Estimating the Impact of Asymptomatic Carriers on the Spread of Infectious Diseases: An Interaction-based Model

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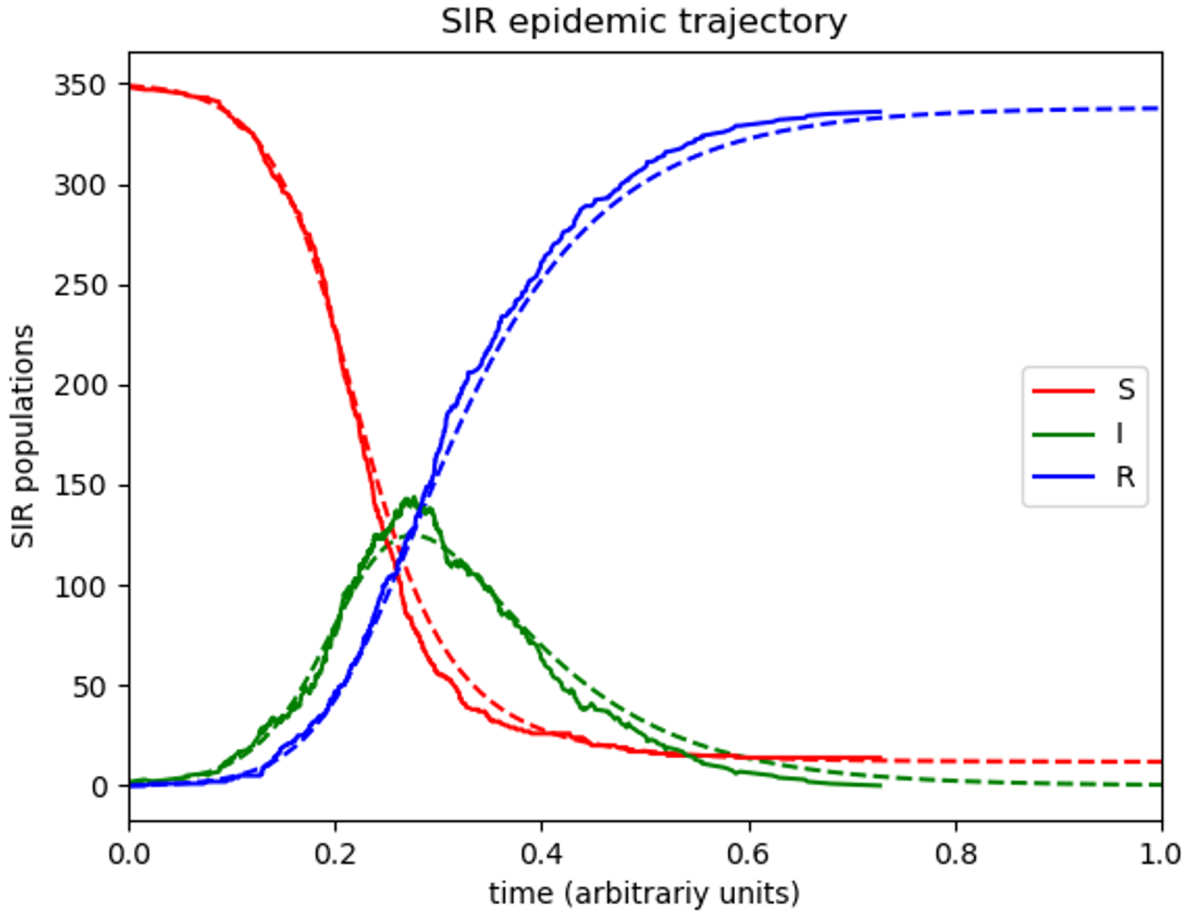
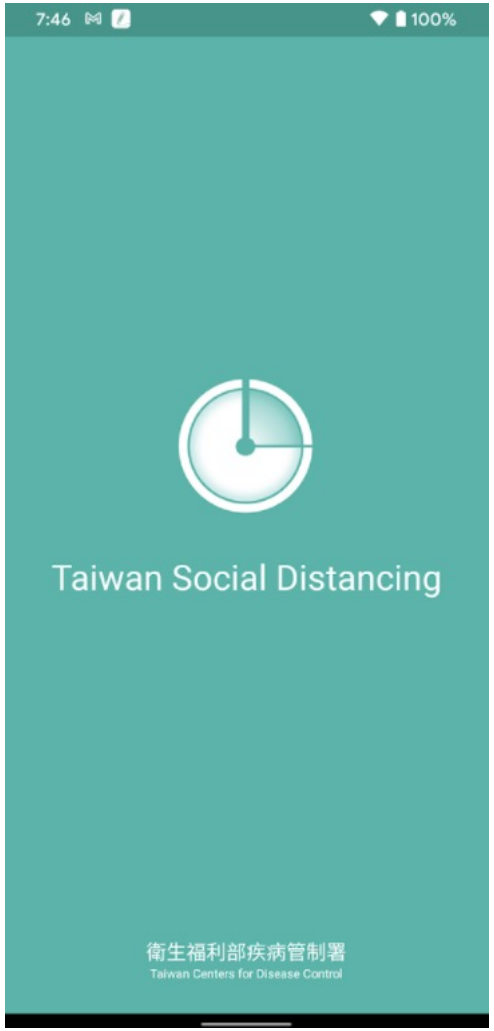
Research Question

