Travel Behavior and Individual Choices in Infectious Disease Spread: Enhancing Activity-Based Models with Awareness and Testing Dynamics

IATBR 2024

Transport and Mobility Laboratory

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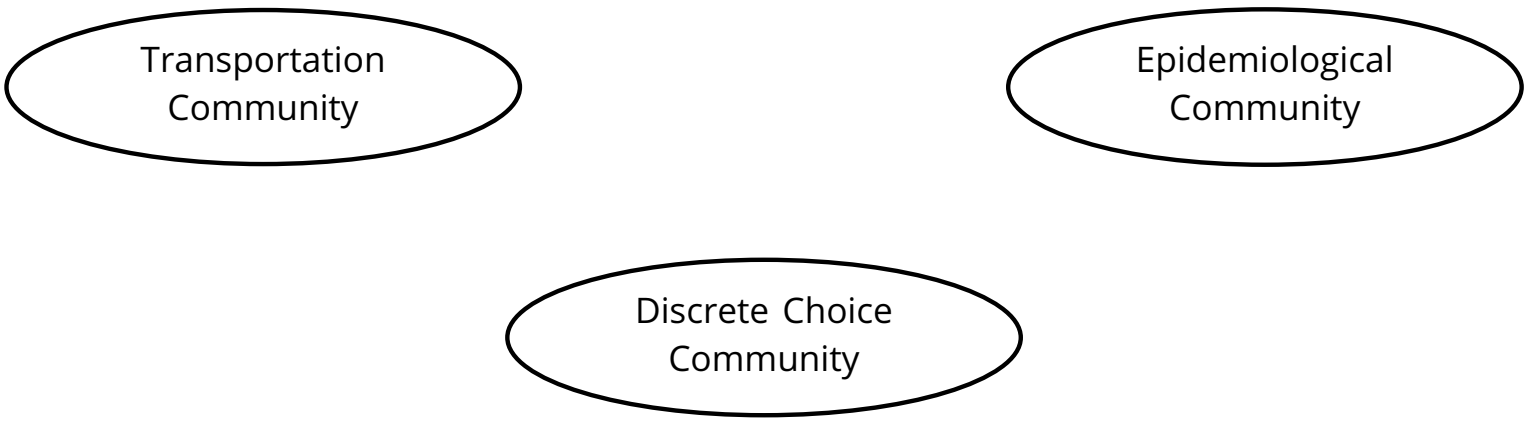
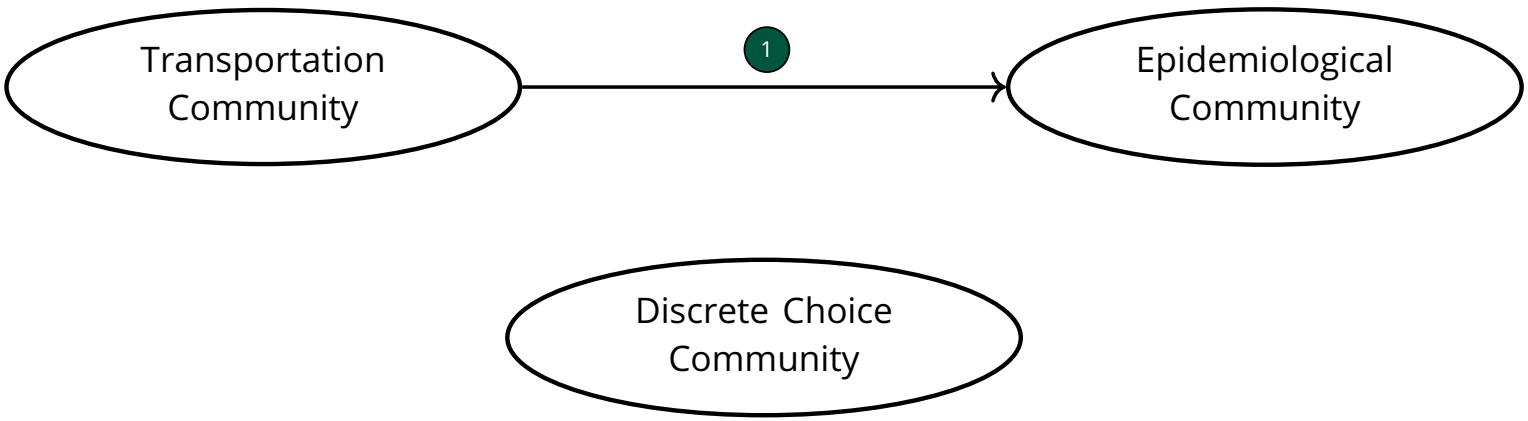
How do we link these communities?



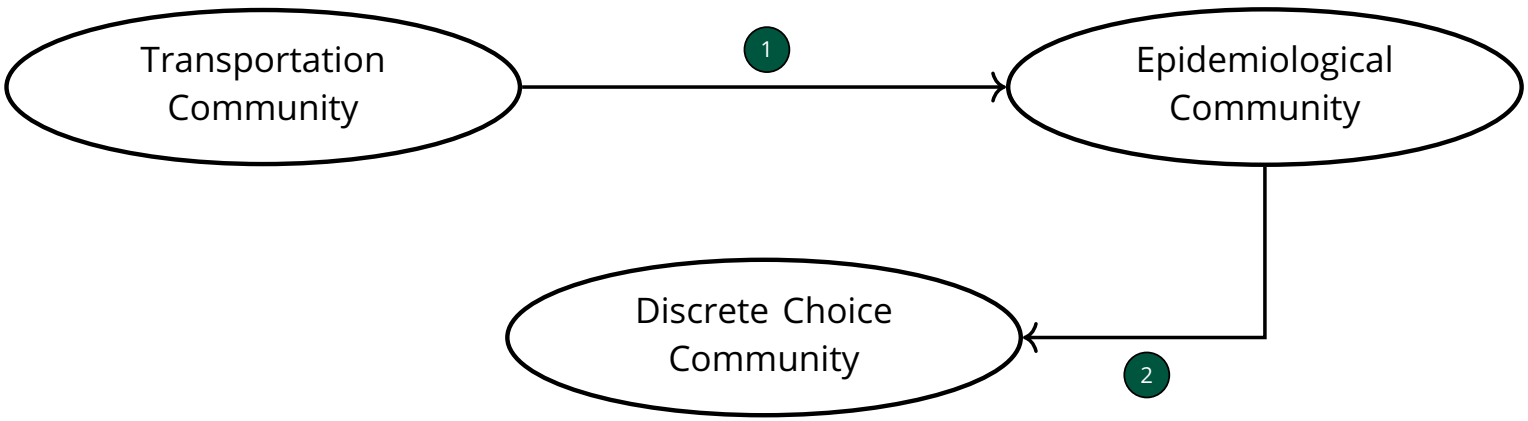
How do we link these communities?

