Mathematical Biology Workshops

BIL 150 & BIL 160

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Contents

Module 1

Introduction to Scilab

1.1 Introduction

MATLAB and Scilab are (mostly) equivalent software packages commonly used to perform scientific computations. Scilab (http://www.scilab.org) is a MATLAB clone and is the open source software we will use throughout the workshops this semester. A full and proper introduction to Scilab requires more time than we have so here we will only go through the very basics.

1.1.1 Some basics

If you feel you need more assistance, type help at the Scilab prompt, or pull down on the Help menu on a PC.

It is important to make sure that your current directory is the directory where you are going to save all your work to. You can click File → Display current directory to see what your current directory is set as. If you want to work

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in a different directory, you can either click File → Change current directory... and select the folder you want to work in, or you can click on the blue folder icon in the toolbar and select the folder you want to work in. (If you do not see the toolbar, you need to click on Preferences → Show/Hide Toolbar.)

1.2   Entering and Executing Scilab Commands

Scilab is an interactive computing language. As with any computing or programming language, you enter and execute commands. Commands have a particular syntax, which means things like punctuation, case and symbols are important and you have to pay attention to the way you type things. This is similar to any spoken language — if the syntax (i.e. spelling and grammar) is not correct, then it is difficult to understand what things mean.

There are a couple of ways you can enter and execute commands in scilab:

Start Scilab and type and execute commands at the Scilab prompt in the command window.

One can also collect commands or functions into a separate file called a .sce file (one can use files other than .sce files but that is all that we will be using). Once you have collected all the commands or functions into your .sce file, you can run these commands or load the functions all at once. In Scilab, the "exec" command is used to execute a .sce file.

> **QUESTION:** Download the file oracle.sce. What is the result of executing the file oracle.sce? Discuss the correct answer with your peers.

1.2.1 Commands within the Scilab software

You can type Scilab commands in the command window at the Scilab command line prompt, which is denoted by $-->$. Press Enter or return to execute commands. For example, at the scilab prompt type in the following command and press Enter.

$$ImportantAnswer = 1/3 + 1/4$$

You can use the up and down arrow keys to easily recall a command, and then edit the command with the left and right arrows. Try it by closing the graphics window which was opened when you executed the oracle.sce file then execute the oracle.sce file again by pressing the up key and not by retyping the "exec" command.

This kind of command is called an **assignment statement**; it is not an equation. It is an action that stores the output of the expression on the right hand side of the equals sign into the variable (a name) given on the left hand side. Not using the assignment statement correctly is one of top 10 errors beginners make.

1.3 Using the Scilab Editor

After downloading a *.sce* file, one can open it from Scilab's editor. Or alternately, one can double click on the file which will open it in the editor.

Download the file introduction_lab.sce and make sure it is in your current directory (check the folder icon and make sure that you see the file in your folder). You can open the editor by typing either of the following commands at the command prompt:

$$-- > edit$$

or

$$-- > editor$$

This command opens the editor. Go to the menu "File → Open a file..." or "File → Open..." and select introduction_lab.sec. The editor shows

```
function y=sum1(n)
// sum1(n) computes the sum of 1 + 2 + ... + n
total = 0;
for i = 1:n,
 total = total + i;
end;
y = total;
endfunction;
```

Go to the command console and execute the following command:

$$-- > exec\ introduction\_lab.sce$$

In general the command *exec* executes a file.

This file defines a function $sum1(n)$. The command $sum1(3)$ returns 6 since $1+2+3 =$

6.

QUESTION: What is the value of $sum1(8)$?

We are going to edit this file. First *save as* introduction_lab2.sce. Then change the name of the function to $sum2(n)$.

$$function\ y = sum2(n)$$

Next change the help line so the integers are squared.

$$sum2(n)\ computes\ the\ sum\ of\ 1^\wedge 2 + 2^\wedge 2 + ... + n^\wedge 2$$

The help line is **ONLY** for reference, to leave a documentation of what is being done. It is optional. We change the code to match, note the i squared.

$$total = total + i^\wedge 2$$

Save and try the code. Try $sum2(3)$ which should be $14 = 1^2 + 2^2 + 3^2 = 1 + 4 + 9$. Remember that you need to execute the file before you can try the code.