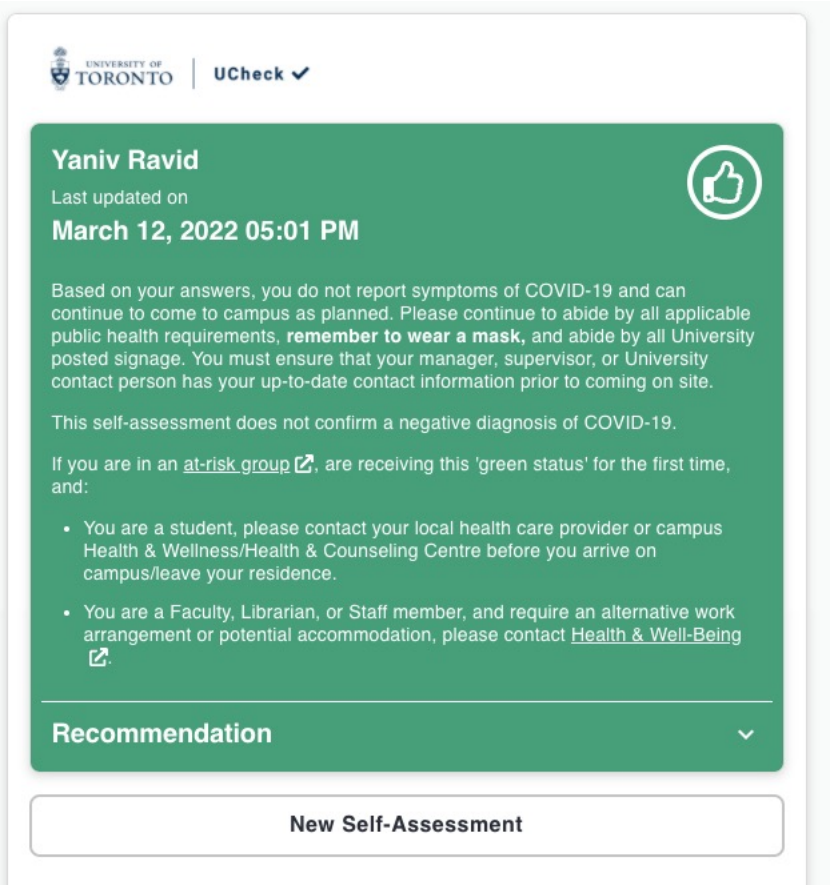
- How can epidemiological models be used to detect specific sub-groups that pose the greatest risk of infection to the population?
  - Can asymptomatic carriers be addressed and targeted by such methodologies?



Research Question



How can epidemiological models help us actively combat the pandemic, and not only describe it?



