Multi-Level Biosensor-based Epidemic Forecasting in Small Areas

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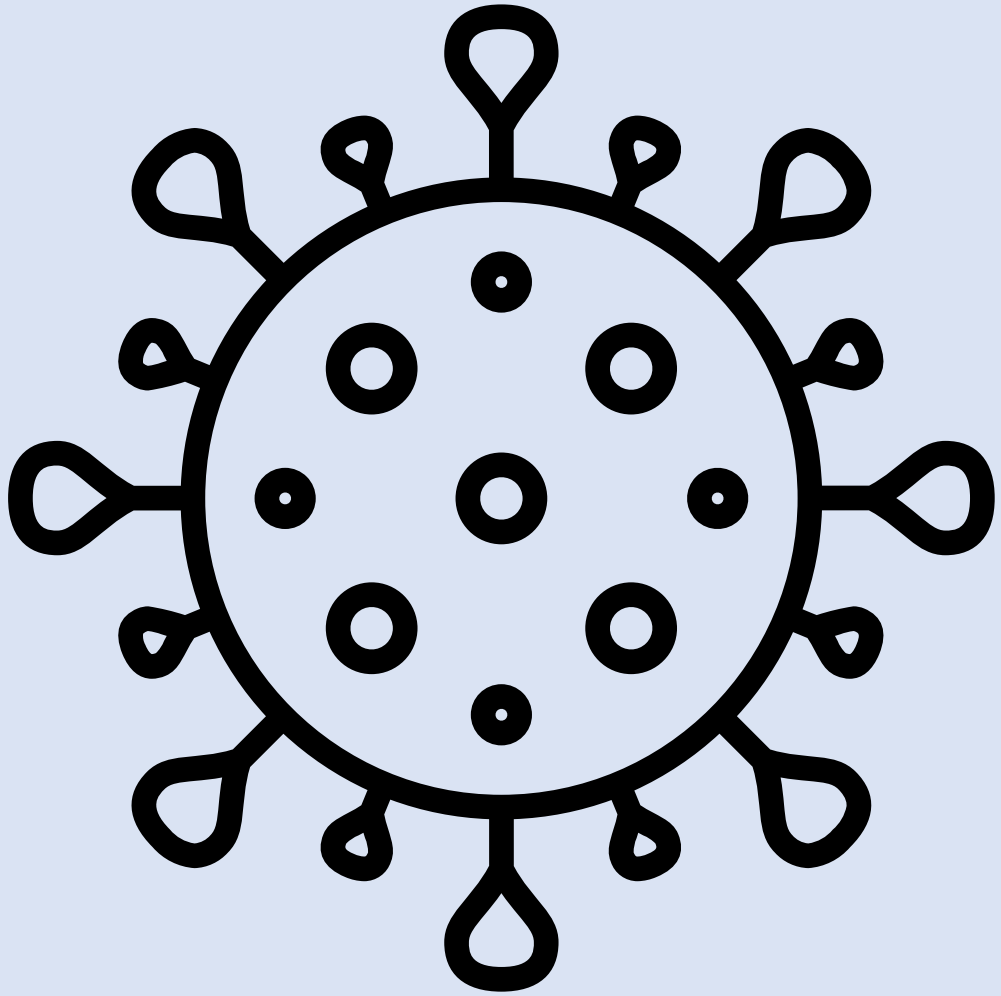


