

## Systems of Differential Equations

### 5.1 Linear Systems

WE CONSIDER THE LINEAR SYSTEM

$$\begin{aligned}x' &= ax + by \\ y' &= cx + dy.\end{aligned}\tag{5.1}$$

This can be modeled using two integrators, one for each equation. Due to the coupling, we have to connect the outputs from the integrators to the inputs.

As an example, we show in Figure 5.1 the case  $a = 0, b = 1, c = -1, d = 0$ . This is the linear system of first order equations for  $x'' + x = 0$ , and  $y = x'$ . We also insert the initial conditions  $x(0) = 1, y(0) = 2$ . Running the model, results in the plots in Figures 5.2 and 5.3.

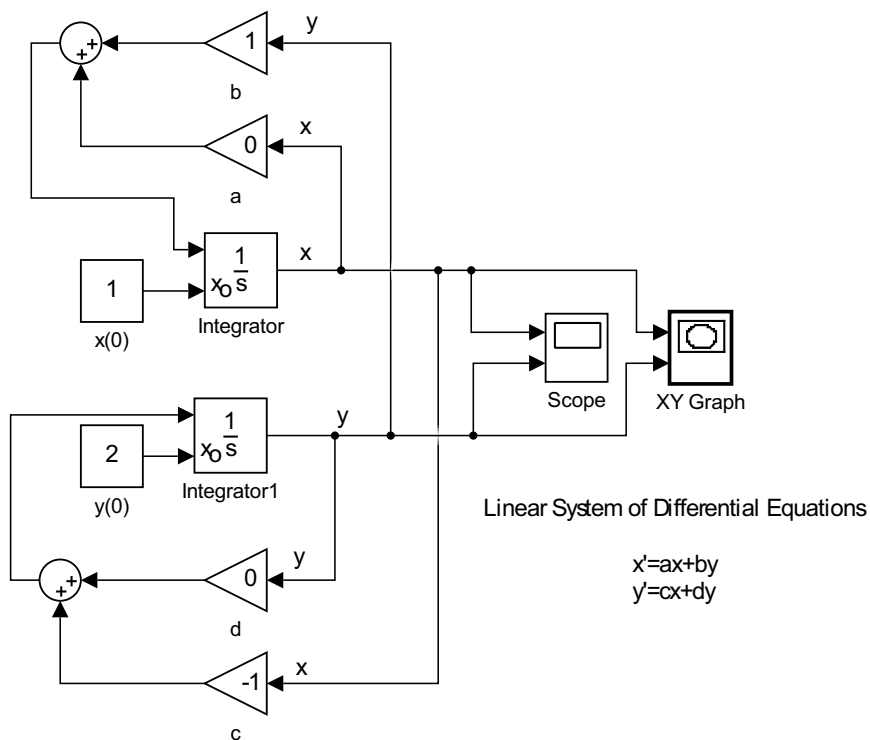


Figure 5.1: Linear system using two integrators.

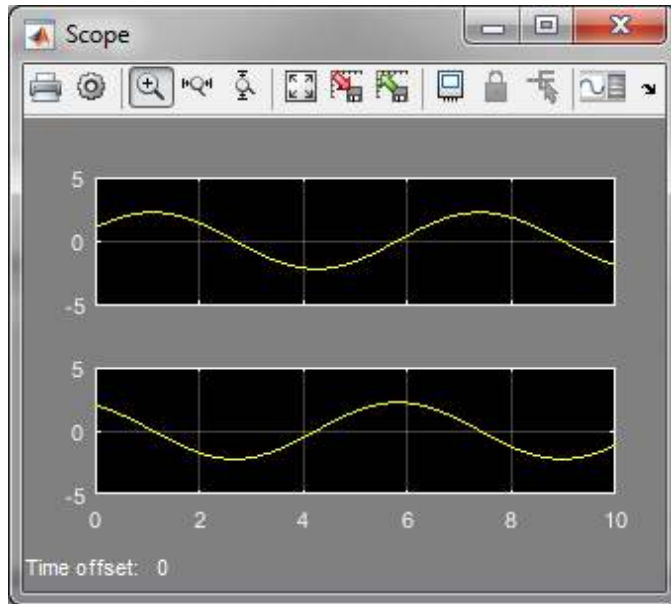


Figure 5.2: Linear system using two integrators.

This system can be put in matrix form,

$$\begin{bmatrix} x \\ y \end{bmatrix}' = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

This can be modeled by introducing matrix multiplication in a gain block as shown in Figure 5.4. The input and output to the **Integrator block** are vectors. The output is split using a **Demux** block to plot  $x$  and  $y$  separately. The **Scope** block plots the two signals separately as functions of  $t$ . The **XY Graph** block is used to plot the phase plane,  $y$  vs  $x$ .

We can also use a **State Space** block to solve this system. This is shown in Figure 5.5. We set the input as  $u = 0$ . In order to output both  $x$  and  $y$ , we set  $A = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix}$ ,  $B = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$ ,  $C = \begin{bmatrix} 1 & 0 \end{bmatrix}$ , and  $D = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$ . We also set the initial conditions to  $\begin{bmatrix} 1 \\ 2 \end{bmatrix}$ . The solution plots are the same as shown in Figures 5.2 and 5.3.

