
Activity-based modeling and simulation of epidemics

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Abstract

The SARS-CoV-2 outburst in March 2020 has led to the lockdown of several countries across the world. Mobility restrictions have been constantly put into action and reversed to find the trade-off between minimizing the number of infections and death and mitigating the inevitable damage to the economy and the societal systems. These emergency measures lead to collateral effects that prove the need for robust and dynamic models for policymakers to make efficient and targeted decisions in short amounts of time. We desire to predict the impact that trips have on the spreading and provide insight into the motivation behind the observed trips to generate a suitable and unbiased response. For this reason, we aim at building a disaggregate model using the agent-based approach to provide insights and forecasts on transport demand and its epidemiological consequences. We will couple people's daily activity schedules and infectious disease spreading. This addition is especially appealing since it includes the different behaviors, contact patterns, and population *heterogeneity* linked to the activities and their consequence of spatial movement, especially during travel. Consequently, we believe that this method will help to guide authorities to ultimately assess the effectiveness of different policy approaches based on socio-economic variables.

Keywords

Agent-based model; SIR model; Policy decision making; SARS-CoV-2.

1 Introduction

There have been many contributions focused on epidemiological models so that disease spread can be better understood, applied to the various viruses that humanity has faced in the last two centuries (see Lemaitre *et al.*, 2020). The SARS-CoV-2 situation has contributed to the publishing of many papers in this direction. However, models that couple mobility of people together with the spreading of a certain disease is a more recent research field. Specifically, there is a gap when coupling public transportation planning and epidemiological disciplines. It seems obvious that it is important to combine these fields if we need to plan for public transportation logistics during and after a pandemic. Public transport is strongly affected by the SARS-CoV-2 situation; their services are either restricted, forced to apply social-distancing and capacity measures, or even temporarily not working, (see Tirachini and Cats, 2020, Douglas *et al.*, 2020, Zheng *et al.*, 2020, Lee and You, 2020). The level of public transport usage, the culture of travelers, or the attributes of the country can influence how the service restrains mitigate the pandemic. However, there is an impact on the ridership since travelers fear infection so they use less public transport and switch to taxis and private cars ((Gerhold, 2020, De Vos, 2020, Baker *et al.*, 2020, Bansal *et al.*, 2021)).

We propose to address this issue at a disaggregate level. The long-term goal is to provide insights that transportation planners and public health authorities can exploit to deal with epidemic situations. For instance, the C2Smart group from NYU ((Wang *et al.*, 2020a)) uses MATSim software ((MATSim, 2021)) together with deep learning to update travel trends and study the impact of proposed phased reopening strategies. Also, in Section 2, we expose the state of the art of this topic. Xinwu Qian ((Qian and Ukkusuri, 2021)) point out the two main challenges facing this kind of model. Firstly, the ability to model different land use and activity patterns. Secondly, while mobility brings people to their activity locations, it also brings massive contact and contagion during travel. Lastly, we need to consider additional assumptions to be able to account for spatial heterogeneity, see (see Qian and Ukkusuri, 2021). Based on the gaps identified in the literature, we attempt to answer these two main research questions:

1. How can we capture the spread of a disease through transportation systems at a disaggregate level?
2. What are the *policy implications* in terms of epidemic crisis management?

We propose an agent-based model coupled to a compartmental model based on disaggregate contact probability dependent on multiple socio-economic and virological variables. The idea is to define the probability of infection accounting for *socio-economic* variables, such as age,

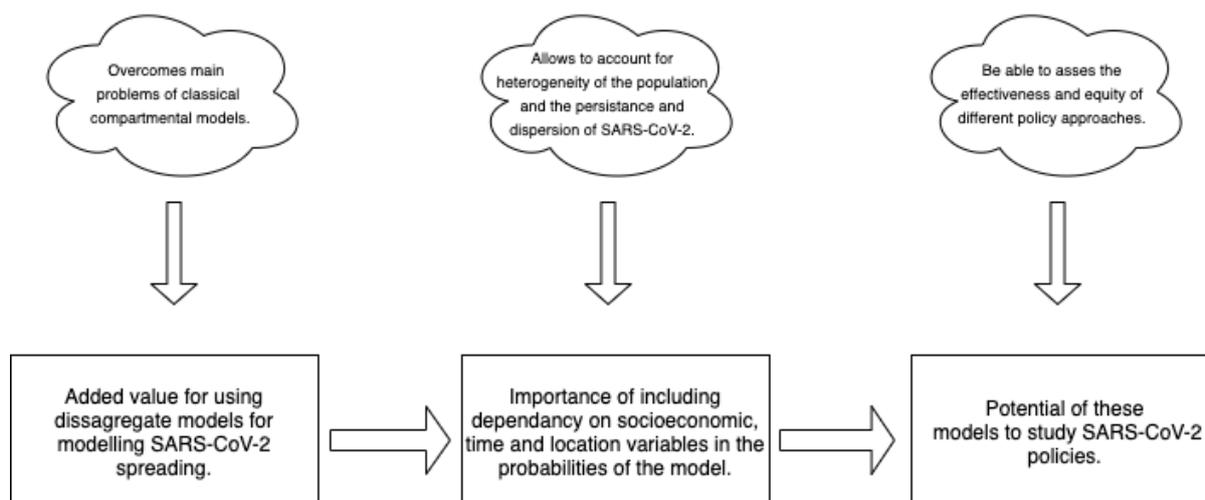


Figure 1: Schematic diagram gaps

income, gender, home address, general state of health, etc., together with variables like the location where the infection is taking place, the surface in m^2 of the activity, number of people, etc. We present a simulation procedure that will allow drawing the most likely infection probability for each agent of the network together as their mobility, the spreading associated with it, their recovery process and how their daily activity choice depends on the level of infection associated with this activity.

