ASIR: Robust Agent-based Representation Of SIR Model

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Preface

As a student double majoring in Computer Science and Data Science, I have always been attracted by the idea behind computer simulation: modeling the real world in programming language, making statistical inference about the real world. I said yes immediately when professor Olivier Marin told me if I was interested in building some bridge between compartmental model (which is based on ordinary differential equation) and agent-based model (which is based on computer simulation.) We only have a vague direction at the beginning, but as we went further in the literature, we were more and more certain about we would like to contribute to. Finally, we proposed the agent-based ASIR that can robustly reproduce the infection curve predicted by the compartmental SIR Model. We are happy to see that ASIR is inspirational for epidemiologists who wish to quickly transform a calibrated SIR model into an agent-based model that retains its prediction without another round of calibration.

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Abstract

Compartmental models (written as CM) and agent-based models (written as AM) are dominant methods in the field of epidemic simulation. But in the literature there lacks discussion on how to build the quantitative relationship between them. In this paper, we propose an agent-based SIR model: ASIR. ASIR can robustly reproduce the infection curve predicted by a given SIR model (the simplest CM.) Notably, one can deduce any parameter of ASIR from parameters of SIR without manual tuning. ASIR offers epidemiologists a method to transform a calibrated SIR model into an agent-based model that inherit SIR’s performance without another round of calibration. The design ASIR is inspirational for building a general quantitative relationship between CM and AM.

Keywords

Computer Simulation; Epidemic Simulation
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1 Introduction

Compartmental models (written as CM) and agent-based models (written as AM) are dominant methods in the field of epidemic simulation. CM capture the population level dynamics by a set of ordinary differential equations. AM capture the individual level dynamics by an agent-based programming environment.

CM and AM have complementary nature. CM are easy to calibrate but have less flexible parameter space to apply a priori; AM have a flexible parameter space to apply a priori, but are hard to calibrate. In the current literature, there lacks discussion on developing the quantitative relationship between CM and AM. Driven by this fact, we wish to bridge the gap between CM and AM by finding an AM that robustly reproduces the infection curve predicted by a CM.

We start from the SIR model (the simplest CM): where \( P_{sir} \) is the set of all parameters; and functions \( S_{sir}(t), I_{sir}(t), R_{sir}(t) \) are the population size of being susceptible, infected and recovered with respect to time \( t \). We propose an agent-based SIR model, ASIR, that achieves the following interesting properties:

1. \( P_{asir} \) only depends on \( P_{sir} \). Any parameter \( p \in P_{asir} \) can be deduced from \( P_{sir} \), i.e. can be written as a determinate expression of \{ \( p_1, p_2, ..., p_k \) \} \( \subset P_{sir} \).

2. ASIR robustly reproduces the infection curve predicted by SIR. ASIR is expected to predict the same \( S(t), I(t), R(t) \) as SIR, i.e. \( \forall t : \mathbb{E}[S_{asir}(t)] = S_{sir}(t); \mathbb{E}[I_{asir}(t)] = I_{sir}(t); \mathbb{E}[R_{asir}(t)] = R_{sir}(t) \)

We validate ASIR’s properties by giving: 1). a proof of robustness, 2). two implementations in GAMA and Agents.jl.

2 Related Work

SIR model is the simplest compartmental model (CM). In [2], the authors give us an overview of the design behind the compartmental model. From this work, we learned that the core idea of CM is to use a set of ordinary differential equations to model the population infection and recovery, and use parameters to control their rate.

In [3], the authors give us an overview of the agent-based simulation’s application in the field of epidemiology. From this work, we learned that representation of "space" is what distinguish
agent-based model (AM) from CM, and drew our attention to the design of agents’ Move behavior.

In [4], the authors describe a general method for the conversion of an equation-based model to an agent-based simulation. Their method was not built on solid mathematics, but the discussion about the relationship between population behavior and individual behavior has greatly inspired our idea behind ASIR. Our model can be seen as translating their rough ideology into rigorous proof in mathematics.

