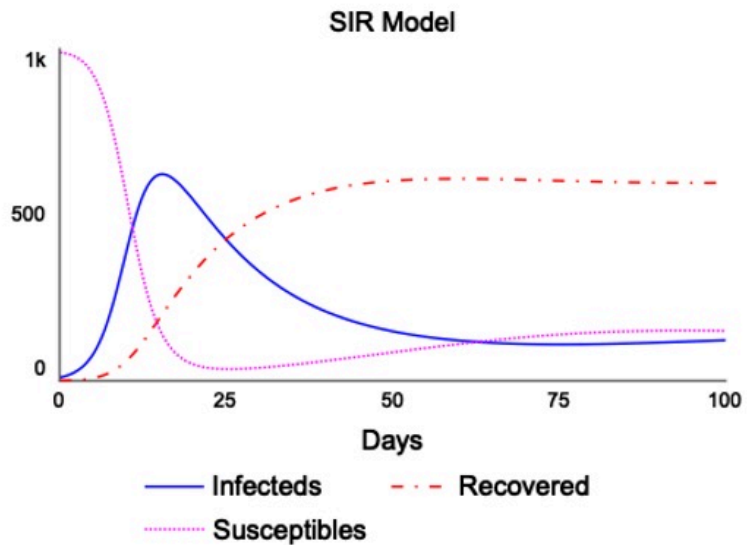


# Computing the Spread: Epidemiology

By Robert Gotwals



Computing CoVID-19: A Presentation of the North Carolina School of Science and Math, Summer 2020

COMPUTING CoVID-19: SUMMER 2020

## COMPUTING THE SPREAD: EPIDEMIOLOGY

*Developer:*  
*Robert Gotwals*  
*June 20, 2020*

COMPUTING CoVID-19. COPYRIGHT HELD BY THE NORTH CAROLINA SCHOOL OF  
SCIENCE AND MATH, MAY 1, 2020. ALL RIGHTS RESERVED.

---

## INTRODUCTION

In this lab, we want to explore the effect of the SARS-CoV-2 virus on a population of people. We are in the middle (some say the beginning!) of a *pandemic*, which is the spread of a disease on a global scale.

To accomplish this, we need an *epidemiology model*, and the most famous epidemiology model was created by Anderson McKendrick and William Kermack in 1927. Their "SIR" model is based on studying the change in three populations of people: susceptibles (those people who are healthy and can get the disease), infecteds, and recovered (those who have been sick but are now better). The populations are represented with a letter, S, I, and R, hence the name of the algorithm. There are several variations on this model. For example, the "SEIR" model adds a population of people who are exposed to the disease, but not yet infected.

---

The Kermack–McKendrick epidemic model of 1927 is an age of infection model, that is, a model in which the infectivity of an individual depends on the time since the individual became infective. A special case, which is formulated as a two-dimensional system of ordinary differential equations, has often been called the Kermack–McKendrick model. One of the products of the SARS epidemic of 2002–2003 was a variety of epidemic models including general contact rates, quarantine, and isolation. These models can be viewed as age of infection epidemic models and analyzed using the approach of the full Kermack–McKendrick model. All these models share the basic properties that there is a threshold between disappearance of the disease and an epidemic outbreak, and that an epidemic will die out without infecting the entire population. ([1])

---

The SIR model is represented using a technique known as *systems dynamics*. A *system* is a collection of interacting parts. In this case, the system is three different types of people. In science, the term *dynamics* means something that changes over time.

Mathematically, we represent the system using a series of three ordinary differential equations. The change in the susceptible population over time is shown in Equation 1. Equation 2 shows infecteds, and Equation 3 shows recovered. The  $\Delta$  symbol is, as you should know, the Greek letter representing "change in".

$$\frac{\Delta S}{\Delta t} = r_B + r_S R_t - r_I S_t I_t \quad (1)$$

$$\frac{\Delta I}{\Delta t} = r_I S_t I_t - r_R I_t - r_D I_t \quad (2)$$

$$\frac{\Delta R}{\Delta t} = r_R I_t - r_S R_t \quad (3)$$

What are the variables here?

