Discrete SIR Model of Epidemics

An Example of a Nonlinear System

CURM Background Material, Fall 2014

In this example, we will consider a disease that is spreading throughout the United States. The Centers for Disease Control and Prevention (CDC) is interested in knowing and experimenting with a model for this new disease before it actually becomes a real epidemic. Their goal is to determine how to prevent such an epidemic.

▼ Step 1: Identify the Problem

Predict the spread of a disease in a region.

▼ Step 2: Identify Relevant Facts about the Problem

- The average length of the disease is two weeks, over which time the person is infectious and can spread the disease.
- Once someone gets the flu, they cannot get it again this year.

▼ Step 3: Choose the Type of Modeling Method

We will use a deterministic model, the discrete SIR model.

▼ Step 4: Make Simplifying Assumptions

Assumptions:

- The population can be considered as divided into three categories: susceptible, infected, and removed.
- No one enters or leaves the community, and there is no contact outside the community.
- Each person is either susceptible (capable of being infected), infected (already has the illness and can spread it), or removed (already had the illness and will not get it again -- includes death).
- Initially, every person is either susceptible or infected.
- Once someone gets the illness, they cannot get it again (e.g., chicken pox).
- The average length of the disease is three weeks, over which time the person is deemed infected and can spread the disease.
- Our time period for the model will be one week.
- The spread of disease is proportional to both the number of susceptible individuals and the number

of infected individuals.
• Initially, assume that the transmission coefficient is constant (actually, it is probabilistic).

Variables: $S(n)$ = the number of people susceptible after time period n
 $I(n)$ = the number of people infected after time period n
 $R(n)$ = the number of people removed after time period n
 n = the number of one-week time periods
 a = the rate at which the disease is spread (the transmission coefficient) (per week)

▼ Step 5: Construct the Model

Since we have assumed that a person is sick for three weeks, one third of the infected people will be removed each week. Therefore, $R(n + 1) = R(n) + \frac{1}{3} \cdot I(n)$.

The value $\frac{1}{3}$ is the removal rate per week, and representes the proportion of infected persons removed from the infected population each week. The population of infected people, $I(n)$, will have terms that both increase and decrease its amount over time (from susceptible individuals becoming infected and from infected individuals becoming removed). So,
$I(n + 1) = I(n) + a \cdot S(n) \cdot I(n) - \frac{1}{3} \cdot I(n)$. Finally, the susceptible population decreases as a result of individuals becoming infected. Therefore, $S(n + 1) = S(n) - a \cdot S(n) \cdot I(n)$.

▼ Step 6: Solve and Interpret the Model

We cannot solve this by hand or analytically at all.

First, we will determine the equilibrium value(s).

restart
$solve\left(\left\{Req = Req + \frac{1}{3} \cdot Ie, \ Ie = Ie + a \cdot Se \cdot Ie - \frac{1}{3} \cdot Ie, \ Se = Se - a \cdot Se \cdot Ie\right\}, \ \{Se, Ie, Req\}\right)$
$$\{Ie = 0, \ Req = Req, \ Se = Se\} \tag{6.1}$$

Thus, there are infinitely many equilibrium solutions. Most importantly, the equilibrium value for the infected population is zero. We must determine if this is a stable equilibrium value.

To get an idea, we will numerically solve the discrete dynamical system with a given set of different initial conditions.

restart
with(*plots*) :

$SIRModel := \mathbf{proc}(x, y, z, g, a, stab)$ **option** *remember*;
local i;
$S(0) := x$;
$Infect(0) := y$;
$R(0) := z$;
for i **from** 1 **to** *stab* **do**