[5] and [6] are the multiagent programming environments we use to implement ASIR. Their design is the direct source of our perception of what is agent-based simulation. ASIR has been influenced by the concepts of "Agent," "Step," and "Map" that were implemented by [5] and [6].

[7] is the book we used as a reference for the necessary condition for the existence of a Markov chain’s stationary distribution.

3 Solution

In this section, we introduce ASIR in the following order: 1). idea behind, 2). model specification, and 3). proof of robustness.

3.1 Idea Behind ASIR

Let us first briefly recap the design of the SIR model.

![Figure 1: Diagram of SIR model](image)

Figure 1: Diagram of SIR model
The SIR model consists of two parameters: \( \{\alpha, \beta\} \) and three ordinary differential equations:

\[
\frac{dS}{dt} = -\frac{\alpha SI}{N} \\
\frac{dI}{dt} = \frac{\alpha SI}{N} - \beta I \\
\frac{dR}{dt} = \beta I
\]  

(1)

(2)

(3)

\( N \) is the total population size. \( S \) is the susceptible population size. \( I \) is the infected population size. \( R \) is the recovered population size. \( \alpha \) controls the transition speed from Susceptible into Infected. \( \beta \) controls the transition speed from Infected into Recovered.

Equation 1 models the transition speed of Susceptible population size. Equation 2 models the transition speed of Infected population size. Equation 3 models the transition speed of Recovered population size.

The intuitions behind ASIR are:

1. **Population infection** is an integral of individual infection.

2. **Population recovery** is an integral of individual recovery.

To translate these intuitions into mathematics, we adopt the theory of probability by treating population infection/recovery as the joint distribution of individual infection/recovery.

The core ideas behind ASIR are:

1. Model individual infection/recovery as mutually independent and identically distributed random events.

2. Use parameters to control the event probability.

3. The transition speed on population-level = the expected value of the integral of event probability on individual-level.

Notably, since a Susceptible individual must be infected by an Infected individual, an individual infection at time \( t + 1 \) is conditional on another individual’s infection at time \( t \) (or ahead of \( t \)). To guarantee independence between each individual’s infection, we model the movement of every agent (or individuals, we are using these words interchangeably) using the same transition matrix \( T_{\text{map}} \). The matrix below shows a simple example where our map consists of three locations:
\[
\begin{pmatrix}
\text{Store} & \text{School} & \text{Stop} \\
0.5 & 0.3 & 0.2 \\
0.3 & 0.3 & 0.4 \\
0.2 & 0.4 & 0.4 \\
\end{pmatrix}
\]

In this example, coordinate \( T_{mn} \) is the probability of moving from \( m \) to \( n \). We focus on the period after every agent’s trajectory reaches \( T_{\text{map}} \)’s stationary distribution. We discuss why stationary distribution is critical for robustness later in this section.

In the following subsection, we introduce ASIR’s detailed specification in the following order: 1). agents’ state, 2). agents’ behavior, 3). model’s parameter setting.

### 3.2 Model Specification

Each agent’s state can be written as a 3-element tuple: \((\text{Timestamp}, \text{Health}, \text{Position})\). "An agent \( a_1 \) has state \((8, I, \text{School})\)" translates as: "at the 8-th timestamp, \( a_1 \) is being Infected at School." In this paper, we will use:

1. \((a_k, h_t)\) or \(H_{a_k}^t\) to denote an agent’s health at timestamp \( t \),
2. \((a_k, p_t)\) or \(P_{a_k}^t\) to denote an agent’s position at timestamp \( t \),
3. \((a_k, h_t, p_t)\) or \((H_{a_k}^t, P_{a_k}^t)\) to denote an agent’s state at timestamp \( t \).

| Meaning                          | Form 1     | Form 2     |
|---------------------------------|------------|------------|
| an agent’s health at timestamp \( t \) | \((a_k, h_t)\) | \(H_{a_k}^t\) |
| an agent’s position at timestamp \( t \) | \((a_k, p_t)\) | \(P_{a_k}^t\) |
| an agent’s state at timestamp \( t \) | \((a_k, h_t, p_t)\) | \((H_{a_k}^t, P_{a_k}^t)\) |

Table 1: Symbol reference for agent state.

