Interdisciplinary Behavioral Model (IBM) for Controlling Infectious Diseases

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Abstract

The COVID-19 pandemic has highlighted the importance of understanding human mobility patterns in controlling the spread of infectious diseases. While compartmental and network-based models are used to analyze the transmission of infectious diseases, their level of aggregation fails to capture individual heterogeneity and activity-travel behavior, which plays a crucial role in the spread of infectious diseases. Therefore, in this paper, we propose an agent-based Interdisciplinary Behavioural Model (IBM) that accounts for individual behavior in both the epidemiological and mobility models. Our approach allows for modeling individual-specific behavior in the selection for testing and measuring the level of infection while tracking daily activities. We argue that this model can provide a better understanding of human mobility and of the impact of activity-travel behavior on infection rates, death rates, and the effectiveness of activity-specific limitations. We also show that capturing behavioral assumptions is critical in analyzing the spread of infectious diseases. To this end, we add latent states in our model to study the impact of individual behavior on the spread of infectious diseases. Overall, our work highlights the importance of interdisciplinary research to address the critical challenge of controlling the spread of infectious diseases.

Keywords

activity-based model, epidemiology, activity-travel behavior, mobility, modeling, simulation.

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1   Introduction

The global COVID-19 pandemic caused by the SARS-CoV-2 coronavirus has resulted in a crisis with significant social and economic impacts. The prevention of infectious diseases is a significant concern for public health officials, and recent events have highlighted the urgent need for effective disease control strategies. To develop effective control strategies, it is essential to understand human mobility patterns, including travel patterns and contact networks. This information can drive the design of targeted interventions, such as quarantine measures, and vaccination campaigns for different segments of the population.

Human mobility is a key factor in the spread of the virus since infected individuals transmit the disease across geographical regions and populations. For this reason, capturing human mobility patterns requires accounting for individual behavior in both the epidemiological and mobility models (Tuomisto *et al.* (2020)). However, developing accurate models of human behavior is challenging as they require large-scale data collection and sophisticated computational techniques. There are three categories of epidemiological models: compartmental(Kermack *et al.* (1927)), network-based (Mancastroppa *et al.* (2020); Eubank *et al.* (2004)), and activity-based (Kerr *et al.* (2020)). Compartmental models are fully aggregated and therefore mathematically simpler and faster to compute. In contrast, network-based and activity-based models are more complex, detailed, and computationally expensive, but they capture better individual behavior, allowing for more accurate forecasting of disease spread.

Although activity-based models are computationally more expensive, they more accurately capture individual behavior, making them an ideal choice for disease spread forecasting (Kerr *et al.* (2020), Tirachini and Cats (2020)). However, current activity-based models (see Kerr *et al.* (2020) and Tirachini and Cats (2020)) only model the probability of infection and do not account for the individual choices, such as deciding to test or being chosen for testing, making the validation process imprecise. Therefore, this study focuses on activity-based models, proposing to include latent states to define the behavior of the agents. Specifically, the spreading process is modeled as a combination of two processes (i.e sub-models): the probability of infection and the probability of an agent being selected for testing as a function of the individual's health and socio-economic characteristics. The two sub-models are coupled in a latter stage. The overall model allows for differentiating between positive individuals that decide non to test and positive tests.

To account for individual choices that lead to different activity-travel or social behavior, a

dynamic fully-disaggregated model is used. Modeling every individual choice as a discrete sequence of events allow us to model the individual-specific behavior of the agents in their selection for testing and to estimate their level of infection while tracking them through their daily activities.