1. Activity-travel behavior impacts the spread of a disease.



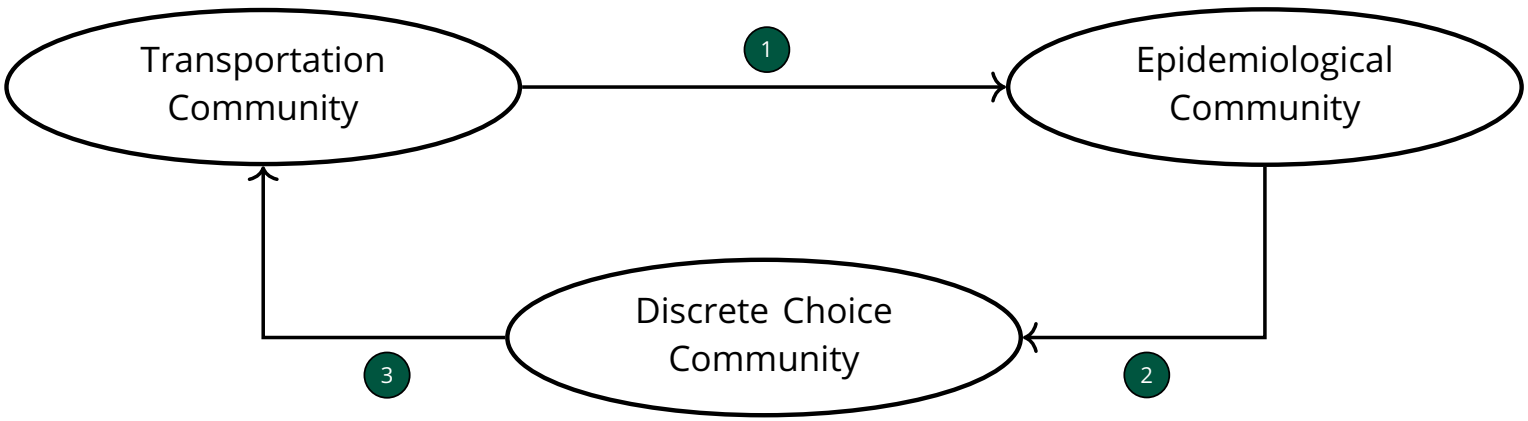
How do we link these communities?

1. Activity-travel behavior impacts the spread of a disease.
2. Being infected is not a choice, testing is.

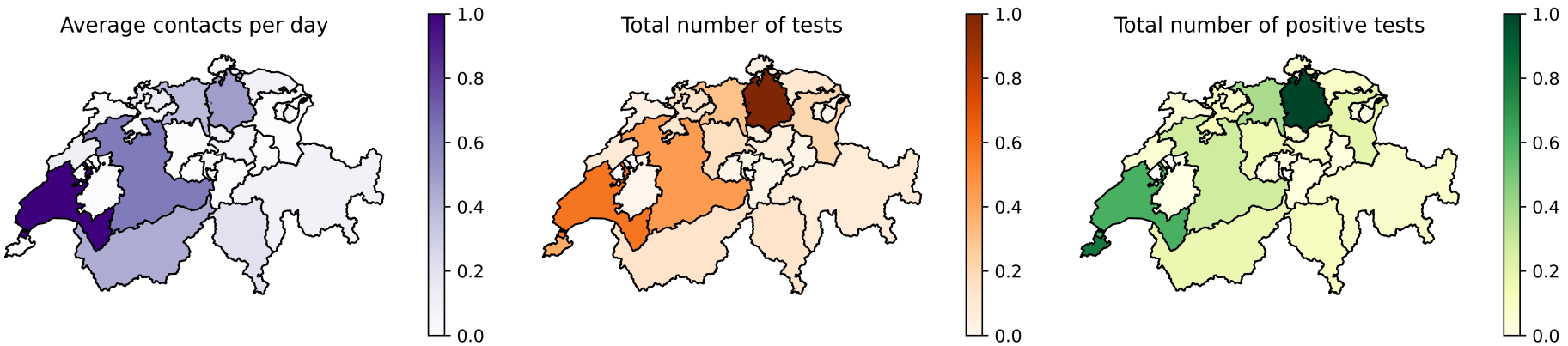


How do we link these communities?

1. Activity-travel behavior impacts the spread of a disease.
2. Being infected is not a choice, testing is.
3. Testing choices change the activity-travel behavior of the individuals, and therefore the spread of a disease.



