Chapter 8 Systems

In this chapter we begin our study of systems of differential equations. While there will be fewer methods to solve them, there will be more interesting applications, and qualitative discussions that explore the nature of solutions.

The SIR model

A simply defined system that has many of the features of nonlinear systems of differential equations is the one describing the spread of an epidemic. In any epidemic of a population of size \( N \), we have the following

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>( t )</td>
<td>Time</td>
</tr>
<tr>
<td>( S(t) )</td>
<td>The population of those susceptible to the disease</td>
</tr>
<tr>
<td>( I(t) )</td>
<td>The population of those infected with the disease</td>
</tr>
<tr>
<td>( R(t) )</td>
<td>The population of those recovered from the disease</td>
</tr>
<tr>
<td>( N )</td>
<td>The total population</td>
</tr>
</tbody>
</table>

Many assumptions can be made about the relation of these variables. And you can experiment with various models drawing your own conclusions. As usual, since these quantities are time variant, we will make our model assumptions about their rates of change. Let \( Q(t) \) be any of the quantities above we will generate our model as follows:

\[
Q'(t) = \text{Increase of number - Decrease of number}
\]

Basic assumptions: There are positive quantities \( a \) and \( b \) so that

1. \( S' = -aSI \)
2. \( I' = aSI - bI \)
3. \( R' = bI \)

As is evident the susceptible population must be decreasing. But why is the dependency on the product of the two population? With the general hypothesis that infection is possible only by a susceptible-infected communication, we see that the proportionality should be to those communications. The diagram below is shows all the possible communications/interactions between the susceptible and infected populations. It is easy to see this number must be the product, \( S(t)I(t) \).
One might argue that all these communications are not possible. The constant of proportionality accounts for that. But one may also argue that there is a geographical factor, a time-delay factor, an incubation factor, and any number of other factors. This is true, but we have promised to keep the model simple.

Thus (1) is justified. To justify (2), note that when the susceptible population decreases, the infected population increases and by roughly the same factor. However, we must also account for the fact that the infected get better. This will be in proportion to the number of infected. Thus, \( I' = aSI - bI \). Again, variations of this model are possible. Finally, the population of those recovered is directly proportional to those infected. So, \( R' = bI \).

This system is nonlinear because of the products and autonomous because there is no explicit time dependence in the equations. There is no explicit solution of this system, and all solutions must be obtained numerically.

**Quantitative results for the SIR model**

In the graphs below, we show results for solutions of this model. First of all, we note that the behavior of the solutions will be affected by initial conditions and the coefficients \( a \) and \( b \). Indeed, it makes sense that if \( b \) is very small, that is few recover, that eventually the entire population will become infected. Similarly, if the disease is highly virulent, that is \( a \) is large in comparison with \( b \), then the population will also become infected. Conversely, if \( b \) is large relative to \( a \), it may be that the population of infected will decrease with insufficient numbers of susceptible to communicate with the infected. Here are some examples.

In the pictures below the red graphs represent susceptible population, while the blue graph represent the infected population. Here the coefficient \( b \) is large, but not too large. In all cases the initial population of susceptible is \( S(0) = 20 \). There are multiple graphs with various \( I(0) \)
On all cases you can see that ultimately the entire population becomes infected. In the next example we increase $b$ to $b = 0.8$, leaving the same $a = 0.1$. Now you can see that the population of susceptible asymptotes above zero. In this scenario, some of the population never becomes infected.

Since the population of susceptibles must always decrease, there are limited
possibilities for the dynamics of these two populations.