## 5.2 Nonlinear Models

### *The Jerk Equation*

IN THIS SECTION we consider modeling a few common nonlinear systems with interesting behaviors in Simulink. These examples stem from a variety of applications such as biological systems, predator-prey models, chemical reactions, such as Michaelis-Menten kinetics, circuits, and other dynamical systems. We begin with the jerk model.

If one denotes  $x(t)$  as the position as a function of time,  $t$ , then we are familiar with the idea that  $x'(t)$  would be the velocity and  $x''(t)$  the acceleration. However, you might not be as familiar with the *jerk*. This is the

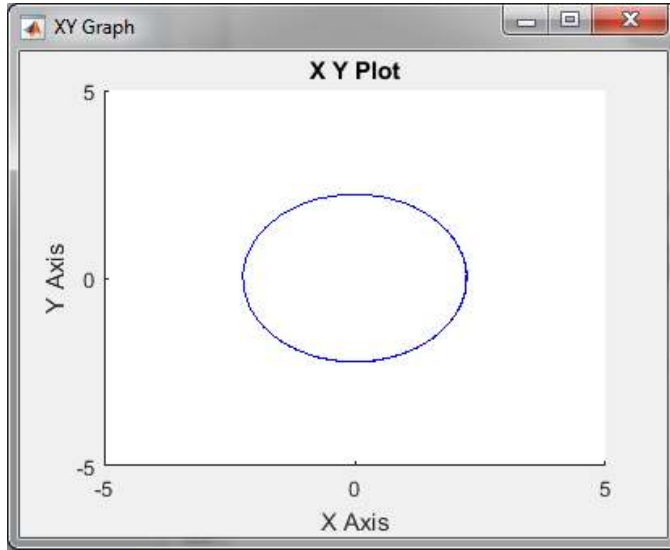


Figure 5.3: Linear system using two integrators.

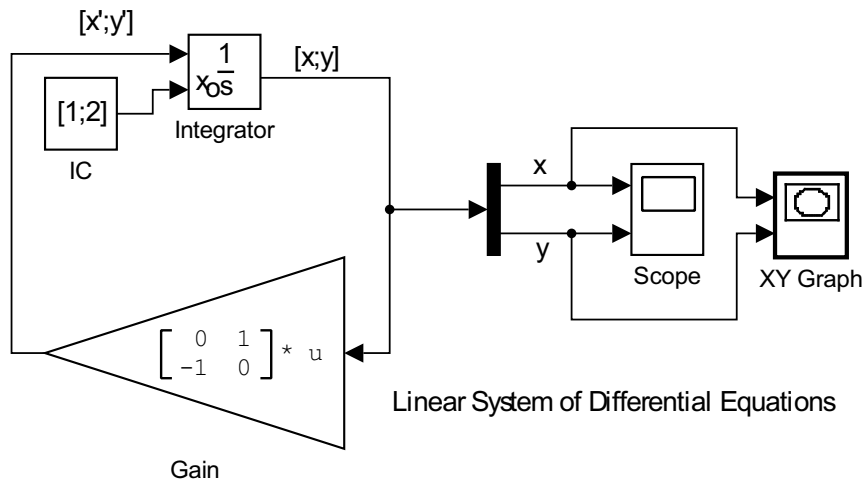


Figure 5.4: Linear system using matrix operation.

third derivative,  $x'''(t)$ . The jerk equation modeled in Figure 5.6 is

$$x''' + cx'' + bx' + ax + x^2 = 0.$$

As a third order equation, one needs initial values for  $x$ ,  $x'$ , and  $x''$ .

### Van der Pol Equation

SOLUTIONS, KNOWN AS LIMIT CYCLES, are common in nature. Rayleigh investigated the problem

$$x'' + c \left( \frac{1}{3}(x')^2 - 1 \right) x' + x = 0 \quad (5.2)$$

in the study of the vibrations of a violin string. Balthasar van der Pol (1889-1959) studied an electrical circuit, modeling this behavior. Limit

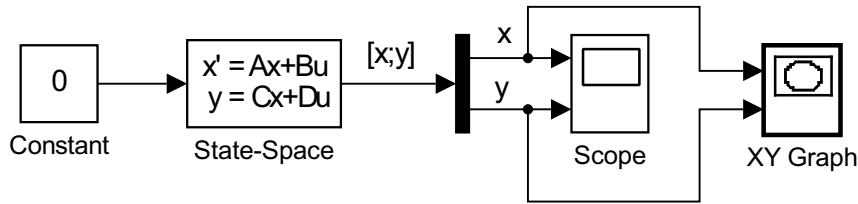


Figure 5.5: Linear system using matrix operation.

