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An Agent-based Framework toward building Epidemic disease simulation based on SIR model

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Abstract. Agent-based models are an important tool that can be used to better understand the dynamics of the epidemic disease outbreak. In many cases, it is impossible to run an experiment to see how a disease will affect a population in the real world so an agent-based model can be used instead. The proposed agent-based framework is based on the modeling of the simple SIR compartmental model. The proposed model involves different types of parameters such as: agent attributes, distribution of population, and patterns of agents interactions. Analysis of modeling result leads to understanding of the mechanisms that affect the spread of disease, and suggest strategies for preventing and minimizing the spread of the disease.

Keywords : Epidemic disease, SIR model, Agent-based framework. Agent-based models.

1 Introduction

Agent-based simulation models are an alternative to equation-based models and can model much richer scenarios. An agent-based simulation model allows agents to interact with other agents and the environment based on a set of rules and it can be an essential part of an epidemiological study when it is not feasible to run an experiment. In this report, we proposed a framework for the design and implementation of models to forecast epidemic diseases in different scenarios. The main idea behind simulations is that for each experiment we use different parameters, including the transmission rate (β), the initial of number of infectious individuals (I), the period of infectiousness (γ). The rest of the report is organized

as follows: Section 2 reviews some epidemiological modeling approaches. Section 3 proposes the general framework and experiments. Section 4 carefully presents the experimental results, and result analysis. Finally, important conclusions are given in Section 5.

2 Epidemiological modeling approaches

We start begin with a classical epidemic model, the so-called Susceptible-Infected-Removed (SIR) model, which is simple and useful when one tries to understand the propagation of many real-life epidemics.

2.1 The SIR model

In this proposed study, we have considered an epidemic model which was developed by Kermack and McKendrick[1] in 1927. This epidemic model is also known as SIR epidemic model. This model have already used successfully in several outbreak diseases like Influenza[2], SARs[3], MERS[4],...

In order to model such an epidemic we divide the population being studied into three classes labeled S, I, and R. Let $S(t)$ denote the number of individuals who are *Susceptible* to the disease, that is, who are not (yet) infected at time t, $I(t)$ denote the number of *Infected* individuals, assumed infectious and able to spread the disease by contact with the susceptibles, $R(t)$ denote the number of individuals who have been infected and have *Recovered*, and then removed from the possibility of being infected again. They may have natural immunity, or they may have recovered from the disease and are immune from getting it again, so they can't transmit the disease to others.

The model we will consider assumes a time scale short enough that births and deaths (other than deaths from this disease) can be neglected and there is a homogeneous population assumption in terms of epidemiology.

In formulating models as differential equations, we assume that the epidemic process is deterministic, that is, that the behavior of a population is determined completely by its history and by the rules which describe the model.

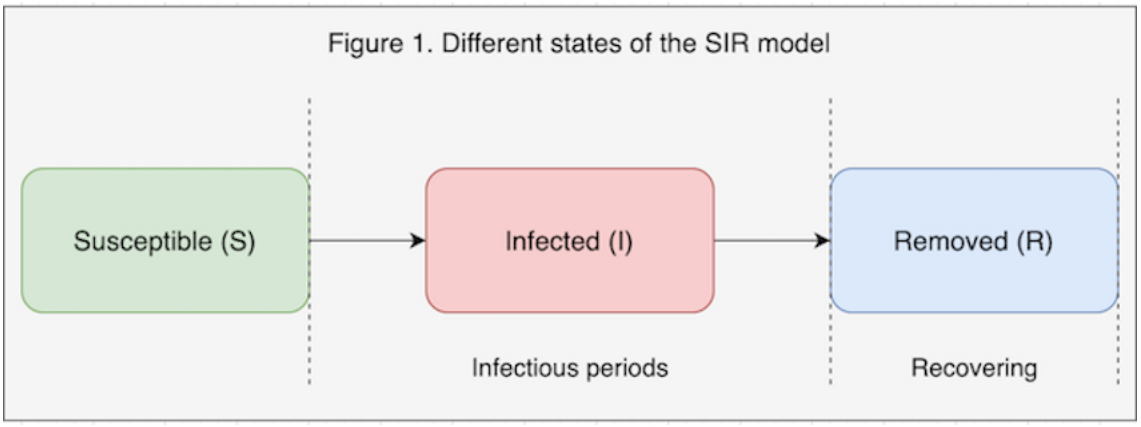
The dynamics of an SIR system is described by the following system of differential equations:

$$\frac{dS}{dt} = -\beta S(t)I(t)$$
$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t)$$
$$\frac{dR}{dt} = \gamma I(t)$$

where β is the *transmission rate* and γ the *removal rate* of infectives.
It is based on the following assumptions:

1. An average member of the population makes contact sufficient to transmit infection with βN others per unit time, where N represents total population size (mass action incidence).
2. Infectives leave the infective class at rate γI per unit time.
3. There is no entry into or departure from the population.

A flow chart of the SIR model is shown in Figure 1.



Explain the model : According to (1), since the probability that a random contact by an infective is with a susceptible, who can then transmit infection, is S/N, the number of new infections in unit time per infective is $(\beta N)(S/N)$, giving a rate of new infections $(\beta N)(S/N)I = \beta SI$. The hypothesis (3) says that the time scale of the disease is much smaller than the time scale of births and deaths so that demographic effects on the population may be ignored. The assumption (2) : Let $u(s)$ denote the number of those who are still infective s time units after being infected. If a fraction γ of these infectious individuals leave the infective class in each unit time then

$$u' = -\gamma u$$

The solution of this elementary differential equation is

$$u(s) = u(0)e^{-\gamma s}$$

Thus, the fraction of infectives remaining infective s time units after becoming infective is $e^{-\gamma s}$, so that the length of the infective period is distributed exponentially with mean

$\int_0^\infty e^{-\gamma s}\,\mathrm{d}s = 1/\gamma$.
In the model, $R(t)$ is determined once $S(t)$ and $I(t)$ are known, and we can drop the R equation from the model, leaving a system of two equations

$$\frac{dS}{dt} = -\beta S(t)I(t) \tag{1}$$
$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) \tag{2}$$

We are unable to solve this system analytically but we learn a great deal about the behavior of its solutions by the following qualitative approach. To begin, remark that the model makes sense only so long as $S(t)$ and $I(t)$ remain non-negative and $S(t)+I(t)+R(t) = N$. From (1), if $S(t)$ and $I(t)$ are non-negative then $I(t)$ decreases. From $\frac{dR}{dt} = \gamma I(t)$, if $I(t)$ is non-negative then $R(t)$ increase. From $\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) = (\beta S - \gamma)I(t)$, consider the $sign()$ of both side.

$$sign(\frac{dI}{dt}) = sign(\beta S - \gamma)$$

If $S < \gamma/\beta$, $I(t)$ decreases to zero (no outbreak), while if $S > \gamma/\beta$, $I(t)$ first increases to a maximum attained when $S = \gamma/\beta$ and then decreases to zero (outbreak).

Basic Reproduction Number : Suppose initially all individuals are S then $S(0) = N$, then there is an infected individual, which has an infection rate of β, so that in the mean infective period $1/\gamma$, this individual can infect $\beta N/\gamma$ other individuals. The quantity $\beta N/\gamma$ is a threshold quantity, called the *basic reproduction number* and denoted by R_0, which determines whether there is an epidemic or not: If $R_0 < 1$ the infection dies out, while if $R_0 > 1$ there is an epidemic.

Instead of trying to solve for S and I as functions of t, we divide the two equations of the model to get

$$\frac{dI}{dS} = \frac{\beta SI - \gamma I}{-\beta SI} = -1 + \frac{\gamma}{\beta S}$$

and integrate to find the orbits

$$I = -S + \frac{\gamma}{\beta}\log S + c \tag{3}$$

where c is an arbitrary constant of integration.