**Remark** Are there equilibrium solutions? These will be values $S$ and $I$ for which $-aSI = 0$ and $aSI - bI = 0$. We must have either $S = 0$ or $I = 0$ for the first equation to be zero. If the former is true, then $I = 0$ is the only solution of the second equation, while if $I = 0$, then any value of $S$ will yield an equilibrium. We may expect therefore that any combination of $I = 0$, and $S$ may actually furnish an asymptotically stable solution. However, we can see that the equilibrium is highly dependent on the initial conditions. Generally speaking, the analysis of stability is extraordinarily difficult. In this particular problem, we can see that if $S(0) > 0$ and $I(0) > 0$ then both populations must be positive. Since $S' < 0$, it $(S(t))$ decreases and therefore we (can) conclude that

$$\lim_{t \to \infty} S(t) = S_\infty \geq 0$$

exists. Correspondingly, if $S(t)$ is asymptotically stable with $S_\infty > 0$, equation (1) shows that $\lim_{t \to \infty} I(t) = 0$. On the other hand if $S_\infty = 0$, then $\lim_{t \to \infty} I(t) = 0$ because there are no more susceptibles to infect.

Here’s an example where the initial population of infected is increasingly large. There results that more and more of the susceptibles eventually succumb to the disease.

\[ a = 0.1 \text{ and } b = 0.8 \]
Equilibrium solutions

Are there equilibrium solutions? These will be values $S$ and $I$ for which $-aSI = 0$ and $aSI - bI = 0$. We must have either $S = 0$ or $I = 0$ for the first equation to be zero. If the former is true, then $I = 0$ is the only solution of the second equation, while if $I = 0$, then any value of $S$ will yield an equilibrium. We may expect therefore that any combination of $I = 0$, and $S$ may actually furnish an asymptotically stable solution. However, we can see that the equilibrium is highly dependent on the initial conditions. Generally speaking, the analysis of stability is extraordinarily difficult. In this particular problem, we can see that if $S(0) > 0$ and $I(0) > 0$ then both populations must be positive. Since $S' < 0$, it decreases and therefore we (can) conclude that

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Computing the solutions

As previously mentioned, there is no explicit solution of this system, and all solutions must be obtained numerically. The following graphs were made with MATLAB using the ode solver code shown below. The for loop is the part that creates the multiple plots.

```matlab
%Using ode45 to solve a system multiple times with varying initial conditions
%To solve a second order differential equation such as y''+y'+4y', you need
%to convert it to a first order system. ODE45 can solve this system
%Now the variable y will be an N x 2 array, where the first variable
clear all
a=0         % initial point
b=15         % final point
n= 15  % number of plots; if you want just one plot set n=1
hold on    %turn on the hold for multiple plots
for i= 1:n  %main loop to generate the plots
    v=i;     [t,y]=ode45('yyy_sir_model',[a,b],[20;1/i]);
    %subplot(3,1,1);
    plot(t,y(:,1),'r')
    %subplot(3,1,2)
    plot (t,y(:,2))
    %subplot(3,1,3)
    %plot(y(:,2),y(:,1))
    drawnow;
    %y(:,1)
end
hold off;
```

The function is given in the following. Call it the file 'yyy_sir_model.m'
function yprime=yyy(t,y)
yprime = [-.1*y(1)*y(2); .1*y(1)*y(2) - .8*y(2)];

Formulation as a system

This part is particularly easy. Form the vector of the susceptible and infected populations, and the vector of their derivatives

\[ u = \begin{bmatrix} S \\ I \end{bmatrix} \quad \text{and} \quad u' = \begin{bmatrix} S' \\ I' \end{bmatrix} \]

Now form the vector of the right side of the differential equations

\[ \begin{bmatrix} -aSI \\ aSI - bI \end{bmatrix} \]

It is common to define a vector function \( f \) of the vector \( u \) to encode this system in a functional form. Thus

\[ f(u) = \begin{bmatrix} -aSI \\ aSI - bI \end{bmatrix} \]

In this way we achieve the system form for the SIR model

\[ u' = f(u) \]

This model is nonlinear (because of the \( SI \) terms and autonomous because \( t \) is not explicitly present.

Prey-Predator models

When one species prey upon another then the signs of the above factors change. Here is the complete set of variables.