The approach that we present in this paper has several advantages over existing epidemiological models in the field. First, all infection probability dimensions (socio-economic and virological) are modeled simultaneously. Second, the model produces an empirical distribution of individual activities vs infection that can be investigated with simulation. Last, the framework is built on first behavioral principles which means that we are able to understand what drives people to act in a certain manner. Also, it can be generalized to complex epidemiological situations, including immunity or vaccination.

2 Background

Mathematical modeling for infectious disease spreading has emerged in the 18th century to study morbidity and mortality of smallpox, see (Gani, 2001). Daniel Bernouilli provided a model describing the spread of smallpox, which was prevalent at the time and argued the advantages of variolation (method of inoculation used to immunize individuals against smallpox). Thenceforth, multiple models have been developed for explaining the spread of a virus in a population.

From simple approaches, like (W. H. Hamer, 1906) who studies the evidence of variability and persistency of type, to early compartmental models like (Kermack and Mckendrick, 1927) or recent and more advanced compartmental models like (Lemaitre *et al.*, 2020). The latest and more complex approaches are the well-known individual or agent-based models, (Eubank *et al.*, 2004a, Mancastropa *et al.*, 2020).

Specifically, deterministic compartmental models rely on differential equations that define the dynamics of the flow between the different compartments. These deterministic models depend on the mass action assumption, see Equation 12, to express the mixing between the various groups of individuals. Network models are able to capture partially the failure of compartmental models to represent the social structure relevant for the disease spreading. This methodology is based on the graph theory, which means that it consists of nodes and links that stand for hosts and their contacts respectively. However, it neglects the quality of the contacts and it is difficult to manage the dynamic approaches for the network. The last category, agent-based models, will be our main focus on the state of the art. They overcome all the disadvantages mentioned for the other two model types. Particularly, we will study how to couple agent-based epidemiological models together with activity-based models to link epidemics and mobility.

2.1 Activity-based models

Activity-based models have started to gain popularity in the last 50 years to advance trip-based models, (see Castiglione *et al.*, 2014, Elston, 2013, Bradley and Bowman, 2004), which do not account for individuals' complex behaviors. The main assumption of these models is that people's mobility is due to their need to perform their daily activities. For that reason, if we can understand the reason and how individuals schedule their week, we can predict their mobility choices and behavior. Therefore, we can state that these models establish that the need to do activities drives travel demand in space and time, (Hägerstrand, 2005, Chapin, 1976). The main roots of ABM are in modeling human social and organizational behavior and individual decision-making. Agents are programmed to react to other agents and the computational environment around them. However, they are engaged in certain behavior rules that go from primitive reactions to complex adaptive AI. All in all, ABM aims to be as behaviorally realistic as possible.

Two different approaches are used to develop ABM, see (Pougala, 2020) . Utility-based models that rely on the assumption that the goal of agents in each step is to manage their schedule at

an optimized level so that their satisfaction is maximized, see (Wang and Timmermans, 2000, Adler and Ben-Akiva, 1979a, Bowman and Ben-Akiva, 2001). The mobility behavior of the agents is represented as the result of discrete choices, usually treated sequentially, and solved with econometric methods like advanced discrete choice models (Bowman and Ben-Akiva, 2001, Wang and Timmermans, 2000), or with micro-simulations, (Recker *et al.*, 1986, Pendyala *et al.*, 2005). The second activity-based model is the computational process model. It refutes the assumption that decision-makers seek the optimal solutions, and argue that they consider context-dependent heuristics (see Arentze and Timmermans, 2004, Golledge *et al.*, 2005).

There exist many in-depth reviews of existing modeling concepts for activity-travel forecasting (e.g. Bradley and Bowman, 2004, Kitamura, 1988, Rasouli and Timmermans, 2013, Axhausen and Gärling, 1992).

2.1.1 Utility-based models

The first utility-based models are based on a *disaggregate* travel demand model system (c.f. Bowman and Ben-Akiva, 2001) and a multinomial logit model for household daily travel patterns (c.f. Adler and Ben-Akiva, 1979b). The model by Adler and Ben-Akiva (1979b) considers that people pick their mobility choices based on their household, the level of service of the transportation system, and the set of economic and social activities. It assumes that the households plan their schedule by optimizing the utility they gain from it, under budget and time constraints. The second model, developed by (Bowman and Ben-Akiva, 2001), uses multinomial logit to compute the choices of the individuals for every mode. These two models consider that the choice set of the activities available and the scheduling decision process follow rules that decrease the number of choices. Because of that, the trade-offs between the activities chosen cannot be accounted for correctly. Habib Nurul (Nurul Habib and Miller, 2009), finds an activity-agenda approach which stands for the set of different activities that pursue a schedule within a specific time frame. This agenda maximizes the utility under the constraints of budget and time. The objective is to capture the trade-off between scheduled and unscheduled activities. Habib Nurul (Nurul Habib, 2011) uses the agenda as an input in a discrete-continuous model that estimates activity choice.