QUESTION: What is the value of $sum2(8)$?

We could go on and define sum3 etc.

1.4   Basic Operations in Scilab

As you have seen, some commands are just like you would type things in a calculator. If you want to refer to the result of the command, you need to give it a name, or in other words, assign the result to a variable. The following command assigns the result to the variable s. (Note that scilab didn't save the true answer $\frac{7}{12}$ but rather a decimal approximation.)

$$-- > s = 1/3 + 1/4$$

$$s \ =$$

$$0.5833333$$

(The command above created a location in Scilab memory that had the address s and now stores the value 0.5833333.)

This is an *assignment statement*.

If a command does not fit on one line, use an ellipsis (three periods), ..., followed by Return/Enter to indicate that the statement continues on the next line. For example,

$$s = 1 - 1/2 + 1/3 - 1/4 + 1/5 - 1/6 + 1/7...$$

$$-1/8 + 1/9 - 1/10 + 1/11 - 1/12$$

$$s \ =$$

$$0.6532107$$

(In the command above, the memory address is s, so it now stores the value 0.6532107. The old value of 0.5833333 was thrown away.) You can always see the value of your variable by just typing the name of the variable and executing it in Scilab.

$$--> s$$

$$s \ =$$

$$0.6532107$$

(The most current value of s is returned.)

1.4.1   Expressions

Like most other programming languages, Scilab provides mathematical expressions. The building blocks of expressions are: Variables, Numbers, Operators, Functions. For example, use the caret symbol (^) to raise something to an exponent.

$$answer = 89^{\wedge}2$$

$$\text{answer} =$$

$$7921.$$

Expressions use familiar arithmetic operators and precedence rules. There are also functions, such as cosine or sine. You surround the input of the function by parenthesis. For example, to calculate the square root of two, you type

$$-- > squareRoot2 = sqrt(2)$$

$$squareRoot2 =$$

$$1.4142136$$

Symbol	Operation
$+$	Addition
$-$	Subtraction
$*$	Multiplication
$/$	Division
$\wedge$	Power
$'$	Complex conjugate transpose
$()$	Specify evaluation order
abs(x)	Absolute value
sqrt(x)	Square root $\sqrt{(x)}$
exp(x)	Exponential function e^x
sin(x)	$\sin(x)$ where x is assumed to be in radians
cos(x)	$\cos(x)$ where x is assumed to be in radians

Taking the square root or logarithm of a negative number is not an error; the appropriate complex result is produced automatically. Scilab also provides many more advanced mathematical functions.

TAKE NOTE: The help browser has a whole section on elementary mathematical functions. Type help in the command console or click on the help icon in the toolbar. It will open the help browser in tree view in a new window. Elementary functions is near the top in the tree view. Several special functions provide values of useful constants. Note that $e = 2.7182818$ is missing from this list. One must use the exp function $exp(x)$ for e^x and $exp(1)$ for e itself.

Constant	Value
%pi	$\pi = 3.1415927$
%i	i, the imaginary unit, $i = \sqrt{(-1)}$
%inf	Inf, Infinity ∞
%nan	Nan, Not-a-number

(Matlab uses pi for π without the % sign and similarly for other constants.)

Infinity is generated by dividing a nonzero value by zero, or by evaluating well defined mathematical expressions that overflow. (Try 10^{310} or $exp(999)$.)

Not-a-number is generated by trying to evaluate expressions like $\frac{0}{0}$ or $\infty - \infty$ that do not have well defined mathematical values.

TAKE NOTE: When assigning names to variables or expressions, it is good practice to make the names useful. Observe that you **CANNOT** have spaces in variable names (ie. no spaces in names on the left hand side of the equals sign). Giving useful names to your variables or output will help you (and the TAs!) keep track of what your are doing.

A popular way of defining variable names is to use capitalization to mark word boundaries. One can also use underscores like rho_sq, but we will avoid them. (They don't cut and paste well.)

1.5   The CLEAR Command

This command clears the internal memory. All the variables are removed; both their current values and their addresses. You don't need to clear memory to change a value of a variable; just assign a new value to the variable by typing variable = 17. The

clear command would never be needed if people were perfect.

