Epidemics travelling across the United States. Credit: Max Planck Institute for Dynamics and Self-organization. MPI is in Germany, hence ‘zeit’ which is German for ‘time’.

1 Instructions

The reporting and submission instructions for this lab are similar to those from Lab 1, and are enumerated below. That said, please note two important points:

- There are some lengthy calculations in this lab that will need to be put in an appendix. Do not include these in the body of the report; do that in the appendix. Instead, reference these calculations and summarize their implications as you present your results within the main body of the report.
Two decimal point accuracy will suffice for this lab.

Labs may be done in groups of **two or three**. You may use any program, but the TAs will only answer coding questions in MATLAB. One report must be turned in for each group and must be in PDF format. **Make sure to read the project writing guidelines on the course webpage.** Labs must include each student’s:

- Name
- Student number
- Section number
- Recitation number

This lab is due on **Thursday, April 21, 2016 at 11:59 p.m.** Each lab must be turned in through D2L on the course page. When you submit the lab please include each group member’s information (name, student number, section number and recitation number) in the comments. This allows us to search for a student’s report. Once the labs are graded, it is **your responsibility** to check that your grade was entered. If you are missing a grade, please **notify your TA within one week of grading.**

The report must be typed (including equations). Be sure to label all graph axes and curves so that, independent of the text, it is clear what is in the graph. Simply answering the lab questions will not earn you a good grade. Take time to write your report as up to 20% of your grade may be based on organization, structure, style, grammar, and spelling.

## 2 Introduction

This lab demonstrates the use of nonlinear systems to model physical processes. In the previous project we saw how a simple diffusion problem could be represented as a system of linear differential equations. Such systems of linear differential equations may be written using matrix notation and are then easily solvable using techniques from linear algebra. When considering **nonlinear** systems, this is not the case, but a much wider range of physical systems and behaviors can be modelled and analyzed using techniques applicable to nonlinear systems. Indeed, many physical systems you will encounter are best described by nonlinear model, and so it is important that we develop techniques for dealing with these systems that allo us to make **qualitative assessments** of the behavior of these systems. Solving these types of systems explicitly (i.e. finding a nice, closed form solution) is generally quite difficult, if not impossible. Therefore when dealing with nonlinear systems, we are typically interested in two things: equilibrium states and their stability.

One area of research that frequently deals with nonlinear systems is the study of disease spread in a population: epidemiology. In this lab we will examine systems of nonlinear differential equations to get a better understanding of the predictions these models make regarding the duration and size of an epidemic. We will determine what conditions allow an outbreak to become a full-blown epidemic, and also examine how large-scale immunity can effect disease dynamics.
3 Epidemics and their Models

For the purposes of this lab we differentiate between an outbreak and an epidemic as follows: an outbreak is a brief incident where a small number of individuals become infected with a disease, while an epidemic refers to a long-term incident where a large fraction of the population will be infected at some point. If 200 people in a small town get the flu for a week or two, it is an outbreak. If that infection spreads to an entire region of the country over the course of several weeks it is an epidemic. Alternately, if the number of infections almost immediately decreases, the event can be considered as an outbreak. If, however, the number of infections increases then we consider the event to be an epidemic. Determining when an outbreak may become an epidemic is a major goal of epidemiology, and one that can be addressed using differential equations.

A wide variety of epidemic models exist, but they can be roughly divided into two camps: stochastic and deterministic. stochastic models incorporate randomness into their structure, whereas deterministic models do not. Deterministic models may be represented by systems of differential equations, and will be the focus of this lab. There are several classic, nonlinear, systems of first-order differential equations that have been developed for the purposes of modelling different types of epidemics. These models are referred to as “bathtub models.”

A bathtub model considers a population of individuals as divided into a small number of categories; individuals move between these categories at rates usually proportional to the number of individuals within each category. This is analogous to a system of water-filled tanks flowing into each other at rates proportional to the water in each tank (hence the name of the model). The number of categories in the model and the linkages between them determine the type of epidemic model. In this lab, we consider models with at most three categories: susceptible, infected, and recovered. Figure 1 shows the general structure of the models that we will be considering.