The main challenge of these models is their computational complexity. That is the reason why micro-simulators started gaining popularity in this field. The difference is that micro-simulators compute a unique schedule for the individual, instead of choices probabilities for the different alternatives. The first activity-based micro simulator that was completely operational was the

STARCHILD, (Recker *et al.*, 1986). The main issue is that this model was fully deterministic, and it does not represent a real decision process (for further literature review on this topic, see Pougala (2020)).

Another example for a micro simulator is the TRANSIMS (Smith *et al.*, 1995) which adopts an activity-based approach to generate individual's activities instead of O-D matrices. It has a module that builds synthetic population based on census and survey data to estimate activities for individuals and households and be able to plan multimodal trips ((Nagel *et al.*, 2002)). The approach used by (Smith *et al.*, 1995, Pendyala *et al.*, 2005), use sequential estimations of the different dimensions of the daily mobility choices. Therefore, the interrelations that arise between choices are difficult to include. To address that, we can cite (Charypar and Nagel, 2005) who generate activity schedules through genetic algorithms. GA can consider activity type, transportation mode, and the location at the same time. The utility fitness function is the sum of the utility of all performed activities and the travel penalties, see equations 14 11 and 3, found in (Charypar and Nagel, 2005):

$$S_{\text{plan}} = \sum_{q=0}^{N-1} S_{\text{act},q} + \sum_{q=0}^{N-1} S_{\text{trav,mode}}(q) \quad (1)$$

The utility of an activity q is defined by:

$$S_{\text{act},q} = S_{\text{dur},q} + S_{\text{wait},q} + S_{\text{late.ar},q} + S_{\text{early.dp},q} + S_{\text{short.dur},q}, \quad (2)$$

and the travel disutility for a leg q is given as

$$S_{\text{trav},q} = C_{\text{mode}(q)} + \beta_{\text{trav,mode}(q)} \cdot t_{\text{trav},q} + \beta_m \cdot \Delta m_q \\ + (\beta_{d,\text{mode}(q)} + \beta_m \cdot \gamma_{d,\text{mode}(q)}) \cdot d_{\text{trav},q} + \beta_{\text{transfer}} \cdot x_{\text{transfer},q} \quad (3)$$

This utility function is notably used in the agent-based micro simulator MATSim (Horni *et al.*, 2016). We will focus on this tool in Section 3.4, called agent-based models that belong to the

epidemiological model section. MATSim allows to add modules straightforwardly, see (mat, 2016).

To conclude, representing decision processes employing utility functions is an important research field. However, there is a potential contribution towards developing a simultaneous estimation approach.

2.1.2 Computational process models

2.2 Epidemiological models

An introduction to the most well known model types used for simulating an infection spreading is in the following subsections together with a description of their advantages and shortcomings. To be specific, we discuss deterministic compartmental models, network models, and individual-based models.

2.2.1 Compartmental models

The SIR model has three compartments: *susceptible* (S), infected (I), and recovered (R), and the SEIR model has an additional compartment of exposed (E). Each compartment is represented by several variables x_i . The dynamics between these compartments are driven by flows, described by differential equations, see (Kelman, 1985). These flows can go from compartment to compartment or from compartment to environment, and they can be expressed as (c.f (Sandberg, 1978):

$$\frac{\partial x_i}{\partial t} = f_{i0} + \sum_{j=1}^n f_{ij} - \sum_{j=1}^n f_{ji} - f_{0i} \quad (4)$$

$$t \geq 0 \quad (5)$$

$$x_i(0) = x_0(i) \quad (6)$$

$$i = 1, 2, \dots, n \quad (7)$$

where x_i is the number of individuals from compartment i ; x_{0i} is the initial value of i ; f_{0i} is the flow from i to the environment, and f_{i0} is the inverse flow; finally, f_{ij} and f_{ji} stands for the flow

from compartment i to j and j to i , respectively.

The SIR epidemic model can be written in the following way(c.f (Kiss *et al.*, 2017)):

$$\frac{\partial S}{\partial t}(t) = -\beta I(t) \frac{S(t)}{N} \quad (8)$$

$$\frac{\partial I}{\partial t}(t) = \beta I(t) \frac{S(t)}{N} - \gamma I(t) \quad (9)$$

$$\frac{\partial R}{\partial t}(t) = \gamma I(t), \quad (10)$$

where $S(t)$, $I(t)$, $R(t)$, denotes the size of the susceptible, infected, and recovered compartment, respectively. We can eliminate one equation by recognizing that $S + I + R = N$. We can see that if $R_0 = \beta/\gamma < 1$, the number of infected people decreases, while if $R_0 > 1$ it will increase if the initial value of susceptible people is close to the total number of the population. We can define R_0 as the average number of new infections caused by individuals that are infected in its early stage inside a completely susceptible population, see (Diekmann and Heesterbeek, 2000, Anderson and Mary, 1992). Note that the system tends to be disease-free when $t \rightarrow \infty$, reaching the steady-state since S and R are bounded between $[0, N]$ and they are monotonic. Therefore, since $\dot{R} \rightarrow 0$ and $I \rightarrow 0$. If we assume that $R(0) = 0$ and that $S(\infty) + R(\infty) = N$, we have equation 11 that we can solve by iteration to an arbitrary accuracy:

$$N - R_\infty = S(0) \exp\left(-\frac{\beta}{N\gamma} R_\infty\right) \quad (11)$$