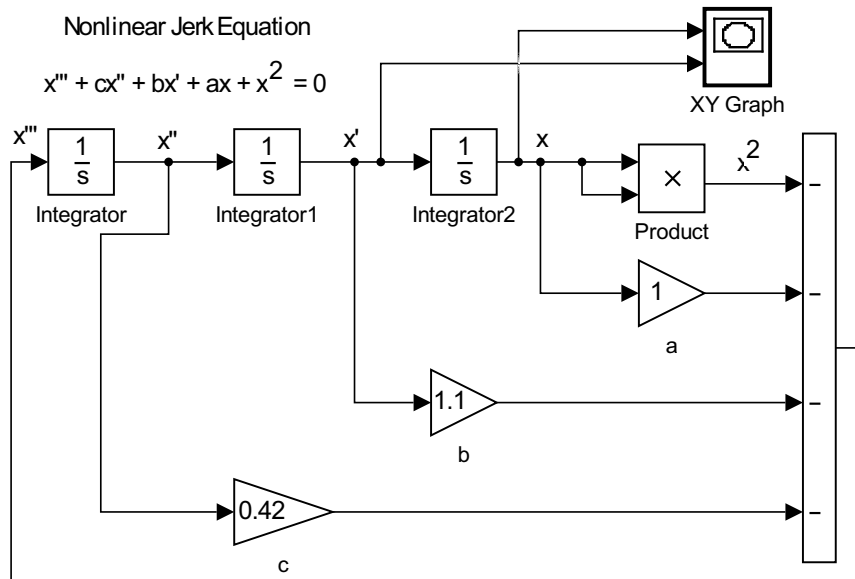


Figure 5.6: Nonlinear jerk model.

cycles are isolated periodic solutions towards which neighboring states might tend when stable. A slight change of the Rayleigh system leads to the van der Pol equation:

$$x'' + c(x^2 - 1)x' + x = 0 \quad (5.3)$$

The limit cycle is found in the model and solutions in Figures 5.7-5.9.

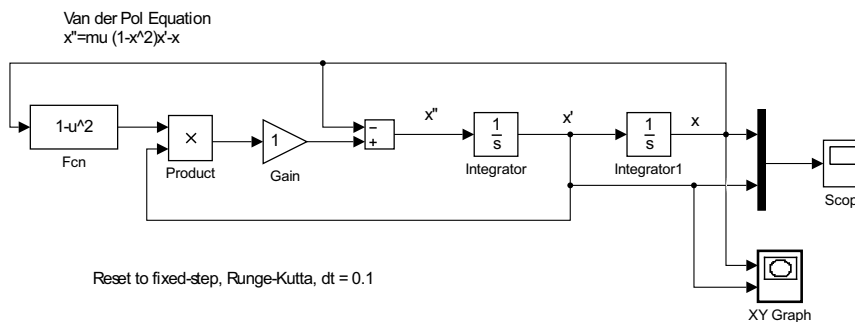


Figure 5.7: van der Pol equation.

### Lorenz Equations

THE LORENZ MODEL IS ANOTHER TYPICAL MODEL used as an example of a nonlinear system. The Lorenz model is a simple model for atmospheric

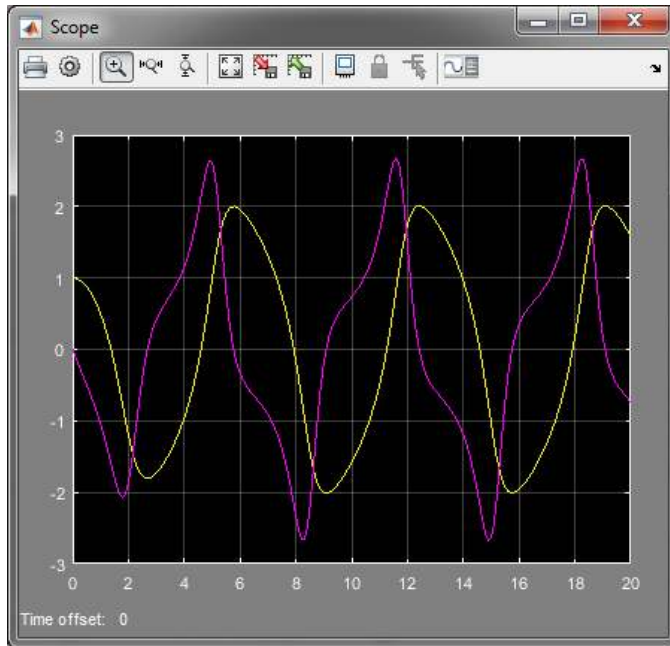


Figure 5.8: Solution plot for the van der Pol equation.

convection developed by Edward Lorenz in 1963. The system is given by the three equations

$$\begin{aligned}\frac{dx}{dt} &= \sigma(y - x) \\ \frac{dy}{dt} &= x(\rho - z) - y \\ \frac{dz}{dt} &= xy - \beta z.\end{aligned}$$

Figures 5.10-5.12 show the models and a famous solution to the Lorenz equations.

Using the data sent to the MATLAB workspace, a three dimensional model can be constructed. The following produces an animation of the data resulting in a 3D plot.

```
Z=simout.data;
N=length(Z(:,1));

figure(3)
axHndl = gca;
figNumber =(gcf);
hdlList = get(figNumber,'UserData');
set(axHndl, ...
    'XLim',[0 50],'YLim',[-20 20],'ZLim',[-30 30], ...
    'XTick',[],'YTick',[],'ZTick',[], ...
    'SortMethod','childorder', ...
    'Visible','on', ...
    'NextPlot','add', ...
```