Research Question



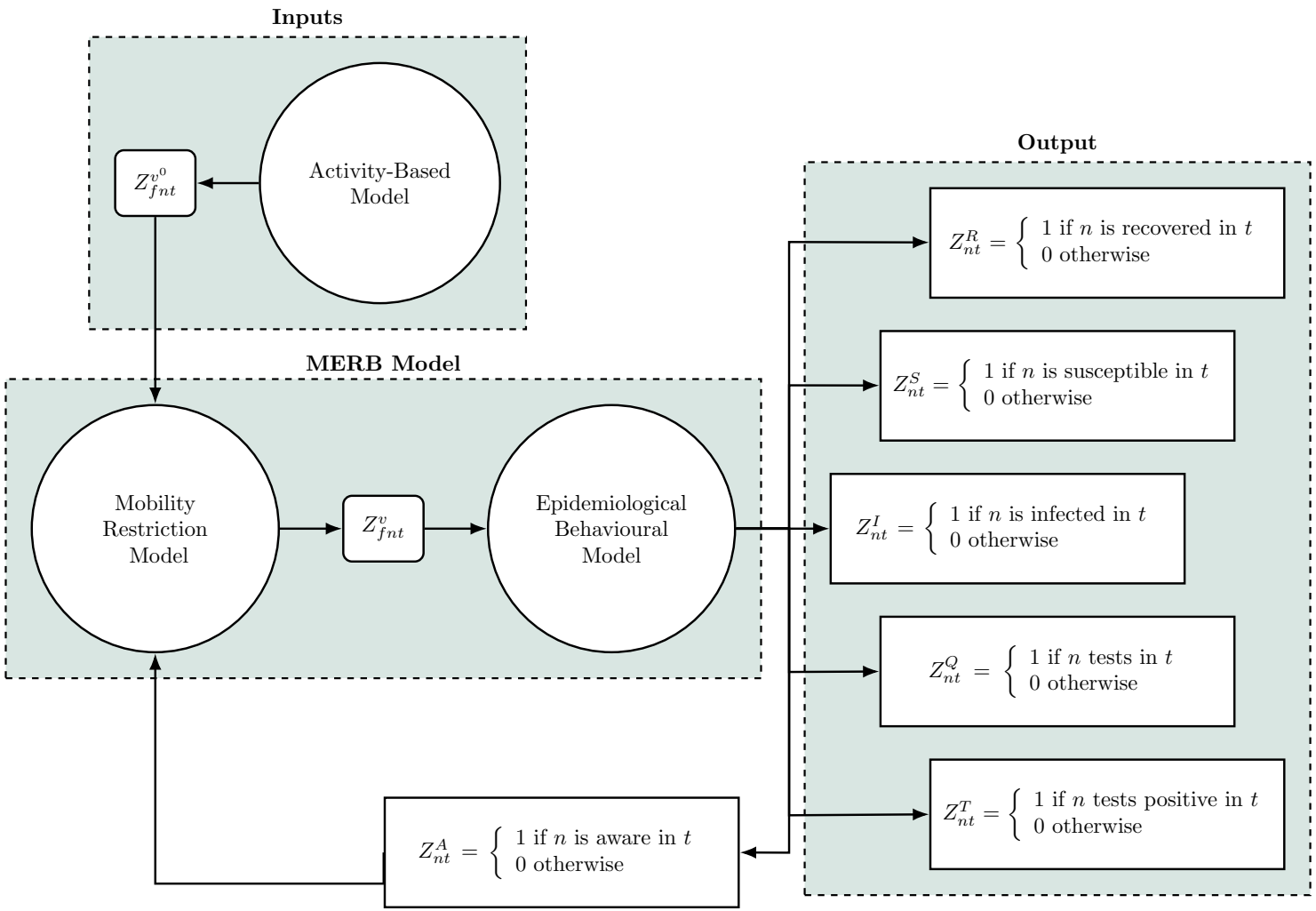
“How do individual testing choices influence activity-travel behavior, and therefore, the dynamics of disease spread?”

Research Gaps

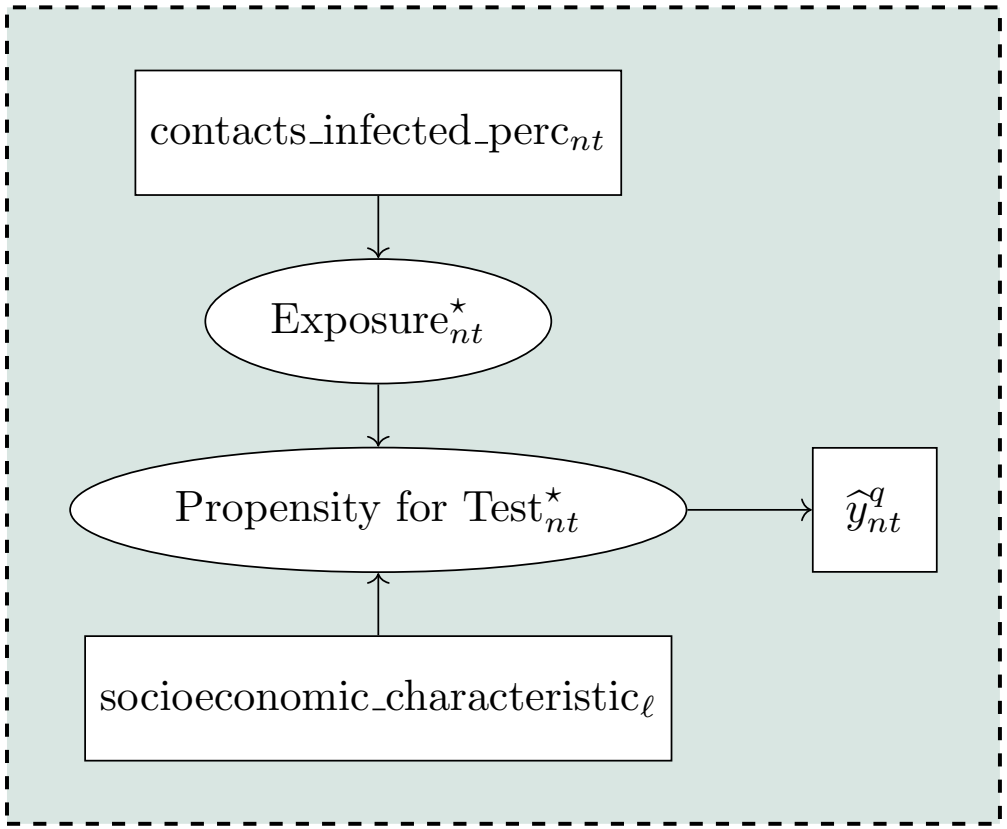
- Traditional models often overlook the **heterogeneity of individual actions** and their impact on the spread of disease (Hackl and Dubernet 2019; Eubank et al. 2004; Perez and Dragicevic 2009).
- Existing research does not fully integrate **socioeconomic and health factors** influencing mobility and epidemiological outcomes.
- There is a **lack of emphasis on individual choices**, particularly regarding testing and the subsequent behavioral adjustments (Cui, Ni, and Shen 2021; Brotherhood et al. 2020).
- Need for models that can **dynamically capture individual decisions** and their effects on the pandemic's trajectory (Tuomisto et al. 2020).