Another way to describe the orbits is to define the function

$$V(S,I) = S + I - \frac{\gamma}{\beta}\log S$$

Each orbit is a curve given implicitly by the equation $V(S,I) = c$ for some choice of the constant c. The constant c is determined by the initial values $S(0)$, $I(0)$ of S and

I, respectively, because $c = V(S(0), I(0)) = S(0) + I(0) - \gamma \log S(0)/\beta$. In particular, $S_\infty = \lim_{t\to\infty} S(t) > 0$, which implies that part of the population escapes infection.
Suppose that size of population is N into which a small number of infectives is introduced, so that $S_0 \approx K$, $I_0 \approx 0$. If we use the fact that $\lim_{t\to\infty} I(t) = 0$, $S_\infty = \lim_{t\to\infty} S(t)$, then the relation $V(S_0, I_0) = V(S_\infty, 0)$ gives

$$N - \frac{\gamma}{\beta} \log S_0 = S_\infty - \frac{\gamma}{\beta} \log S_\infty$$

from which we obtain an expression for β/γ in terms of the measurable quantities S_0 and S_∞, namely

$$\frac{\beta}{\gamma} = \frac{\log S_0 - \log S_\infty}{N - S_\infty}$$

We may rewrite this in terms of R_0 as the final size relation

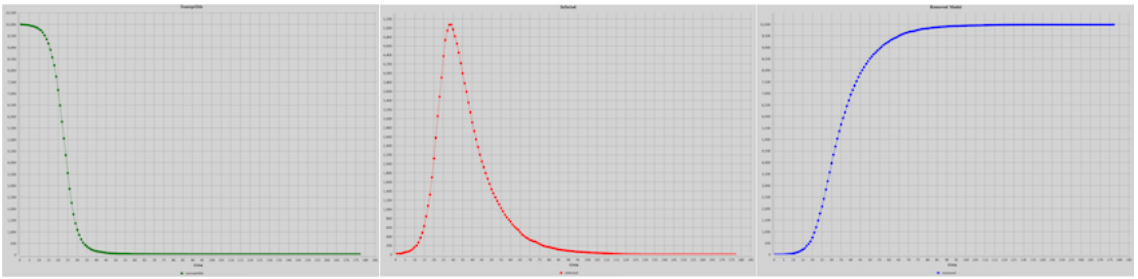
$$\log S_0 - \log S_\infty = R_0[1 - \frac{S_\infty}{N}]$$

In particular, since the right-hand side is finite, the left-hand side is also finite, and this shows that $S_\infty > 0$. The maximum number of infectives at any time is the number of infectives when the derivative of I is zero, that is, when $S = \gamma/\beta$. This maximum is given by

$$I_{max} = S_0 + I_0 - \frac{\gamma}{\beta} + \frac{\gamma}{\beta} \log \frac{\gamma}{\beta S_0}$$

obtained by substituting $S = \gamma/\beta$ into (3).

The behaviors of S, I and R as functions in t are illustrated in the figures below.



Susceptible *Infected* *Removed*

3 Modeling framework and experiments

3.1 Aim

We build a framework for epidemic simulation that should be flexible enough to be applied to different populations, different situations, and on different diseases with different transmission rates.

3.2 Agent-based modeling platform

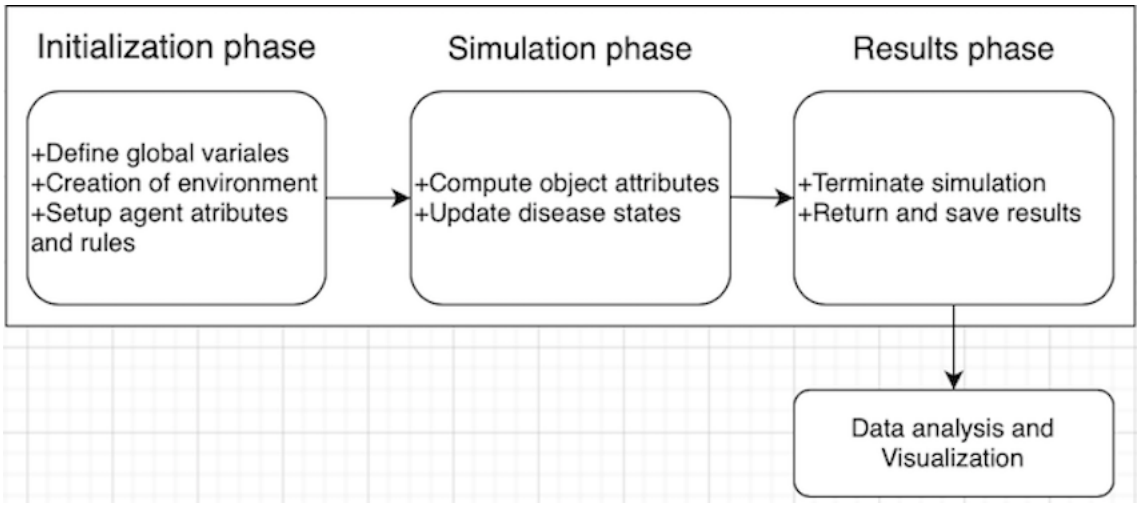
In order to implement the design of framework, GAMA platform[5] was used. GAMA is a modeling and simulation development environment for building spatially explicit agent-based simulations. Additionally, we use python for statistical analysis of the results. Code of the framework can be found in my personal repository[6].