However, for debugging purposes, this is useful to use at the start of any script file (or any Lab problem!) to make sure the values of all variables have been cleared. This is particularly important if you are going to use the same variable names over and over for different problems. By using the clear command between problems you can ensure that values from one problem are not used in another problem. It is easier to find and fix a undefined variable error than a strange error caused by using a matrix of the wrong size which was left over from the previous problem.

Syntax: clear

Description: Erase values of all previously declared variable

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1.6   Additional Help

There is lots of help available through the menus. Additionally you can type help at the scilab prompt. The help browser called by just the command help has sections on Elementary Functions,the graphics library and many other sections. The use of help command-name will give you help on a specific command. For example, help plot. There are lots of Internet resources available too. This concludes the first part of the introductory lab module.

1.7   A note to Mac Users

While Scilab on the Mac is officially supported in version 5.2 it only runs on newer Intel based Mac's and not on the older PPC processors. (But it has been several years since Apple has sold a PPC processor.) One can obtain older versions of Scilab

for the Mac which work on PPC processors. They require you to install X11, which is on system disc, but not installed by default.

1.8   Plotting

Now we introduce how to do plotting using Scilab, especially using the plot command and its enhancements such as the title, labels and the legend. Drawing the graph is important. It is also important to add information so that the graph can stand on its own. You can and should enhance your graphs with axis labels, titles, color, and legends, if appropriate. Often scientific papers have figures (graphs) that "float". They are moved to make good looking page breaks and can be disconnected from where they are discussed in the text.

Often we want to graph functions, like $f(t) = t^2$ or $g(t) = \sin(t)$ and Scilab has aids to help us. The most confusing aid for new comers are the elementwise operations which are different from the matrix ones. We will sometimes need to use '.∗' (dot star) and ' .ˆ' (dot power) where you are used to using just star or power. On the plus side, most Scilab functions $f(x)$ are vectorized, so if x is a vector, then $y = f(x)$ is also a vector. This is very handy indeed.

1.8.1   Plot basics

The basic plot command has vectors of x and y data and an optional way of giving the color, marker and/or linestyle. As a simple example, suppose

$$x = [1, 2, 4, 5]$$

and

$$y = [1, 4, 16, 20]$$

then

$$plot(x, y,' ro-')$$

will give a graph like Figure 1. This is called plotting y vs x, the range versus the domain. The $'ro-'$ is optional, but it gives us control over the drawing. (In the text, Figure 1 was defined next.)
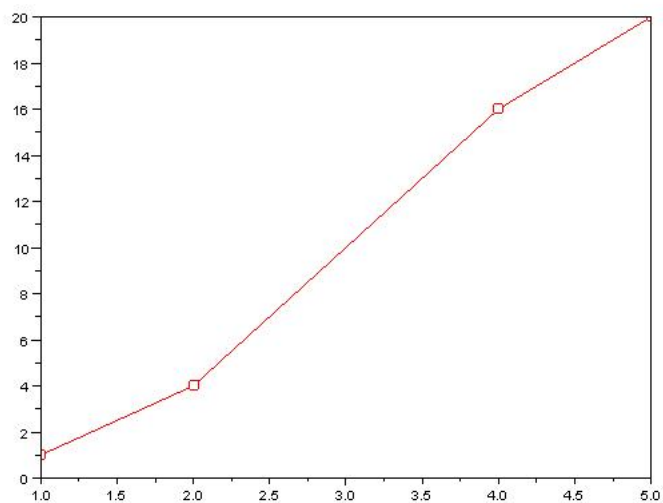
Figure 1:Result of

$$plot\left([1, 2, 4, 5], [1, 4, 16, 20],' ro-'\right)$$

Figure 1.1: *

This command plots the points $(1, 1)$, $(2, 4)$, $(4, 16)$ and $(5, 20)$, puts circles at these locations, and connects them with a solid line. The graph is sized to barely hold the data. There are ticks and values on both the $x-$ and $y-$axes. The $'ro-'$ tells Scilab to plot the graph in color red (because of the r), to put a circle (called a marker) at each data point, and to connect the points with a solid line (because of the $-$). There are many possible replacements for $'ro-'$ described below in syntax for color, marker, linestyle characters.