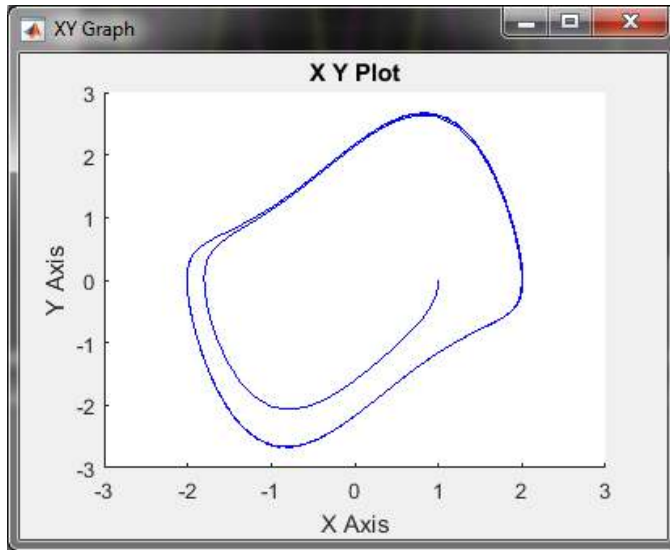


Figure 5.9: Phase plane plot for the van der Pol equation.

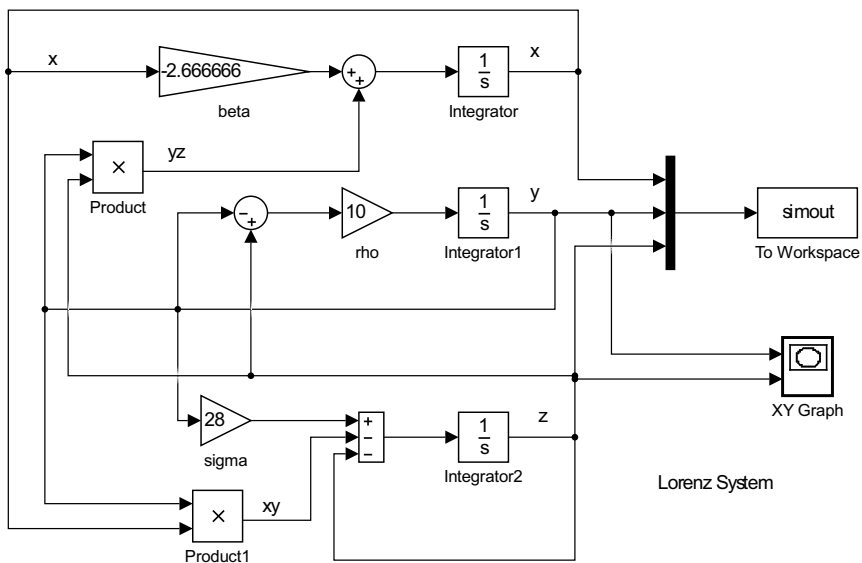


Figure 5.10: Model for Lorenz equations.

```
'View',[-37.5,30], ...
'Clipping','off');
xlabel('x');
ylabel('y');
zlabel('z');
```

```
y(1) = Z(1,1);
y(2) = Z(1,2);
y(3) = Z(1,3);
```

```
L = 5;
Y = y*ones(1,L);
```

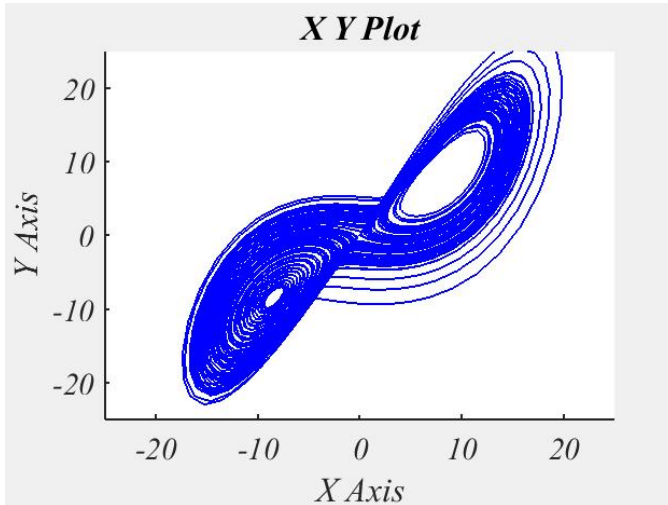


Figure 5.11: XY plot for the Lorenz model.

```

cla;
head = line('color','r', 'Marker','.', 'MarkerSize',10, 'LineStyle','none', ...
            'XData',y(1), 'YData',y(2), 'ZData',y(3)) ;
body = animatedline('color','b', 'LineStyle','--') ;
tail = animatedline('color','b', 'LineStyle','--') ;

for j=2:N
    y(1) = Z(j,1);
    y(2) = Z(j,2);
    y(3) = Z(j,3);

    % Update the plot
    Y = [y Y(:,1:L-1)];
    set(head, 'XData', Y(1,1), 'YData', Y(2,1), 'ZData', Y(3,1));
    addpoints(body, Y(1,2), Y(2,2), Y(3,2));
    addpoints(tail, Y(1,L), Y(2,L), Y(3,L));
    pause(0.1)

    % Update the animation every ten steps
    if ~mod(j,10)
        drawnow;
    end
end
end