<table>
<thead>
<tr>
<th>Model</th>
<th>Prey-Preditor model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Description</td>
</tr>
<tr>
<td>( t )</td>
<td>Time</td>
</tr>
<tr>
<td>( P_1(t) )</td>
<td>The population of prey species</td>
</tr>
<tr>
<td>( P_2(t) )</td>
<td>The population of predator species</td>
</tr>
<tr>
<td>( a ) and ( c )</td>
<td>Growth rates (positive)</td>
</tr>
<tr>
<td>( c ) and ( d )</td>
<td>Competing factors (positive)</td>
</tr>
<tr>
<td>( e ) and ( f )</td>
<td>Crowding factors (positive)</td>
</tr>
</tbody>
</table>

The basic differential equations of population variation do not include crowding. They are
\[ P'_1 = aP_1 - bP_1P_2 \]
\[ P'_2 = -cP_2 + dP_1P_2 \]

The behavior of the solution is quite different from the SIR model. Examining the differential field plot, we see a "circulation" of the vectors. This means that solutions will generally circulate in orbits. Thus populations will fluctuate in sort of a periodic way. For the specific example

\[ P'_1 = 2P_1 - P_1P_2 \]
\[ P'_2 = -P_2 + P_1P_2 \]

we obtain the differential field plot

(The Maple command to do this is:
fieldplot([(2-y)*t,(t-1)*y],t=0..2,y=0..3,arrows=large,
color=red);)

Solutions for this simple model look much like the following.
The initial populations were \((100, 200)\) and the differential equations for this are 
\[ P_1' = P_1 - 0.02P_1P_2 \quad \text{and} \quad P_2' = -P_2 + 0.01P_1P_2. \]
There seems to be a need to make the interaction coefficients small in comparison with the growth factors to gain this circular appearance of the orbits.

As we have indicated earlier when studying first order differential equations (not systems), the plane is divided into an infinite set of solution curves to the solution. In the next plot you can see the orbits of the same differential for several initial conditions.
You should be able to see the orbital type of behavior of the solution. Note also that the solution appears to approach very close to zero. This is possible, but does not always occur. Remember, if this is applied to specific species it is necessary to calibrate the model by determining the coefficients. This may prove to be difficult.

Plotting both populations versus time over several periods gives a periodic (though not sinusoidal) variation as shown below.

There are equilibrium solutions for the Prey-Predator model. Solve the system

\[ aP_1 - bP_1P_2 = 0 \]
\[ -cP_2 + dP_1P_2 = 0 \]

to get the solution set \((0, 0)\) and \((c/d, a/b)\). For the specific example
\[2P_1 - P_1P_2 = 0\]
\[-P_2 + P_1P_2 = 0\]

the equilibrium solution are: \(\{P_1 = 0, P_2 = 0\}\) and \(\{P_1 = 1, P_2 = 2\}\). The stability properties here are interesting: \textit{We may say the solution are asymptotically stable but do not approach the equilibrium solution. Interesting???

Crowding

The addition of crowding makes important changes to the orbits. At this time we consider the general model

\[P_1' = aP_1 - bP_1P_2 - eP_1^2\]
\[P_2' = -cP_2 + dP_1P_2 - fP_2^2\]

Here is a specific example, \(P_1' = P_1 - 0.01P_1P_2 - 0.0001P_1^2\) and \(P_2' = -0.18P_2 + 0.001P_1P_2 - 0.0002P_2^2\), with the resulting graphs

As is apparent, the crowding seems to create an asymptotically stable equilibrium. Remember though nothing has been proved. We can solve the system

\[P_1 - 0.01P_1P_2 - 0.0001P_1^2 = 0\]
\[-0.18P_2 + 0.001P_1P_2 - 0.0002P_2^2 = 0\]

to obtain the equilibrium solutions \(\{P_1 = 0, P_2 = 0\}\), \(\{P_1 = 0, P_2 = -900.0\}\),
\{P_2 = 0, P_1 = 10000.0\}, \text{ and } \{P_2 = 98.00399202, P_1 = 199.6007984\} \text{ One thing is apparent: the solution seems to be tending toward the fourth solution. By the way these are relatively easy to find. You merely solve two coupled quadratic equations. In the following graph we show the actual points computed. The remaining part of the graph consists of connective lines.}

![Graph showing actual points computed](image)

Even the slightest crowding factors give behavior like this, though perhaps the convergence is not completely to the equilibrium solution. Consider the phase plane plot when crowding factors a tenth the size of the previous example.