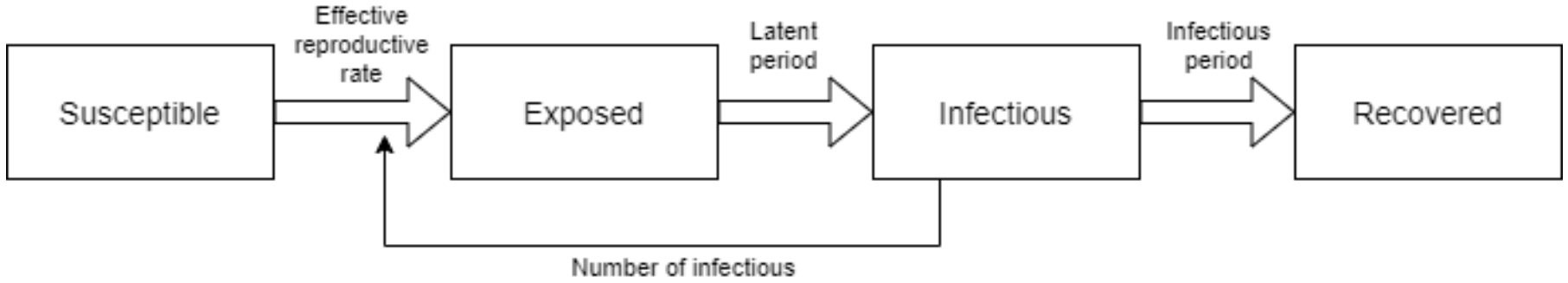
Current Epidemic Forecasting

SEIR: Standard model, tracks change in population of different “compartments” in the region

Implement as **Linear Dynamical System**:

$$x_{t+1} = A_t x_t$$

SEIR Model, graphically



Current Epidemic Forecasting

SEIR: Standard model, tracks change in population of different “compartments” in the region

Implement as **Linear Dynamical System**:

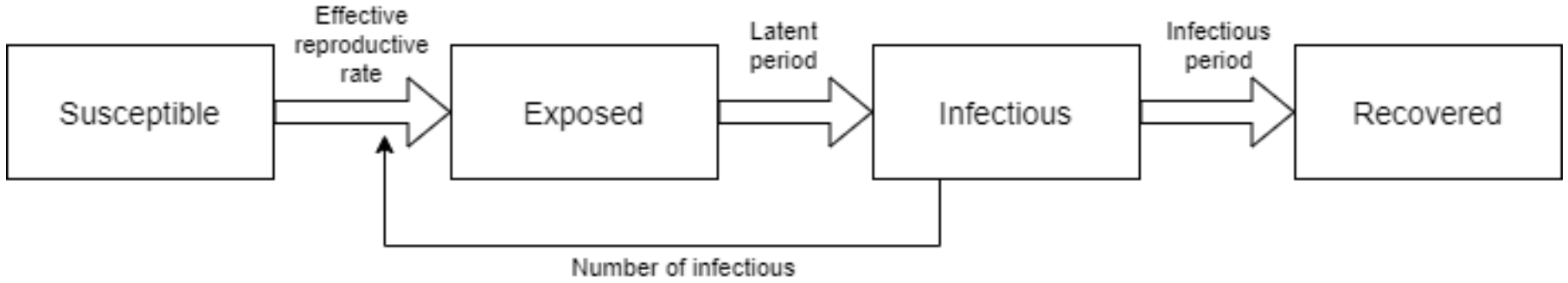
$$x_{t+1} = A_t x_t$$

Challenges using SEIR:

- Assume closed system
- Rely on potentially delayed tests
- Suboptimal for small areas (universities, towns, etc.)

How can we overcome these challenges?

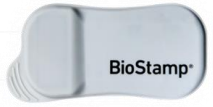
SEIR Model, graphically



The m-ADBio Model

Improves on SEIR by incorporating novel data sources into compartmental model

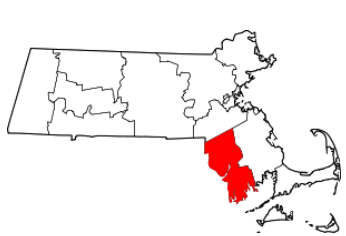
Biosensor Data – more accurate case estimates