Background

Classic epidemiological models: population is split into groups and a transition diagram specifies the flow from one group to another

1. Susceptible (S)
2. Exposed (E)
3. Infected (I)
4. Recovered/Removed (R)

Transition rates and model parameters dictate the evolution of each group:

$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$

$$\frac{dE}{dt} = \beta SI - (\mu + \alpha)E$$

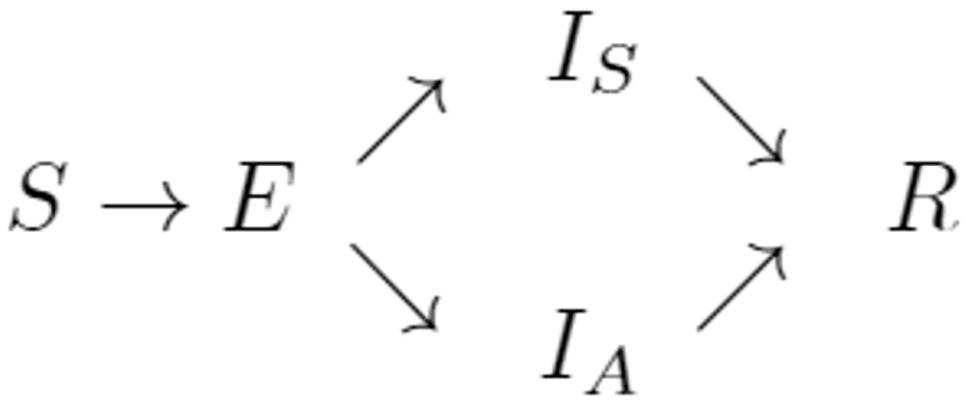
Problem Statement

Can individuals be differentiated from one another, and can active infectious vectors be isolated from the rest?

Specifically, can asymptomatic carriers be identified among the population? If so, with what accuracy can this classification be made?

Proposed Solution & Modifications to SEIR

Split the infectious group into symptomatic and asymptomatic:



Model the group's evolution in accordance with classical models:

both infectious groups can expose others

$$\frac{dS}{dt} = \mu - \beta S(I_S + I_A) - \mu S$$

$$\frac{dE}{dt} = \beta S(I_S + I_A) - (\mu + \alpha)E$$

rate of flow into the two new groups

$$\frac{dI_S}{dt} = \alpha p E - (\mu + \gamma_S)I_S$$

rate of recovery (1/infectious period)

$$\frac{dI_A}{dt} = \alpha(1-p)E - (\mu + \gamma_A)I_A$$

$$S + E + I_S + I_A + R = 1$$

Proposed Solution & Modifications to SEIR

Additional Assumptions:

1. Births and deaths are negligible. This would be equivalent to setting $\mu = 0$ in the original SEIR model.
2. Contact occurs in discrete times, not continuously.
3. At every time interval t, the susceptible (S), exposed (E), symptomatic (I_S) and asymptomatic (I_A) populations are spread among $n_{cells}(t)$ infection cell. Individuals can only contact others who are in the same infection cells as them. Additionally, all contact between individuals is known and stored as historical data.
4. When a susceptible interacts with an infected individual, the susceptible entity becomes exposed with probability p_{expose} or remains susceptible with probability $1 - p_{expose}$. This exposure parameter is similar in nature to β in the SEIR model.

Proposed Solution & Modifications to SEIR

Additional assumptions:

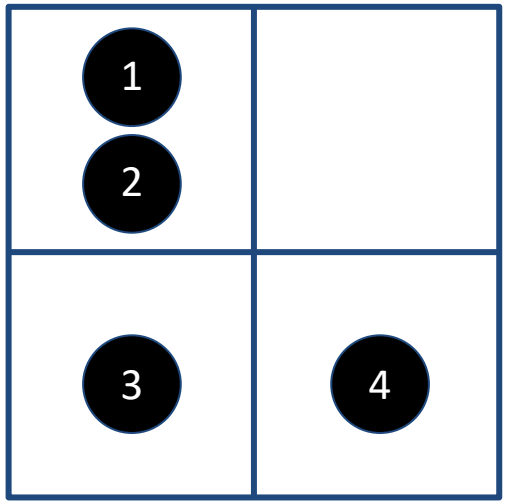
5. When a susceptible individual becomes exposed, an incubation period of t_{inc} discrete time steps begins. During this period, an exposed individual cannot transmit the disease to others. After this incubation period, two possible outcomes can occur:

   (a) With probability p_{sympt}, the exposed individual begins to show symptoms and is isolated after t_{sympt} periods of infectiousness. Isolation is comprised of complete removal from the system and no further interactions with others. However, during the initial t_{sympt} incubation period, the individual can expose the virus to other entities it contacts. We note that all isolated symptomatic individuals are known, identifiable and countable.