![Phase plane plot](image)

In this case the equilibrium solutions to
\[
P_1 - 0.01P_1P_2 - 0.00001P_1^2 = 0 \\
-0.18P_2 + 0.001P_1P_2 - 0.00002P_2^2 = 0
\]
are \{P_1 = 0, P_2 = 0\}, \{P_1 = 0, P_2 = -9000.0\}, \{P_2 = 0, P_1 = 100000.0\}, and \{P_1 = 181.9963601, P_2 = 99.81800364\}

**MATLAB code**

The MATLAB code that generated these plots follows.
%Using ode45 to solve a system multiple times with varying initial conditions
%To solve a second order differential equation such as \(y''+y'+4y\), you need
%to convert it to a first order system. ODE45 can solve this system
%Now the variable \(y\) will be an \(N \times 2\) array, where the first variable

```matlab
clf;
a=0                 % initial point
b=155                % final point
hold on  %for idn=2:2 %turn on the hold for multiple plots
%clear all
[t,y]=ode45('yyy_predprey_model',[a,b],[100;150]); %solve the problem %Use subplot command to divide the
plot plane into segments
subplot(2,1,1);     %Create subplot
hold on;
plot(t,y(:,1),'r')  %plot the prey population
plot (t,y(:,2))     %Create subplots
xlabel('Time ')     %Add labels
ylabel('Prey-red; Predator-blue')
subplot(2,1,2)      %Create subplot
hold on
plot(y(:,1),y(:,2)) %Make phase portrait plot
xlabel('Prey ')     %Add labels
ylabel('Predator')  %Add labels
grid on             %Add grid
drawnow;
%figure If the "%%" is removed the animation is on a separate graph.
hold on
%Now begin and animation
lh=plot( y(1,1),y(1,2),'.r'); %Define plot handle
grid on             %Add grid
axis([0 max(y(:,1))*1.2 0 max(y(:,2))*1.2]); %Create axes bounds
xlabel('Prey ')     %Make x-label
ylabel('Predator')  %Make y-label
set(lh,'EraseMode', 'none', 'MarkerSize', 10); %What are the mode and marker of the plot handle
% Now animate the phase-portrait plot.
for idn=2:length(y(:,1))
pause(.1)       %Pause .2 seconds between graphs
set(lh,'xdata',y(idn,1),'ydata',y(idn,2));
drawnow;
end
min(y(:,1)) %Print minimum of Prey
min(y(:,2)) %Print minimum of Prey
max(y(:,1)) %Print maximum of Prey
max(y(:,2)) %Print maximum of Prey
hold off;
```

It is also posted to the Internet. Look on the news page. One reason we used MATLAB instead of Maple is that MATLAB is very much easier to use for this kind of example. I’ve written a similar version for Maple but using a finite difference scheme.* You will note that it is a level of complexity greater. But it works. Check out the link on the news page.

*Finite difference schemes:* Even the MATLAB ode45 solver is a finite difference scheme. A more basic scheme, akin to Euler’s method, was used in the Maple code. This is basically the situation when we view time in discrete pieces. If you recall how the Fibonacci sequence was derived as a population model, you will note that is was also a finite difference scheme based on discrete time.