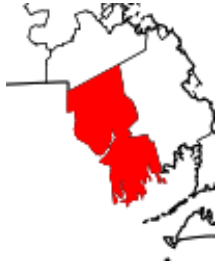


Courtesy of MC10.
https://www.mc10inc.com/

Courtesy of BioIntellisense.
https://biointellisense.com/

Estimate Local Virus Parameters – State-level+ informs community-level





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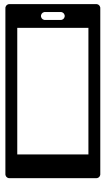
m-ADBio case forecast using linear dynamical system

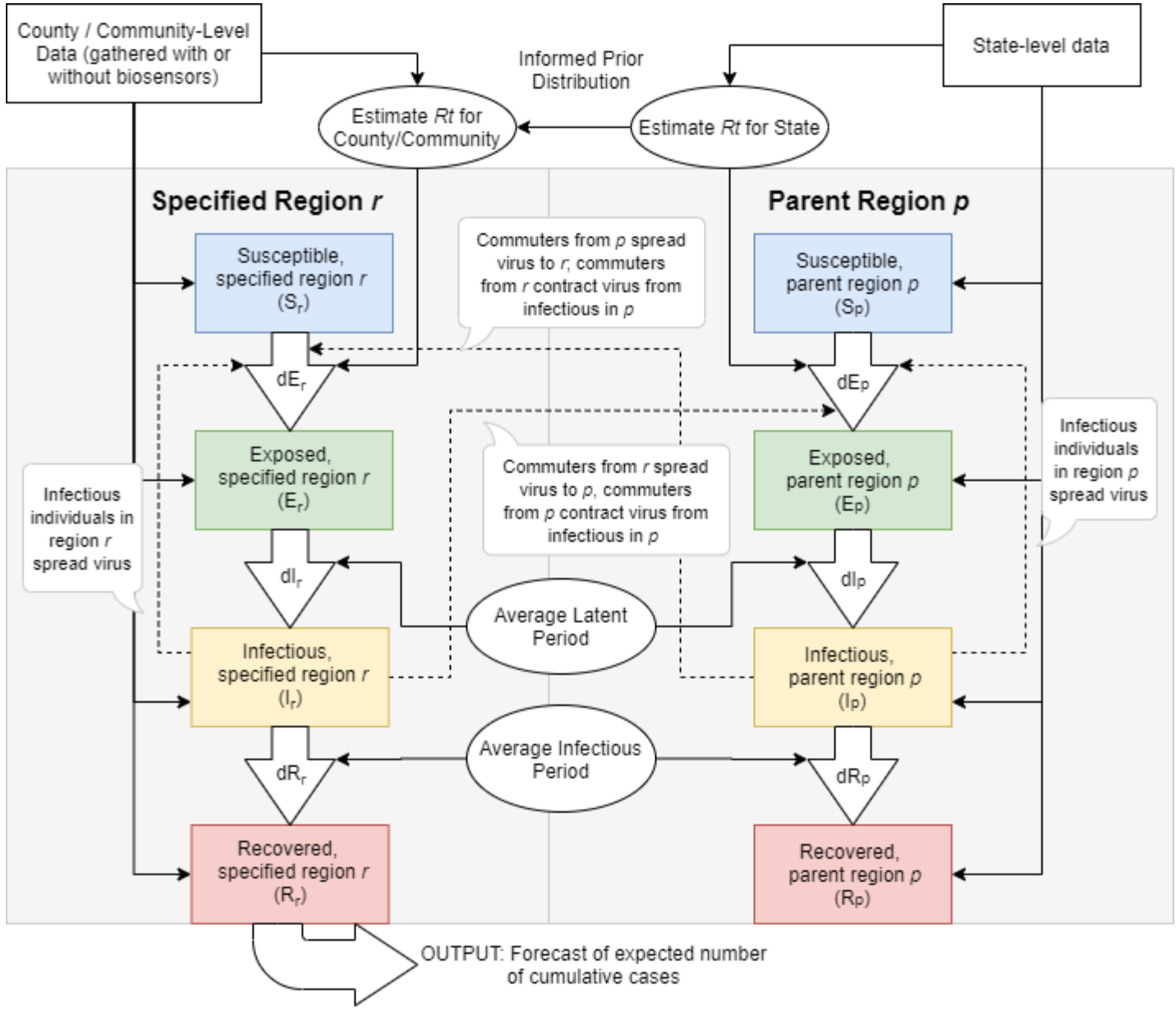
$$x_{t+1} = A_t x_t$$

Commuting effect – outsiders may carry virus into target region



Courtesy of US Census Bureau.
https://commons.wikimedia.org/wiki/

The m-ADBio Model, graphically



Parameters of m-ADBio

Var.	Name	Description
w	Population vector	$w_k :=$ the population of geography k