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S(i) := evalf(S(i − 1) − a·S(i − 1)·Infect(i − 1));
Infect(i) := evalf(Infect(i − 1) − g·Infect(i − 1) + a·S(i − 1)·Infect(i − 1));
R(i) := evalf(R(i − 1) + g·Infect(i − 1));
 end do;
 end;
```

proc$(x, y, z, g, a, stab)$ **(6.2)**

    option *remember*;

    local i;

    $S(0) := x$;

    $Infect(0) := y$;

    $R(0) := z$;

    for i **to** $stab$ **do**

        $S(i) := evalf(S(i − 1) − a * S(i − 1) * Infect(i − 1));$

        $Infect(i) := evalf(Infect(i − 1) − g * Infect(i − 1) + a * S(i − 1) * Infect(i − 1));$

        $R(i) := evalf(R(i − 1) + g * Infect(i − 1))$

    end do

end proc

Assume that $a = 0.00167$, and $I(0) = 3$, $S(0) = 997$, and $R(0) = 0$ (so the total population is 1,000).

$$SIRModel\left(997, 3, 0, evalf\left(\frac{1}{3}\right), 0.00167, 30\right)$$

                               999.8656890   **(6.3)**

$seq([i, R(i), Infect(i), S(i)], i = 0 .. 30)$

$[0, 0, 3, 997], [1, 0.9999999999, 6.994970000, 992.00503], [2, 3.331656666, 16.25151919,$ **(6.4)**
    $980.4168241], [3, 8.748829729, 37.44289505, 953.8082752], [4, 21.22979475,$
    $84.60321310, 894.1669921], [5, 49.43086578, 182.7366411, 767.8324931], [6,$
    $110.3430795, 356.1440156, 533.5129049], [7, 229.0577514, 554.7417490,$
    $216.2004996], [8, 413.9716677, 570.1200230, 15.9083093], [9, 604.0116753,$
    $395.2263237, 0.76200104], [10, 735.7537832, 263.9871578, 0.2590590475], [11,$
    $823.7495025, 176.1056469, 0.1448506505], [12, 882.4513848, 117.4463647,$
    $0.1022505913], [13, 921.6001730, 78.31763143, 0.08219562770], [14, 947.7060501,$
