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Mobility and Individual Choices in the Spread of Infectious Diseases: Enhancing Activity-Based Models with Awareness and Testing Dynamics

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Abstract

The SARS-CoV-2 epidemic outbreak has left a deep impact on society, highlighting the urgent need to fully understand the role of human mobility in infectious disease spread and control [1]. For this reason, being able to model the behavior of individuals is key to understanding the impact of mobility in the context of infectious diseases, leading to an increase in the amount of literature developing epidemiological models.

Epidemiological models are essential tools used to predict disease dynamics and can be classified into three main types: compartmental [2], network-based [3, 4], and activity-based [5]. Each type offers a different perspective on disease transmission, from more aggregated observations (compartmental) to more individual-based indicators (activity-based). Compartmental models are based on aggregated compartments where individuals belong: for example, susceptible $\mathtt{S}$, infected $\mathtt{I}$, and recovered $\mathtt{R}$, neglecting the heterogeneity of the population. Network-based models focus on interactions between individuals within a network, making them computationally expensive to extend to large-scale populations. Activity-based models, the focus of our research, despite being CPU-intensive, offer a more detailed representation of individual behaviors, which is crucial for understanding disease spread in a real-world context. While activity-based epidemiological models have been widely used to guide public health responses during the pandemic, they have some limitations. Specifically, the literature indicates that activity-based models, although providing a more detailed perspective on individuals, tend to focus primarily on infection probabilities [6], overlooking personal choices such as test decisions. This oversight can lead to incomplete insights into how diseases spread and how people respond to their infection status.

Our research aims to address this gap by introducing the choice of testing of each individual and the concept of "awareness" into the modeling framework, providing a more comprehensive view of how diseases spread within the population. In this paper, we introduce a novel approach, which takes into account not only infection probabilities but also individual testing decisions. We propose an activity-based epidemiological model that adds two latent states for agents' behavior: the level of exposure $\mathtt{E}^\star$, and the propensity to test $\mathtt{Q}^\star$. Also, it introduces the concept of awareness as the key mobility-epidemiological indicator in an individual's journey through a disease. The probability of an individual being infected is modeled using a logit. The logit is defined by the individual's exposure level,

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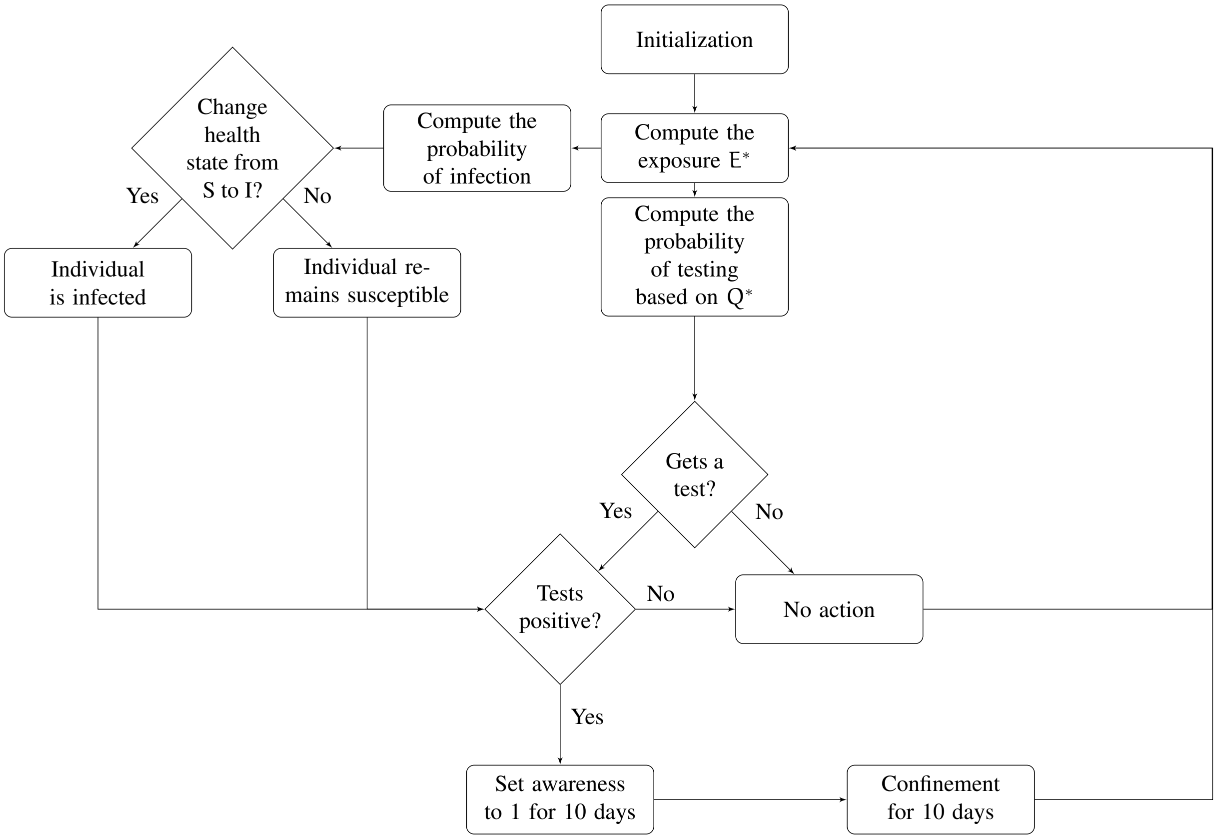