2 Methodology

2.1 General framework

2.1.1 Input variables

The input variables consist of the agent's characteristics and their daily schedule (activities and transportation modes). The characteristics of each individual $n \in 1, ..., N$ include social, demographic, health, and economic information of the individual. To account for the mobility of the population, we use the output of an Activity-Based Model (ABM) to obtain the synthetic scheduling of every individual throughout the day. The scheduling file includes, for every time step $t \in 1, ..., D$, with $t = 30[\text{min}]$, the facility f where each individual n is located. The discretization of time is fixed at 30 minutes to capture the trade-off between computational cost and activity-travel behavior accuracy. The facilities $f \in 1, ..., F$ are defined as locations where agents can perform an activity, or transit. We define a binary variable $F_{f,n,t}$ as follows:

$$F_{f,n,t} = \begin{cases} 1 & \text{if individual } n \text{ is in } f \text{ at time } t \\ 0 & \text{otherwise.} \end{cases} \tag{1}$$

Moreover, we divide the agent characteristics in the following classes:

i) The agents' social, economic, and demographic characteristics $\boldsymbol{X}_n^{\text{soceco}}$.
ii) The agents' activity profiles: the time intervals when they perform each activity $\boldsymbol{X}_{n,t}^{\text{act}}$.
iii) The agents' transportation profiles: time intervals when they use a mode of transportation $\boldsymbol{X}_{n,t}^{\text{tran}}$.

iv) The agents' health characteristics $\boldsymbol{X}_{\boldsymbol{n}}^{\text{health}}$.

2.1.2 State variables

At each time step t, we assume the state of the system to be defined by the following variables:

- The location of each individual, i.e. $F_{f,n,t} \; \forall n$.
- The health state of each individual , i.e. $H_{n,t}$,

where $H_{n,t}$ is captured by three binary variables $S_{n,t}$, $I_{n,t}$ and $R_{n,t}$, such that:

$$S_{n,t} + I_{n,t} + R_{n,t} = 1 \quad \forall n, t. \tag{2}$$

$S_{n,t}$, $I_{n,t}$ and $R_{n,t}$ take the value 1 if individual n is susceptible, infected, or recovered (respectively) at time t,

2.1.3 Output variables

The output variables of the simulation are:

- The infection status of each individual $Z_{n,t}^{I}$, describing if individual n is infected at time step t in facility f:

$$Z_{n,t}^{I} = \begin{cases} 1 & \text{if individual } n \text{ is infected at time } t \\ 0 & \text{otherwise.} \end{cases} \tag{3}$$

- The selection of testing of the individual, describing if the individual has been selected (self-selection or imposed selection) to get tested:

$$Z_{n,t}^{T} = \begin{cases} 1 & \text{if individual } n \text{ is selected for testing at time } t \\ 0 & \text{otherwise.} \end{cases} \tag{4}$$

- The testing results:

$$Z_{n,t}^+ \begin{cases} 1 & \text{if individual } n \text{ testes positive at time } t \\ 0 & \text{otherwise.} \end{cases} \tag{5}$$

2.1.4 Other modeling parameters

- The duration D of the simulation.
- The recovery rate $\gamma_{n,t}$. This recovery time is drawn from a log-normal distribution with a mean of 384 periods, and a deviation of 96 periods of the normal distribution (Wölfel *et al.* (2020)).

2.2 State transmission model for activity-travel behavior dependent states

The framework we propose simulates the state of individuals, or agents, over a number of discrete time steps. The model focuses on two types of calculations: the probability that a given agent changes from one state to another at a given time step, and the selection of individuals to be tested at a given time step.

Our primary goal is to model the transition probabilities between states based on the agent's activity and travel behavior. We use a logistic equation to model the activity-travel-dependent transition probabilities, which are transitions that lead to an infectious state, i.e. from $S_{n,t} = 1$, $I_{n,t} = 0$ to $S_{n,t+1} = 0$, $I_{n,t+1} = 1$. For the other transitions (such as the recovering process) we refer to existing literature (Kerr *et al.* (2020); Wölfel *et al.* (2020)). The recovery time for an individual n at time step t is computed by:

$$\gamma_{n,t} \sim \text{lognormal}(384, 96) \tag{6}$$

To capture the impact of individual behavior on the spread of infectious diseases, we include two latent states in our model. The first latent state is a continuous variable capturing the level of infection of each individual at each period of time. It is denoted as $I_{n,t}^*$. The second latent state is a continuous state capturing the likelihood of an individual

to be tested at a given point in time. It is denoted as $T_{n,t}^*$. The structural equations of the two latent states are defined below.