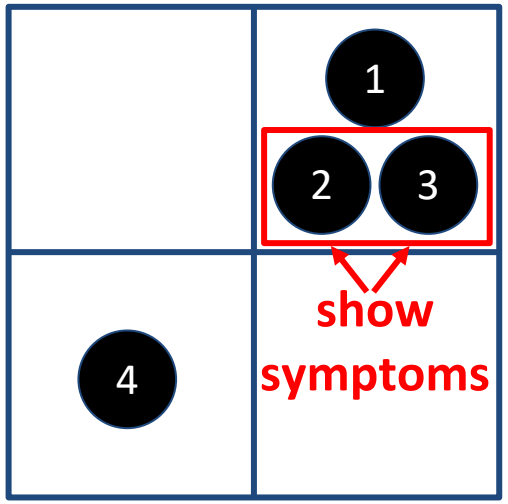
   (b) Alternatively, with probability $p_{asympt} = 1 - p_{sympt}$, once incubation is complete, the individual might not show symptoms. During t_{asympt} periods after incubation, the individual can expose other entities it interacts with to the virus. After this period, the asymptomatic carrier recovers and cannot infect others or get re-infected.

Classification Model: Interaction Counting

$t = t_0$



$t = t_0+1$



$V = \Sigma Y_i \quad \forall$ *symptomatic i*

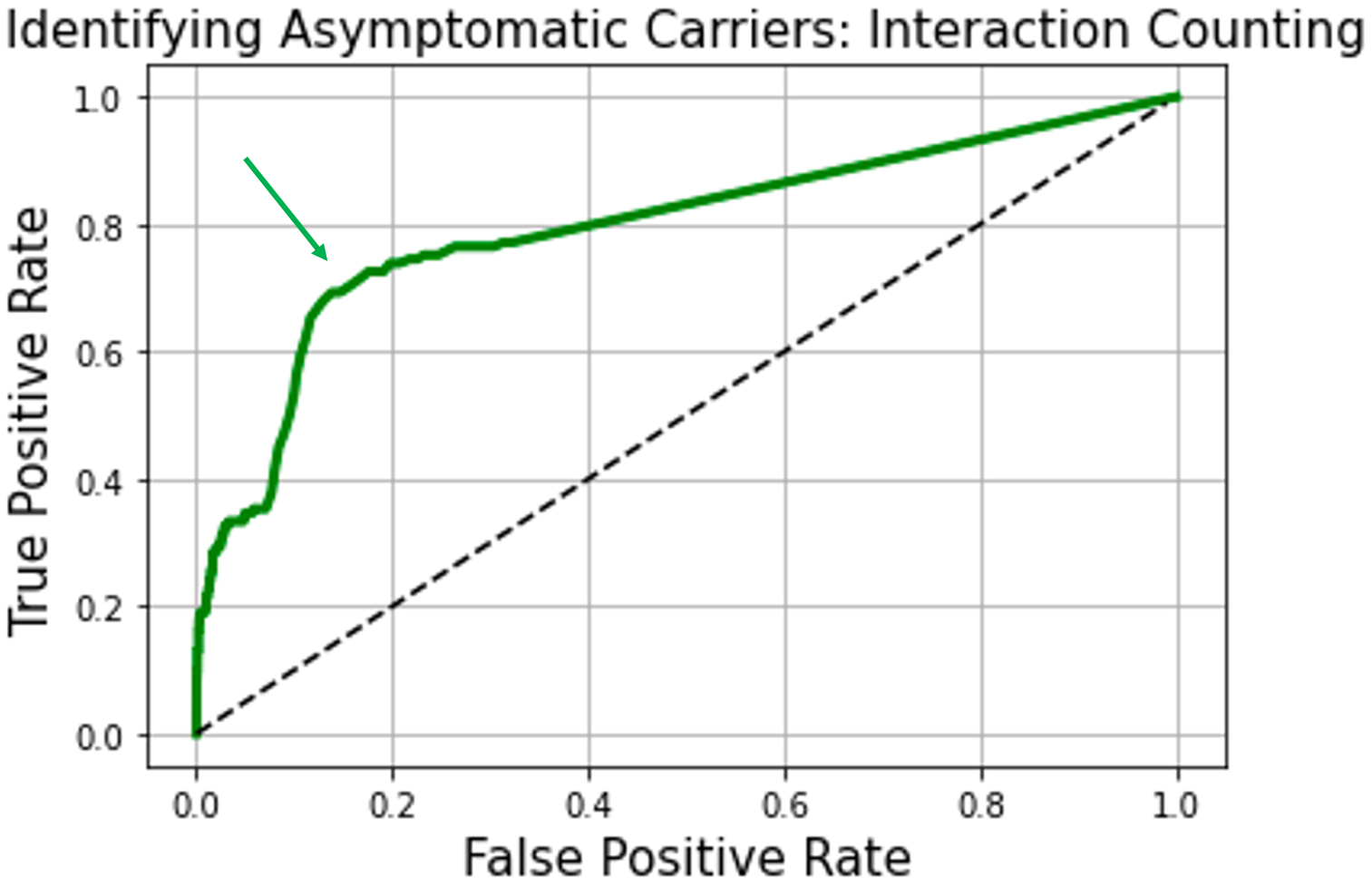
$= \begin{pmatrix} 3 & 1 & 1 & 0 \end{pmatrix}$