Main Problem: Lack of disaggregated data available.

Overall framework



Epidemiological-Behavioural Model



Structural model

- L socioeconomic characteristics: age, employment, income, level of education, etc.
- $\widehat{y}^{q}_{nt}$ binary observed data, 1 if the individual n tested at timestep t.
- contacts_infected_perc$_{nt}$: the proportion of infected individuals that individual n encounters in a facility f at timestep t, where $x^{v}_{nt} = \sum_{f} \sum_{m \neq n} Z^{v}_{fnt} Z^{v}_{fmt} Z^{i}_{mt}$.

Epidemiological-Behavioural Model: Structural equations

Exposure State

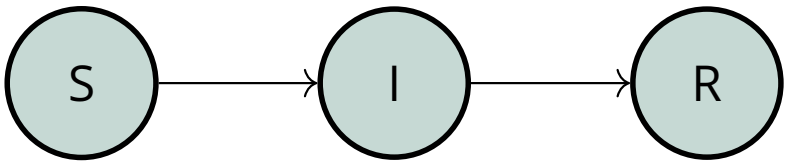
$$E^*_{nt} = \beta_v x^v_{nt} + \varepsilon_{E^\star}$$

Propensity to Test

$$Q^\star_{nt} = \beta^0_{Q^\star} + \sum_{\ell=1}^{L-1} \beta_\ell x^\ell_n + \eta_{E^\star} E^\star_{nt} + \varepsilon_{Q^\star}$$

- x^ℓ_n: L socioeconomic characteristics of indiviudal n.
- x^v_{nt}: is the number of contacts_infected_perc$_{nt}$.
- $\beta^0_{Q^\star}$, β_v, β_ℓ, $\eta_{E^\star}$, $\varepsilon_{E^\star}$, and $\varepsilon_{Q^\star}$ are parameters to be calibrated.

Dynamics of the MERB model: Health State Transition



A **hidden Markov chain** is employed to model the **transitions** between **health states**. The **state transition matrix** $\mathbb{B}$ is:

$$\begin{bmatrix} P(Z^s_{n(t+1)} = 1 | Z^s_{nt} = 1) & P(Z^i_{n(t+1)} = 1 | Z^s_{nt} = 1) & 0 \\ 0 & P(Z^i_{n(t+1)} = 1 | Z^i_{nt} = 1) & P(Z^r_{n(t+1)} = 1 | Z^i_{nt} = 1) \\ P(Z^s_{n(t+1)} = 1 | Z^r_{nt} = 1) & 0 & P(Z^r_{n(t+1)} = 1 | Z^r_{nt} = 1) \end{bmatrix}$$

Dynamics of the MERB model: Health State Transition

Is the individual **becoming infected or remaining susceptible**?

$$P(Z^{i}_{n(t+1)} = 1 | Z^{s}_{nt} = 1) = E^{\star}_{nt} \tag{1}$$

$$P(Z^{s}_{n(t+1)} = 1 | Z^{s}_{nt} = 1) = 1 - P(Z^{i}_{n(t+1)} = 1 | Z^{s}_{nt} = 1) \tag{2}$$

$$Z^{i}_{n(t+1)} = \begin{cases} 1, & \text{if } \pi < P(Z^{i}_{n(t+1)} = 1 | Z^{s}_{nt} = 1) \\ 0, & \text{otherwise.} \end{cases} \tag{3}$$

π: random uniform value

Dynamics of the MERB model: Health State Transition

Is the individual **becoming recovered or remaining infected**?

$$P(Z^r_{n(t+1)} = 1 | Z^i_{nt} = 1) = \Phi_{\gamma_n}(t - t^i_n)$$

Φ_{γ_n}: cumulative distribution function of the log-normal distribution of γ_n (recovery rate (Kerr et al. 2020)).
$t - t^i_n$: number of timesteps that satisfy $Z^i_n = 1$.

For each infected individual n at time t, we decide if they will be recovered by time t given that they were infected at time t^i_n, by computing:

$$Z^r_{n(t+1)} = \begin{cases} 1, & \text{if } \pi < P(Z^r_{n(t+1)} = 1 | Z^i_{nt} = 1) \\ 0, & \text{otherwise.} \end{cases} \quad (4)$$

Dynamics of the MERB model: Health State Transition

Finally, we assume that an individual who recovers remains recovered until the end of the simulation.

$$P(Z^r_{n(t+1)} = 1 | Z^r_{nt} = 1) = 0,$$

$$P(Z^s_{n(t+1)} = 1 | Z^r_{nt} = 1) = 0.$$

Dynamics of the MERB model: Testing process

What about the testing process?

We model the probability of an individual to test through a logit:

$$P(Z^q_{n(t+1)} = 1) = \frac{1}{1 + e^{-\mu Q^\star_{nt}}}, \tag{5}$$

and each individual n at time t, decides to get tested by generating π, and following:

$$Z^q_{n(t+1)} = \begin{cases} 1, \text{if } \pi < P(Z^q_{nt}) \\ 0, \text{otherwise.} \end{cases} \tag{6}$$

Dynamics of the MERB model: Mobility Restriction Model - What about awareness?

Assumption:

Only people that are infected and test positive will quarantine.

$$Z^a_{nt} = Z^i_{nt} Z^+_{nt} \tag{7}$$

Now, we apply the mobility restriction model, and the new dynamics can be written as:

$$Z^v_{fn(t+1)} = \begin{cases} Z^v_{fnt} & \text{if individual's } n \text{ outcome is 0, and} \\ 0 & \text{otherwise.} \end{cases} \tag{8}$$

Results: Case Study - Population of Vaud

Study Focus

- Our study examines the population of **Vaud in Switzerland** (**823'456 individuals**).
- A **synthetic population** is generated to simulate **socio-economic characteristics** and **daily schedules** for each individual (Horl and Balac 2021).

Data requirements

- **Open-source data** including **number of tested individuals** ($\widehat{y}^{q}_{gw}$) and **positive tests** ($\widehat{y}^{+}_{gw}$) individuals (CloudPlatform 2021).
- Data from **Federal Office of Public Health** including the **tested positive** individuals ($\widehat{y}^{+}_{hjk\ell}$) with their **age, gender and municipality** information (Riou et al. 2021).