2.2.1 Level of infection

The level of infection is computed for every individual n, for every time step t, in a facility f. We use four groups of explanatory variables to model $I_{n,t}^*$:

- Socio-economic characteristics of individual n ($\boldsymbol{X_n^{\text{soceco}}}$).
- Health characteristics of individual n ($\boldsymbol{X_n^{\text{health}}}$).
- The transportation profile of individual n ($\boldsymbol{X_{n,t}^{\text{tran}}}$).
- The activity profile of individual n ($\boldsymbol{X_{n,t}^{\text{act}}}$).

where $\boldsymbol{X_n^{\text{soceco}}}, \boldsymbol{X_n^{\text{health}}}, \boldsymbol{X_{n,t}^{\text{tran}}}, \boldsymbol{X_{n,t}^{\text{act}}}$ are vectors of the different characteristics. To model the level of infection, we define the discrete model from Figure 1. $I_{n,t}^*$ is modeled by Equation 7.

$$I_{n,t}^* = \beta_{\text{inf}} \frac{\text{infectious agents in } f(t)}{\text{total number of agents in } f(t)} + \boldsymbol{\beta}^{\text{soceco}} \boldsymbol{X_n^{\text{soceco}}} + \boldsymbol{\beta}^{\text{health}} \boldsymbol{X_n^{\text{health}}} \\ + \boldsymbol{\beta}^{\text{tran}} \boldsymbol{X_{n,t}^{\text{tran}}} + \boldsymbol{\beta}^{\text{act}} \boldsymbol{X_{n,t}^{\text{act}}} + \varepsilon_{n,t}^{I^*}. \tag{7}$$

where $\boldsymbol{\beta}^{\text{soceco}}, \boldsymbol{\beta}^{\text{health}}, \boldsymbol{\beta}^{\text{tran}}, \boldsymbol{\beta}^{\text{act}}$ are the parameters for $\boldsymbol{X_n^{\text{soceco}}}, \boldsymbol{X_n^{\text{health}}}, \boldsymbol{X_{n,t}^{\text{tran}}}, \boldsymbol{X_{n,t}^{\text{act}}}$, respectively. β_{inf}, is the parameter of the ratio between infected individuals in a facility f at time t, and the total number of individuals. $\varepsilon_{n,t}^{I^*}$ is a random error term.

Figure 1: Discrete model for the level of infection.
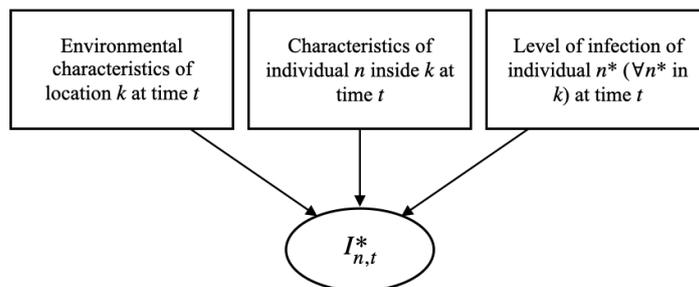
2.2.2 Selection for testing

Figure 2 shows the modeling of the unobserved latent state of the selection for testing $T^*_{n,t}$. As previously mentioned, agents get infected depending on their surroundings, their contacts and their health characteristics. We assume that agents do not modify their schedule, except if they test positive. Hence, it is important to include the selection for testing.