At timestamp \( t \), each agent \( a_k \) has three (potential) behaviors:
1. **Move.** $a_k$ moves from $p_{t-1}$ to $p_t$ (which can be the same position as $p_{t-1}$). Written as:

$$P_{a_k}^{t-1} \rightarrow P_{a_k}^t$$ (5)

As mentioned in the introduction, we model the movement of every agent using the same transition matrix $T_{\text{map}}$. The trajectory of every agent forms a Markov chain as the example below shows:

![Figure 2: Markov chain of the sample $T_{\text{map}}$](image)

We insist on focusing on the period after every agent’s position reaches $T_{\text{map}}$’s stationary distribution, because the stationary distribution offers us the following critical property to deduce ASIR’s robustness:

**Property.** When every agent’s position reaches the $T_{\text{map}}$’s stationary distribution, the probability that any two agents become neighbor at time $t$ (i.e. stay at the same position $p_t$) equals to a constant $P(\text{meetup})$. $P(\text{meetup})$ is completely determined by $T_{\text{map}}$.

The proof is trivial. An intuition is that agents’ locations are mutually independent and identically distributed, therefore $\forall j, k, m, n$, $P(a_k \text{ meets } a_j) = P(a_m \text{ meets } a_n)$

2. **Turn infected.** When $a_k$ was Susceptible before moving to position $X$, it has a chance to turn infected when there is an "Infected neighbor" at $X$, or more precisely, $\exists_{a_j \neq a_k} H_{a_j}^t = I, P_{a_j} = P_{a_k}$. Written as:

$$\left( H_{a_k}^{t-1} \rightarrow H_{a_k}^t = S \rightarrow I \mid \exists_{a_j \neq a_k} H_{a_j}^t = I, P_{a_j} = P_{a_k} \right)$$ (6)

or simply:

9
\[ (H_{a_k}^{t-1} \rightarrow H_{a_k}^t = S \rightarrow I \mid a_k \text{ has an infected neighbor at } t) \] (7)

\[ (H_{a_k}^{t-1} \rightarrow H_{a_k}^t = I \rightarrow R \mid H_{a_k}^{t-1} = I) \] (8)

or simply:

\[ H_{a_k}^{t-1} \rightarrow H_{a_k}^t = I \rightarrow R \] (9)

Figure 3: Individual infection process in ASIR model.
\( \alpha' \) is the infection probability

3. **Turn recovered.** When \( a_k \) was Infected at time \( t - 1 \) it has a chance to turn Recovered at time \( t \). Written as:

\[ (H_{a_k}^{t-1} \rightarrow H_{a_k}^t = I \rightarrow R) \]

Figure 4: Individual recovery process in the ASIR model.
\( \beta' \) is the recovery probability

As mentioned in the introduction, a core idea supporting ASIR to robustly reproduce SIR’s prediction is using parameters to control the event probability. In our model, there are only two types of random events that involve transition in individual health state \( H_{a_k}^t \): 1. **turn**
infected: \((H_{ak}^{t-1} \rightarrow H_{ak}^t) = (S \rightarrow I)\), and 2). turn recovered: \((H_{ak}^{t-1} \rightarrow H_{ak}^t) = (I \rightarrow R)\).

We are using two parameters \(\{\alpha', \beta'\}\) to control their probability in the following way:

1. \(a_k\)'s probability of being infected at \(t\) is proportional to the count of infected neighbor, with the ratio equals to parameter \(\alpha'\)

\[
\frac{\mathbb{P}(H_{ak}^{t-1} \rightarrow H_{ak}^t = S \rightarrow I)}{\sum_{a_j} 1_{\{H_{aj}^t = I, P_{aj}^t = p_{st}\} \cap H_{ak}^{t-1} = S}} = \mathbb{I}_{\{H_{ak}^{t-1} = S\}} \cdot \alpha'
\]

or simply,

\[
\frac{\mathbb{P}(H_{ak}^{t-1} \rightarrow H_{ak}^t = S \rightarrow I)}{\sum_{a_j} 1_{a_j \text{ is infected neighbor of } a_k \text{ at } t}} = \alpha'
\]

Notably, here we are making an assumption that:

\[
\mathbb{P}(1 < \alpha' \cdot \sum_{a_j} 1_{a_j \text{ is infected neighbor of } a_k \text{ at } t}) = 0
\]

This means we are requiring the agent density at any location to be reasonably low in order to reflect the reality that people almost never stay in a place that has absolute causality in terms of infection.