Results: Case Study - Population of Vaud

Data and Model Development

Due to the unavailability of disaggregated data:

- The exposure level of an individual (E^*_{nt}) is calculated as:

$$E^*_{nt} = \beta^v x^v_{nt}, \tag{9}$$

- The propensity to test of an individual ($Q^\star_{nt}$) is calculated as:

$$Q^\star_{nt} = \beta^0_{Q^\star} + \beta_{\text{age}} x^{\text{age}}_n + \beta_{\text{employment}} x^{\text{employment}}_n + \eta_{E^\star} E^\star_{nt}, \tag{10}$$

where:

- x^{age}_n represents the age, and $x^{\text{employment}}_n$ represents the employment status of the individual.
- β_{age}, $\beta_{\text{employment}}$, β^v,$\beta^0_{Q^\star}$ and η are parameters to be estimated.

Measurement equations

Since available **data** tends to be **aggregated**,

we link the tests performed for each individual and timestep, with the observed number of tests by defining:

$$P^q_{gw} = \sum_{n \in g} \sum_{t=1}^{7T} P(Z^q_{nt} = 1), \tag{11}$$

$$P^+_{hjk\ell} = \sum_{i \in h,j,k\ell} \sum_{t=1}^{T} P(Z^+_{nt} = 1). \tag{12}$$

Beware: The lack of panel data presents a challenge because the modeling of testing choices is influenced by preceding ones.

Epidemiological-Behavioural Model: Measurement equations

Data & Likelihood functions

We use the **negative binomial distribution** for modeling the count data.

$\mathcal{L}_1(\theta)$ - testing

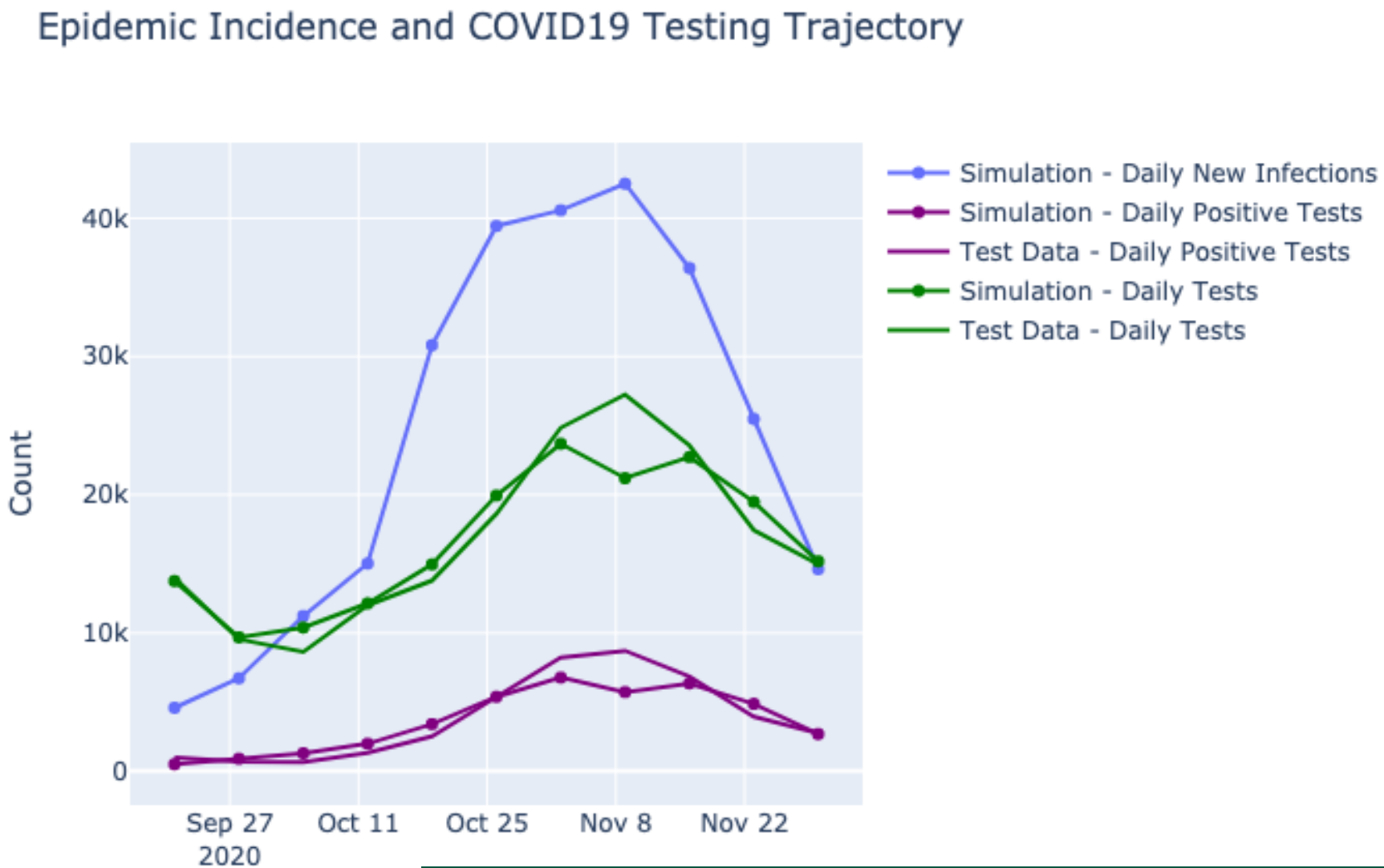
$$= \sum_{i \in g} \sum_{w \in W} \Big(\log \Gamma(\widehat{y}^q_{gw} + r_1) - \log \Gamma(r_1) - \log \Gamma(\widehat{y}^q_{gw} + 1) + r_1 \cdot \log \left(\frac{r_1}{r_1 + P^q_{gw}} \right) + \widehat{y}^q_{gw} \cdot \log \frac{P^q_{gw}}{r_1 + P^q_{gw}} \Big),$$