1: likely infectious *4: likely susceptible*

$$Y(t_0) = \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

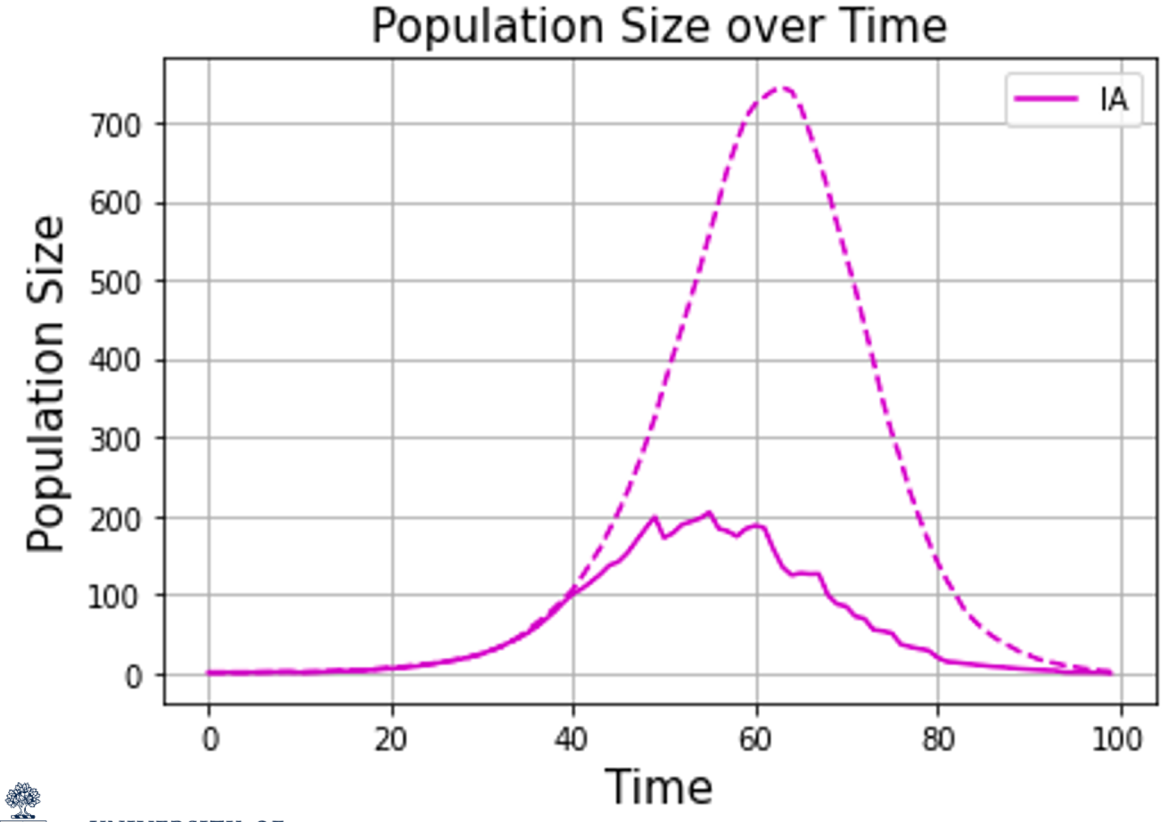
$$Y(t_0+1) = \begin{pmatrix} 0 & 2 & 1 & 0 \\ 2 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \begin{matrix} \\ Y_2 \\ Y_3 \\ \\ \end{matrix}$$