2. An Infected \(a_k\)'s probability of being recovered at any time \(t\) is constant, which equals to parameter \(\beta'\)

\[
\mathbb{P}(H_{ak}^{t-1} \rightarrow H_{ak}^t = I \rightarrow R) = \mathbb{I}_{\{H_{ak}^{t-1} = I\}} \cdot \beta'
\]

or simply:

\[
\mathbb{P}(H_{ak}^{t-1} \rightarrow H_{ak}^t = I \rightarrow R) = \beta'
\]

Based on the ASIR specification above, we propose the following theorem:

**Theorem 1.** (ASIR Robustness theorem) ASIR robustly reproduce the infection curve predicted by SIR, i.e. \(\forall t: \mathbb{E}[S_{asir}(t)] = S_{sir}(t); \mathbb{E}[I_{asir}(t)] = I_{sir}(t); \mathbb{E}[R_{asir}(t)] = R_{sir}(t)\), if:
1. \( S_{\text{asir}}(0) = S_{\text{sir}}(0); \ \ I_{\text{asir}}(0) = I_{\text{sir}}(0); \ \ R_{\text{asir}}(0) = R_{\text{sir}}(0), \) and

2. \( \alpha = \alpha' \cdot P(\text{meetup}) \cdot N; \ P(\text{meetup}) \) is determined by \( \text{ASIR}'s \) transition matrix \( T_{\text{map}} \), \( N \) is the population size, and

3. \( \beta = \beta' \)

We will give the proof in the "Proof of Robustness" section.

### 3.3 Proof of Robustness

Let us give the proof for theorem 1. We write "period \((t,t+k)\)" when we refer to the period since \( t \) till \( t+k \). We are using \( \Delta \) to denote the change in \( S_{\text{sir}}(t) \) during the period \((t,t+k)\):

\[
\Delta S_{\text{sir}}|_{t}^{t+k} = S_{\text{sir}}(t+k) - S_{\text{sir}}(t)
\] (15)

\[
\Delta I_{\text{sir}}|_{t}^{t+k} = I_{\text{sir}}(t+k) - I_{\text{sir}}(t)
\] (16)

\[
\Delta R_{\text{sir}}|_{t}^{t+k} = R_{\text{sir}}(t+k) - R_{\text{sir}}(t)
\] (17)

Similarly, we are using \( \Delta S_{\text{asir}}|_{t}^{t+k} \) to denote the change in \( S_{\text{asir}}(t) \) during the period \((t,t+k)\):

\[
\Delta S_{\text{asir}}|_{t}^{t+k} = S_{\text{asir}}(t+k) - S_{\text{asir}}(t)
\] (18)

\[
\Delta I_{\text{asir}}|_{t}^{t+k} = I_{\text{asir}}(t+k) - I_{\text{asir}}(t)
\] (19)

\[
\Delta R_{\text{asir}}|_{t}^{t+k} = R_{\text{asir}}(t+k) - R_{\text{asir}}(t)
\] (20)

We prove theorem 1 by proving theorems 2, 3:

**Theorem 3 → Theorem 2 → Theorem 1**
2. \( E[\Delta I_{\text{sir}}|_t^{t+k}] = \Delta I_{\text{sir}}|_t^{t+k}, \) and

3. \( E[\Delta R_{\text{sir}}|_t^{t+k}] = \Delta R_{\text{sir}}|_t^{t+k} \)

Proof. Take period \((0, t), \)

1. \( E[S_{\text{sir}}(t)] = E[\Delta S_{\text{sir}}|_0^{t}] + S_{\text{sir}}(0) = \Delta S_{\text{sir}}|_0^{t} + S_{\text{sir}}(0) = S_{\text{sir}}(t), \) and

