A TypeScript Based Agentbased Disease Mode

A Disease Model in TypeScript

Introduction

The background of Disease Prediction Models

Introduction

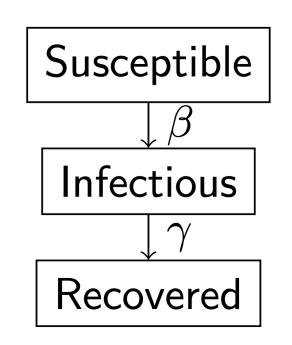
The background of Disease Prediction Models

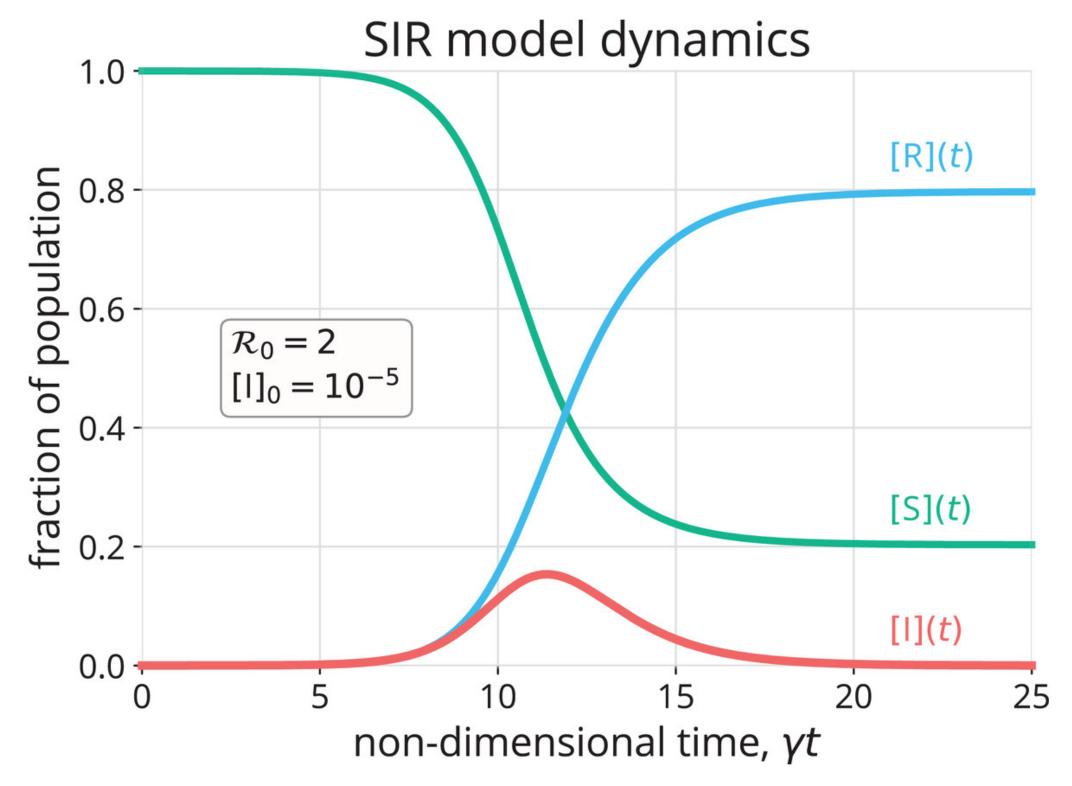
- SIR model
- A set of differential equations
- Describes the number of people
 - Susceptible (S, not infected)
 - Infected (I)
 - Recovered (R, recovered, not susceptible)