Figure 2: Selection for testing.
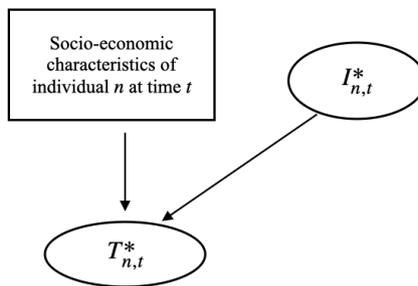
$T^*_{n,t}$ is measured by the level of infection of the individual and its socioeconomic characteristics (see Equation (8)):

$$T^*_{n,t} = \boldsymbol{\beta}^{\text{soceco}} \boldsymbol{X}^{\text{soceco}}_{\boldsymbol{n}} + \beta^{\text{acttype}}\text{acttype}_{n,t} + \gamma^{LI} I^*_{n,t} + \varepsilon^{T^*}_{n,t} \qquad (8)$$

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.

2.2.3 Measurements of the LI and ST models

The LI and ST models are connected by means of a measurement equation that uses as an observation the probability of testing positive for an individual n at time step t (see Equation (9)).

$$P(Z_{n,t}^+ = 1) =$$

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = I) P(Z_{n,t}^+ = 1 \text{ and } H_{n,t} = I) +$$

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = R) P(Z_{n,t}^+ = 1 \text{ and } H_{n,t} = R) + \tag{9}$$

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = S) P(Z_{n,t}^+ = 1 \text{ and } H_{n,t} = S)$$

The joint probability of the sequence of T observations for the same individual is (Equation (10)):

$$P\left(Z_{n,t}^+, Z_{n,2}^+, \ldots, Z_{n,T}^+\right) = \Pi_{t=1}^T \Pi_{n=1}^N P\left(Z_{n,t}^+ = 1\right)^{y_{n,t}^{\text{test}+}}. \tag{10}$$

2.3   Dynamics of the model

This section describes the full methodology to update agents schedule and health state. As described in Section 2.1.3, the output variables of the simulation are $Z_{n,t}^I$, $Z_{n,t}^T$ and $Z_{n,t}^+$ describing the infection status, the selection testing, and the testing result for each individual, at each time step. The full procedure is summarized in Algorithm 1.

First, we update the location f of each agent based on their daily activities (obtained from the output of an activity-based model), and we update the health state of each agent as follows:

- If an agent n is in health state S, that is if $H_{n,t} = S$, there are two possibilities: to remain in state S (susceptible) or to transition to state I (infected). The probability that agent n transitions to state I at time $t+1$ conditional on S at time t is given by a logistic model, (see Equation (11)):

$$P(H_{n,t+1} = I | H_{n,t} = S) = \frac{1}{1 + e^{-\mu I_{n,t}^*}} \tag{11}$$

$$P(H_{n,t+1} = S | H_{n,t} = S) = 1 - P(H_{n,t+1} = I | H_{n,t} = S) \tag{12}$$

where $I_{n,t}^*$ is defined in Equation (7). Then, we draw a random binary variable $Z_{n,t}^I$ from the probabilities defined by Eq. (11) and (12), which is an indicator that takes

Algorithm 1 Dynamics of the model

1: **procedure**
2:     **Input:** Population, scheduling, etc.
3:     **for** each $t \in 1, \ldots, D$ **do**
4:         Update the location $F_{f,n,t} \forall f, n$
5:         **for** each n in the population **do**
6:             Update the Health state $H_{n,t}$:
7:             **if** $H_{n,t} = S$ **then**
8:                 Compute $P(H_{n,t+1} = I | H_{n,t} = S)$ with Eq. (11)
9:                 Draw a binary variable $Z_{n,t}^I$ with $P(H_{n,t+1} = I | H_{n,t} = S)$
10:            **end if**
11:            **if** $H_{n,t} = I$ **then**
12:                Consider the recovery time distribution γ from (Wölfel *et al.* (2020))
13:                Draw the recovery time γ_n for n randomly from the distribution γ
14:                **if** $H_{n,t-\gamma_n} = I$ **then**
15:                    Set $H_{n,t} = R$
16:                **else**
17:                    Set $H_{n,t} = I$
18:                **end if**
19:            **end if**
20:            **if** $H_{n,t} = R$ **then**
21:                Keep $H_{n,t} = R$
22:            **end if**
23:            Evaluate the selection for testing:
24:            Compute $P_{n,t,f}^T$ by means of Eq. (8)
25:            Draw a random binary variable $Z_{n,t}^T$ with probability $P_{n,t,f}^T$
26:            Compute $Z_{n,t}^+$ using Equations (14)-(16)
27:        **end for**
28:        **Output:** $Z_{n,t}^I, Z_{n,t}^T$ and $Z_{n,t}^+$ for all n a time t
29:    **end for**
30: **end procedure**