r	Effective reproductive rate vector	$r_k :=$ the effective reproductive rate of geography k
p_E	Latent period	Mean days until infectious once exposed
p_I	Recovery period	Mean days to recover once infectious
C	Commuting matrix	$C_{i,j} :=$ population commuting from i to j
X_0	Initial value matrix	A 4 x m matrix, the column $X_i :=$ Number of Susceptible, Exposed, Infectious, and Recovered individuals respectively.

Table 1: Constant variables in the m-ADBio model

m-ADBio as a Linear Dynamical System

$$A_t = \begin{bmatrix} -\alpha_i & 0 & 0 & 0 \\ \alpha_i & \frac{-1}{p_E} & 0 & 0 \\ 0 & \frac{1}{p_E} & \frac{-1}{p_I} & 0 \\ 0 & 0 & \frac{1}{p_I} & 1 \end{bmatrix}$$

Transition Matrix

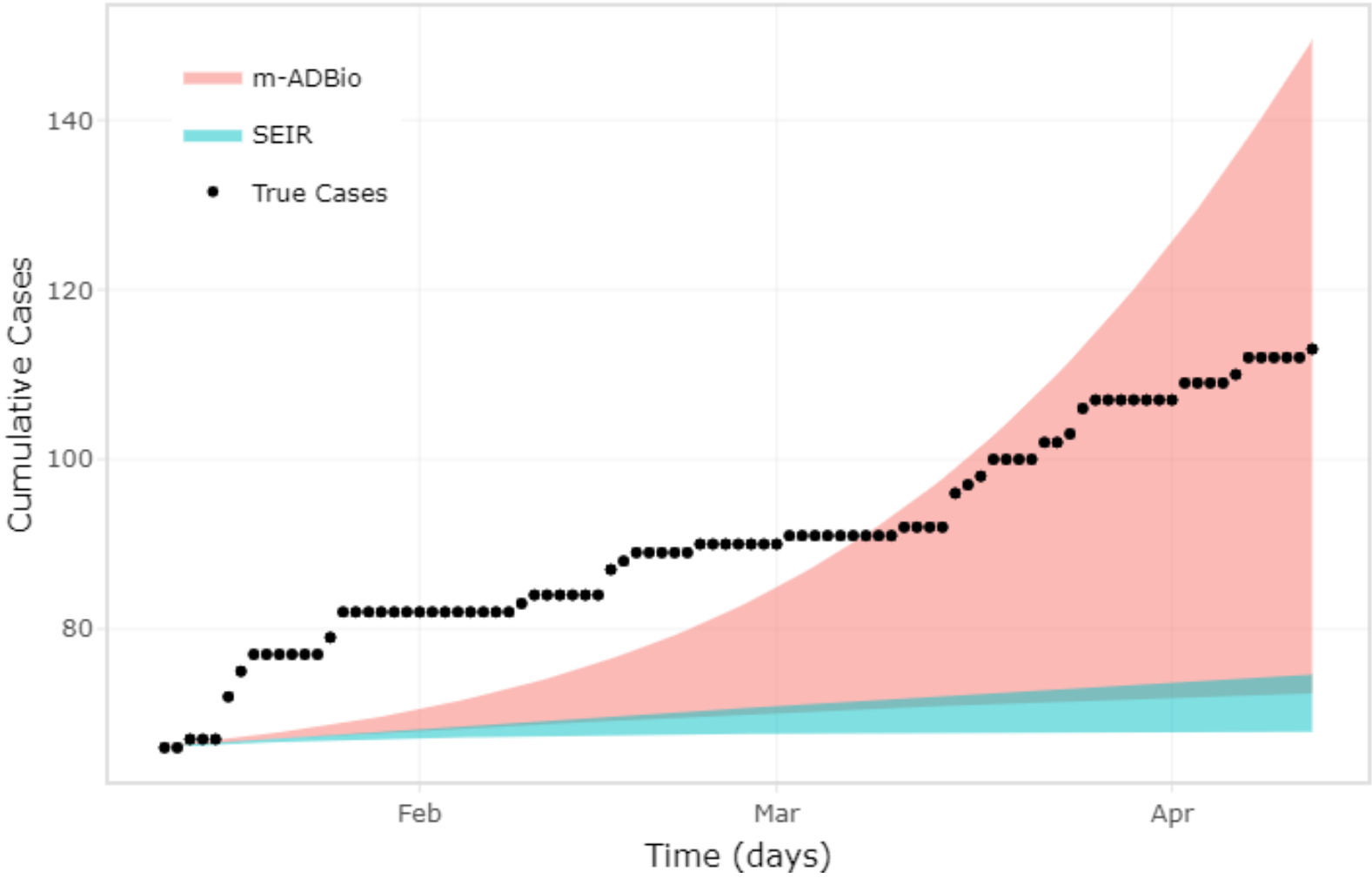
$$M_{i,j} = \frac{C_{i,j} I_i r_i}{p_I w_i w_j}$$