```

### *Lotka-Volterra Predator-Prey Model*

TWO WELL-KNOWN NONLINEAR POPULATION MODELS are the predator-prey and competing species models. In the predator-prey model, one typically has one species, the predator, feeding on the other, the prey. We will

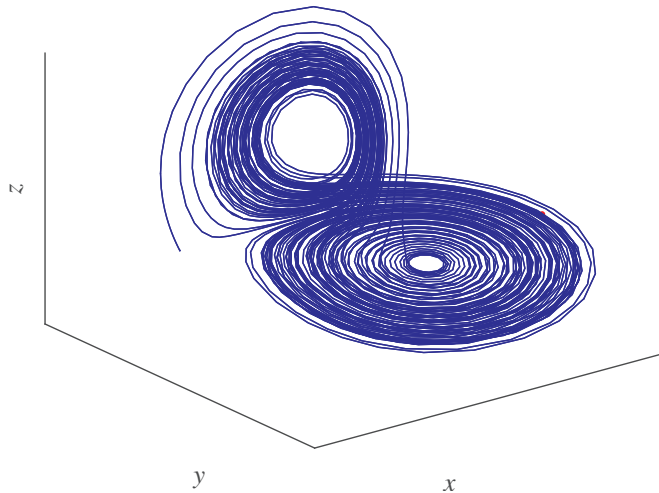


Figure 5.12: Three dimensional plot for the Lorenz model.

look at the standard Lotka-Volterra model in this section. The competing species model looks similar, except there are a few sign changes, since one species is not feeding on the other. Also, we can build in logistic terms into our model. We will save this latter type of model for the homework.

The Lotka-Volterra model takes the form

$$\begin{aligned}\dot{x} &= ax - bxy, \\ \dot{y} &= -dy + cxy,\end{aligned}\tag{5.4}$$

where  $a$ ,  $b$ ,  $c$ , and  $d$  are positive constants. In this model, we can think of  $x$  as the population of rabbits (prey) and  $y$  is the population of foxes (predators). Choosing all constants to be positive, we can describe the terms.

- $ax$ : When left alone, the rabbit population will grow. Thus  $a$  is the natural growth rate without predators.
- $-dy$ : When there are no rabbits, the fox population should decay. Thus, the coefficient needs to be negative.
- $-bxy$ : We add a nonlinear term corresponding to the depletion of the rabbits when the foxes are around.
- $cxy$ : The more rabbits there are, the more food for the foxes. So, we add a nonlinear term giving rise to an increase in fox population.

The Lotka-Volterra model is named after Alfred James Lotka (1880-1949) and Vito Volterra (1860-1940).

The Lotka-Volterra model of population dynamics.

### *SIR Model of Disease*

ANOTHER INTERESTING AREA OF APPLICATION of differential equation is in predicting the spread of disease. Typically, one has a population of susceptible people or animals. Several infected individuals are introduced into the population and one is interested in how the infection spreads and



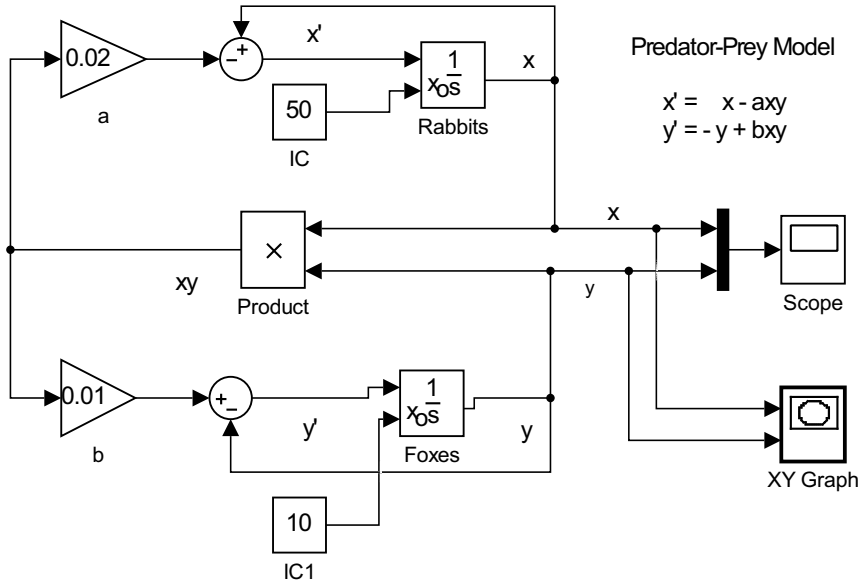


Figure 5.13: Predator-Prey model.

if the number of infected people drastically increases or dies off. In the SIR model one uses a compartmental analysis by breaking the population into three classes. First, we let  $S(t)$  represent the healthy people, who are susceptible to infection. Let  $I(t)$  be the number of infected people. Of these infected people, some will die from the infection and others could recover. We will consider the case that initially there is one infected person and the rest, say  $N$ , are healthy. Can we predict how many deaths have occurred by time  $t$ ?