**Competing species models.**

When two species compete in an environment, it is very possible that one of them will become extinct. Here are the variables.
The differential equations of motion

\[ P_1' = aP_1 - bP_1P_2 \]
\[ P_2' = cP_2 - dP_1P_2 \]

As you can see rates of growth for both species decline upon interactions. Presumably, the competition is that both species feed on the same food source. An example would be the hawk and the eagle, both of which feed on various rodents. Other examples include predatory cats such as the leopard and lion, though the competition may be more limited here. Various plants also compete for soil nutrients and for sunlight. Below is a graphic showing a very typical result of what happens when species compete.

\[ P_1' = 0.2P_1 - 0.011P_1P_2 \]
\[ P_2' = 0.18P_2 - 0.02P_1P_2 \]
As you can see one of the species becomes extinct and the other grows indefinitely. The possibilities are of considerable variety and depend on the coefficients of the system, as you know, but also very much on the initial conditions. Here is another example — in fact the same example, the difference being the initial conditions.

Competing species with crowding
It makes perfect sense that a population cannot grow without bounds. Crowding must play a role. We account for crowding in the same way as usual. The effects of crowding within the system has the equations

\[ P_1' = aP_1 - bP_1P_2 - eP_1^2 \]
\[ P_2' = cP_2 - dP_1P_2 - fP_2^2 \]

Now let us take the same system we just considered and add a "dash" of crowding to obtain a phase plane portrait as we see below.

As you see one of the species becomes extinct, while the other grows logistically. We ask under what conditions can the two competing species co-exist? But competing species do co-exist, this we know. Can you conjecture some changes to the model that may assure this is so?

**Qualitative Analysis**

We begin our study differential systems by citing some very important theorems about the solutions of systems of differential equations. As previously mentioned, most systems cannot be solve explicitly or implicitly for that matter. However, there are many general statement that can be made about systems.

Our setting is this: \( \mathbf{x} \) is a vector in \( \mathbb{R}^n \) which is usually written in set notation as \( \mathbf{x} \in \mathbb{R}^n \). There is a function \( \mathbf{f}(t, \mathbf{x}) \) that takes values in \( \mathbb{R}^n \). The differential system to be considered is

\[ \mathbf{x}' = \mathbf{f}(t, \mathbf{x}) \quad (\ast) \]

and the region over which it is considered is
\[ R = I \times U = \{(t, x) \mid a < t < b, \ x \in U\} \]

where \( U \) is an open set in \( \mathbb{R}^n \). To get to the heart of a qualitative analysis of the solutions, we need to know that a solution exists and that it is unique.

**Theorem** Suppose that \( f(t, x) \) is defined and continuously differentiable in the region \( R \). If \( (t, x_0) \in R \) then there exists a unique solution to (*) that satisfies the initial condition \( x(t_0) = x_0 \). This solution remains valid while in \( R \).

This is the "ticket" that will validate our future statements. Solutions of system can have very non-function like appearance in the phase plane.

Note that the solutions need not be functions in any sense except that each of the components of the vector \( x(t) \) is a function of \( t \). For completeness we suppose that all vectors are column vectors

\[ x = \begin{bmatrix} x_1 \\ x_2 \\ \vdots \\ x_n \end{bmatrix} \]

also written in transpose form \( x = [x_1, x_2, \ldots, x_n]^T \)

**Autonomous systems**

A very special and important result is true for autonomous systems \( x' = f(x) \). Our result is that if two solutions intersect they must follow the same curve. That is to say we cannot have the situation in the figure above, but rather solutions must look more like those in the figures below. The argument that they cannot cross is reasonably simple. However the autonomous condition is necessary for this. cannot cross one another.
We remark that the prey-predator model, also known as the Lotka-Volterra model, is autonomous and you may recall the solutions above very much resemble the solutions for various initial conditions.

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**Linear Systems of Differential Equations**

We will now take up systems of differential equations in general. Instead of looking at solutions per se, we will look at structural aspects of systems and state the very important theorems that will give important information about how to find solutions. We will always take $t$ to be the single independent variable. For the most part the dependent variables will be $x_1, x_2, \ldots, x_n$.