$\mathcal{L}_2(\theta)$ - testing positive

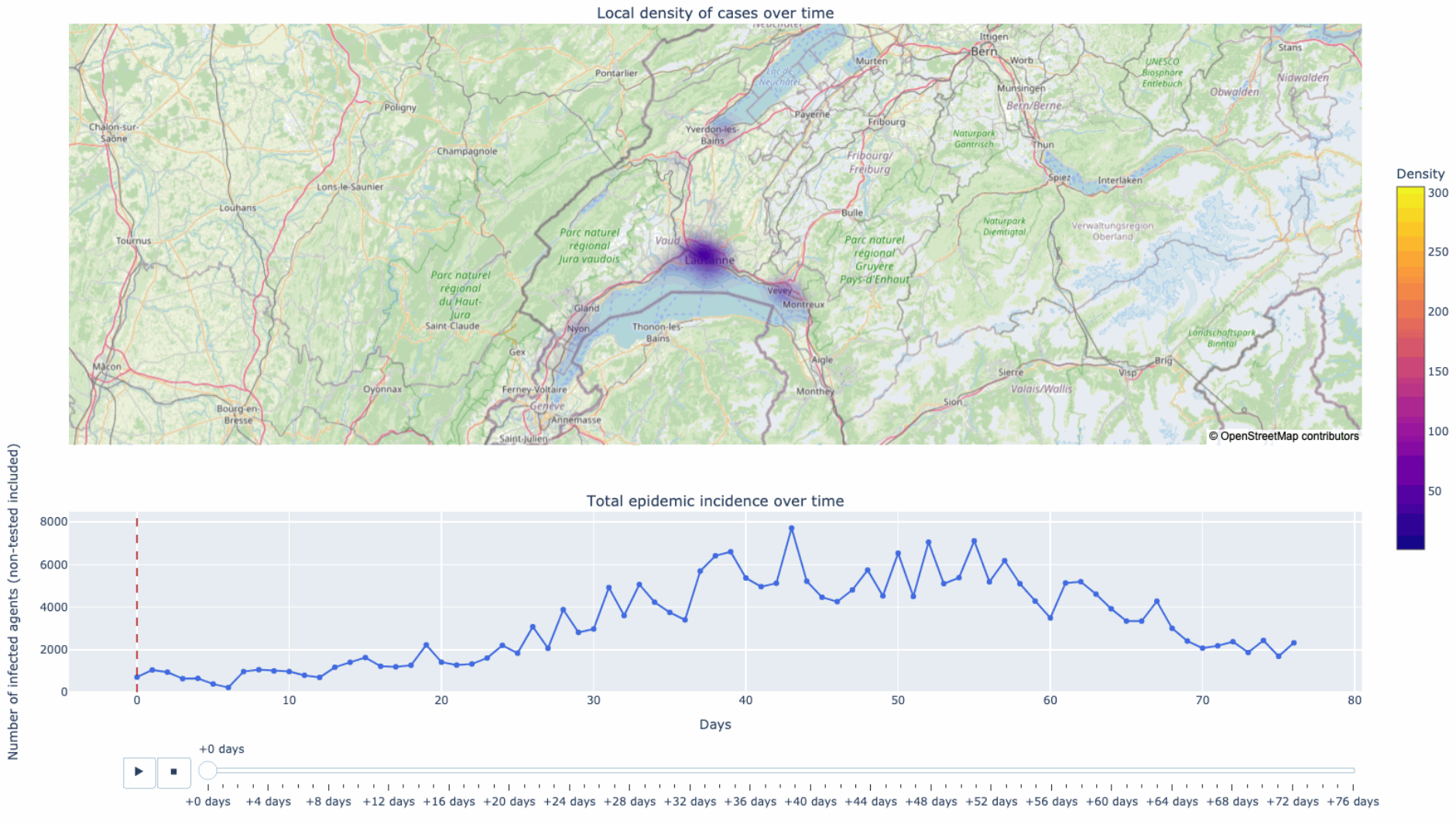
$$= \sum_{i \in h,j,k\ell} \sum_{\ell \in L} \Big(\log \Gamma(\widehat{y}^+_{hjk\ell} + r_2) - \log \Gamma(r_2) - \log \Gamma(\widehat{y}^+_{hjk\ell} + 1) + r_2 \cdot \log \left(\frac{r_2}{r_2 + P^+_{hjk\ell}} \right) + \widehat{y}^+_{hjk\ell} \cdot \log \frac{P^+_{hjk\ell}}{r_2 + P^+_{hjk\ell}} \Big).$$

where r_1 and r_2 are the parameters of the negative binomial, $\widehat{y}^+_{gw}$ are the positive tests per age group, g, and week w, and $\widehat{y}^+_{hjk\ell}$ are the positive tests per age, h, gender, j, and municipality k, per day ℓ.