We can first look into a linear model. We assume that the rate of change of any population would be due to those entering the group less those leaving the group. For example, the number of healthy people decreases due to infection and can increase when some of the infected group recovers. Let's assume that a) the rate of infection is proportional to the number of healthy people,  $aS$ , and b) the number who recover is proportional to the number of infected people,  $rI$ . Thus, the rate of change of healthy people is found as

$$\frac{dS}{dt} = -aS + rI.$$

Let the number of deaths be  $D(t)$ . Then, the death rate could be taken to be proportional to the number of infected people. So,

$$\frac{dD}{dt} = dI$$

Finally, the rate of change of infected people is due to healthy people getting infected and the infected people who either recover or die. Using the corresponding terms in the other equations, we can write the rate of change of infected people as

$$\frac{dI}{dt} = aS - rI - dI.$$

This linear system of differential equations can be written in matrix form.

$$\frac{d}{dt} \begin{pmatrix} S \\ I \\ D \end{pmatrix} = \begin{pmatrix} -a & r & 0 \\ a & -d-r & 0 \\ 0 & d & 0 \end{pmatrix} \begin{pmatrix} S \\ I \\ D \end{pmatrix}. \quad (5.5)$$

The commonly used nonlinear SIR model is given by

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I, \end{aligned} \quad (5.6)$$

where  $S$  is the number of susceptible individuals,  $I$  is the number of infected individuals, and  $R$  are the number who have been removed from the the other groups, either by recovering or dying. The Simulink model is given in Figure 5.14.

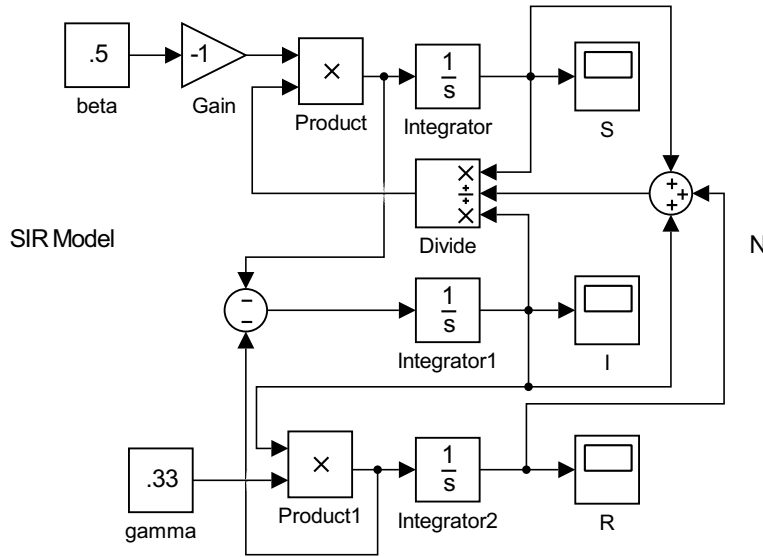
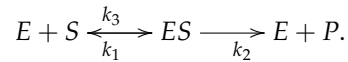


Figure 5.14: SIR epidemic model.

### Michaelis-Menten Kinetics

THE MICHAELIS-MENTEN KINETICS REACTION is given by



This approximates the dynamics under the assumption that the concentration of the enzyme remains constant. The enzyme interacts with the substrate to form an enzyme–substrate complex, leading to a release of enzyme.  $E$ ,  $S$ , and  $P$  are the enzyme, substrate, and product, respectively. The system of differential equations corresponding to the dynamics of these reactions is

$$\begin{aligned}
\frac{d[S]}{dt} &= -k_1[E][S] + k_3[ES], \\
\frac{d[E]}{dt} &= -k_1[E][S] + (k_2 + k_3)[ES], \\
\frac{d[ES]}{dt} &= k_1[E][S] - (k_2 + k_3)[ES], \\
\frac{d[P]}{dt} &= k_3[ES].
\end{aligned} \tag{5.7}$$

In chemical kinetics one seeks to determine the rate of product formation ( $v = d[P]/dt = k_3[ES]$ ). Assuming that  $[ES]$  is a constant, one seeks  $v$  as a function of  $[S]$  and the total enzyme concentration  $[E_T] = [E] + [ES]$ .

### The Chua Circuit

THE CHUA CIRCUIT, as shown in Figure 5.15, consists of an inductor, a resistor, two capacitors and a nonlinear resistor, or other nonlinear component. The system of differential equations is found using Kirchoff's circuit laws. There are two junctions, labeled as 1 and 2. The total current into each node equals the current leaving the node. There are three loops over which one sums the potential rises and drops.

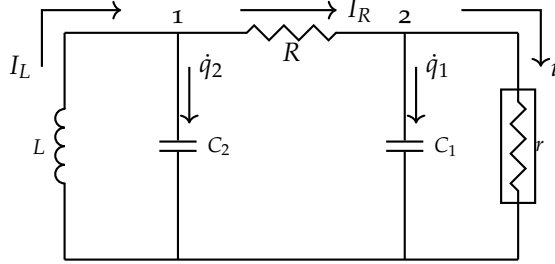


Figure 5.15: The Chua circuit used in this note.