Mean Infection Risk

$$\alpha = \frac{1}{2}(M + M^T) \begin{bmatrix} 1 \\ \dots \\ 1 \end{bmatrix}$$

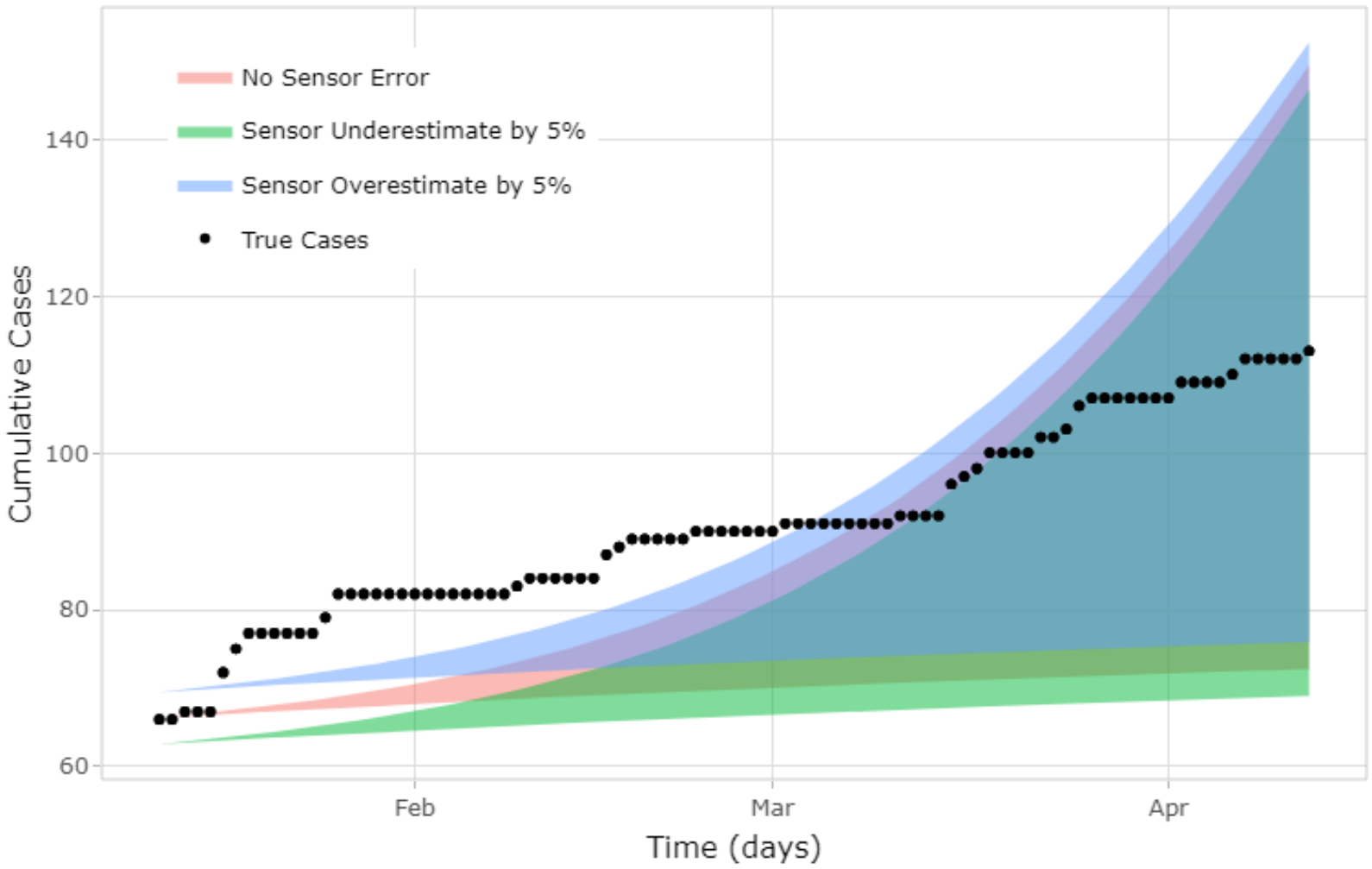
Calculating the alpha vector

Results



Forecast of COVID-19 cases at University of Massachusetts Dartmouth during Spring Semester: *m-ADBio* compared to *SEIR*

Results



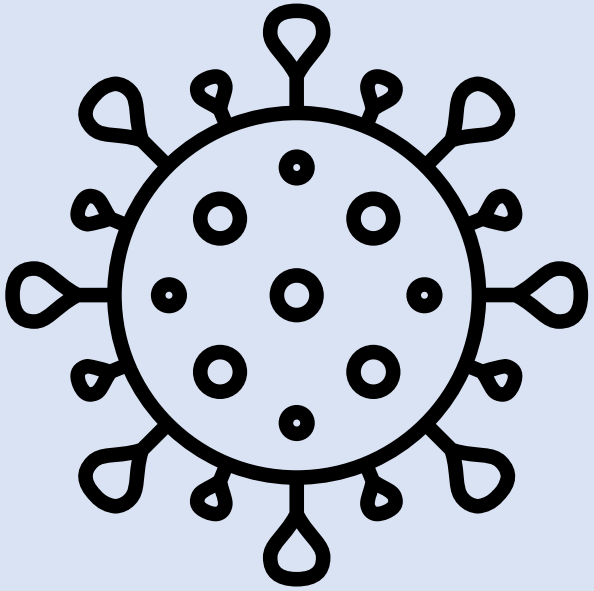
Forecast of COVID-19 cases at University of Massachusetts Dartmouth during Spring Semester: *m-ADBio* using sensors of varying error rates

Using the model yourself: The **madbio** R package

- R package available on GitHub
- Visualizes cases over time
- Can compare different…
  - Models
  - Sensor-based starting values
  - Reproductive rates

Future Work

- Expand R package to allow additional model parameters
- Test model on geographies beyond University of Massachusetts Dartmouth
- Improve estimation of effective reproductive rate R_t for small regions



Thank you for listening!