3.1 Part I: A Simple Model

The simplest model of an epidemic is the SI model (sometimes called the SIS model) in a closed population, so-called because it has only two categories of individuals: susceptible and infected. We say that it occurs in a ‘closed population’ if we do not consider births or deaths in the population. This is a rather crude model, but it works fairly well for non-lethal diseases that an individual might acquire multiple times, such as the common cold. The SI model is expressed as:

\[
\begin{align*}
\frac{dS}{dt} &= \frac{\rho I}{N} - \frac{\beta SI}{N} \\
\frac{dI}{dt} &= \frac{\beta SI}{N} - \frac{\rho I}{N}
\end{align*}
\]  

(1)

Observe that \(S\) and \(I\) are the dynamic variables, while \(\rho\), \(\beta\), and \(N\) are constants, i.e. parameters of the system. The variable \(S\) denotes the number of susceptible individuals and the variable \(I\) denotes the number of infected individuals. The parameter \(\rho\) is the recovery rate of infected individuals, \(\beta\) is the contact rate between susceptible and infected individuals, and \(N\) is the total number of individuals in the population. Assume that all variables and
parameters are positive. Note that $S + I = N$ is a constant, since we are dealing with a closed population. We will skip the derivation of the models in this lab, but if you are interested, this model (and all models we will consider in this lab) can be derived from a stochastic, ‘Continuous Time Markov Chain model’ by way of the ‘mean field approximation’.

**Exercises I**

Please do not use a computer for these questions. You may use software to confirm your answers while writing the lab, but show your work by hand in your report.

1. This system has two equilibrium points. The first occurs when $I = 0$ and hence $S = N$. This is called the *disease free equilibrium*. Please find the other equilibrium point in terms of the parameters $\beta$, $\rho$, and $N$. What does the existence of a second equilibrium mean in terms of an epidemic?

   *Please read the Appendix on linearization before continuing to Problem 2.*

2. Please find the Jacobian for the SI model (Eq. 1) and evaluate it at each of the equilibrium points. You should find one matrix for each equilibrium point.

3. Find the eigenvalues and eigenvectors of each of the resulting matrices in terms of the parameters $\beta$, $\rho$, and $N$.

   In most epidemic models the *basic reproduction rate*, $R_0$, is an important quantity in determining whether an outbreak stays contained, or if the outbreak will grow into an epidemic. In our SI model $R_0 = \frac{\beta N}{\rho}$. 

Figure 1: Some simple epidemic models with categories for Susceptible, Infected, and Recovered individuals.
4. We can think of an outbreak as a small displacement from the disease free equilibrium, and an epidemic as an outbreak that results in increasing infections. Using the eigenvalues and eigenvectors from Problem 3, discuss how the stability of the disease free equilibrium depends on $R_0$.

Note: For guidance you may wish to consult the examples worked in some of the “Borderline Cases” in Section 6.4 in your textbook. Also when working in the phase plane keep in mind that in our system, $S$ and $I$ are confined to the line $S + I = N$ in the positive quadrant, where $S, I, N > 0$.

5. In your discussion include at least one paragraph explaining these results to someone who has no knowledge of differential equations, and a limited understanding of calculus. Make sure to provide an interpretation of $R_0$ in the context of an epidemic. Do not repeat my description above, explain $R_0$ in terms of its units and what that means for an epidemic outbreak. You may wish to consult outside sources for perspective, but sure to provide citations if you do so and keep in mind that you must provide your own insights.

### 3.2 Part II: A Less Simple Model

Slightly more elaborate than the SI model is the SIR model. Here we add a third category for ‘removed’ individuals. Removed individuals are no longer infectious or susceptible and may have achieved this through immunity, permanent recovery, or death. This type of model does a good job capturing infectious disease dynamics for epidemics like chicken pox, where an infection typically occurs only once in a lifetime. They also allow us to analyze the theoretical justification for immunity through vaccination, which we will explore numerically. The model looks like this:

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta SI}{N} \\
\frac{dI}{dt} &= \frac{\beta SI}{N} - \frac{\gamma I}{N} \\
\frac{dR}{dt} &= \frac{\gamma I}{N}
\end{align*}
\]

(2)

Where $S$, $I$, and $R$ are the total number of individuals in each category, $\beta$ is the rate of infection, and $\gamma$ is the rate of removal in the system. This model is a little gnarly, so for our purposes it will be useful to rewrite it in a non-dimensionalized form. That is, we re-write these equations not in terms of total individuals $S$, $I$, and $R$, but as percentages of the population $s$, $i$, and $r$:

\[
\begin{align*}
\frac{ds}{dt} &= -R_0si \\
\frac{di}{dt} &= R_0si - i \\
\frac{dr}{dt} &= i
\end{align*}
\]

(3)
Where \( R_0 = \frac{\beta N}{\gamma} \), and now \( s + i + r = 1 \). Observe that in this system, we have still have three dynamic variables, but only one parameter, \( R_0 \). We will deal with this non-dimensional system going forward.