Using junction rules, we have at nodes 1 and 2:

$$I_L = \dot{q}_2 + I_R, \tag{5.8}$$

$$I_R = \dot{q}_1 + i. \tag{5.9}$$

Kirchoff's Loop rules for the three small loops are

$$L \frac{dI_L}{dt} = -V_2, \tag{5.10}$$

$$I_R R = V_2 - V_1, \tag{5.11}$$

$$V_r = \frac{q_1}{C_1}. \tag{5.12}$$

We seek a system of differential equations for  $V_1$ ,  $V_2$ , and  $I_L$ . Noting that  $q_i = C_i V_i$ , for  $i = 1, 2$ , we find from Equations (5.8) and (5.11):

$$C_2 \dot{V}_2 = I_L - R^{-1}(V_2 - V_1).$$

From Equation (5.9) we have, using Equation (5.11),

$$C_1 \dot{V}_1 = R^{-1}(V_2 - V_1) - g(V_1),$$

where  $g(x)$  gives the characteristics of the nonlinear component in the circuit. This is typically of the form

$$g(x) = ax + \frac{1}{2}b(|x+1| - |x-1|).$$

This function is show in Figures 5.16-5.17 for  $a = 0$  and  $a \neq 0$ .

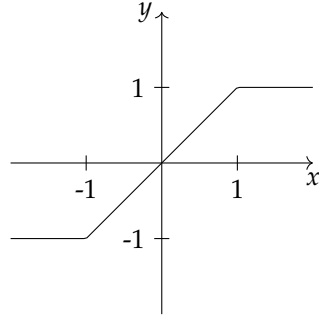


Figure 5.16:  $g(x) = \frac{1}{2}(|x+1| - |x-1|)$ .

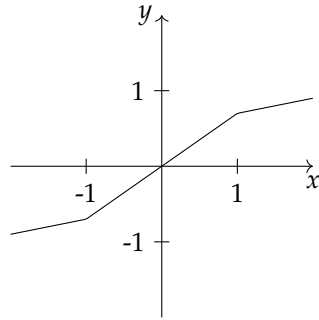


Figure 5.17:  $g(x) = ax + \frac{1}{2}b(|x+1| - |x-1|)$ .

The last equation comes from Equation (5.10) and often a term  $-rI_L$  is added. So, we have

$$C_1 \dot{V}_1 = R^{-1}(V_2 - V_1) - g(V_1), \quad (5.13)$$

$$C_2 \dot{V}_2 = I_L - R^{-1}(V_2 - V_1), \quad (5.14)$$

$$L \dot{I}_L = -V_2 - rI_L. \quad (5.15)$$

These equations are made dimensionless by introducing some characteristic scales. Let  $C_1$  and  $R_1$  be characteristic scales of capacitance and resistance. We let  $\alpha^{-1} = R/R_1$ ,  $\bar{r} = r/R_1$ , and define

$$x = \frac{V_1}{V_C}, \quad y = \frac{V_2}{V_C}, \quad z = \frac{I_L R_1}{V_C}.$$

This gives

$$R_1 C_1 \dot{x} = \alpha(y - x) - g(V_1)/V_C, \quad (5.16)$$

$$R_1 C_2 \dot{y} = z - \alpha(y - x), \quad (5.17)$$

$$\frac{L}{R_1} \dot{z} = -y - \bar{r}z. \quad (5.18)$$

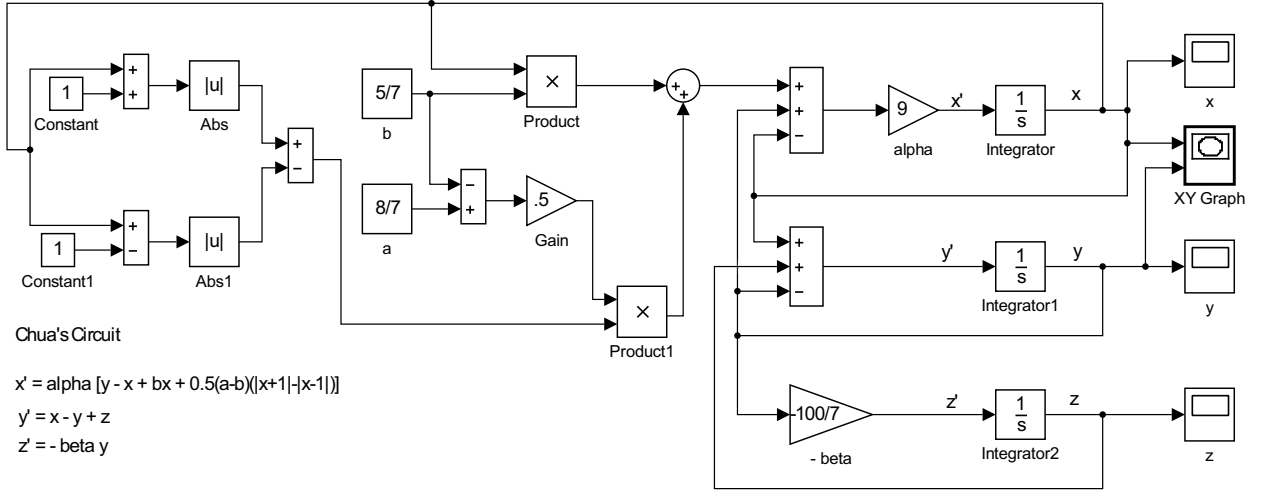


Figure 5.18: Nonlinear Chua model.