Compartmental models applied to the epidemiological field rely on the idea of mass action coming from chemical kinetics. The mass action principle defines the reaction rate v of a chemical reaction:

$$v = k \cdot [A] \cdot [B] \quad (12)$$

If reactants A and B are well-mixed, then k is a constant rate. In "The law of mass-action in epidemiology: A historical perspective" (Heesterbeek, 2005) we can find the origin of the analogy between chemical collisions leading to chemical reactions and people's collisions leading to infection.

The main advantage of these models is their mathematical simplicity. Due to this characteristic, compartmental models can be examined analytically which means that they are easy to manage as well as interesting for scientific theorizing. However, this oversimplicity of considering that

every compartment is fully mixed, neglects, as Soper (Soper, 1929) said in 1929, the 'imperfect mixture'. This can be defined as a difficulty to express heterogeneity, complex behavior, and contact patterns between individuals. Many authors (see (Smieszek, 2009), (Edmunds *et al.*, 2006), (Edmunds *et al.*, 1997) and (Liljeros *et al.*, 2007)) have stated the importance of taking into consideration characteristics of the contacts, such as transient contacts, long-term relations, variability between the contacts that people have, etc. Not considering this might lead to erroneous conclusions from simulation results. In addition to the simplicity in the social aspect, there are also a few in the biological one. For instance, pre-existing immunity or different levels of virus shedding (Smieszek, 2009). Also, the infectious period $1/\gamma$ is exponentially distributed which does not show its central tendency for most diseases.

2.2.2 Network models

Network models overcome the weakness of compartmental models to simulate social heterogeneity. We can find these complex representations in many different research fields, like the cell, predator-prey relations, the Internet, a network of routers and computers connected by physical links or language, among others. Authors (see Albert and Barabasi, 2001, Zverovich, 2021, MORRIS, 1993) present a careful analysis of structured mixing in network models to study the spread of AIDS.

Real-world networks rely on graph theory (Bondy and Murty, 2008). Their components are nodes that represent the individuals, or also known as hosts, and the links that define the contact structure between the two hosts. Depending on the system that we need to simulate, these graphs can be undirected, directed, weighted, time-dependent, or combinations of these types. Also, in "Spread of the epidemic disease on networks" (Newman, 2002) introduces an example of a bipartite population in which he assumes a heterosexual population, and therefore, the only possibility is to link two nodes of different sex.

If we want to define mathematically a graph G by a pair (V, E) , where V is the set of nodes in the network, and $E \subset V \times V$ is the set of pairs of nodes, that are computed in the adjacency matrix whose entry g_{ij} is 1, if $(i, j) \in E$, and zero otherwise.

One of the most studied random graph models is the Erdos-Renyi model, see Gilbert (1959)

and Renyi (1959). The graph G is defined by n vertices, and m edges: $\{G_1, G_2, \dots, G_n\}$, where $n = \binom{M}{m}$ with $M = N(N - 1)/2$, and the probability of picking each graph is the same, namely $1/n$. The traditional Erdos Renyi models are essentially static graphs, which means that the random graph is drawn just once, and does not change over time. However, in Mandjes *et al.* (2019) we can find two varieties of dynamic versions of the classical Erdos-Renyi graph.

Characterizing the network is extremely useful when studying the disease evolution in a particular scenario. Essentially, it is complex to find the correct adjacency matrix. Two cities can have similarities in the spreading of disease but complete different adjacency matrices. Therefore, it is convenient to have a few measures to quantify networks, for example, the degree of distribution, assortative and disassortative mixing, clustering and higher-order structure, shortest path length, and strong connectedness and cycles and tree graphs (see (Kiss *et al.*, 2017)).

There are advantages that network models can provide, like for instance the addition of heterogeneity. However, there are a few challenges that are not solvable. The first one is that it is difficult to use them in densely populated areas since it becomes a computationally intractable environment. Except if we can find symmetries in the network and then lumping techniques (see Nicola, 2021) can be applied. Moreover, if we want to ameliorate this aspect and be able to understand the interaction of two individuals, we could use a mean-field approach (see Matsuda and Sato, 1992, Keeling *et al.*, 1997, Rand, 1999). The second disadvantage is the quality of the contacts between two individuals. The adjacency matrices are binary. Therefore, they do not consider the characteristics of the contact action between two people, like its duration or the intensity. Generally, we can fix this by weighing the links by their transmission probability. However, as aforementioned, the intensity variable and the duration depend on the time, so a dynamic representation is required. The third weakness involves the static character of network models. While compartmental models assume that the contacts change constantly, network models assume a completely stable structure. Both have an unrealistic approach since stable, long-term relationships tend to have high frequencies of contagion, whilst transient encounters will likely never be repeated.