2. \( E[I_{\text{sir}}(t)] = E[\Delta I_{\text{sir}}|_0^{t}] + I_{\text{sir}}(0) = \Delta I_{\text{sir}}|_0^{t} + I_{\text{sir}}(0) = I_{\text{sir}}(t), \) and

3. \( E[R_{\text{sir}}(t)] = E[\Delta R_{\text{sir}}|_0^{t}] + R_{\text{sir}}(0) = \Delta R_{\text{sir}}|_0^{t} + R_{\text{sir}}(0) = R_{\text{sir}}(t) \)

\[
\text{Theorem 3. For any period } (t, t+k): \\
1. \( E[\Delta S_{\text{sir}}|_t^{t+k}] = \Delta S_{\text{sir}}|_t^{t+k} \)
2. \( E[\Delta I_{\text{sir}}|_t^{t+k}] = \Delta I_{\text{sir}}|_t^{t+k} \)
3. \( E[\Delta R_{\text{sir}}|_t^{t+k}] = \Delta R_{\text{sir}}|_t^{t+k} \)
\]

if:

1. \( S_{\text{sir}}(0) = S_{\text{sir}}(0); \ I_{\text{sir}}(0) = I_{\text{sir}}(0); \ R_{\text{sir}}(0) = R_{\text{sir}}(0), \) and

2. \( \alpha = \alpha' \cdot \mathbb{P}(\text{meetup}) \cdot N; \mathbb{P}(\text{meetup}) \) is determined by ASIR’s transition matrix \( T_{\text{map}}, \) \( N \) is the population size, and

3. \( \beta = \beta' \)

Proof. In SIR,

\[
\Delta S_{\text{sir}}|_t^{t+1} = \int_t^{t+1} \frac{dS}{dt} dt = -\frac{\alpha}{N} \cdot S_{\text{sir}}(t) I_{\text{sir}}(t) \cdot \int_t^{t+1} dt = -\frac{\alpha}{N} \cdot S_{\text{sir}}(t) I_{\text{sir}}(t) \tag{22}
\]

\[
\Delta R_{\text{sir}}|_t^{t+1} = \int_t^{t+1} \frac{dR}{dt} dt = \beta \cdot I_{\text{sir}}(t) \cdot \int_t^{t+1} dt = \beta \cdot I_{\text{sir}}(t) \tag{23}
\]

\[
\Delta I_{\text{sir}}|_t^{t+1} = -\Delta S_{\text{sir}}|_t^{t+1} - \Delta R_{\text{sir}}|_t^{t+1} = \frac{\alpha}{N} \cdot S_{\text{sir}}(t) I_{\text{sir}}(t) - \beta \cdot I_{\text{sir}}(t) \tag{24}
\]
In ASIR,

\[
\mathbb{E}[\Delta S_{asir}^{t+1}] = - \sum_{a_k \mid H^n_{a_k} = s} \sum_{a_j \mid H^n_{a_j} = t} \mathbb{1}_{(F_{\alpha}^{a_j} = F_{\alpha}^{a_k})} \cdot \mathbb{1}_{(H^n_{a_k} \rightarrow H^{n+1}_{a_k} = S \rightarrow I)}
\]

\[
= - \sum_{a_k \mid H^n_{a_k} = s} \sum_{a_j \mid H^n_{a_j} = t} \mathbb{P}(\text{meetup}) \cdot \alpha'
\]

\[
= - \alpha' \cdot \mathbb{P}(\text{meetup}) \cdot \mathbb{E}[S_{asir}(t)] \cdot \mathbb{E}[I_{asir}(t)]
\]

\[
= - \frac{\alpha}{N} \cdot \mathbb{E}[S_{asir}(t)] \cdot \mathbb{E}[I_{asir}(t)]
\]  