This plot is incomplete. It needs a title. If x and y have names or units, there should be axis labels. One can plot two or more graphs at the same time using a template like $plot(x1, y1,' ro-', x2, y2,' b :')$ which combines $plot(x1, y1, \ 'ro-')$ with $plot(x2, y2, \ 'b :')$. (More than 2 is also possible) If the plot has multiple graphs, then a legend is often required. These are described below in label basics.

1.8.2 Label basics

To add a title to your plot use

$$title('\text{The title in single quotes}')$$

To label the $x-$ or $y-$axes

$$xlabel('\text{time t in fortnights}')$$

$$ylabel('\text{distance y in furlongs}')$$

The legend is the hardest of these commands. Legend requires you to label each graph

and has an optional location. If you plotted both x^2 and x^3 and then you might use

$$legend\,('x\char`^2','x\char`^3',2)$$

Sometimes the legend will block part of the graph and need to be moved. A full list of legend locations is given by using the **help legends** command (see Scilab command list below).

1.9 The Graphics Window

Scilab has a graphic environment where the plot is displayed in a separate graphic window. This window has ways for interactively labeling a graph, including titles, axis labels, creating legends, color bars, etc. But we will not use these features in this class.

You may need to create a graphics window and then plot your graph. Type the following commands at the Scilab prompt.

$$scf(0);$$
$$x = 0 : 0.01 : 2 * \%pi;$$
$$y = sin(x);$$
$$plot(x, y)$$

If you were to type commands in Scilab for a new plot, they will appear in the pre-

vious window. If you want them to appear in a new figure window, then you would type the command

$$scf(1)$$

before doing the plot command to create a new (second figure window). The most recent figure window that you specify will be where your graphs are plotted. So, to plot in a previous window, you need to specify that window using the figure command.

Saving your Figure

If you want to save the drawing in the graphics window, there are many ways of exporting your graph into another document.

1. If you want to save graphics window number n, then from the command line, use the command

$$xs2png(n,'plot.png')$$

which will save a copy of graphics window n into the file plot.png in the current directory. The plots for last week's lesson were made this way. The command

$$xs2jpg(n,'plot.jpg')$$

will save the graphics window n as a jpeg in the file plot.jpg in the current directory. There are more possibilities: xs2eps, s2ps, xs2pdf, etc. but xs2pdf is buggy.

2. Alternatively, File → Export allows you to save the plot in a graphics format, such a png, jpg, or eps. You can select the format by selecting the appropriate format in the "Format Selection" area in the Export dialog window.

1.10   Appendix – Details

1.10.1   Syntax for color, marker, linestyle, characters

It is possible to specify color, linestyle, and markers, such as plus signs or circles, with a string of 1-4 characters inside single quotes. Color and marker are always one character, while linestyle can be one or two characters.

$plot(x1, y1,' ColorMarkerStyle1', x2, y2,' ColorMarkerStyle2')$

The color characters are 'b' for blue, 'c' for cyan, 'g' for green, 'k' for black, 'm' for magenta, 'r' for red, and finally 'y' for yellow which doesn't print well. Both letters and symbols are used for markers. The letters are 'd' for diamonds ($\Diamond$), 'h' for hexagrams (six pointed stars), 'o' for circles ($\circ$), 'p' for pentagrams (five pointed stars $\star$), 's' for squares ($\square$), 'v' for triangles pointing down (∇), and 'x' for x-marks $\times$) The symbols are '+' for plus (+), '.' for point ($\cdot$), '*' for (eight pointed stars), '^' for triangles pointing up ($\triangle$), '>' for triangles pointing right ($\triangleright$), and '<' for triangles pointing left ($\triangleleft$). Finally there are the linestyles '-' for solid, ':' for dotted, '-.' for dashdot and '–' for dashed. This list of commands are repeated by the command: help plot.

It is suggested that you always use the order: color, marker, linestyle for the charac-

ters. Scilab can usually figure out other orders, but not always (compare 'b.-' with 'b-.'). If you leave out the color, Scilab will pick one for you. If you leave out the marker, there will be no markers. If you leave off the linestyle but have marker, then no line is drawn. If you leave off the linestyle and the marker, Scilab will pick a linestyle for you.