**Exercises II**

6. Find all of the equilibrium points for this system in the \( s, i, r \) phase space keeping in mind that \( s + i + r = 1 \).

7. Discuss how these equilibrium points differ from those of the SI model and explain why they are different.

One useful measure of the severity of an SIR epidemic is its size, the number of people that were infected over the entire run of the epidemic. Since in our model all individuals who become infected eventually become removed, and no individuals leave the removed category, the size of the epidemic with \( r(0) = r_0 \) is just \( \sigma = \lim_{t \to \infty} r(t) - r_0 \); in practice this limit will be achieved fairly rapidly. We will now look at how the value of \( R_0 \) impacts the size of an epidemic. **For the remainder of the lab you will need to use a software aid (eg. MATLAB).**

8. Set \( R_0 = 1.5 \) and use the MATLAB package ode45 (or an equivalent numerical, differential equation solver) to numerically find the size of the epidemic, \( \sigma \), resulting from the outbreak \( s(0) = .9, i(0) = .1, \) and \( r(0) = 0 \). Set \( R_0 = .5 \) and repeat the simulation. Discuss your results and compare them to your conclusions for \( R_0 \) in the SI model.

Let us now consider how giving susceptibles immunity can affect the size of an epidemic. Vaccines are commonly accepted as one method to provide large portions of the susceptible population with immunity. We are going to consider an idealized model of a vaccine, where a fraction \( p \) of the initial susceptibles \( s(0) = s_0 \) are given permanent immunity through vaccination. This means that we can write our initials conditions generally as \( s(0) = (1 - p)s_0, i(0) = i_0, \) and \( r(0) = ps_0 \). Note that our model assumes that vaccines do not change the magnitude of an outbreak, \( i_0 \).

9. Set \( R_0 = 1.5, s_0 = .9, \) and \( i_0 = .1 \). For several (ie. \( \geq 5 \)) values of \( p \) between 0 and 1 plot \( \sigma \) vs. \( p \). Explain your results.

10. For each value of \( p \) used in the previous problem also plot each curve \( i(t) \) (it’s fine to overlay them, you don’t need to make 5+ separate plots). The duration of an epidemic is the first time \( \tau \) that \( i(\tau) = 0 \) (assuming that the outbreak occurs at \( t = 0 \)). Discuss how the duration of the epidemic depends on \( p \).

11. There is a bifurcation value \( \hat{p} \) such that when \( p < \hat{p} \) an outbreak becomes an epidemic, but for \( p > \hat{p} \) no epidemic occurs. Please estimate this value to two decimal places.

12. Please discuss any shortcomings you see in these models. Propose some ways that this model could be extended.
Appendix: Linearization

In a system of linear differential equations \( \frac{d\vec{x}}{dt} = A\vec{x} \) we have seen that the stability of equilibrium points is determined using the eigenvalues of the matrix \( A \). However our SI model is not a system of linear differential equation and therefore we cannot use this approach. Fortunately it turns out that for every equilibrium point we can construct a linear system of differential equations that behaves almost identically to the nonlinear system near the equilibrium. In other words, if the equilibrium is stable in the linear system, then it is also stable in the nonlinear system. This technique is called linearization. Below is a brief summary of the technique, but a more comprehensive discussion can be found in section 7.2 of your textbook.

For a suitably nice function of one variable you should be familiar with the Taylor Series; Taylor allows us to re-write our function as a (potentially infinite-degree) polynomial with coefficients determined by the derivative of the function at some arbitrary point \( x_0 \). Mathematically we write:

\[
f(x) = \sum_{n=0}^{\infty} \frac{f^{(n)}(x_0)(x-x_0)^n}{n!} \tag{4}
\]

Where \( f^{(n)}(x_0) \) denotes the \( n^{th} \) derivative of \( f(x) \) evaluated at \( x_0 \). Previously in the course we used Taylor Series to find approximate solutions to differential equations, now we can use them to examine the stability of differential equations.