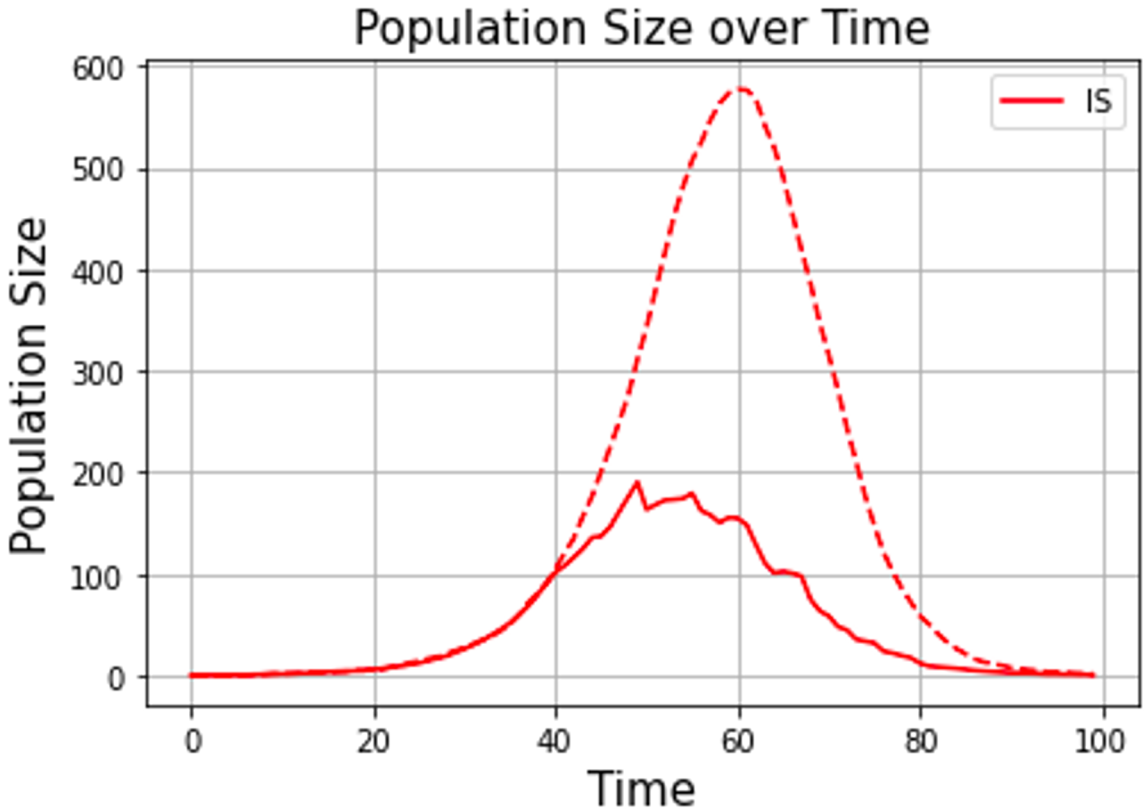
Classification Model: Interaction Counting



Policy Proposal: Removing Asymptomatics

Experiment: remove 10% of suspected asymptomatics using the proposed classifier





Thank you!

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