To conclude, network models work well for calculating disease outbreaks, understanding the disease dynamics, and understanding the interaction between two individuals given a distribution. Therefore, these models are more suitable for the analysis of diseases that spread in relatively small populations such as sexually transmitted diseases. However, we can not study what triggers people to go from one node to another, which characteristics in the population

drive people to perform an activity, or the impact of getting infected to using a bus link instead of a car link. We would need a very complicated and computational expensive model to study a few socio-economics parameters.

2.3 Individual-centric models

Individual-centric or agent-based models applied to the field of epidemiology are widely used to study the spread of infectious disease, see (Boots and Sasaki, 1999, Carpenter and Sattenspiel, 2009, Cauchemez *et al.*, 2008, Atti *et al.*, 2008, Das *et al.*, 2007, Eubank *et al.*, 2004b, Ferguson *et al.*, 2005, 2006). These models provide flexibility for epidemiological modelers and they overcome the challenges mentioned in the previous two models.

The model works by following people over time at an individual level through the different stages of the disease. The agent is the unit of analysis in these types of models; they perform on their own and interact with the environment, (Weiss, 2000, Quesada, 2007). Their interactions lead to outcomes that we define using probability distributions. Agents are the ones that pick up the pathogens with their behavior, carry them, and spread disease by releasing them. That is why one of the main advantages of these models is that they are intuitive to understand, which makes communication with decision-makers efficient.

Contrary to compartmental model and network models, there is no easy boundary to define individual-based models. This is because there are similar kinds of approaches that take the individual as the main unit of analysis. However, we can find two main characteristics specific for individual-based models, see (Holland, 2006). The first one is parallelism, which means that the dynamics of the model are based on the interactions of the individual. They have a role towards the environment and at the same time, the environment affects them. The second one is that actions are conditional to the signals that the individual receives from the environment. These reactions can be fully deterministic or include an error term to make it stochastic. However, they follow a rule-based process: if an individual is susceptible and it has contact with an infected agent, it becomes infected with a probability p .

In short, individual-based models are flexible and easy to interpret intuitively. Moreover, we can deal with the aggregation error. We can define the aggregation error as the intuitive idea that if we aggregate multiple individual behaviors, collectives will start acting accordingly. Also, it is straightforward to include considerations of activities, location choice, complex mechanisms,

etc. On the other hand, it is difficult to parametrize these models because of the lack of data. For that reason, sensitivity analyses are more laborious than for other models. Besides the fact that the level of detail is higher, also because of their stochasticity they can not be dealt with analytically. It means high computing time and storage capacity.

As we have seen, there exist many in-depth reviews of existing modeling concepts for infectious disease spreading. We will focus on the most advanced level of agent-based models, as well as possible model expansions to include social interactions and methodologies to estimate or infer policies optimization. Note that the difference between individual- and agent-based models lies in the learning process. The latest has the capability of learning, evolving, and adapting to the environment. (Johnson, 2001) defines it as the ability of low-level components of a population to self-organize into a higher-level system of sophistication and awareness, and he presents five fundamental principles to his hypothesis: more is different, ignorance is useful, encourage random encounters, look for patterns and pay attention to your neighbors.

2.3.1 Synthesis

Agent-based models are the most advanced models for studying the spreading of infectious diseases. The agent-based approach is well suited for implementing realistic and accurate modeling of contact tracing and policies put into place. These models provide a more realistic interaction between agents, by taking into account their daily activities, such as workplace, education, their travel mode as well as socio-economic characteristics as gender, age or income.

Multiple authors, (like Hackl and Dubernet, 2019, Müller *et al.*, 2020, Aleta *et al.*, 2020, Tuomisto *et al.*, 2020), have shown that the most accurate results for obtaining policies are obtained by simulating the spread of the epidemic coupled to a human mobility model. We model how individuals move to know where they are at every timestep of the simulation. On the other hand, we diffuse the virus and track the specifics of people's interaction to assess how the virus is spreading, to whom and where. As a result, this gives us a high level of disaggregation that allows us to change specific aspects of the population or the virus effortlessly.

One of the most known activity-based models to forecast human mobility models is MATSim (Horni *et al.*, 2016). This simulation model has been used to study the impact of the COVID-19

on the New York City (NYC) transportation system (Wang *et al.*, 2020b) or on the metropolitan area of Berlin, Germany (Müller *et al.*, 2020), among others. Using an agent-based mobility simulation allows following population over time at an individual level while delivering the network of co-presence for one day at their different activities over the whole agent population. Agent-based modeling can capture complex behavior patterns and provide valuable information about the dynamics of the real-world system that it imitates. Each agent has its parameters and makes decisions based on a set of rules of their everyday dynamics (Bonabeau, 2002). Using agent-based simulations for studying the mobility of a population allows overcoming problems as not having data of a certain population.