(25)

\[
\mathbb{E}[\Delta R_{asir}^{t+1}] = \sum_{a_k \mid H^n_{a_k} = t} \mathbb{1}_{(H^{n+1}_{a_k} = I \rightarrow R)}
\]

\[
= \sum_{a_k \mid H^n_{a_k} = t} \beta'
\]

\[
= \mathbb{E}[I_{asir}(t)] \cdot \beta'
\]  

(26)

\[
\mathbb{E}[\Delta I_{asir}^{t+1}] = - \mathbb{E}[\Delta S_{asir}^{t+1}] - \mathbb{E}[\Delta R_{asir}^{t+1}]
\]

\[
= - \frac{\alpha}{N} \cdot \mathbb{E}[S_{asir}(t)] \cdot \mathbb{E}[I_{asir}(t)] - \mathbb{E}[I_{asir}(t)] \cdot \beta'
\]  

(27)

When \( t = 0 \),

\[
\mathbb{E}[S_{asir}(1)] = \mathbb{E}[S_{asir}(0)] + \mathbb{E}[\Delta S_{asir}^{t}]
\]

\[
= S_{asir}(0) + \frac{\alpha}{N} \cdot \mathbb{E}[S_{asir}(0)] \cdot \mathbb{E}[I_{asir}(0)]
\]

\[
= S_{asir}(0) + \frac{\alpha}{N} \cdot S_{asir}(0) \cdot I_{asir}(0)
\]

\[
= S_{asir}(0) + \Delta S_{asir}^{0}
\]

\[
= S_{asir}(1)
\]  

(28)
\[ \mathbb{E}\left[ R_{\text{asir}}(1) \right] = \mathbb{E}\left[ R_{\text{asir}}(0) \right] + \mathbb{E}\left[ \Delta R_{\text{asir}} \right] \]
\[ = \mathbb{E}\left[ R_{\text{asir}}(0) \right] + \mathbb{E}\left[ I_{\text{asir}}(0) \right] \cdot \beta' \]
\[ = R_{\text{asir}}(0) + \beta' \cdot I_{\text{asir}}(0) \]
\[ = R_{\text{sir}}(0) + \Delta R_{\text{sir}} \cdot 1 \]
\[ = R_{\text{sir}}(1) \]

(29)

\[ \mathbb{E}\left[ I_{\text{asir}}(1) \right] = N - \mathbb{E}\left[ S_{\text{asir}}(1) \right] - \mathbb{E}\left[ R_{\text{asir}}(1) \right] \]
\[ = N - S_{\text{sir}}(1) - R_{\text{sir}}(1) \]
\[ = I_{\text{sir}}(1) \]

(30)

When \( t > 0 \), assume \( \mathbb{E}[S_{\text{asir}}(t-1)] = S_{\text{sir}}(t-1) \), \( \mathbb{E}[I_{\text{asir}}(t-1)] = I_{\text{sir}}(t-1) \), and \( \mathbb{E}[R_{\text{asir}}(t-1)] = R_{\text{sir}}(t-1) \),

\[ \mathbb{E}\left[ S_{\text{asir}}(t) \right] = \mathbb{E}\left[ S_{\text{asir}}(t - 1) \right] + \mathbb{E}\left[ \Delta S_{\text{asir}} \right] \]
\[ = \mathbb{E}\left[ S_{\text{asir}}(t - 1) \right] - \frac{\alpha'}{N} \cdot \mathbb{E}\left[ S_{\text{asir}}(t - 1) \right] \cdot \mathbb{E}\left[ I_{\text{asir}}(t - 1) \right] \]
\[ = S_{\text{sir}}(t - 1) - \frac{\alpha}{N} \cdot S_{\text{sir}}(t - 1) \cdot I_{\text{sir}}(t - 1) \]
\[ = S_{\text{sir}}(t) \]

(31)

\[ \mathbb{E}\left[ R_{\text{asir}}(t) \right] = \mathbb{E}\left[ R_{\text{asir}}(t - 1) \right] + \mathbb{E}\left[ \Delta R_{\text{asir}} \right] \]
\[ = \mathbb{E}\left[ R_{\text{asir}}(t - 1) \right] + \mathbb{E}\left[ I_{\text{asir}}(t - 1) \right] \cdot \beta' \]
\[ = S_{\text{sir}}(t - 1) + I_{\text{sir}}(t - 1) \cdot \beta \]
\[ = R_{\text{sir}}(t) \]