a value of 1 if individual n is infected, and 0 otherwise.

- The process of an agent moving from the Infectious state to the Recovered state does not depend on activity-travel behavior (the transition from $I_{n,t}$ to $R_{n,t}$). For this reason, we base it on a predetermined recovery time, γ_n, assigned to each agent upon entering the Infectious state. This healing time is drawn randomly from a log-normal distribution with a mean of 8 days and a standard deviation of 2 days (Wölfel *et al.* (2020)). Specifically, if the agent n is infected at time t, we draw γ_n from the log-normal distribution and define $H_{n,s} = I$ for $s = t, \ldots t + g_n$, and $H_{n,s} = R$ for $s = t + g_n + 1, \ldots, T$. While personal health characteristics do influence the severity of the disease and the healing time, this model simplifies the process to reduce the number of parameters to calibrate. The model may consider more

detailed states in the future but, for now, the objective is to estimate the impact of behavior on the spread of the virus.

Once the health state is updated, we run the testing model to estimate whether the agents get tested or not. To evaluate the selection for testing of n we use a binary choice model. We obtain $P_{n,t,f}^T$ (see Equation (13)):

$$P_{n,t,f}^T = \frac{1}{1 + e^{-\mu T_{n,t}^*}} \tag{13}$$

We draw a random binary variable $Z_{n,t}^T$ with probability $P_{n,t,f}^T$, and observe the test result where $Z_{n,t}^T$ is an indicator that takes a value of 1 if individual n is tested, and 0 otherwise.

The test output can be positive or negative if an agent is selected for the testing process. This output can be determined by a logical combination of the output of the two models. We simulate $Z_{n,t}^+$ as a random variable with two values: positive 1 and negative 0. For the sake of simplicity, we define the probabilities constant through the simulation, across n and t (Ai *et al.* (2020)). The ranges in parentheses correspond to the 95% confidence intervals.

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = I) = 0.65 \pm (0.62 - 0.68) \tag{14}$$

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = S) = 0.17 \pm (0.10 - 0.23) \tag{15}$$

$$P(Z_{n,t}^+ = 1 | Z_{n,t}^T = 1 \text{ and } H_{n,t} = R) = 0.17 \pm (0.10 - 0.23) \tag{16}$$

Finally, we apply activity reduction policies, such as quarantine or social distancing measures, which modify the probability of disease transmission across the contact network of each infectious agent.

3   Results and discussion

3.1   Data availability

The model requires input data that includes activity-travel behavior information, socioeconomic and health characteristics, and COVID-19-related data about individuals. However, no single dataset in the literature includes all the necessary features, so different datasets are used:

- The Federal Office of Public Health (FOPH) dataset, covering mid-February 2020 to mid-September 2021, contains information on positive COVID-19 tests in Switzerland and the tested individuals. This dataset includes age, gender, municipality, vaccination doses, hospitalization, and casualties (Office of Public Health (2020)).
- Open-source data from Google was used to determine the share of positive tests per age group, with age groups defined in intervals of 10 years (CloudPlatform (2021)).
- The Swiss Health Survey provides information on the health status of the Swiss population, including physical, mental, and social well-being, physical disorders and diseases, accidents, disabilities, lifestyle and health behaviors, use of health system services, living conditions, health determinants, health resources, and health insurance (fédéral de la statistique (2016)).
- A calibrated MATSim simulation output from ETH Zurich was used, which includes synthetic information about the population's attributes, activities, and trips (Horl and Balac (2021)).
  By combining these datasets, the model is able to account for each individual's daily activity plan, socioeconomic characteristics, health characteristics, and COVID-19-related medical information.