3.3 Model framework structure

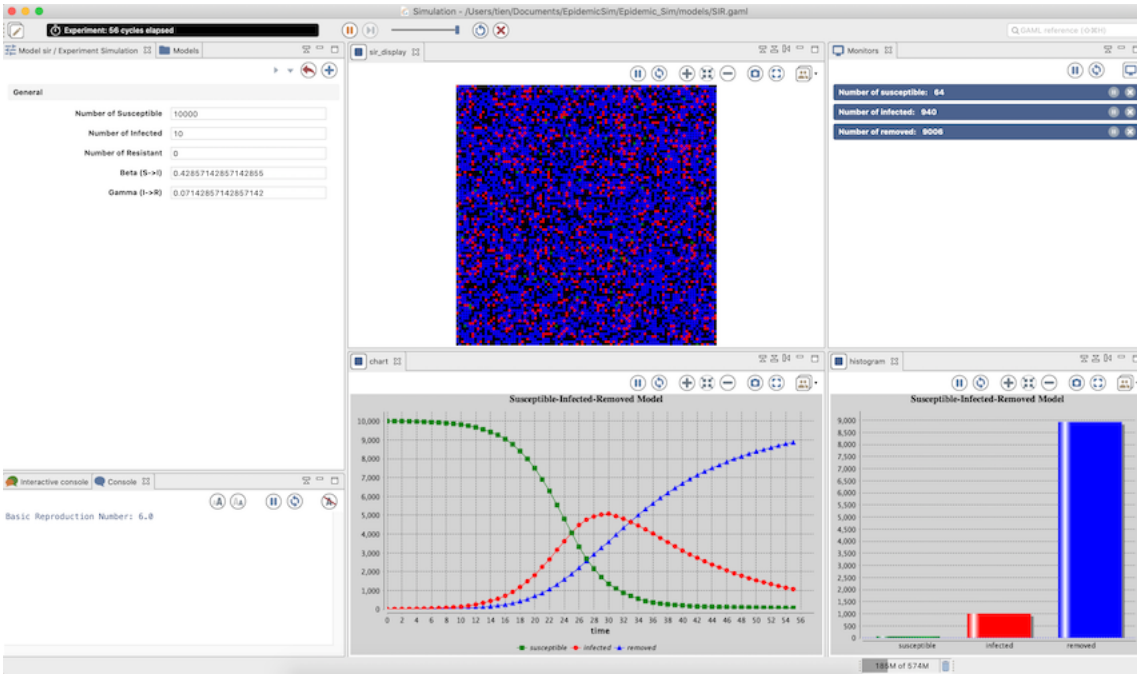
A typical agent-based model consists of three different sections: **global**, **species and grid**, and **experiment**

- **global**: Defines the "world" agent, a special agent of a GAMA model. It represents all that is global to the model: dynamics, variables, actions. In addition, it allows to initialize the simulation (init block).
- **species and grid**: Agent species, several species blocks can be defined.
- **experiment**: Simulation execution context, in particular inputs and outputs. Several experiment blocks can be defined.

Overview of phases and simulation of the agent-based Epidemic framework is described in Figure 3.



Graphical User Interface developed for model implementation is described in Figure 4.