For example in the POLYMOD study (Prem *et al.*, 2017), the objective is to provide estimates of age-specific contact rates for countries where data are not yet available. This is done by combining data from 8 European countries used to project over 144 other countries, using Bayesian hierarchical model to estimate the proclivity to provide projections of age-specific contact patterns for all the other ones. These estimations are limited by the fact that using data from European countries to represent non-European societies is not suited. Implementing an agent-based model to deliver the contact rates is much more appropriate than estimating mobility data from contact surveys. Based on this model, an epidemiological model can be added and implemented on top of the mobility simulation. For instance, in the Berlin study (Müller *et al.*, 2020), the disease progression model is described by the division of the population into six categories: namely *Exposed*, *Infectious*, Showing Symptoms, Seriously Sick, Critical and *Recovered*. The probability for person n to become infected by this interaction in a time step t is 13 (c.f Smieszek, 2009):

$$P_{n,t} = 1 - \exp \left[-\Theta \cdot \sum_{m=1}^I q_{m,t} \cdot ci_{nm,t} \cdot in_{n,t} \cdot \tau_{nm,t} \right], \quad (13)$$

where the parameters are I that is the total number of infectors (i.e. sum of all other persons); $q_{m,t} [s^{-1}]$ the shedding rate (microbial load) of infector m at simulation time step t ; $ci_{nm,t}$ the contact intensity between the infector and the susceptible individual; $i_{n,t}$ the intake (reduced for example by a mask); $\tau_{nm,t} [s]$ the duration of interaction between the individuals n and m during time step t and Θ the calibration parameters that account for all relevant factors that are not explicitly represented (for example the survival probability of the infectious agent).

Several other parameters can then be added to build a more detailed disease model being able to add any number of interventions on the model timeline (e.g., physical isolation, testing, tracing, and controlling the number of cases entering the area), see REINA model (Tuomisto *et al.*, 2020).

The Berlin study appears to be the most complete, as it implements a detailed agent-based model combined with an individual-based compartmental model for the dynamics of the virus simulated over the metropolitan area of Berlin. The study was conducted for determining changes in the reinfection rate depending on the interventions put in place, such as reduction in activity participation, wearing of masks, contact tracing, or quarantine-at-home. In "An agent-based epidemic model reina for covid-19" (Tuomisto *et al.*, 2020) we can see that the contact intensities differ for each activity and location as well as per age group. Also, (see Lemaitre *et al.*, 2020), we can observe the difference between each canton in Switzerland and each hospital's procedures and protocols have been shown to cause differences between modeled and observed results.

Mathematical models and computer simulations often assume a constant, generic transmission probability (c.f. Müller *et al.*, 2020) while ignoring the fact that, for example, a short interaction between two people in a public bus is less likely to transmit the virus than an interaction that lasted several hours in a more enclosed space. Considering all contacts as having the same contact intensity may lead to a misrepresentation of the results and changing the predictions of the interventions. In T. Smieszek's paper (Smieszek, 2009) there is evidence for the need of differentiating contact intensities and proposes an approach to differentiate the potential contagious contacts. It shows why the duration and the intensity of different contacts should be included in the epidemiological model. In the agent-based epidemic model REINA (Tuomisto *et al.*, 2020), the agent has a list of individual properties as well as an age-specific probability distribution of the number of contacts per day. In real life, contacts are clustered for example by family relations, school, and work environments. The contact intensity differs for each location and each age group, so each set has a different contact pattern and therefore a particular probability of getting infected. In their paper, Tuomisto *et al.* (Tuomisto *et al.*, 2020) consider the different probabilities of transitioning from each category of the SEIR epidemic model differentiated by age group. These probabilities are shown in Table 1 of (Tuomisto *et al.*, 2020) paper. Another variable of interest is studied by Dattner *et al.* (Dattner *et al.*, 2020). They show that children are less susceptible to infection than adults and that they display fewer symptoms than adults when infected with the SARS-CoV-2 virus.

In summary, using epidemiological models to represent the spreading of an infectious disease is widely used. However, there is still a significant potential for contribution, especially implementing a methodology to consider the fitting variables and including them in the infection probability as explanatory variables that can be interpreted. This *disaggregate level* will allow us to assess

the choices of the population of their transportation mode, what socio-economic characteristics incentives their trips, how can we plan the transportation of a city in a post-pandemic world, etc.

3 Methodology

In this paper, we seek to extend a basic SIR model with its heterogeneity variation to develop a realistic disease tool. We expect to understand disease dynamics in specific groups of the population. In this Section we will present the characteristics of the dataset, the activity model and the epidemiological model.

3.0.1 Context of the dataset

We will analyze surveillance data reported to the Federal Office of Public Health. FOPH is the swiss government's federal entity for public health. Their main activity is to develop national health policy. However, they also represent Switzerland interests within international health organizations (for example, OECD or the World Health Organization). We anticipate to have access to their data.

3.1 Dataset

3.1.1 Variables and descriptive statistics

We expect to receive individual data that reads for each individual, its age, gender, home address (to calculate the average income of the person), if it is infected and when it was tested positive, the vaccine and when this vaccine was provided. Descriptions of the available variables are reported in Table 1.