3.2   Validation and evaluation

The proposed approach is validated using a simplified case study of the canton of Vaud. Due to the unavailability of health data from the OFS, we use the MATSim and FOPH data mentioned in Section 3.1 to produce a disaggregated database, taking advantage of the methodology developed in Balcells *et al.* (2022). The contact mechanisms are computed using a calibrated MATSim simulation from ETH Zurich, which includes the

socio-economic characteristics of individuals such as gender, age, municipality, and daily schedules. The epidemic trajectory, as shown in Figure 3, is obtained by coupling the private and public data.

Only age is considered as agent characteristic, so that Equation (7) can be simplified as follows:

$$I_{n,t}^* = \beta_{\text{inf}}\text{shareinfectedindividuals}_t + \beta_{\text{inf}}^{\text{age}}\text{age}_n\text{shareinfectedindividuals}_t, \qquad (17)$$

where β_{inf} and $\beta_{\text{inf}}^{\text{age}}$ are coefficients, age_n is the age of the individual, and $\text{shareinfectedindividuals}_t$ (see Equation (7)) is the proportion of infected individuals at time t. Considering only the age as a characteristic of the individual, Equation (8) becomes:

$$T_{n,t}^* = \beta^{\text{age}}X_n^{\text{age}} + \gamma^{LI}I_{n,t}^*. \qquad (18)$$

where β^{age} and γ^{LI} are coefficients, age_n is the age of the individual, and $I_{n,t}^*$ is the level of infection.

3.3   Inital conditions

The initial conditions of the framework have an impact on the results of simulation, as the trajectory of an epidemic is directly linked to the number of initial cases. We assume the model to be run after a few days from the start of the pandemic. For this reason, the initial conditions for the first days of simulations, are not determined by the model, but rather taken directly from the data. This allows the model to best capture the actual initial conditions of a wave of COVID-19, and the number of infected individuals at the end of D is relatively close to the actual number. However, one significant drawback of this method is that it is only possible to know the number of confirmed cases and not the actual number of infections. Therefore, the initial infections in the model will always be lower than in reality, leading to deviation in the simulation results.

In Figure 3, we show the geographical distribution of new infections at the beginning of the