3.4 Experimental Scenarios

We built 6 different experimental scenarios, each scenario is run 50 times, the common parameter values of the scenarios are: $N_0 = 10000$, $I_0 = 10$, $\gamma = \frac{1}{14}$ (average duration of infectiousness is 14 days):

- Scenario 1: $\beta_1 = \frac{6}{14}$
- Scenario 2: $\beta_2 = \frac{4}{14}$
- Scenario 3: $\beta_3 = \frac{2}{14}$
- Scenario 4: $\beta_4 = \frac{1.5}{14}$
- Scenario 5: $\beta_5 = \frac{1}{14}$

- Scenario 6: $\beta_6 = \frac{0.5}{14}$

The results are then processed with python. With each scenario, we calculate the final size of the disease outbreak, mean of infected, distribution of individuals, maximum of Infected, and the number of susceptible.

4 Result analysis and discussion

Table 1. Final size of disease (when I = 0)			
Scenarios	Mean(S)	Mean(R)	Mean(Time)
1. $\beta_1 = \frac{6}{14}$	26.18	9983.82	160.66
2. $\beta_1 = \frac{4}{14}$	233.82	9776.2	188.14
3. $\beta_1 = \frac{2}{14}$	2438.68	7571.32	319.38
4. $\beta_1 = \frac{1.5}{14}$	4881.44	5128.56	492.14
5. $\beta_1 = \frac{1}{14}$	9906.12	103.88	154.68
6. $\beta_1 = \frac{0.5}{14}$	9991.04	18.96	60.98

Table 2. Final size of disease (when I = 0)			
Scenarios	Std(S)	Std(R)	Std(Time)
1. $\beta_1 = \frac{6}{14}$	5.05	5.05	21.45
2. $\beta_2 = \frac{4}{14}$	20.57	20.57	21.48
3. $\beta_3 = \frac{2}{14}$	99.60	99.60	43.71
4. $\beta_4 = \frac{1.5}{14}$	186.42	186.42	49.81
5. $\beta_5 = \frac{1}{14}$	129.02	129.02	105.90
6. $\beta_6 = \frac{0.5}{14}$	6.22	6.22	27.24

Table 3. I maximum			
Scenarios	Mean(S)	Mean(I)	Mean(Time)
1. $\beta_1 = \frac{6}{14}$	1618.14	4989.94	29.8
2. $\beta_2 = \frac{4}{14}$	2539.02	3621.66	45.16
3. $\beta_3 = \frac{2}{14}$	5374.24	1234.72	112.36
4. $\beta_4 = \frac{1.5}{14}$	7115.09	454.72	198.9
5. $\beta_5 = \frac{1}{14}$	9953.17	16.92	45.64
6. $\beta_6 = \frac{0.5}{14}$	9995.77	10.82	3.04

Table 4. I maximum			
Scenarios	Std(S)	Std(I)	Std(Time)
1. $\beta_1 = \frac{6}{14}$	163.5	64.78	2.12
2. $\beta_2 = \frac{4}{14}$	211.54	94.06	2.53
3. $\beta_3 = \frac{2}{14}$	358.18	60.05	13.32
4. $\beta_4 = \frac{1.5}{14}$	350.09	55.00	31.18
5. $\beta_5 = \frac{1}{14}$	78.10	11.22	57.25
6. $\beta_6 = \frac{0.5}{14}$	3.45	1.38	5.75