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

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$



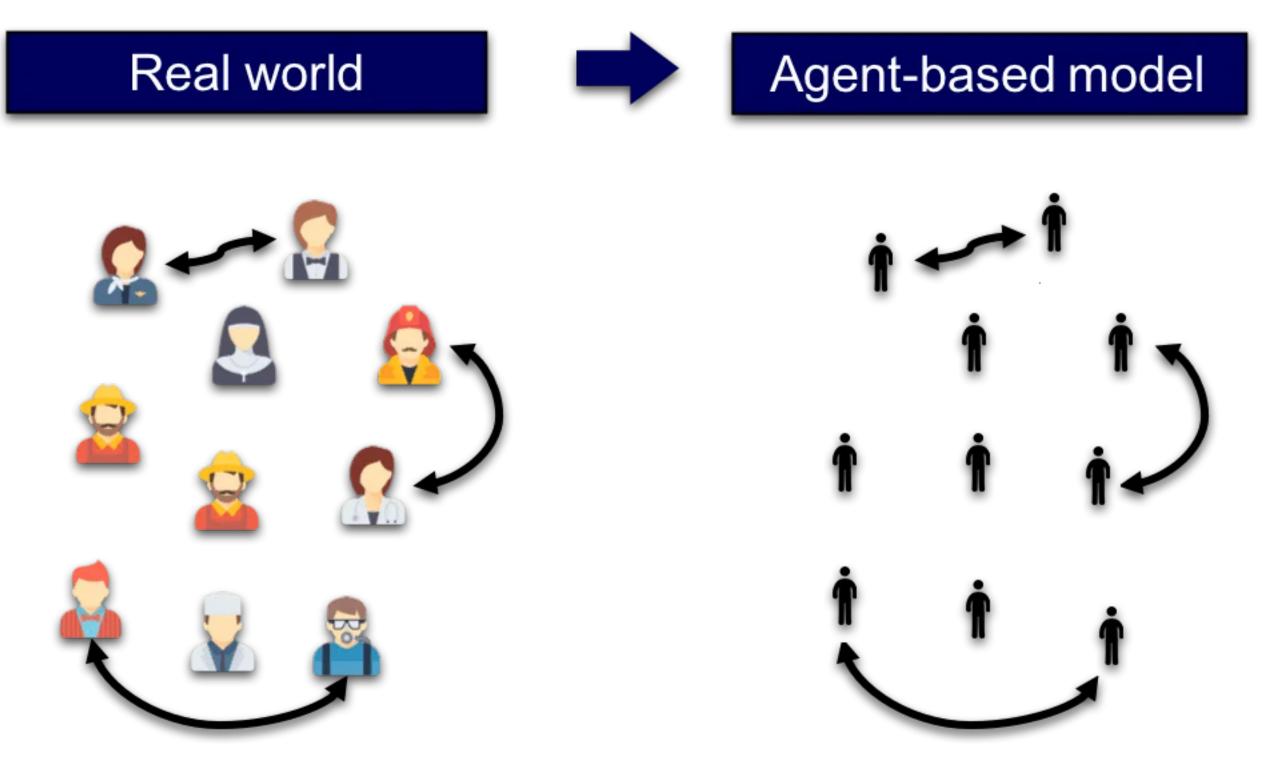


This image comes from: https://peerj.com/articles/pchem-14/

Introduction

The background of Disease Prediction Models

- Agent-based model
 - A computer simulation of the interaction of agents (people)
 - Used to predict and demonstrate the spread of diseases
- Agent is associated with certain attributes



This image comes from: https://www.synlabs.io/post/top-5-significant-use-cases-of-agent-based-modeling-simulation

Methodology

Constructing the Agent-based Model

Agent-based Model Building blocks

- Components:
 - Agents: Collections of properties (name, age, gender, health, etc.)
 - Behaviours: Daily routines and interactions.
 - Environment: Space where agents reside and interact.