1.10.2   Scilab command list

Here are the list commands used in this lab:

Syntax: $plot(X, Y)$ Description: The$plot(X, Y)$ command plots vector Y versus vector X.   This produces a graph of Y versus X.   Can be combined and used like $plot(x1, y1,' Color Marker Style1', x2, y2,' Color Marker Style2')$ so you can specify the appearance of each curve within the command.
Syntax: $scf(n)$;   Description: Makes graphics window number n the current graphics window. If it is not visible one can use the *show_window* command to raise it above all other windows on the screen. If graphics n does not exist, and n is an integer, a new graphics n is created.
Graph Title Syntax: $title('text')$ When giving titles to graphs, the convention is to list the dependent variable (y) first. For example, if $x = time$ and $y = speed$, a valid graph title would be "Speed Versus Time", or alternatively, "y versus x"
Axis Label Syntax: $xlabel('text')$ and $ylabel('text')$

Axis Scaling Syntax: $a = gca(); a.data_bounds = $ [xmin xmax ymin ymax];

Text in Graph at location (x, y) Syntax: $xstring(x, y,' text')$

Legend Syntax:

$legend('text1',' text2', ...)$ or $legend('text1',' text2', LOC)$ uses the specified 'text' as labels in the legend. If the number LOC is include, the location of the legend is indicated by the value of LOC. Common values for LOC are 1 for upper right, 2 for upper left, 3 for lower left, 4 for lower right. These correspond to inside plot top right (default), inside plot top left, inside plot top, etc, for the best location inside the plot to least conflict with data in the plot. A full list of these options can be found at: **help legends**

Syntax: $xs2eps(n,' figure.eps')$

Description: Stores a color postscript version of the graphics window n in the file figure.eps. Similar commands exist for formats like pdf, jpeg and png.

1.11 Notes

This module was adapted from two modules originally made by Juan Gutierrez (http://people.mbi.ohio-state.edu/jgutierrez/jbg_personal/index_en.html).

Module 2

The Cell and Biomolecules

2.1 Biological Introduction

The chemical environment inside living cells differs markedly from the environment outside the cell. **Cell membranes** regulate the ongoing exchange between the intracellular and extra-cellular environments, making it possible for cells to get vital raw materials (examples: oxygen, sugars, amino acids), rid themselves of wastes (examples: carbon dioxide, urea), and maintain a healthy electrical balance (membrane potential). It is the objective of this module to gain a deeper understanding of cell membrane structure and the processes of **transport** that systematically move molecules in and out of cells. Especially we will focus here on diffusion and **osmosis**, two passive means of exchange. Prepare for your workshop by reading in your textbook (ex. Campbell, 7th edition, Chapter 7) and completing the Pre-Workshop Activities posted on Blackboard as part of module 2b. Answers to any mathematical questions completed below should be submitted to your workshop leader in written form.

