the spreading



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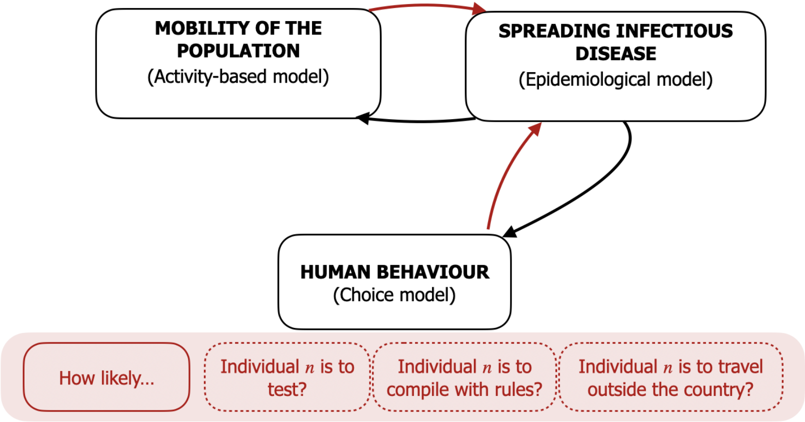
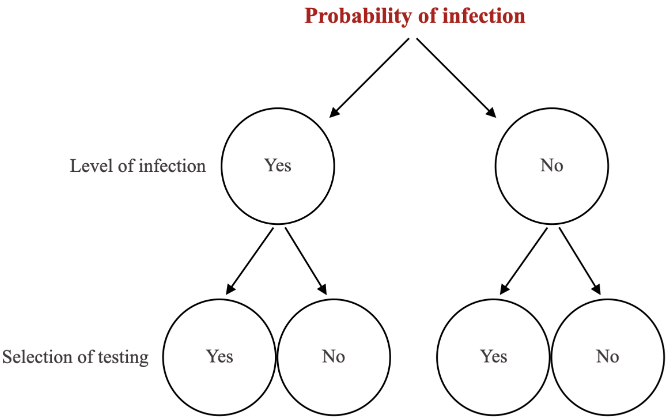


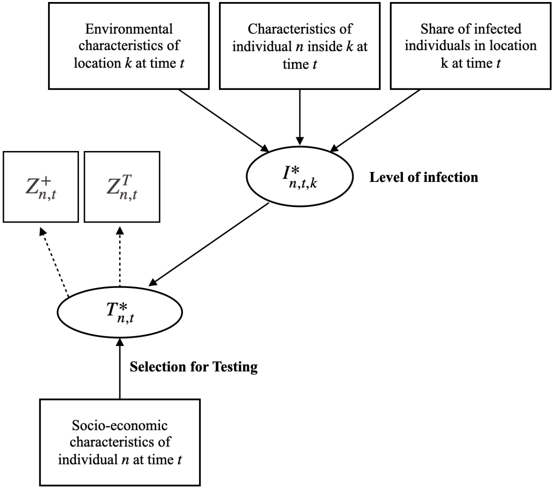
Interdisciplinary Behavioral Model (IBM)



First IBM iteration: we include two latent states

- Level of infection
- Selection for testing

Interdisciplinary Behavioral Model (IBM)



Added value

- Level of infection depends on the socio-economic characteristics, activities performed, and environmental conditions.
- Selection for testing is modeled. We do not have real data on the infections but on positive tests!

Level of infection

$$I^*_{n,t} = \beta_{\text{inf}} \frac{\text{infectious agents in } f(t)}{\text{total number of agents in } f(t)} + \boldsymbol{\beta}^{\text{soceco}} \boldsymbol{X}^{\text{soceco}}_{\boldsymbol{n}} + \boldsymbol{\beta}^{\text{health}} \boldsymbol{X}^{\text{health}}_{\boldsymbol{n}} + \boldsymbol{\beta}^{\text{tran}} \boldsymbol{X}^{\text{tran}}_{\boldsymbol{n,t}} + \boldsymbol{\beta}^{\text{act}} \boldsymbol{X}^{\text{act}}_{\boldsymbol{n,t}} + \varepsilon^{I^*}_{n,t}.$$

where:

- $\boldsymbol{\beta}^{\text{soceco}}, \boldsymbol{\beta}^{\text{health}}, \boldsymbol{\beta}^{\text{tran}}, \boldsymbol{\beta}^{\text{act}}$ are the parameters for $\boldsymbol{X}^{\text{soceco}}_{\boldsymbol{n}}, \boldsymbol{X}^{\text{health}}_{\boldsymbol{n}}, \boldsymbol{X}^{\text{tran}}_{\boldsymbol{n,t}}, \boldsymbol{X}^{\text{act}}_{\boldsymbol{n,t}}$, respectively.

Selection for testing

$$T^*_{n,t} = \boldsymbol{\beta}^{\text{soceco}} \boldsymbol{X}^{\text{soceco}}_{\boldsymbol{n}} + \beta^{\text{acttype}} \text{acttype}_{n,t} + \gamma^{LI} I^*_{n,t} + \varepsilon^{T^*}_{n,t}$$

where:

- $\boldsymbol{\beta}^{\text{soceco}}$ and $\boldsymbol{X}^{\text{soceco}}_{\boldsymbol{n}}$ are vectors of the socio-econommic characteristics of the individual and the corresponding parameters, respectively.
- β^{acttype} and $\text{acttype}_{n,t}$ is the type of activity performed during the time step, and its parameter.
- $I^*_{n,t}$ is the level of infection of the individual, and γ^{LI} is its parameter.
- $\varepsilon^{T^*}_{n,t}$ is a random error term.

Dynamics of the model: infection process

An agent n can be in 3 different health S Susceptible, I Infected, and R Recovered.

If an agent n is in health state S,

$$P(H_{n,t+1} = I | H_{n,t} = S) = \frac{1}{1 + e^{-\mu I^{*}_{n,t}}} \tag{1}$$

$$P(H_{n,t+1} = S | H_{n,t} = S) = 1 - P(H_{n,t+1} = I | H_{n,t} = S) \tag{2}$$

We draw a random binary variable $Z^{I}_{n,t}$ with probability $P(H_{n,t+1} = I | H_{n,t})$.

If an agent n is in health state I,

- Does not depend on activity-travel behavior.
- Drawn from a log-normal distribution with a mean of 8 days and a standard deviation of

Dynamics of the model: testing process

Once the health state is updated, we run the testing model:

$$P^T_{n,t,f} = \frac{1}{1 + e^{-\mu T^*_{n,t}}} \tag{3}$$

We draw a random binary variable $Z^T_{n,t}$ with probability $P^T_{n,t,f}$.

The test outcome can be positive or negative [AYH+20]:

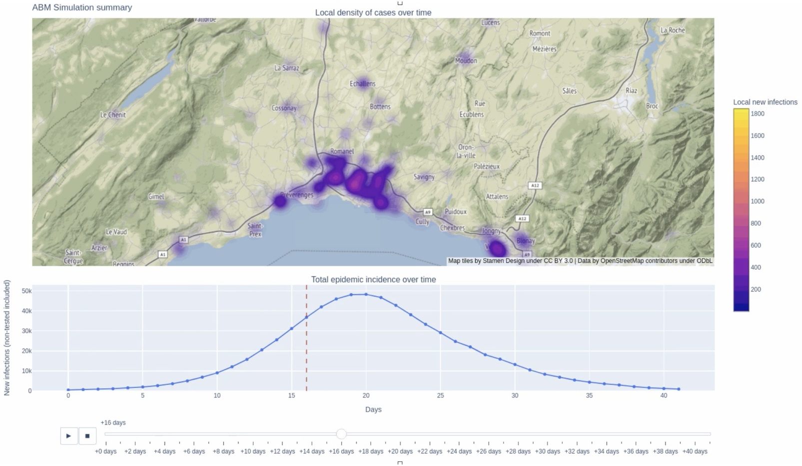
$$P(Z^+_{n,t} = 1 | Z^T_{n,t} = 1 \text{ and } H_{n,t} = I) = 0.65 \pm (0.62 - 0.68) \tag{4}$$