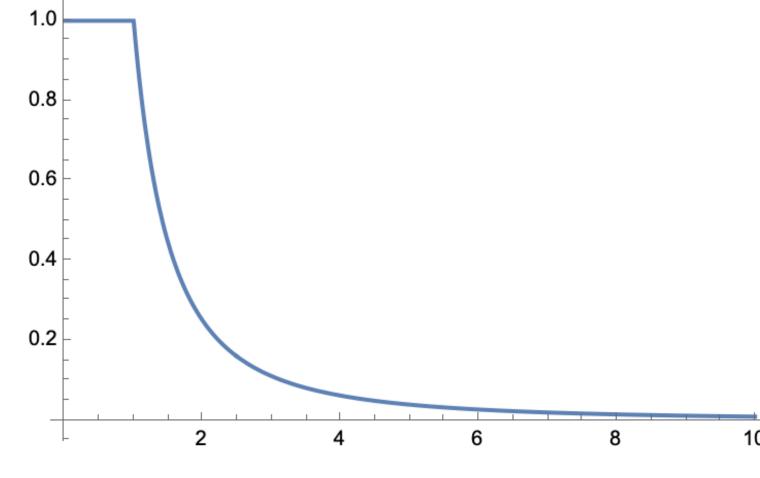
Machinist of Infection

The process that the disease spread

- The risk of infection will be increased as:
 - The susceptible agents moved close to the infected agents.

$$\mathbb{P}(\mathsf{Infection}) = \begin{cases} \frac{1}{d^2} & (\mathsf{for}\,d > 1) \\ 1 & (\mathsf{for}\,d \leq 1) \end{cases} \quad (d \text{ is the between the agents})$$

- A timer will start if the agents get infected.
- Agents will recover if the timer reaches zero.