Calibrated model: aggregated validation

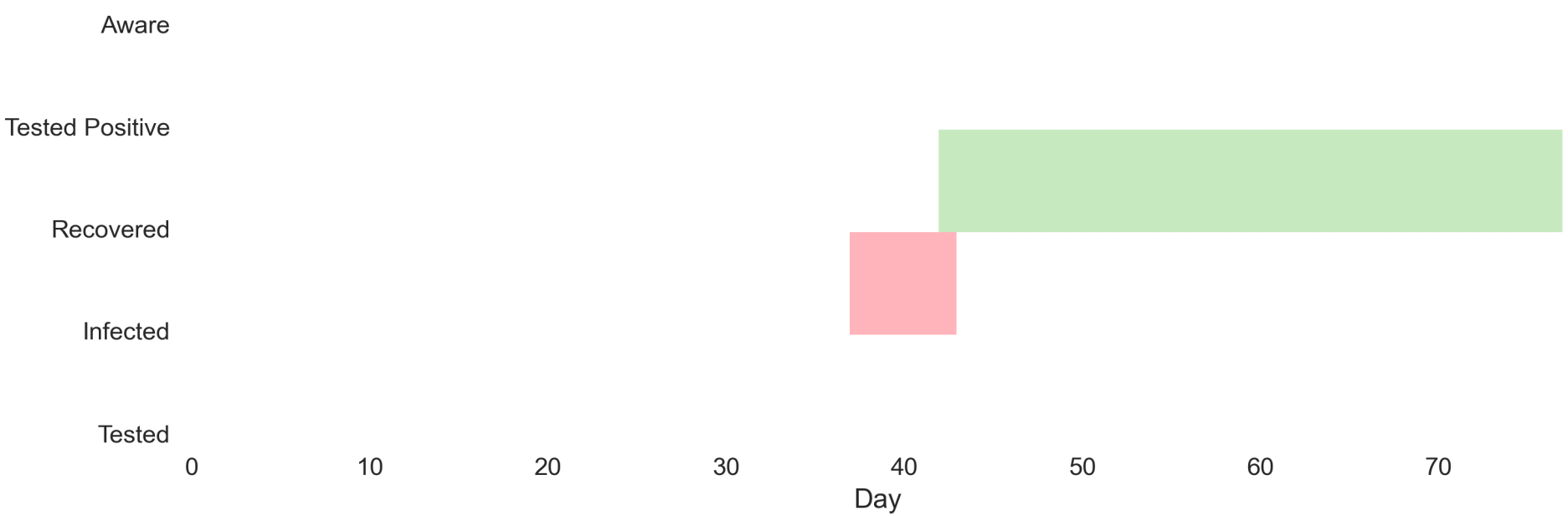


Results across geographical area



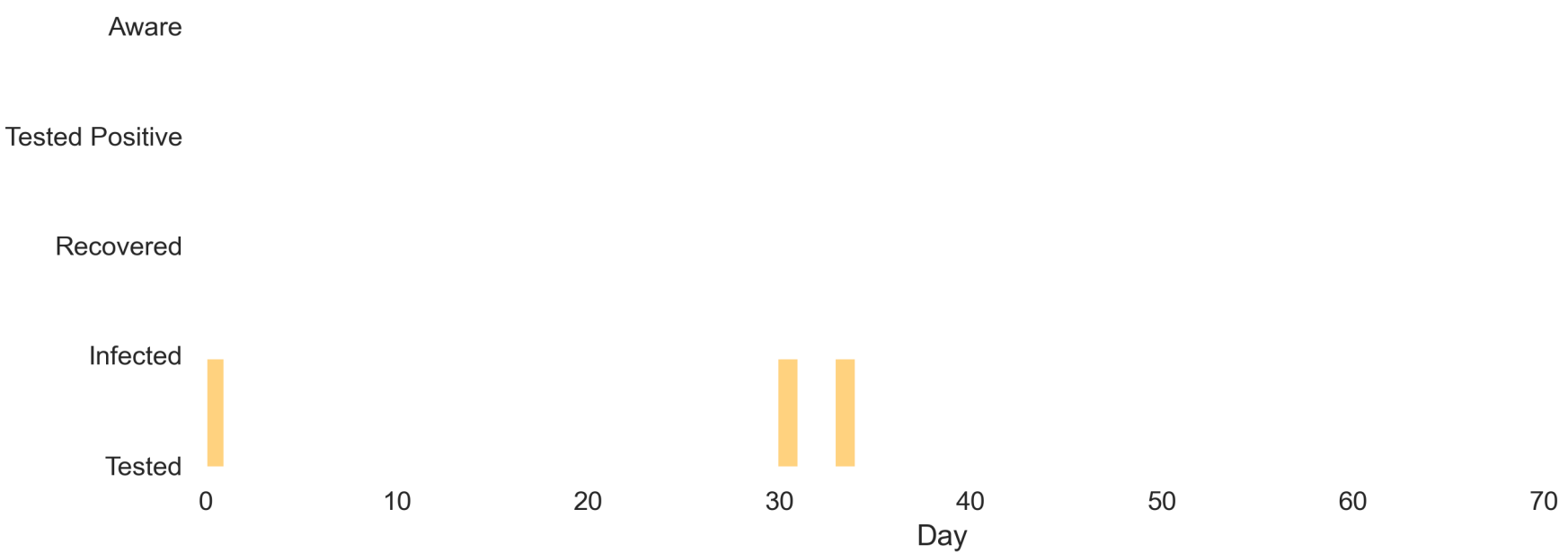
Results across individuals: insights on behavior

The 'unaware' behavior:



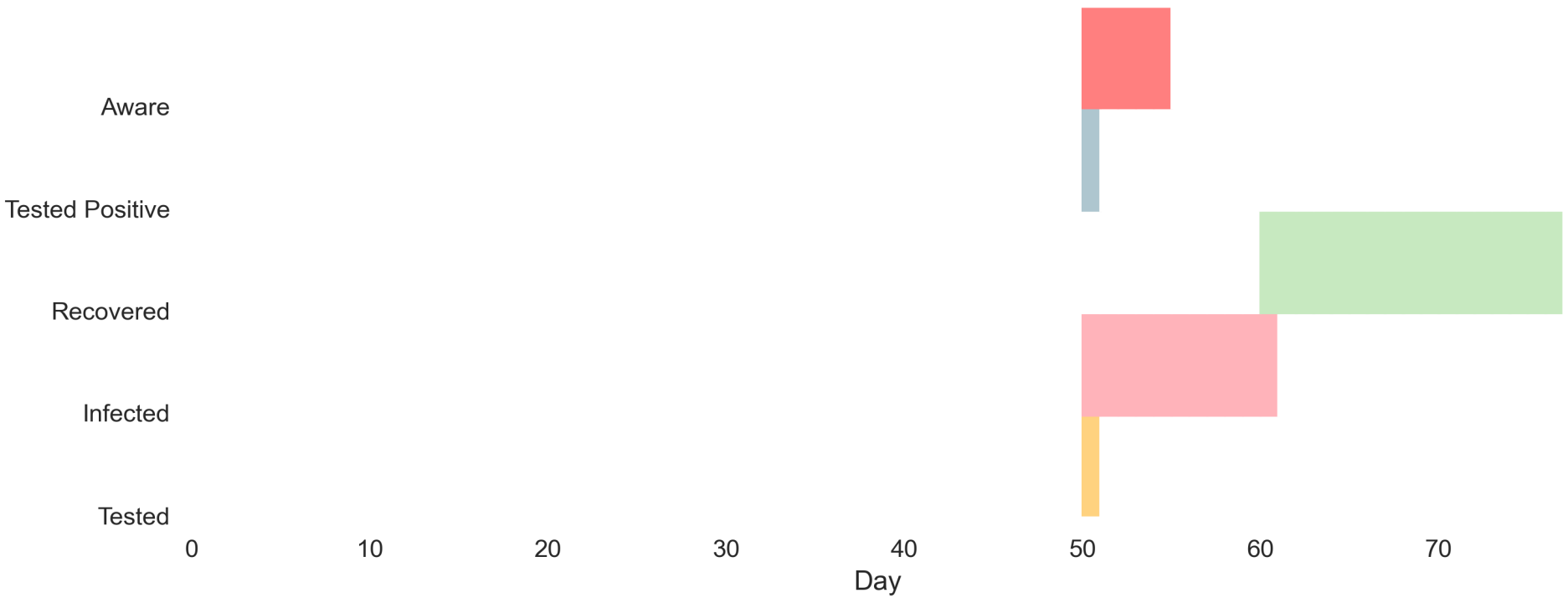
Results across individuals: insights on behavior