Finally, we can rescale the time as  $\tau = t/R_1C_1$ , where  $R_1C_1$  is the characteristic time constant. Then,

$$\frac{d}{dt} = \frac{d\tau}{dt} \frac{d}{d\tau} = \frac{1}{R_1C_1} \frac{d}{d\tau}.$$

So,

$$\dot{x} = \alpha(y - x) - g(V_1)/V_C, \quad (5.19)$$

$$\frac{C_2}{C_1} \dot{y} = z - \alpha(y - x), \quad (5.20)$$

$$\frac{L}{R_1^2C_1} \dot{z} = -y - \bar{r}z. \quad (5.21)$$

So, we define  $\sigma = \frac{C_1}{C_2}$ ,  $\beta = \frac{R_1^2C_1}{L}$ ,  $\gamma = \bar{r}$ , and

$$f(x) = g(V_1)/aV_C.$$

Then,

$$\dot{x} = \alpha(y - x - f(x)), \quad (5.22)$$

$$\dot{y} = \sigma(z - \alpha(y - x)), \quad (5.23)$$

$$\dot{z} = -\beta y - \gamma z. \quad (5.24)$$

Finally, many models have no parameters in the second equation. So, we let  $x = \mu X$ ,  $y = \mu Y$  and  $z = \nu Z$  to see if this is possible. Then,

$$\mu \dot{X} = \alpha \mu (Y - X) - \alpha f(\mu X), \quad (5.25)$$

$$\mu \dot{Y} = \sigma (\nu Z - \alpha \mu (Y - X)), \quad (5.26)$$

$$\nu \dot{Z} = -\beta \mu Y - \gamma \nu Z. \quad (5.27)$$

Simplifying, we have

$$\dot{X} = \alpha (Y - X) - \frac{\alpha}{\mu} f(\mu X), \quad (5.28)$$

$$\dot{Y} = \sigma\left(\frac{\nu}{\mu}Z - \alpha(Y - X)\right), \quad (5.29)$$

$$\dot{Z} = -\frac{\beta\mu}{\nu}Y - \gamma Z. \quad (5.30)$$

So, we need to chose  $\sigma = \alpha^{-1}$  and  $\frac{\mu}{\nu} = \sigma$ .

$$\dot{X} = \alpha(Y - X - \bar{f}(X)), \quad (5.31)$$

$$\dot{Y} = Z - Y + X, \quad (5.32)$$

$$\dot{Z} = -\bar{\beta}Y - \gamma Z, \quad (5.33)$$

where  $\bar{\beta} = \beta\sigma$  and  $\bar{f}(X) = \mu f(\mu X)$ . This is the version of the model we can explore.

We have obtained a dimensionless set of first order differential equations of the form

$$\dot{x} = \alpha(y - x - f(x)), \quad (5.34)$$

$$\dot{y} = z - y + x, \quad (5.35)$$

$$\dot{z} = -\beta y - \gamma z, \quad (5.36)$$

where

$$f(x) = ax + \frac{1}{2}b(|x+1| - |x-1|).$$

We can write this system in matrix form as

$$\frac{d\mathbf{x}}{dt} = \begin{pmatrix} -\alpha & \alpha & 0 \\ 1 & -1 & 1 \\ 0 & -\beta & -\gamma \end{pmatrix} \mathbf{x} + \begin{pmatrix} -\alpha f(x) \\ 0 \\ 0 \end{pmatrix},$$

where

$$\mathbf{x} = \begin{pmatrix} x \\ y \\ z \end{pmatrix}.$$

We can model this in Simulink as shown in Figure 5.19. The linear part of the system is encoded as a subsystem. The subsystem is shown in Figure 5.20.

The subsystem takes inputs of the variables  $\alpha$ ,  $\beta$ , and  $\gamma$  and outputs the matrix in the linear part of the system,  $L$ . Then, the nonlinear part of the system is added to  $Lx$ . This is integrated with given initial conditions to arrive at the solution. A sample of the solutions is given in Figures 5.21 and 5.22.

The plots in Figures 5.21 and 5.22 were created by using the **to Workspace** block. The variable name was changed to **chuaput** and the data was sent to the MATLAB workspace. Then the following code was used to plot the data.

```
% Plot x, y, z vs t
figure(1)
```



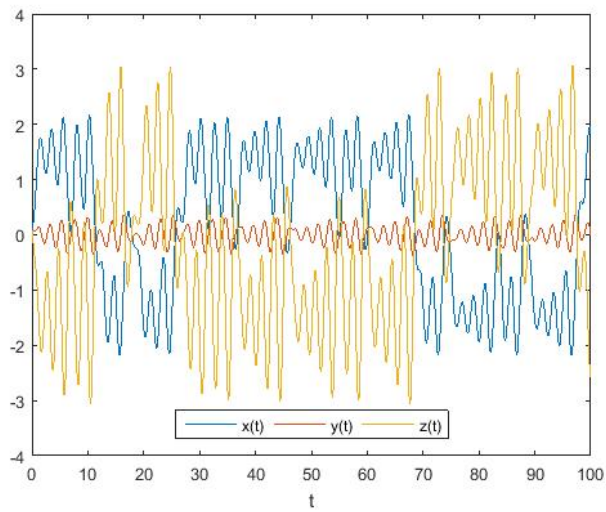


Figure 5.21: Solutions of Chua model as a function of time.

Figure 5.22: 3d plot of Chua solutions.