**Definition** A linear differential system of equations has the form

$$
\begin{align*}
    x_1' &= a_{11}(t)x_1 + a_{12}(t)x_2 + \cdots + a_{1n}(t)x_n + f_1(t) \\
    & \quad \vdots \\
    x_n' &= a_{n1}(t)x_1 + a_{n2}(t)x_2 + \cdots + a_{nn}(t)x_n + f_n(t)
\end{align*}
$$

The coefficients are the $a_{ij}(t)$. The functions $f_i(t)$ are the forcing terms. All conditions of continuity, etc, are assumed taken on the interval $I = (a, b)$.

**Example** Most examples look something like this

$$
\begin{align*}
    x_1' &= 2x_1 - 3x_2 \\
    x_2' &= 4x_1 + x_2
\end{align*}
$$

Using the matrix notation

$$
A(t) = \begin{bmatrix}
    a_{11}(t) & a_{12}(t) & \cdots & a_{1n}(t) \\
    a_{21}(t) & a_{22}(t) & \cdots & a_{2n}(t) \\
    \vdots & \ddots & \vdots \\
    a_{n1}(t) & a_{n2}(t) & \cdots & a_{nn}(t)
\end{bmatrix}
$$

the linear differential system has the much simpler appearance
\[ x' = A(t)x' + f(t) \]

The example above becomes
\[ x' = \begin{bmatrix} 2 & -3 \\ 4 & 1 \end{bmatrix} x' \]

**Solutions**

Our goal is generally to solve
\[ x' = f(t, x), \quad x(t_0) = x_0 \]
and a good part of our task ahead is to find solutions. For linear systems, \( x' = A(t)x' \), the task will be simpler, and for linear systems with constant coefficients \( x' = Ax' \), we can reduce the problem solving to the analysis of matrices. For the system
\[ x' = \begin{bmatrix} 2 & -3 \\ 0 & 1 \end{bmatrix} x' \]
the solutions are
\[ x_1 = e^{2t} \begin{bmatrix} 1 \\ 0 \end{bmatrix} \quad \text{and} \quad x_2 = e^t \begin{bmatrix} 3 \\ 1 \end{bmatrix} \]

The question is how was this solution found? We will take this up soon, but in the mean time we want to make three important — critical — statements about solutions of linear systems.

1. **(Superposition)** For linear homogeneous differential systems \( x' = A(t)x' \), sums and scalar multiples of solutions are also solutions. Thus, if \( x_1 \) and \( x_2 \) are solutions, then so also is
\[ x = c_1 x_1 + c_2 x_2 \]
for any two scalars \( c_1 \) and \( c_2 \).

2. **(All or nothing on linear independence)** If a set of solutions \( \{x_1, x_2, \ldots, x_n\} \) to \( x' = A(t)x' \) is linearly independent at one point it is linearly independent at every point. Similarly, if a set of solutions \( \{x_1, x_2, \ldots, x_n\} \) to \( x' = A(t)x' \) is linearly dependent at one point it is linearly dependent at every point.

3. **(Representation)** If \( A(t) \) is an \( n \times n \) matrix and \( \{x_1, x_2, \ldots, x_n\} \) is a linearly independent set of solutions, then every solution to the differential system \( x' = A(t)x' \) can be expressed as a linear combination of these solutions.
\[ x = c_1 x_1 + c_2 x_2 + \cdots + c_n x_n \]
where of course \( c_1, \ldots, c_n \) are scalars.

The last result makes the situation abundantly clear that we need to find a linearly independent set of solutions. This will also be called a fundamental set of solutions. The good news is that there is a procedure to find this set in the case that \( A(t) \) does
not depend on time. Thus, the analogy with the solution of second order differential
equations is easily recognized.

We are now left with a large set of hows

- How to find the fundamental set?
- How to determine if a set is linearly independent?
- How to actually solve the initial value problem?

The next section will answer these "how to" questions and the answers are contained in matrix theory. Be sure to sharpen your skills on matrices and in particular eigenvalues and eigenvectors.

\[ f(t,x) \]
\[ x' = f(x) \]
\[ x' = f(t,x) \]
\[ x(t_0) = x_0 \]