1.  $S_t$ : this is the number of susceptibles at any given time. At the beginning of the epidemic ( $S_0$ , when time = 0), we'll set the number at 990 people.
2.  $I_t$ : number of infecteds at any given time.  $I_0$  is 10.
3.  $R_t$ : number of recovered at any given time.  $R_0$  is 0.
4.  $r_B$ : the number of new people – births, immigrants, etc. – coming into the model. We'll set this at a constant rate of three (3) people per unit time.
5.  $r_S$ : the loss of immunity of the recovered people. We'll set this at a constant rate of 0.01 (1%) per unit time.
6.  $r_I$ : the infection rate. We'll set this at a constant rate of 0.0005 (0.05%) per unit time.
7.  $r_R$ : the rate at which immunity is acquired. We'll set this at a constant rate of 0.05 (5%) per unit time.
8.  $r_D$ : the rate at which infected people die from the disease. We'll set this at a constant rate of 0.02 (2%) per unit time.

To model these conditions, we'll use a software program called STELLA ([2]), a visually-oriented program that is designed specifically to do systems dynamics (and nothing else). The model for SIR will be demonstrated in the webinar, and is shown in Figure 2 at the end of the file.

We want to run the model for 100 days, with updates coming every 3 hours. Accordingly, we'll set the *step size*, the value of time in  $\Delta t$ , at 0.125 (24 hours in a day x 0.125 = 3 hours).

Since we are using differential equations, we need to apply integral calculus to solve them. There are several different integration methods. If you have studied calculus, you are familiar with Euler's method. We'd rather use a more powerful integration technique, so we'll use Runge-Kutta 4 (RK4) for our method.

Figure 1 shows the model run settings for this model:

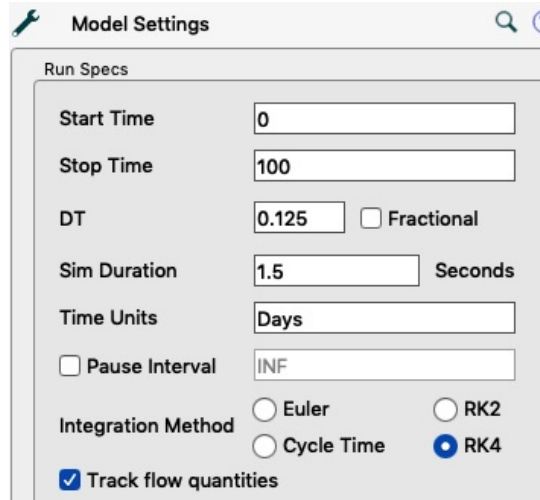


Figure 1: Screenshot of model run settings

Now, let's change the model. We want to add the effect of quarantining those people who are infected. What happens if 10% of the sick people are quarantined? 25%? More? We will add the factor of  $-r_Q I_t$  to the infected population, where  $r_Q$  is the percentage of infecteds quarantined. In the original model, we did not include that factor, so of course it is zero.

$$\frac{\Delta I}{\Delta t} = r_I S_t I_t - r_R I_t - r_D I_t - r_Q I_t \quad (4)$$

(5)

---

## STUDENT ACTIVITY

**NOTE! The majority of the steps for the activity will be demonstrated in the webinar.**

### 2.1 STUDENT ACTIVITY: BASIC SIR MODEL

For this activity, you want to build the model as demonstrated in the webinar! Then, you want to use the model to answer this question:

**What is the effect of increasing the percentage of infected people who are quarantined when sick?**

You want to find the *maximum* number of people who are infected with these rates of  $r_Q$  (the quarantine rate):

1. 0%
2. 5% (0.05)
3. 10% (0.10)
4. 20% (0.20)
5. 25% (0.25)

Once you have determined your value, enter the maximum value on the Canvas lab activity

### 2.2 STUDENT ACTIVITY: USING AN ADVANCED COVID-19 SIMULATOR

For this activity, we'll use a larger, more complex model written in STELLA. You can find this model on Canvas.

Following the example in the webinar, your task is to:

1. create a *sensitivity* analysis using the infectivity rate. We will start at a rate of 0.40 (40%), increasing by 0.01 (10%5) for five runs, up to 0.60 (60%).
2. Plot a comparative graph of severely infected persons over the course of a year.

# REFERENCES

- [1] Brauer, Fred. "The Kermack–McKendrick epidemic model revisited." Mathematical biosciences 198.2 (2005): 119-131.
- [2] STELLA software, ISEE Systems, <https://www.iseesystems.com>, accessed June 25, 2020.
- [3] Voit, Eberhard. A first course in systems biology. Garland Science, 2017.