$$P(Z^+_{n,t} = 1 | Z^T_{n,t} = 1 \text{ and } H_{n,t} = S) = 0.17 \pm (0.10 - 0.23) \tag{5}$$

$$P(Z^+_{n,t} = 1 | Z^T_{n,t} = 1 \text{ and } H_{n,t} = R) = 0.17 \pm (0.10 - 0.23) \tag{6}$$

We simulate $Z^+_{n,t}$ as a random variable with two values: positive 1 and negative 0.

Results: validation



- We test the population of Vaud (around 2M people).
- We can see the spatial dimension of the model.
- 2.6 GHz 6-Core Intel Core i7, it takes 149.942 s for 3 months and 2M people.

Results: calibration

- We calibrate the parameters by using a Variable Neighbourhood Search algorithm: that allows for multiobjective optimization.
- We use an MSE on the shares of positive tests and another one for the positive tests.

Conclusions and future work

- **Understanding** of **human behavior** to better capture the **spread** of a disease in a **given population**.
- Most existing research focuses on an **aggregated approach** to estimate the various parameters that define the spread of an infectious disease. It is important to account for **heterogeneity**.
- **IBM** model allows for **assessing** and **targetting** better policies based on changing human behavior in different segments of the population.
- Calibrate the model and connect all the arrows in the cycle to understand the spreading.

Thank you

References I

[AYH+20] Tao Ai, Zhenlu Yang, Hongyan Hou, Chenao Zhan, Chong Chen, Wenzhi Lv, Qian Tao, Ziyong Sun, and Liming Xia. Correlation of Chest CT and RT-PCR Testing for Coronavirus Disease 2019 (COVID-19) in China: A Report of 1014 Cases. *Radiology*, 296(2):E32–E40, August 2020.

[CPK+21] Serina Chang, Emma Pierson, Pang Wei Koh, Jaline Gerardin, Beth Redbird, David Grusky, and Jure Leskovec. Mobility network models of COVID-19 explain inequities and inform reopening. *Nature*, 589(7840):82–87, January 2021.

[MBCV20] Marco Mancastroppa, Raffaella Burioni, Vittoria Colizza, and Alessandro Vezzani. Active and inactive quarantine in epidemic spreading on adaptive activity-driven networks. *Physical Review E*, 102(2):020301, August 2020.

[SACB20] Sravani Singu, Arpan Acharya, Kishore Challagundla, and Siddappa N. Byrareddy. Impact of Social Determinants of Health on the Emerging COVID-19 Pandemic in the United States. *Frontiers in Public Health*, 8:406, July 2020.

[TYK+20] Jouni T. Tuomisto, Juha Yrjola, Mikko Kolehmainen, Juhani Bonsdorff, Jami Pekkanen, and Tero Tikkanen. An agent-based epidemic model REINA for COVID-19 to identify destructive policies. preprint, Infectious Diseases (except HIV/AIDS), April 2020.

References II

[WCG+20] Roman Wölfel, Victor M. Corman, Wolfgang Guggemos, Michael Seilmaier, Sabine Zange, Marcel A. Müller, Daniela Niemeyer, Terry C. Jones, Patrick Vollmar, Camilla Rothe, Michael Hoelscher, Tobias Bleicker, Sebastian Brünink, Julia Schneider, Rosina Ehmann, Katrin Zwirglmaier, Christian Drosten, and Clemens Wendtner. Virological assessment of hospitalized patients with COVID-2019. *Nature*, 581(7809):465–469, May 2020. Number: 7809 Publisher: Nature Publishing Group.

[XLH+23] Haoning Xi, Qin Li, David A. Hensher, John D. Nelson, and Chinh Ho. Quantifying the impact of COVID-19 on travel behavior in different socio-economic segments. *Transport Policy*, 136:98–112, June 2023.