2.2   Cell membrane

Use the figure below for the next portion of the workshop. In turn, each member of the group should identify the structure described. As a group you should answer the associated the questions. Many but not all of the structures are identified by white boxes.
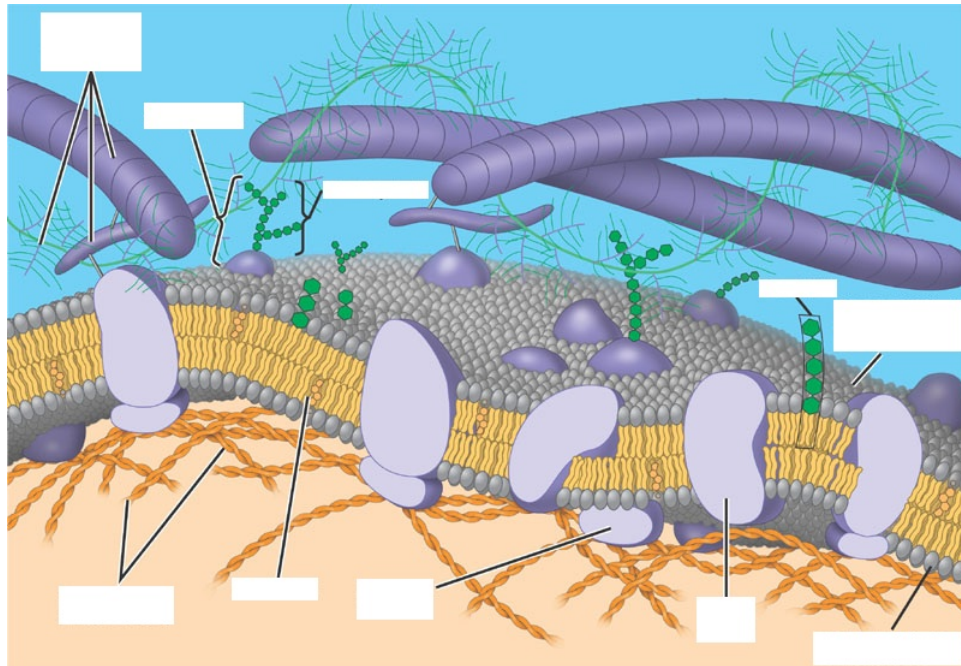
(1) Identify the phospholipid bilayer. Which is the hydrophilic side? Which is the hydrophobic side? How does this contribute to the structure of cellular membranes? Identify the cytoplasmic and extracellular fluid on either side of the membrane.

(2) Identify a transmembrane protein that could act as a gated channel. Explain what it does. Suggest one molecule or ion that might cross it.

(3) Identify a receptor protein with a bound ligand. Explain the process that goes on here.

(4) Identify a recognition proteina glycoprotein. Explain what it does.

(5) Identify an integral protein that spans the entire membrane. This protein is an electrogenic pump. Explain what it does and give an example.

(6) Identify several cholesterol molecules in the membrane. Take note of their general shape. What purpose for these molecules serve for the membrane?

(7) Identify some cytoskeletal elements in the picture above. Note how they are attached to the membrane. What is their role in maintaining membrane structure?

(8) Assume that immediately outside the picture is a cell membrane belonging to another cell. These two cells membranes are connected by a gap junction. What function does this junction serve for the two cells?

(9) If the gated channel in item 2 were open and conducted Na+ ions, what would happen if 8 Na+ ions were outside the cell and 2 Na+ ions were inside the cell? What process is involved?

(10) Assume the channel in item 8 is closed and conducts K+ ions. If there were 8 K+ ions in the cell and 2 K+ ions outside the cell, what will happen when the gate opens?

(11) What is the difference between the two channels described in items 8 and 9 and the sodium-pottasium pump pictured below? Describe the process in the picture below including the type of energy used?
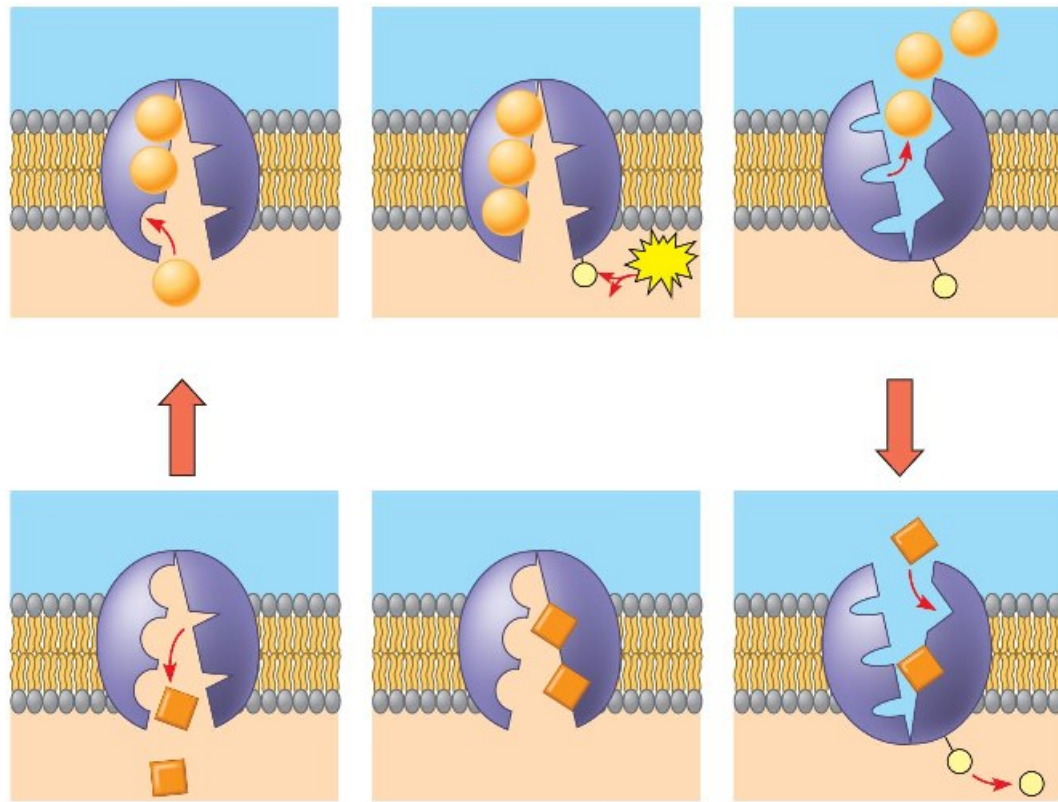
2.3   Transport Process