## 2.3 STELLA MODEL

Figure 2 shows the model for the SIR algorithms. Parameters come from Voit ([3]).

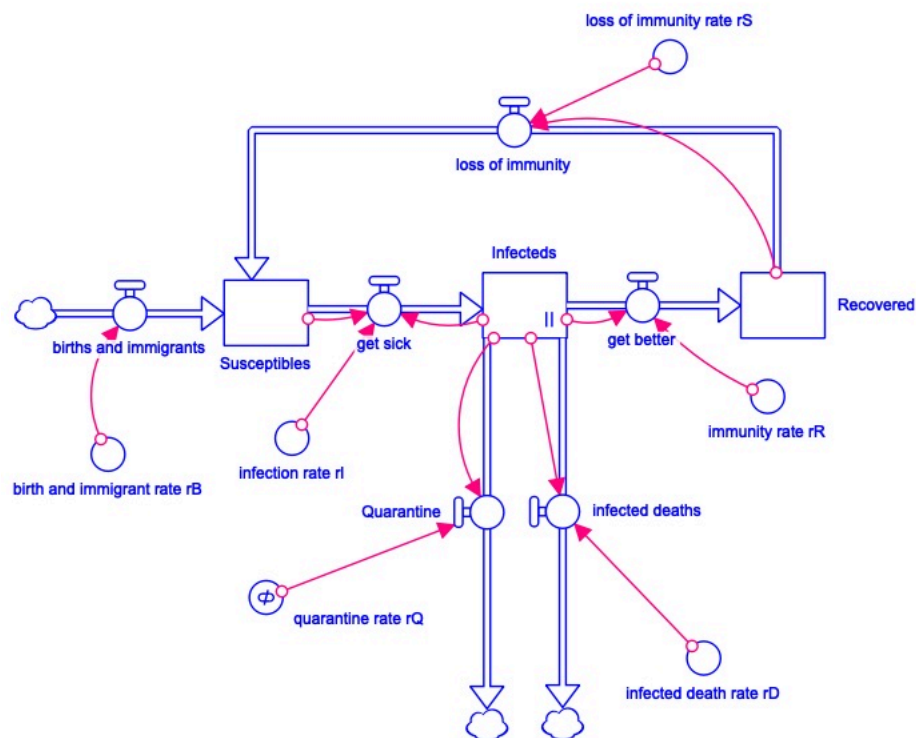


Figure 2: SIR Model in STELLA[2]

Top-Level Model:

```

Infecteds(t) = Infecteds(t - dt) + (get_sick - get_better
- infected_deaths - Quarantine) * dt
INIT Infecteds = 10
  
```

```

INFLOWS:
    get_sick = infection_rate_rI*Susceptibles*Infecteds
OUTFLOWS:
    get_better = immunity_rate_rR*Infecteds
    infected_deaths = infected_death_rate_rD*Infecteds
    Quarantine = quarantine_rate_rQ*Infecteds
Recovered(t) = Recovered(t - dt) +
(get_better - loss_of_immunity) * dt
INIT Recovered = 0
INFLOWS:
    get_better = immunity_rate_rR*Infecteds
OUTFLOWS:
    loss_of_immunity = loss_of_immunity_rate_rS*Recovered
Susceptibles(t) = Susceptibles(t - dt) + (births_and_immigrants + loss_of_immunity
INIT Susceptibles = 990
INFLOWS:
    births_and_immigrants = birth_and_immigrant_rate_rB
    loss_of_immunity = loss_of_immunity_rate_rS*Recovered
OUTFLOWS:
    get_sick = infection_rate_rI*Susceptibles*Infecteds
birth_and_immigrant_rate_rB = 3
immunity_rate_rR = 0.05
infected_death_rate_rD = 0.02
infection_rate_rI = 0.0005
loss_of_immunity_rate_rS = 0.01
quarantine_rate_rQ = 0.1
{ The model has 15 (15) variables (array expansion in parens).
  In root model and 0 additional modules with 0 sectors.
  Stocks: 3 (3) Flows: 6 (6) Converters: 6 (6)
  Constants: 6 (6) Equations: 6 (6) Graphicals: 0 (0)
}

```