(32)

\[ \mathbb{E}\left[ I_{\text{asir}}(t) \right] = N - \mathbb{E}\left[ S_{\text{asir}}(t) \right] - \mathbb{E}\left[ R_{\text{asir}}(t) \right] \]
\[ = N - S_{\text{sir}}(t) - R_{\text{sir}}(t) \]
\[ = I_{\text{sir}}(t) \]

(33)
By mathematical induction, for any period \((t, t+k)\): 
\[
\mathbb{E} [\Delta S_{\text{sir}} |_{t}^{t+k}] = \Delta S_{\text{sir}} |_{t}^{t+k}, \quad \mathbb{E} [\Delta I_{\text{sir}} |_{t}^{t+k}] = \Delta I_{\text{sir}} |_{t}^{t+k}, \quad \mathbb{E} [\Delta R_{\text{sir}} |_{t}^{t+k}] = \Delta R_{\text{sir}} |_{t}^{t+k}.
\]

Proof of Robustness:

Proof. Theorem 3 implies theorem 2; theorem 2 implies theorem 1. □

4 Results

In this section, we will discuss the outcome of our imperfect ASIR implementations in two multiagent programming environments: GAMA and Agents.jl.

4.1 ASIR implementation in GAMA

Our ASIR implementation in GAMA uses a small map (50 \(\times\) 50 grid) and large population size \((N = 500)\). We observe a perfect reproduction of the corresponding SIR’s infection curve. We think this is because \(P(\text{meetup})\) and \(\text{step size map size}\) is high enough to quickly reach \(T_{\text{map}}\)’s stationary distribution.

4.2 ASIR implementation in Agents.jl

However, our ASIR implementation in Agents.jl with a larger map (100 \(\times\) 100 grid) and the same population size \((N = 100)\) fails to robustly reproduce the infection curve of the same benchmark SIR we used in GAMA. (As Figure 7 illustrates.) The initial Infected agents recover before infecting enough Susceptible agents; so both \(I_{\text{sir}}(t)\) and \(R_{\text{sir}}(t)\) full curves remain flat to 0.

When we play back the trajectory of agents, we find agents are loosely distributed, and their trajectories have few intersections (\(P(\text{meetup}) \approx 0, \text{step size map size} \approx 0\)).

We think this is a counterexample where \(T_{\text{map}}\)’s stationary distribution can not be reached in finite steps. A primitive explanation is: when \(\text{step size map size} \approx 0\), positions that are too far away are nearly inaccessible to each other in finite steps; for example, an agent will take nearly infinite steps to move from the top-left corner to the bottom-right corner. This breaks one

\(^1\)This happened because those implementations were crafted before we mature the model design and completed the Proof of Robustness.

\(^2\)Agents.jl is more flexible and programmable than GAMA. We shift to Agents.jl to examine if the robustness we observed in GAMA retains under different environment.
Figure 6: ASIR implementation on GAMA perfectly reproduce the infection curve of the given SIR. On bottom-left is ASIR’s infection curve; on top-right is SIR’s infection curve; on bottom-right is a comparison between the two.

of the necessary conditions that "there is only one communication class" for $T_{\text{map}}$’s stationary distribution to exist in finite steps.

5 Discussion

In this section, we will discuss the primary imperfection of our ASIR implementations.

The primary imperfection of our implementations is: they does not guarantee agents to reach the $T_{\text{map}}$’s stationary distribution at time $t = 0$. This is because we did not implement the Move behavior in a direct form of transition matrix $T_{\text{map}}$, but as "at each timestamp $t$, randomly choose one direction from (up, down, left, right), then move one unit distance accordingly." Though theoretically, this implementation of the Move behavior has a transition matrix $T_{\text{map}}$ representation which has a stationary distribution. The problem is: we cannot determine, after which $t$, agents’ positions will reach $T_{\text{map}}$’s stationary distribution. Also, we have to estimate but not deduce the value of $P(\text{meetup})$.