Figure 3: Evolution of infected people over time in the canton of Vaud.
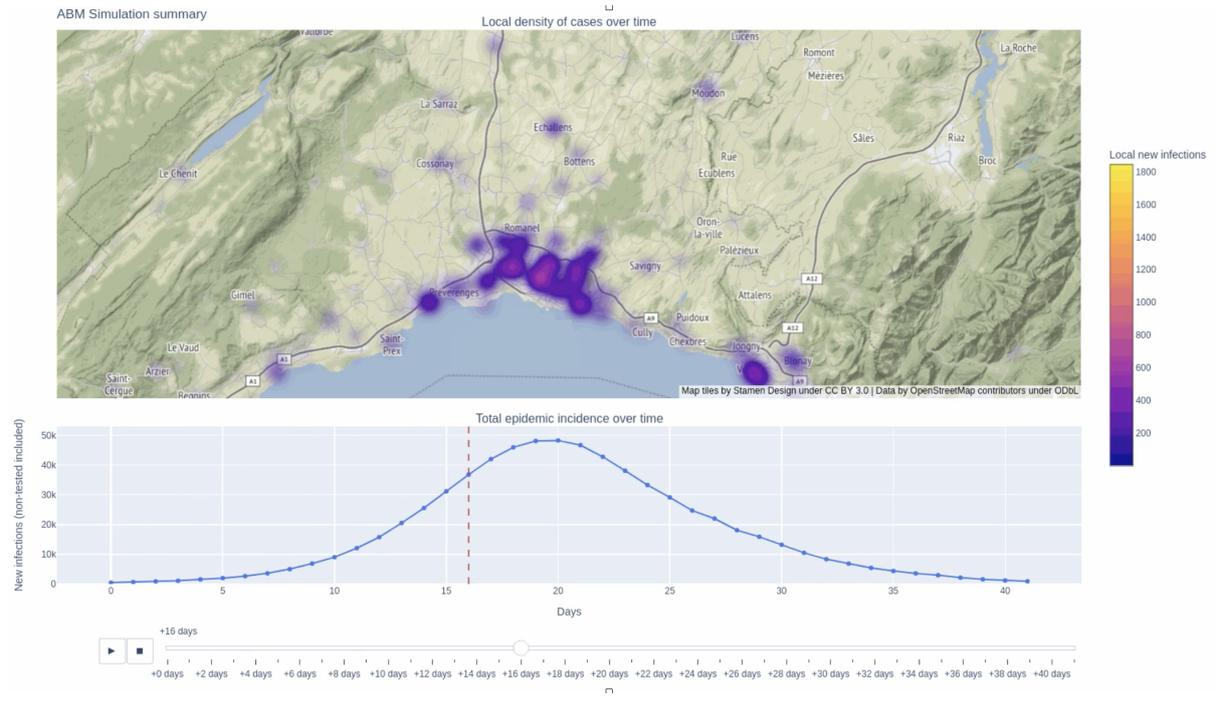
pandemic in the canton of Vaud. The figure indicates that areas with higher population density tend to generate more contacts between agents, resulting in a greater number of infectious individuals. These findings underscore the critical role of human mobility in studying pandemic evolution.

3.4 Calibration

This study aims to test the model rather than draw any conclusions from the results. Nonetheless, the data preparation stage of this calibration can be useful for future model calibration. The calibration procedure involved isolating FOPH data from mid-August 2020 to October 29, 2020, the rising phase of the second wave of Covid-19, with no restrictions or vaccination at that time. The simulation and target data are geographically limited to the canton of Vaud, which has approximately 800,000 inhabitants. The 7-day rolling average of the target data is used instead of the raw data to reduce computation complexity. The model is constructed without additional infection risk factors or test probabilities, relying only on the strength of infection, the baseline probability of being tested, and the additional test factor related to the risk of infection, with only the baseline

probability of being tested being calibrated. As it is out of the scope of this paper to provide a full methodology on how to calibrate such models, the parameters: $\beta^{\mathrm{age}}, \gamma^{LI}$ and $\beta_{\mathrm{inf}}^{\mathrm{age}}$ are considered constant during the calibration process. Their value is obtained following the methodology developed in Balcells *et al.* (2022).

First, we initialize the model as explained in Section 3.3. Then, the Mean Squared Error (MSE) is considered as objective function to estimate the difference between the simulation's predicted trajectory and the trajectory that real data follow for the positive tests, in order to calibrate β_{inf}.

$$MSE = \sum_{d} \left(Z_{n,t}^{+} - Z_{n,t}^{+\mathrm{sim}} \right)^2 . \tag{19}$$