The 'cautious' behavior:

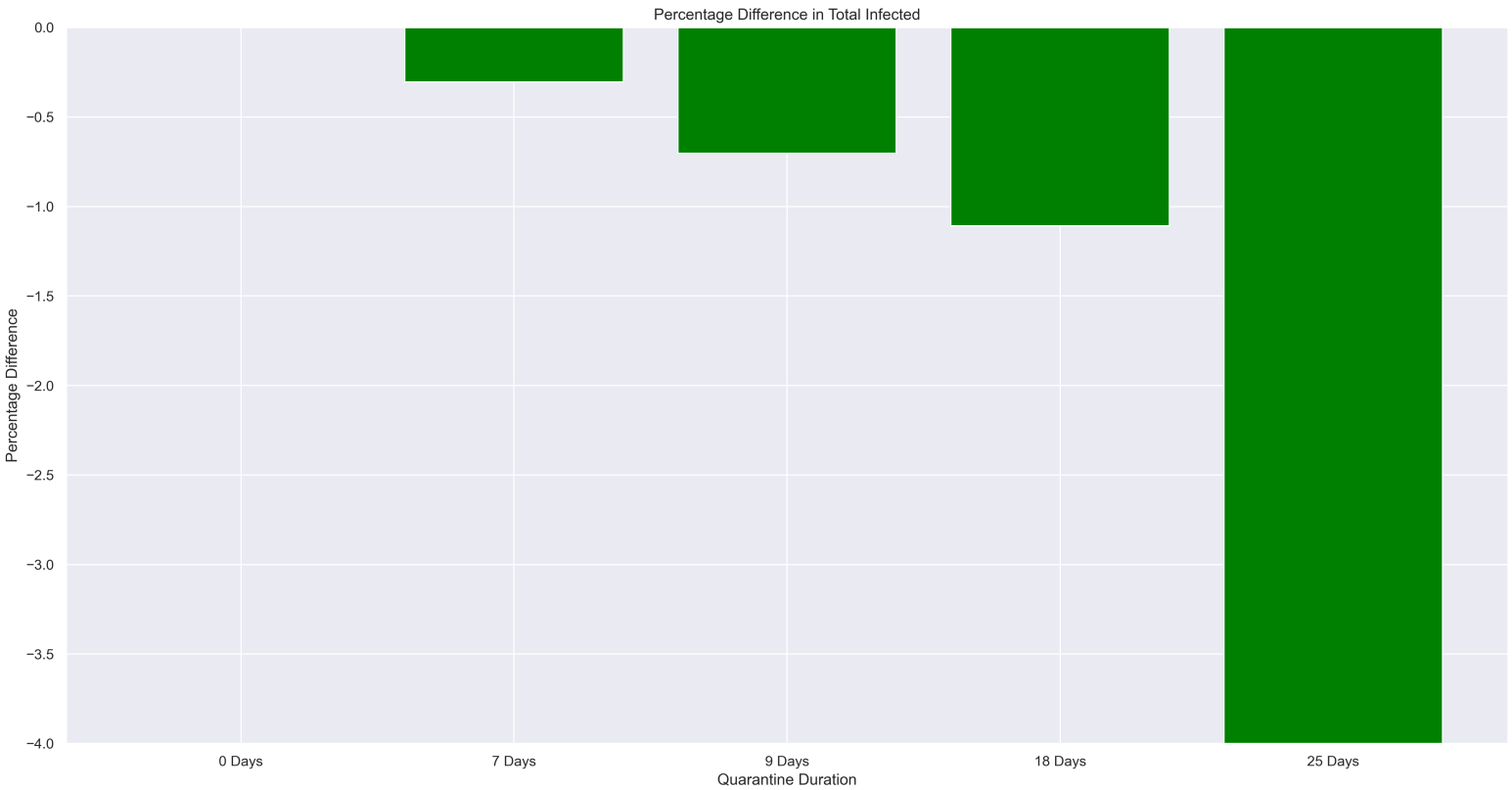


Results across individuals: insights on behavior

The 'full package' behavior:



Results by applying different confinements



Conclusion and Future Work

Conclusions:

1. Tool that effectively models the individual dynamic choice of testing, and the impact on activity-travel behaviour.
2. We are able to predict the actual infected individuals (in our case study are around 3 times higher than the tracked data).
3. A computationally efficient tool (1m 11s for 800k individuals and 90 days with a timestep of 30m).
4. Lack of disaggregated data always makes it hard to calibrate the models.
5. Bridging epidemiology, transportation, and discrete choice communities for a interdisciplinary model that can better explain how and why a spreading occurs.

Future work:

1. Include health characteristics and calibrate the model.
2. Run this model together with the policy optimization framework from Cortes Balcells 2021.
3. Run the model for different cantons and see how the testing behavior impacts the spreading.

Thank you for your attention

Testing process

The outcome of the test is computed by:

$$P(Z^+_{nt} = 1|Z^i_{nt} = 1) = P(Z^+_{nt} = 1|Z^q_{nt} = 1 \text{ and } Z^i_{nt} = 1)P(Z^q_{nt} = 1 \text{ and } Z^i_{nt} = 1) =$$
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