    $52.22250469, 0.07144522501], [15, 965.1135517, 34.82123398, 0.06521437385], [16,$
    $976.7206297, 23.21794830, 0.06142206275], [17, 984.4599458, 15.48101378,$
    $0.05904048531], [18, 989.6202837, 10.32220224, 0.05751409434], [19, 993.0610178,$
    $6.882459592, 0.05652266191], [20, 995.3551710, 4.588956050, 0.05587300697], [21,$
    $996.8848230, 3.059732219, 0.05544482102], [22, 997.9047337, 2.040104788,$
    $0.05516151169], [23, 998.5847686, 1.360257793, 0.05497357780], [24, 999.0381879,$
    $0.9069634084, 0.05484869814], [25, 999.3405090, 0.6047253477, 0.05476562272],$
    $[26, 999.5420841, 0.4032055391, 0.05471031539], [27, 999.6764859, 0.2688405321,$
    $0.05467347602], [28, 999.7660994, 0.1792515678, 0.05464892961], [29, 999.8258499,$
    $0.1195174044, 0.05463257045], [30, 999.8656890, 0.07968917394, 0.05462166611]$

$pointplot(\{seq([i, S(i)], i = 0 .. 30)\}, symbol = solidcircle, labeldirections = [horizontal, vertical],$
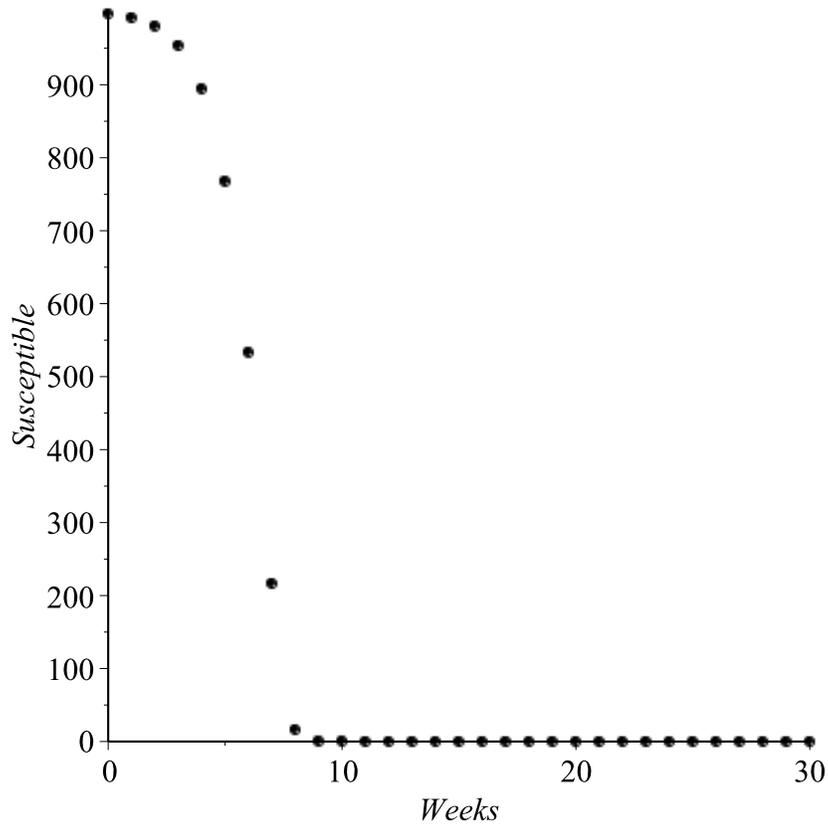
pointplot({*seq*([*i, Infect*(*i*)], *i* = 0 ..30) }, *symbol* = *solidcircle, labeldirections* = [*horizontal, vertical*], *labels* = [*Weeks, Infected*])
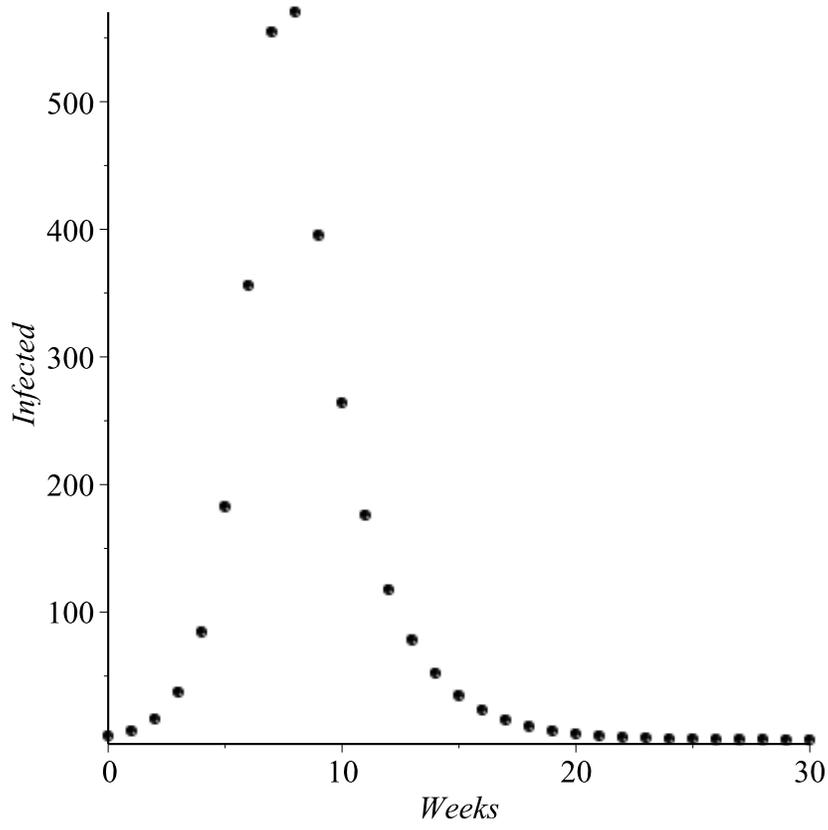
$pointplot(\{seq([i, R(i)], i = 0..30)\}, symbol = solidcircle, labeldirections = [horizontal, vertical],$
$\quad labels = [Weeks, Removed])$
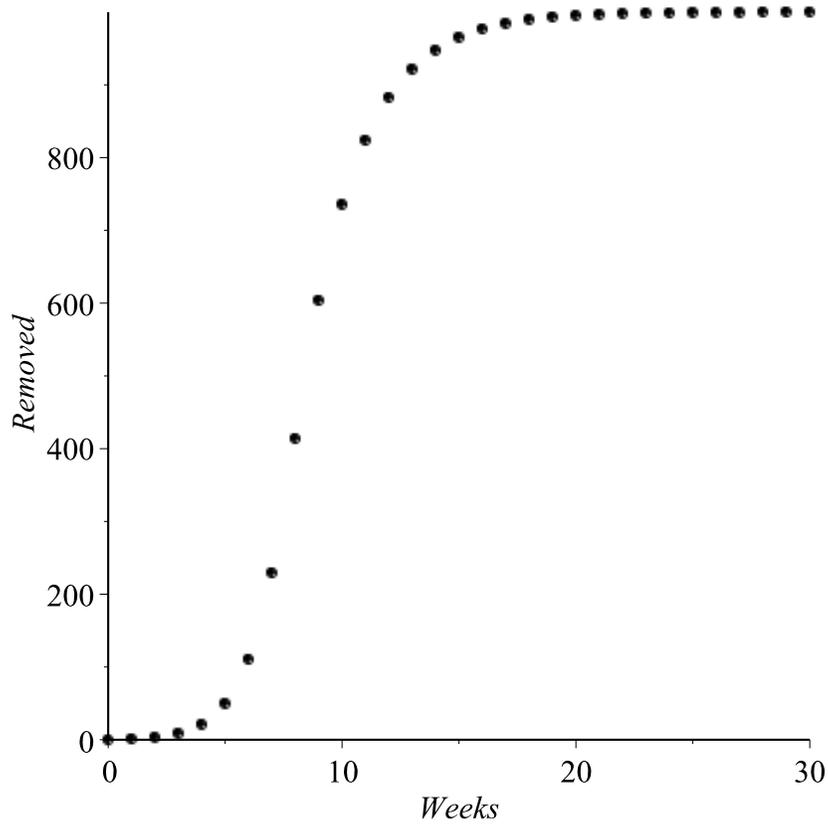
It appears that the infection peaks at approximately 8 weeks. Checking:

Infect(7)

$$554.7417490 \tag{6.5}$$

Infect(8)

$$570.1200230 \tag{6.6}$$

Infect(9)

$$395.2263237 \tag{6.7}$$

It appears that the infection does, in fact, peak at 8 weeks.