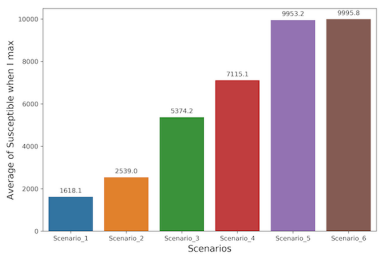


Fig 6.1.S_{Imax}

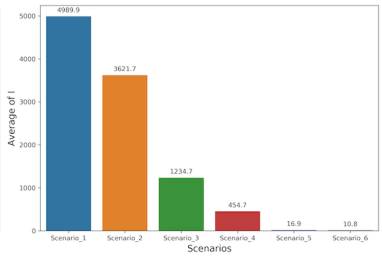


Fig 6.2.I_{Imax}

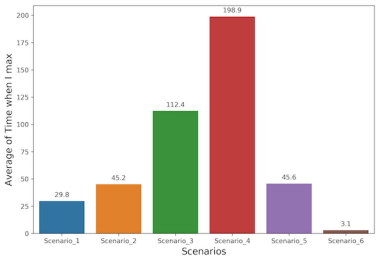


Fig 6.3.$Time_{Imax}$

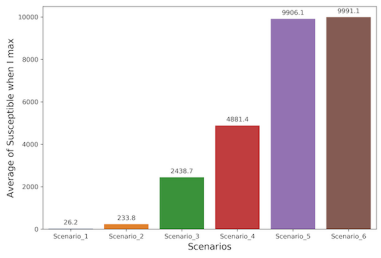


Fig 6.4.$S_{I=0}$

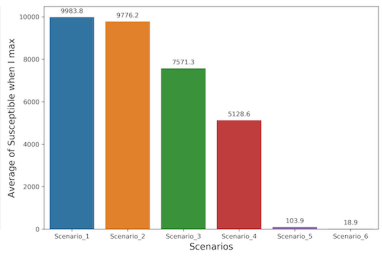


Fig 6.5.$R_{I=0}$

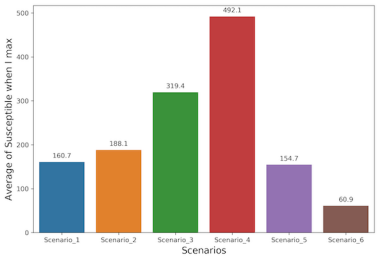


Fig 6.6.$Time_{I=0}$

In experiments, we will run different scenarios of applied control strategies (changing of the infectious rate β). The results of the scenarios are plotted and listed in Figures 6.1-6.6, Tables 1-4. We notice that the peak of the infection decrease based on the decrease of the infectious rate β. Also, as the decrease of the infectious rate, the number of *Removed* decreases, the number of *Susceptible* increases at the end of the disease, the epidemic duration increase from scenario 1 to scenario 4 and then decrease.

For the first scenario, with $\beta = \frac{6}{14}$ the peak of the epidemic started early from day number 30, the maximum number of infected is 4989.94 individuals (49.85% of population) (Table 3). After 160.66 days, at the end of the epidemic, the number of *Removed* is 9983.82 individuals, and the part of the population escapes infection is 26.18 individuals (Table 1).

In the second scenario, with $\beta = \frac{4}{14}$, the peak of the infection was on the 45th day, the maximum of infected is 3621.66 individuals (36.18%of population) (Table 3). which means that it has reduced the prevalence of infection with comparison to the first scenario. The duration is 188.14 days, the number of *Removed* is 9776.2 individuals and the number of *Susceptible* is 233.82 individuals (Table 1).

In the third scenario, with x$\beta = \frac{2}{14}$, the peak of the infection was on the 112th day, the maximum of infected is 1234.72 individuals (12.33% of population) (Table 3). the duration of the disease is 319.38 days, the number of *Removed* is 7571.32 individuals and the number of *Susceptible* is 2438.58 individuals (Table 1).

In the scenario 4, 5 and 6, with $\beta = \frac{1.5}{14}, \frac{1}{14}, \frac{0.5}{14}$ corresponding, the peak of the infection was on the 199th, 45th, and 3th, the maximum of infected is 454.72 individuals (4.5% of population) (Table 3), 16.92 individuals (0.16% of population), 10.82 individuals (0.10% of population) corresponding. The duration of the disease is 492.14, 154.68, and 60.98 days, the number of *Removed* is 5128.56, 103.88, 18.96 individuals and the number of *Susceptile* is 4881.44, 9906.12, 9991.04 individuals corresponding (Table 1).
In the study presented, we get the following observations
1. If R_0 is large (β is large), the peak of the disease come soon, but the number of infected is large.
2. As the decrease of R_0, the maximum of infected decreases.
3. If $R_0 < 1$, No outbreaks occurred.

5 Conclusions

We have presented a general framework to build agent-based epidemic disease simulation based on Susceptible-Infected-Removed model. The framework is general and flexible to be applied to different scenarios and disease outbreaks. The SIR model discussed here does not consider the percentage of the population who are exposed to the disease, but do not show any symptoms. When the incubation time i.e, the time elapsed before developing symptoms is significant, the SIR model will not be able to capture it.