3.2 Notation

For each individual i we define the notation in Table 2:

Variable	Description
Individual	Id of the individual.
Age	Age of the individual.
Gender	Gender of the individual.
Home	Coordinates of the individual home
Infected	If the SARS-CoV-2 test was positive or not
Vaccinated	If the individual was vaccinated
Vaccinationdate	When was the individual vaccinated

Table 1: Description of respondent specific variables

Notation	Description Variables
S	Susceptible population.
I	Infected population.
R	The population who recovered from the disease and got immunity.
Δt	The time-step of the simulation.
X_m	Explanatory variables from the dataset.
H	Total number of individuals in the population.
l_i^{met}	Number of individuals crossed by individual i .
H_i^{met}	Number of total crossings between two individuals.
ϵ_i	Error term explanatory variables of β_i .
μ_i	Error term explanatory variables of γ_i .
α_m	Parameters of the explanatory variables.
θ_m	Parameters of the explanatory variables.
β_i	Contagion rate between S and I.
$1/\gamma_i$	Length of the infectious period for population I .

Table 2: Table of notation

3.3 Activity model: event file

In agent-based modeling (ABM), a system is modeled as a collection of autonomous decision-making entities called agents. Each agent individually assesses their situation and makes decisions based on a set of rules. Agents may execute various behaviors appropriate for the system they represent. For example, producing, consuming, moving, and most importantly interacting with other agents. Agent-based models work in a disaggregate way (probability of infections are computed between individual agents), whereas compartmental models work in an aggregate way. They can be described as extensions of compartmental modeling with a stochastic framework.

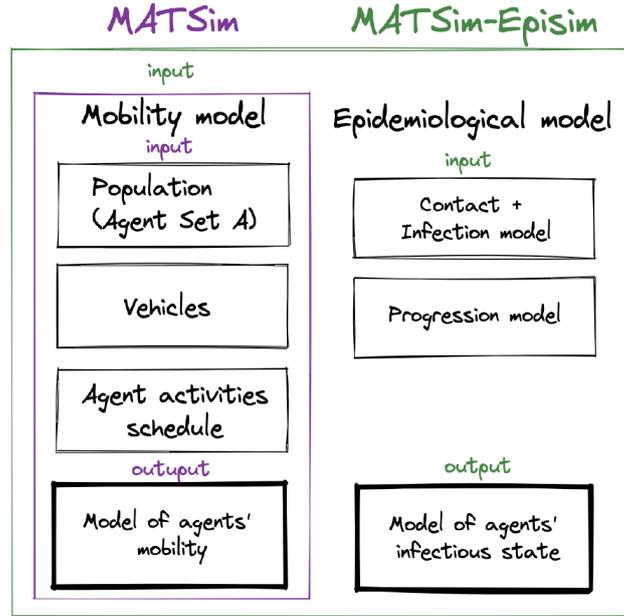


Figure 2: MATSim events output for travel by individual vehicle (on top) and for travel by public transport (at the bottom), (MATSim, 2021)

We use an activity model (MATSim, 2021) to produce the event files of each individual of our simulation. Its agent-based modeling provides a fine-grained modular framework. As we can see in Figure 2, we have the schedule of each individual for every day. This information is completed by the definition of the different activities, such as the transportation mode, leisure, home, errands and work. Also, another file defines the characteristics of the population which are introduced in Equations 19 and 21 as the explanatory variables X_m . The input data is taken from the Berlin OpenModel data which are mostly public.

Our goal is to study how the disease impacts the choice of activities. For that reason, we will modify the utility scoring function from the activity-based model to introduce the epidemiological penalty. (Charypar and Nagel, 2005) define the utility of a plan as Equation 14, and the utility of an activity as Equation 15.

$$S_{\text{plan}} = \sum_{q=0}^{N-1} S_{\text{act},q} + \sum_{q=0}^{N-1} S_{\text{trav, mode}(q)}. \quad (14)$$

$$S_{\text{act},q} = S_{\text{dur},q} + S_{\text{wait},q} + S_{\text{late.ar},q} + S_{\text{early.dp},q} + S_{\text{short.dur},q}. \quad (15)$$

We will add in Equation 15 another term called $S_{\text{level of virus load}}$ to define the impact that an epidemic has on the choice of activities, including travel mode. To estimate the parameters of the model we are planning to use already-existing methodologies like maximum likelihood or Bayesian methods.

We intend to keep working with the dataset provided by the OFSP. However, this dataset is too limited for a few applications (for example, an activity where infection occurs, biological characteristics of the virus, etc.). We will investigate other data sources. Also, we will validate this disaggregate model at the aggregate level.

3.4 Epidemiological model overview

Individuals can move through each compartment of the model during the disease following the distribution of the disease parameters. We characterize each disease by its state transition parameters. These parameters differ from virus to virus. For instance, we observe that for SARS-CoV-2, people are infected relatively early through the disease. In later stages, the infection can become more severe but appears to be less contagious to other people. The contagion rate controls the speed of spreading. We define it as the probability of contracting the disease between a susceptible and an infectious individual. When susceptible and infectious individuals meet, there is a certain probability that the susceptible person becomes infected and transitions from one state to the other. During the simulation, every susceptible individual i , at time t , has a probability, see Equation 16, of becoming infected.

$$\dot{P}_{S \rightarrow I}(t) = 1 - \exp\left(-\beta_i \frac{I}{H} dt\right) \quad (16)$$

Once this person is infected it has a probability of being recovered, see Equation 17. We consider that the individuals that are not recovered follow the distribution represented in Equation 18 to death.