Figure 1: Overall dynamics of the discrete choice models inside the framework

which depends on the encounters with infected individuals and health characteristics. Once we compute the probabilities, we generate a random variable that determines the binary outcome of remaining susceptible or becoming infected. The process of someone deciding to get tested is modeled as a discrete choice model. An individual's likelihood of getting tested is predicted using a logit function that considers their underlying propensity to test. This propensity is influenced by the person's socioeconomic factors, their level of exposure to the virus, and the activities they perform. The output of these models allows us to compute the awareness indicator. Awareness represents when an individual not only contracts the virus, but also tests positive for it. From a mobility standpoint, this indicator is crucial because it deeply influences an individual's behavior. Once aware of their infection, individuals are likely to alter their activity-travel behavior, reduce interactions, and seek medical care. Currently, we assume that all the aware individuals go under a 10-day quarantine. The dynamics of the model are shown in Figure 1.

As input to the model, we employ an activity-based microscopic modeling technique [7], which provides us with detailed schedules and the socioeconomic characteristics of the individuals in our population. Furthermore, to ensure the reliability and precision of our framework, we calibrate the parameters of the latent states using real-world infection data. Regarding infection data, we dispose of daily positive tests in Switzerland and information about tested individuals from the Federal Office of Public Health (FOPH) from mid-February 2020 to mid-September 2021 [8]. It includes age, sex, municipality, vaccination doses, hospitalizations, and causalities. Furthermore, we use open-source aggregated data [9], including positive, negative, and tested counts, per age group. This calibration process allows us to estimate the model parameters, aligning its final disease dynamics with the ones observed in the data.

One of the most significant findings of our research challenges a common assumption in disease modeling: that an individual's positive test is equivalent to an active infection of the individual. This assumption neglects the underlying behavioral reaction of individuals not being aware of the infection, and therefore not changing their behavior. Our approach offers the possibility of distinguishing between the individuals who do not test positive and, therefore, do not alter their behavior, those who take measures upon receiving a positive result, or those who are scared and test very often with no positive results. This distinction is key for a comprehensive understanding of disease spread and its impact on activity-travel behavior, or even to forecast medical supplies. Furthermore, the framework also shows high computational efficiency: It runs in around 3 seconds for three months of simulation and 800,000 individuals. The computationally efficient aspect makes our model suitable for large-scale simulations and real-time decision support, and consequently for both researchers and policymakers.

In conclusion, our activity-based epidemiological model offers a fresh perspective on understanding the spread of the disease, not only during the SARS-CoV-2 pandemic but also for future infectious diseases. By accounting for the likelihood of infection and testing and the awareness of the individual, we can bridge the gap between human mobility patterns and individual behaviors, providing a deeper insight into how diseases propagate. As a behavioral-epidemiological tool that explains the intricate relationship between human behavior and disease dynamics, our model can help assess the process of developing targeted interventions to mitigate the impact of infectious diseases. Its practicality and efficiency make it a valuable asset to guide real-time decision-making in public health crises. Our approach integrates insights from various fields, including epidemiology, transportation, and discrete choice analyzes, bridging different research communities to provide an interdisciplinary approach.

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