The future studies will be focusing on improving the framework in a number of ways: extend baseline SIR with Exposed periods, and SIR with general contact rates.

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[5] Https://gama-platform.github.io
[6] Https://github.com/huutiendang/EpidemicSim

Appendix

The source code of the program is described in detail below:

Global block : World attributes

```
global {
    int number_S <- 10000; // init number of Susceptible
    int number_I <- 10 ;
    int number_R <- 0 ;
    int number_individuals<- number_S + number_I + number_R;
   float beta <- 4/14 ;
   float gamma <- 1/14;
   float R0 ;
   geometry shape <- square(200);
   init {
      create Host number: number_S {
```

```
            is_susceptible <- true;
            is_infected <- false;
               is_immune <- false;
               color <- #green;
        }
        create Host number: number_I {
            is_susceptible <- false;
            is_infected <- true;
            is_immune <- false;
            color <- #red;
       }
       create Host number: number_R {
            is_susceptible <- false;
            is_infected <- false;
            is_immune <- true;
            color <- #blue;
       }
   }
   reflex compute_nb_infected {
        number_I <- Host count each.is_infected;}
   reflex compute_nb_susceptible {
        number_S <- Host count (each.is_susceptible);}
   reflex compute_nb_removed {
        number_R <- Host count (each.is_immune);}
   reflex stop_simulation when: number_I = 0 {
       do pause;}
}
```

Species block : Road and building agents.

```
//Grid used to discretize space
grid sir_grid width: 100 height: 100 use_individual_shapes: true
    use_regular_agents: false frequency: 0{
   rgb color <- #black;
}

species Host {
   //Booleans to represent the state of the host agent
   bool is_susceptible <- true;
   bool is_infected <- false;
    bool is_immune <- false;
    rgb color <- #green;
    sir_grid myPlace;

    init {
      //Place the agent randomly among the grid
```

```
    myPlace <- one_of (sir_grid as list);
    location <- myPlace.location;
  }

  reflex become_infected when: is_susceptible{
    float rate <- beta*number_I/number_individuals;
    bool results <- flip(rate);
    if(results){
          is_susceptible <- false;
         is_infected <- true;
         is_immune <- false;
         color <- #red;
        }
  }

  reflex become_immune when: (is_infected and flip(gamma)) {
    is_susceptible <- false;
    is_infected <- false;
      is_immune <- true;
      color <- #blue;
  }

  aspect basic {
      draw circle(1) color: color;
  }

}
```

Experiment block : output definition.

```
experiment Simulation type: gui{
   parameter "Number of Susceptible" var: number_S ;
   parameter "Number of Infected" var: number_I ; // The number of infected
     parameter "Number of Resistant" var:number_R ; // The number of removed
   parameter "Beta (S->I)" var:beta;  // The parameter Beta
   parameter "Gamma (I->R)" var: gamma; // The parameter gamma
   init{
    }
    reflex end_of_runs {
    int cpt <- 0;
    ask simulation{
        save ( ""+ cycle + "," + number_S + "," + number_I + "," + number_R)
         to: "result1"  type: "text" rewrite: false;
      }
      cpt <- cpt + 1;
  }
```

```
  output {
      display sir_display {
         grid sir_grid lines: #black;
         species Host aspect: basic;
      }
        display histogram refresh: every(1#cycle) {
           chart "Susceptible-Infected-Removed Model" type: histogram background:
               #lightgray style: exploded {
              data "susceptible" value: Host count (each.is_susceptible) color:
                  #green;
              data "infected" value: Host count (each.is_infected) color: #red;
              data "removed" value: Host count (each.is_immune) color: #blue;
           }

        }
        display chart refresh: every(1#cycle) {
           chart "Susceptible-Infected-Removed Model" type: series background:
               #lightgray style: exploded {
              data "susceptible" value: Host count (each.is_susceptible) color:
                  #green;
              data "infected" value: Host count (each.is_infected) color: #red;
              data "removed" value: Host count (each.is_immune) color: #blue;
           }
        }
        monitor "Number of susceptible" value: number_S;
           monitor "Number of infected" value: number_I;
           monitor "Number of removed" value: number_R;}
}
```