As a correction of our present approach, we would implement the Move behavior in direct form of $T_{\text{map}}$ so that we can 1). guarantee each agents’ position will state reach $T_{\text{map}}$’s stationary
Figure 7: ASIR implementation on Agents.jl fails to reproduce the infection curve of the given SIR; both $I_{asir}(t)$ and $R_{asir}(t)$ full curves remain flat to 0.

distribution at $t = 0$, 2). deduce the exact value of $P(\text{meetup})$.

6 Conclusion

We propose an agent-based SIR model, ASIR, that achieves the following interesting properties:

1. Parameters of ASIR can be deduced from (i.e. written as a determinate expression of) parameters of SIR.

2. ASIR robustly reproduce the infection curve predicted by SIR (i.e. the expectation values of the population size of being susceptible, infected and recovered equal to SIR’s prediction.)

We validated ASIR’s properties by giving: 1). a proof of robustness, 2). two implementations in GAMA and Agents.jl.

There are two interesting directions to extend our work:

1. Find robust agent-based representations for other compartmental models (SEIR, SEIS, …) We could start with describing new types of states and behaviors in the algebraic language we use (like Table 1) and give a proof of robustness.
2. Construct the transition matrix $T_{\text{map}}$ based on real data, check if the deduced value of $\alpha'$ comply with intuition. We could start with finding a calibrated $SIR$ model in the literature, where both real infection data and transportation data are applicable; then use MCMC algorithms like Gibbs sampling to construct the according transition matrix $T_{\text{map}}$. 
References

[1] V. Grimm, U. Berger, F. Bastiansen, S. Eliassen, V. Ginot, J. Giske, J. Goss-Custard, T. Grand, S. K. Heinz, G. Huse, A. Huth, J. U. Jepsen, C. Jørgensen, W. M. Mooij, B. Müller, G. Pe’er, C. Piou, S. F. Railsback, A. M. Robbins, M. M. Robbins, E. Rossmanith, N. Rüger, E. Strand, S. Souissi, R. A. Stillman, R. Vabø, U. Visser, and D. L. DeAngelis, “A standard protocol for describing individual-based and agent-based models,” *Ecological Modelling*, vol. 198, no. 1, p. 115–126, 2006.

[2] A. Menon, N. K. Rajendran, A. Chandrachud, and G. Sethur, “Modelling and simulation of covid-19 propagation in a large population with specific reference to india,” *medRxiv*, 2020. [Online]. Available: https://www.medrxiv.org/content/early/2020/05/05/2020.04.30.20086306

[3] L. Perez and S. Dragicevic, “An agent-based approach for modeling dynamics of contagious disease spread,” *International Journal of Health Geographics*, vol. 8, no. 1, p. 50, Aug 2009. [Online]. Available: https://doi.org/10.1186/1476-072X-8-50

[4] M. Crossley and M. Amos, “Simzombie: A case-study in agent-based simulation construction,” in *Agent and Multi-Agent Systems: Technologies and Applications*, J. O’Shea, N. T. Nguyen, K. Crockett, R. J. Howlett, and L. C. Jain, Eds. Berlin, Heidelberg: Springer Berlin Heidelberg, 2011, pp. 514–523.

[5] P. Taillardand, B. Gaudou, A. Grignard, Q.-N. Huynh, N. Marilleau, P. Caillou, D. Philippon, and A. Drogoul, “Building, composing and experimenting complex spatial models with the gama platform,” *Geoinformatica*, vol. 23, no. 2, p. 299–322, apr 2019. [Online]. Available: https://doi.org/10.1007/s10707-018-00339-6

[6] G. Datseris, A. R. Valdai, and T. C. DuBois, “Agents.jl: a performant and feature-full agent-based modeling software of minimal code complexity,” *SIMULATION*, vol. 0, no. 0, p. 00375497211068820, Jan. 2022. [Online]. Available: https://doi.org/10.1177/00375497211068820

[7] R. F. Serfozo, “Basics of applied stochastic processes,” 2012.