Consider the simple, toy example \( \frac{dx}{dt} = f(x) = x^2 - 1 \). Clearly this differential equation has an equilibrium at \( x^* = 1 \), which we can see is unstable by considering values of \( x \) above and below 1. However for the sake of education let’s Taylor expand the right hand side of the differential equation to two terms, with \( x_0 = x^* \):

\[
x' = f(x^*) + f'(x^*)(x-x^*) + \sum_{n=2}^{\infty} \frac{f^{(n)}(x^*)(x-x^*)^n}{n!} \\
= 0 + 2(1)(x - 1) + \sum_{n=2}^{\infty} \frac{f^{(n)}(1)(x - 1)^n}{n!} \tag{5}
\]

This is very convenient, because as \( x \to 1 \) all of the terms \( (x - 1)^n \) with \( n > 1 \) go to zero much faster than \( (x - 1) \), so near the equilibrium we can approximate our nonlinear differential equation with the linear differential equation \( \frac{dx}{dt} = 2(x - 1) \), which we call the linearization. Almost immediately we can see that \( x^* = 1 \) is unstable in the linear differential equation, which corresponds to our initial analysis.

For a one-dimensional differential equation, it is usually straightforward to check stability by examining values near the equilibrium, but in higher dimensions this quickly becomes tedious. Using the appropriate Taylor series for higher dimensional functions we can construct a linearization for a system that is analogous to the one-dimensional case. Consider the general system of two, nonlinear differential equations:

\[
x' = f(x, y) \\
y' = g(x, y)
\]
We define the Jacobian Matrix $J(x, y)$ to be:

$$J(x, y) = \begin{bmatrix} f_x(x, y) & f_y(x, y) \\ g_x(x, y) & g_y(x, y) \end{bmatrix}$$

(6)

Here the $f_x(x, y)$ notation denotes the partial derivative $\frac{\partial f(x,y)}{\partial x}$ the partial derivative of a function of two variables is just the derivative with respect to one variable, treating the other as a constant). Eq’n (4) can be thought of as being analogous to $f'(x)$ in the Taylor expansion. Furthermore we would like to shift our linearized system so that the equilibrium of interest is located at the origin. Hence the linearization of our system about an equilibrium point $(x^*, y^*)$ is:

$$\begin{bmatrix} \frac{du}{dt} \\ \frac{dv}{dt} \end{bmatrix} = J(x^*, y^*) \begin{bmatrix} u \\ v \end{bmatrix}$$

(7)

Where $u = x - x^*$ and $v = y - y^*$. Now we can analyze the linearized system using the eigenvalues and eigenvectors of $J(x^*, y^*)$ to determine the stability of the equilibrium in the nonlinear system. Let’s see an example:

Consider the system of nonlinear differential equations:

$$\begin{align*}
\frac{dx}{dt} &= 2(x-1)y \\
\frac{dy}{dt} &= 3(y-2)x
\end{align*}$$

Here we have $f(x, y) = 2(x-1)y$ and $g(x, y) = 3(y-2)x$. Setting $f(x, y) = 0$ and $g(x, y) = 0$ we see that we have two equilibrium points, one at $(0, 0)$ and the other at $(1, 2)$. Let’s analyze the stability of $(1, 2)$. First we will need to find the Jacobian matrix:

$$J(x, y) = \begin{bmatrix} f_x(x, y) & f_y(x, y) \\ g_x(x, y) & g_y(x, y) \end{bmatrix} = \begin{bmatrix} 2y & 2(x-1) \\ 3(y-2) & 3x \end{bmatrix}$$

Now we evaluate the Jacobian at the equilibrium point $(1, 2)$:

$$J(1, 2) = \begin{bmatrix} 2(2) & 2(1-1) \\ 3(2-2) & 3(1) \end{bmatrix} = \begin{bmatrix} 4 & 0 \\ 0 & 3 \end{bmatrix}$$

Therefore our linearized system about $(1, 2)$ is:

$$\begin{bmatrix} \frac{du}{dt} \\ \frac{dv}{dt} \end{bmatrix} = \begin{bmatrix} 4 & 0 \\ 0 & 3 \end{bmatrix} \begin{bmatrix} u \\ v \end{bmatrix}$$

Note that the equilibrium of this linear system, $u = v = 0$ corresponds to $u = x - 1 = 0$ and $v = y - 2 = 0$, ie. $x = 1$ and $y = 2$. Now we find the eigenvalues of the Jacobian by setting $\det(J(1, 2) - \lambda I) = 0$.

$$\begin{vmatrix} 4 - \lambda & 0 \\ 0 & 3 - \lambda \end{vmatrix} = (4 - \lambda)(3 - \lambda) = 0$$

Therefore our eigenvalues are $\lambda_1 = 4$ and $\lambda_2 = 3$. Since both of our eigenvalues are real and positive we know that the equilibrium $u = v = 0$ is unstable in the linear system. We conclude that the equilibrium $x = 1$ and $y = 2$ in the nonlinear system is also unstable. See section 6.4 in your textbook for a more complete discussion of how eigenvalues determine stability.
References