$$\dot{P}_{I \rightarrow R}(t) = 1 - \exp\left(-\frac{1}{\gamma_i} dt\right) \quad (17)$$

$$\dot{P}_{NR \rightarrow D}(t) = 1 - \exp(-\lambda dt) \quad (18)$$

The β'_i , Equation 19 is defined as the sum of the different factors that make an agent recover (characteristics of the individual and virological attributes. Individual attributes can include age, gender, income, etc. By virological attributes, we understand parameters like viral load, contact intensity, ventilation characteristics, etc.

$$\beta'_i = \sum_{j=1}^m \alpha_m X_m + \epsilon_i \quad (19)$$

$$\beta_i = \beta'_i \frac{l_{met}}{H_{met}} \quad (20)$$

The $1/\gamma_i$, Equation 21 is defined as the sum of the contagion risks coming from the different sources of infections (characteristics of the individual and biological attributes).

$$\gamma_i = \sum_{j=1}^m \theta_m X_m + \mu_i \quad (21)$$

3.4.1 Vaccination

We introduce vaccination in our model by adding the effectiveness of the different vaccines against SARS-CoV-2, (Roa, 2021).

Vaccine	Effectiveness in %
NVX-CoV2373	96.0
Comirnaty	95.0
mRNA-1273	94.1
Sputnik V/Gam-Covid-Vac	91.6
BBIBP-CorV	79.0
AZD1222/Covishield	76.0
Ad26.COV2.S	72.0

Table 3: Effectiveness of vaccines against SARS-CoV-2, (Roa, 2021)

We generate random assignments of the vaccine following the different types of vaccines in each canton and the total number of doses. In Switzerland, three of the vaccines exposed on Table 3 have been distributed: BioNTech/Pfizer, Moderna and Johnson & Johnson.

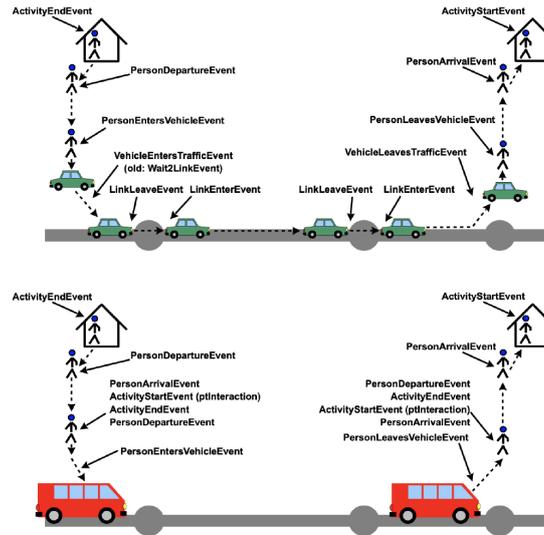


Figure 3: High-level description of the models' hierarchy

3.5 Simulation framework

3.5.1 MATSim-Episisim

In (Müller *et al.*, 2020) they use the term model to define two different entities. A model (agent-based) that is a disaggregated algorithmic description of a phenomenon. It includes a simulation, data-structures and is defined from the bottom-up. On the other side, a model (SEIR) is an aggregated mathematical description of a phenomenon from a top-down approach. Moreover, it defines two distinct agent-based models:

1. a mobility model describes the travel and activity behavior of the agent. The used framework is MATSim.
2. an epidemiological model describes the propagation of a virus in a given population based on a mobility model, a virus-transmission mathematical model and a compartmental mathematical model. The used framework is MATSim-Episisim.

In Figure 3 we can see a high-level description of this model. They are coupled by means of an input-output relationship. In other words, MATSim's output, the event file of the agents is used as the Episisim input, that models the infection spread of the agents.

4 Conclusions and future work

The objective of this paper is to provide a literature review for transportation and urban planners of epidemiological models. Also, a description of the preliminary considerations and presentation of the model. This model aims to predict the probability of the infection spreading process for a given population. This probability will be later implemented in a fully functional activity-based epidemiological model to assess the decision-making process in public transportation planning during an epidemic. The outcome would be a tool to forecast daily mobility and disease infection for given populations that share socioeconomic characteristics like age range or income.

Moreover, the activity-based approach will allow us to take into consideration how the epidemic phenomenon affects mobility behaviors. As already aforementioned, we expect to observe a reduced amount of trips using PT. The cause can be the subjective level of safety of public transport and mental comfort of the users. We intent to analyze this effect in different groups of the population that share socioeconomic attributes.

There are many potential contributions that align with this paper. We have identified several gaps in the literature that we will try to address at a further stage:

1. There is no consensus on how to best represent the infectiousness of a disease in a given population. Many assumptions try to explain how and why individuals get infected, some being difficult to verify with currently available data.
2. Most existing research in epidemiological modeling 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. We argue that diseases do not spread equally to every individual and in every activity, but might have a more dynamic process that is flexible towards feedback and trade-offs between each agent and its location.
3. Epidemiological models are a crucial element for public transportation planning and activity-travel behavior, especially during or after a pandemic. However, there is a lack of research focused on evaluating public transportation policies for a targeted group that considers at the same time the disease spreading and the travel mode chosen.

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