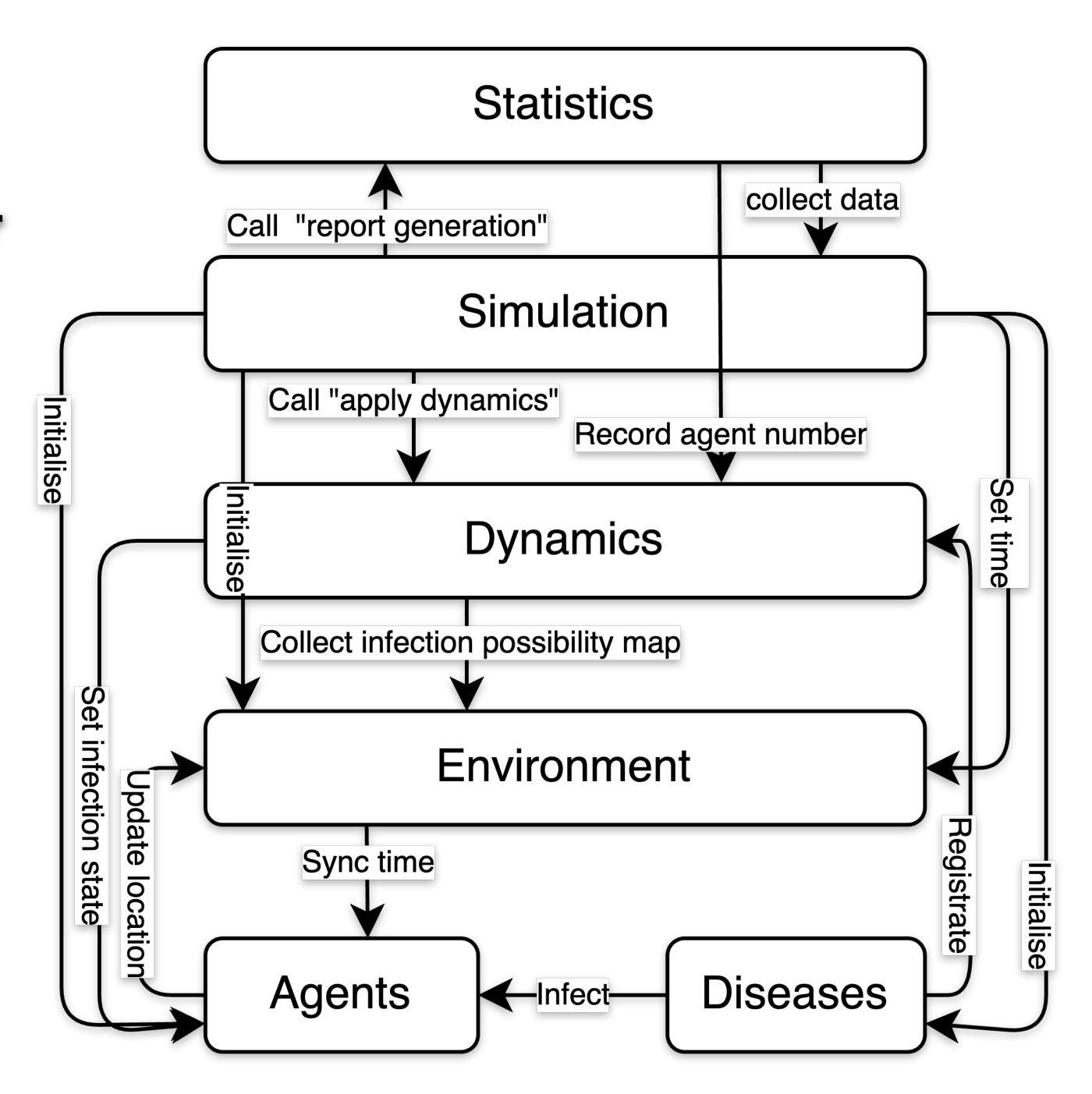


The plot for the possibility function

Model

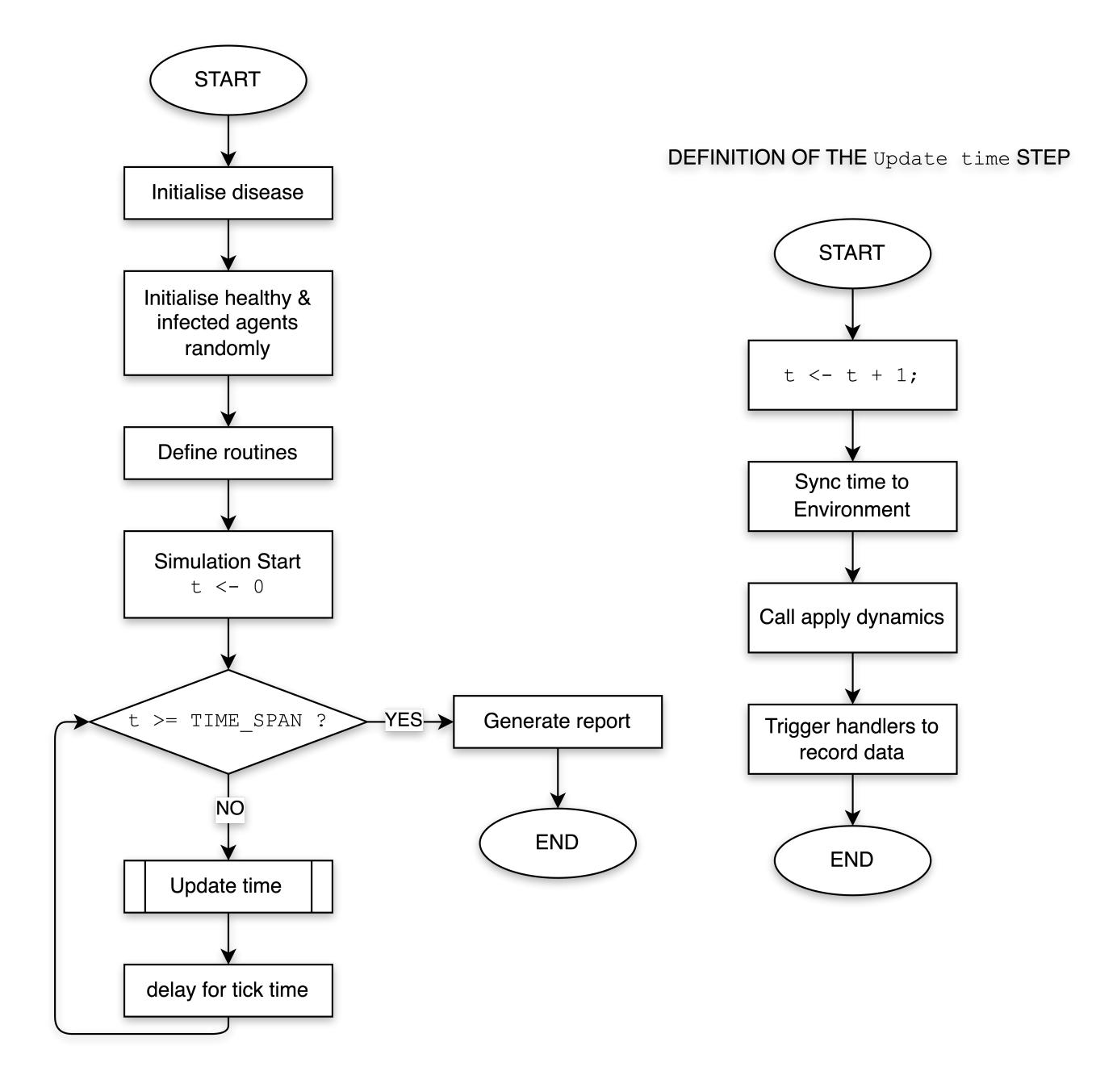
How the modules work together

- This diagram shows how the components (modules) interact with each other.
- Each rectangle represents a module
- Arrow represents action done by the module to another.



Model How the model works

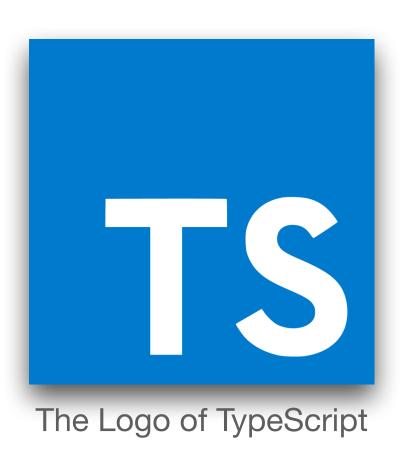
- The flow chart shows how the model works
- Major steps
 - Initialisation
 - Simulation by tick
 - Generate report



Implementation

Some coding works

- Programming languages used:
 - TypeScript: For type safety and structure.
 - More familiar with TypeScript
 - R: For graphing using ggplot2 library.





Results

The Outcomes from the Model with the Specific Parameters

ResultsThe parameters & diagram

• Simulation Parameters:

• Time: 60

Agent Number: 40

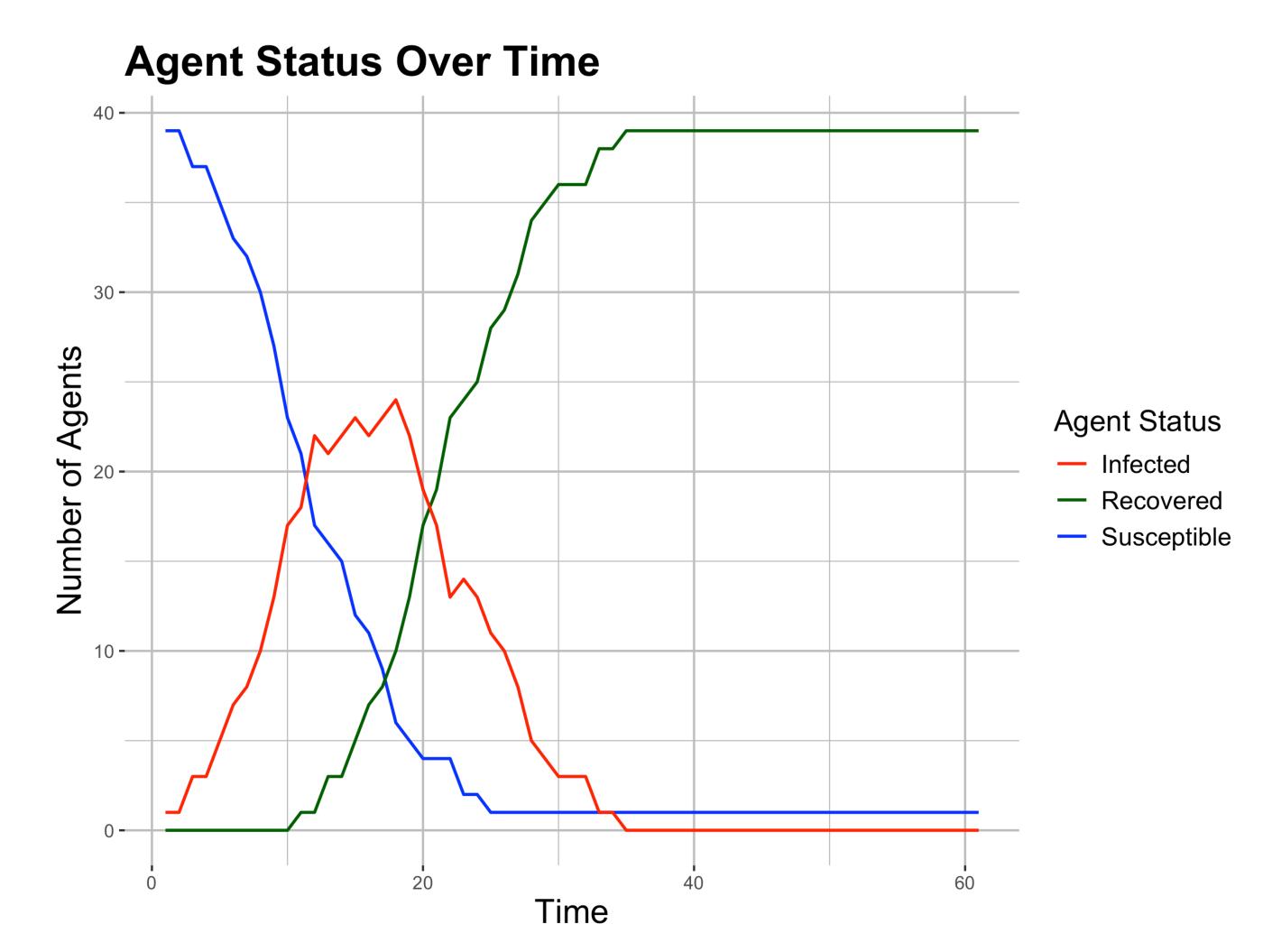
• Room Size: 40

• **Disease** Parameters:

Name: Cold

• Severity: 100

• Time to Restore: 10

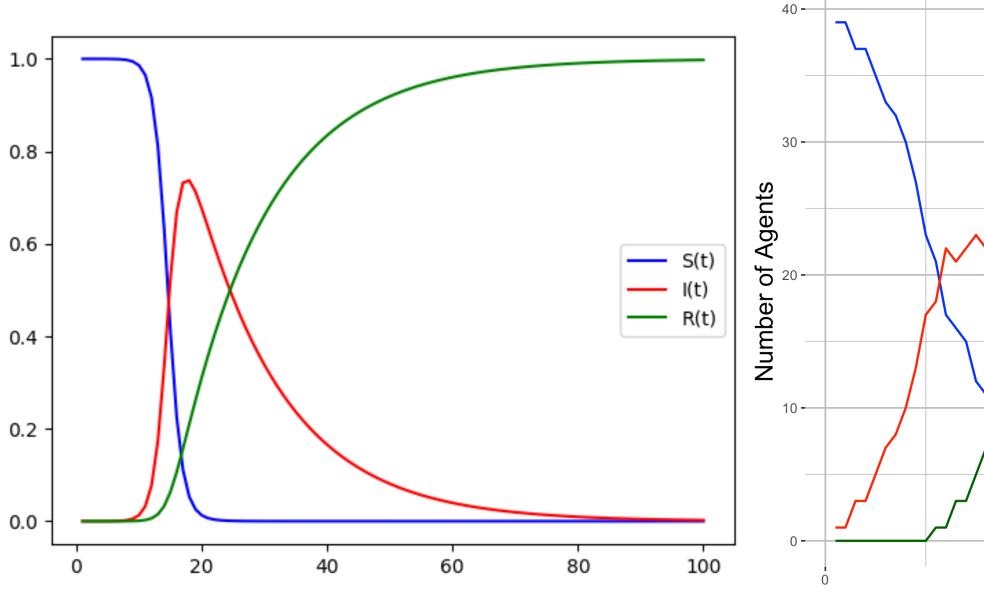


Results

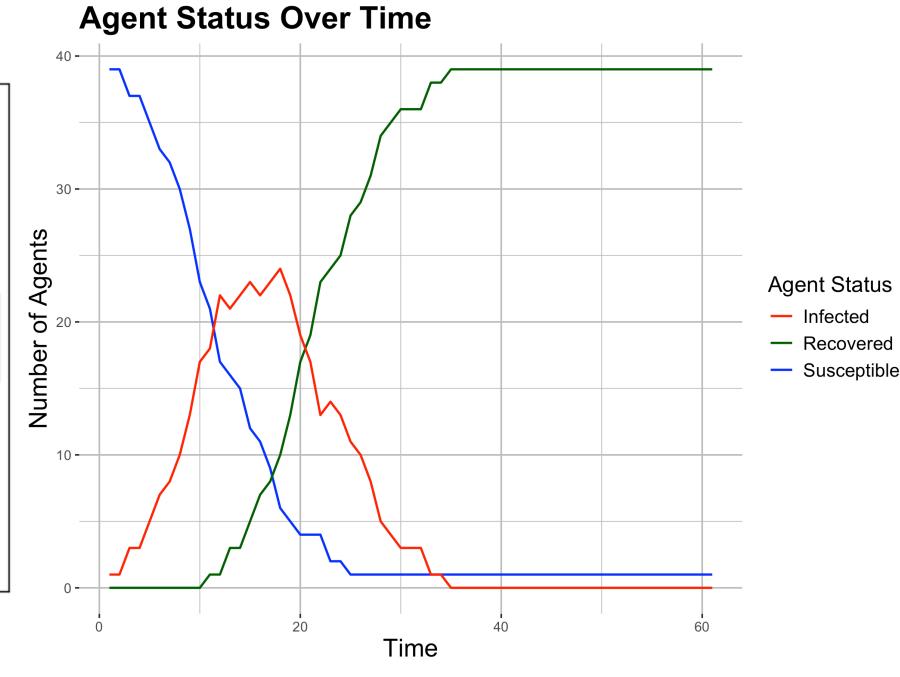
Compare the predictions from SIR model to this model

This model is:

- Capable of partially simulating the spread of the disease
- Due to the similarity
- Depict outbreaks and extinctions



The plot for SIR model, β = 1, γ = 0.1



The plot for previous agent based model

Discussion

Advantages & Drawbacks

Discussion Advantages & Drawbacks

• Strengths:

- Effective for simple disease spread simulation.
- Maintainable code due to TypeScript.

Limitations:

- Lacks simulation of multiple diseases with complex dynamics.
- Use recover time, not recover possibility
- Lacks features of migrating parameters from SIR model to this model
- Lacks simulation for some complex mechanisms between the infection possibility and the age, health of the agents, the severity of the disease, etc.

Conclusion

To Summarise the Insights from the Disease Prediction Model

Conclusion To summarise

- Summary:
 - Model simulates disease spread, outbreaks, and extinctions accurately.
 - Future work includes enhancing complexity and dynamic features

Thanks for Listening

Thank You for Your Attention

The source code of the model is available on Github:

https://github.com/Anson2251/camp-agent-base-model

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