Figure 4: Calibration of β_{inf} using the positive tests (upper figure) and the share of positive tests (lower figure) over time in the canton of Vaud.
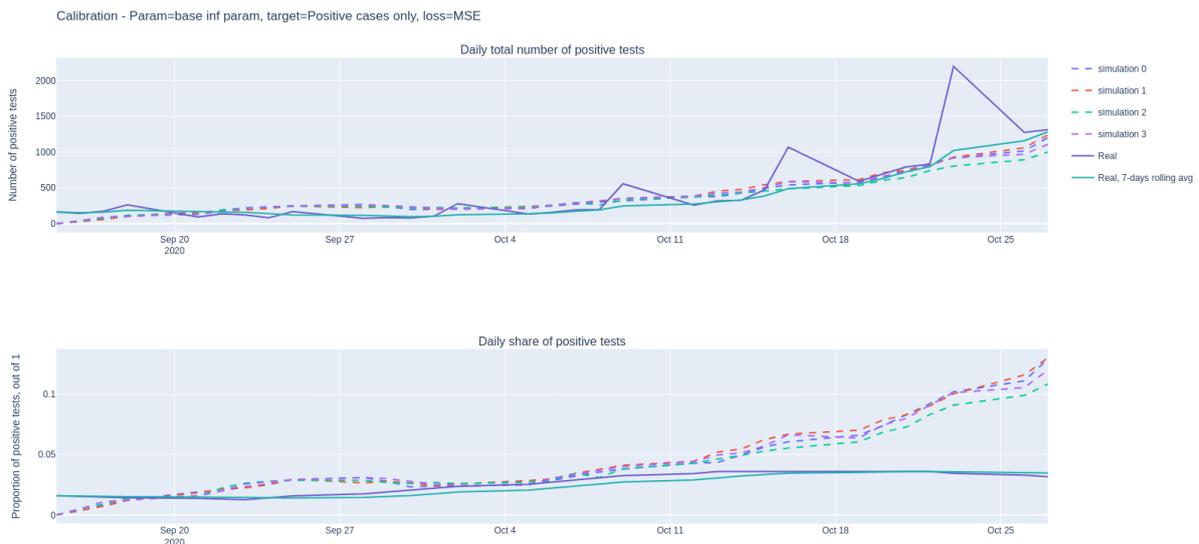
The results, visible in Figure 4, demonstrate the proposed approach's efficacy using two distributions in a case study. The daily total number of positive tests over one month for various simulations and the confirmed cases are shown in the upper plot, with peaks on Mondays, indicating laboratory closures over weekends. A rolling average over a week is computed to improve interpretability, demonstrating that the simulation results followed the actual data trend.

The lower plot represents the positive test proportion data on the aggregate level and the disaggregated FOPH data on age, gender, and municipality. As the parameters related to

the selection for testing are not calibrated but taken from the literature, the simulated scenarios do not correspond to the measured data. This underlines the need for a more accurate calibration process, taking into consideration many parameters and a more complex objective function.

4   Conclusions

In conclusion, this paper addresses the critical issue of human mobility and its role in the spread of infectious diseases, with a particular focus on the COVID-19 pandemic. The paper proposes an activity-based epidemiological model that accounts for the heterogeneity of individual behavior and its impact on the dynamics of disease spread. By tracking individuals through their daily activities, the model enables the analysis of the impact of activity-travel behavior on the infection mechanism and testing process. The paper argues that a better understanding of human mobility is crucial for developing effective control strategies to mitigate the impact of infectious diseases and that interdisciplinary research is essential for addressing this critical challenge.

The proposed model provides a preliminary framework for future research that includes adding relevant parameters to define the level of infection and the selection for testing, introducing activity restrictions, and considering the vaccination effect. We propose for the first time the coupling of different latent states (i.e. I^* and T^*) to explain the spreading of infectious disease, even if more data is required to provide full validation of the disaggregated model. Once the input of the model is pre-processed, the computational time for Vaud with a time step of 30 min for a period of 2 months, is around 8 min with a processor of 2.6 GHz 6-Core. Even though the model is not fully calibrated, the computational time suggests that disaggregated models can be used to capture the influence of human behavior for epidemiological purposes. In addition, future work aims to explore the change in activity-travel behavior due to the presence of a virus. By accounting for the heterogeneity of individual behavior and its impact on disease spread, this paper contributes to the development of more accurate and effective disease control strategies.

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