Each pair of students take one of the following problems. Spend 5 min working on them. When the group is reassembled, the pair should present their solutions to the rest of the group and answer questions and make corrections if needed.

1. A one-celled organism called an Amoeba encounters a particle of food moving through its watery environment. The particle is too large to pass through its cell membrane. The Amoeba is able to ingest it anyway.

   a. Suggest how the particle is taken in. Explain your suggestion.

   b. Draw a simple diagram of the process using several sketches to show the stages.

c. Describe where in the cell the particle is located after being ingested. Be specific.

d. Suggest what might happen to the particle next so the Amoeba can use it for food.

2. Small molecules are passing from inside the cell across the membrane to the extracellular fluid. The cell expends no energy, nor are there any special channels involved. The rate of movement is rapid for a while and then slows to a steady rate.

a. Suggest the type of transport moving the molecules. Explain your suggestion.

b. Draw a simple diagram of the process using several sketches to show the stages.

c. Propose the conditions (energy, gradients, metabolic activity) that must exist for the rapid and slow steady phases of molecular movement.

d. Think of a cell in which this transport might occur in the rapid and steady phases.

3. A large protein is secreted by a cell. It was manufactured in the ER.

a. Suggest a type of transport for getting the large protein out of the cell.

b. Draw a simple diagram of the process using several sketches to show the stages.

c. Discuss the role of membranes in this transport process.

d. Give an example of a substance that is transported in this manner.

4. A cell has too many Na+ ions in its cytoplasm and must use energy to lower the internal concentration back to normal levels since the Na+ concentration is higher outside the cell than in.

a. Suggest a type of transport for getting the Na+ out of the cell. Explain your suggestion.

b. Draw a simple diagram of the process using several sketches to show the stages.

c. Explain how this type of transport differs from simple diffusion.

d. Give an example of this type of transport in cells.

e. Suggest the electrical consequences of moving Na+ out of the cell.

5. A cell has many more potassium ions (K+) in its cytoplasm than in the extracellular fluid. The cell membrane has low permeability to potassium normally and very little leaves. Suddenly a large number of K+ ions rush out of the cell, and then the transport stops again.

a. Suggest what type of transport is responsible for the outward rush of K+ ions.

b. Draw a simple diagram of the process using several sketches to show the stages.

c. Identify the conditions (energy, gradients, stimuli, etc.) that must be present in the cell for this type of transport to occur.

d. Propose a way that the K+ ions might get back in the cell.

6. The figure in the next section is based upon the model of sucrose uptake by cells. Assume that cells have a lower concentration of hydronium ions (H+) inside as compared to outside the cell.

a. What effect would increasing the extra-cellular sucrose concentration have on the rate of sucrose transport into the cell?

b. What effect would lowering the extracellular pH have on the rate of transport of sucrose into the cell? Be careful!! Remember what happens with lowering pH?

c. What effect would adding an inhibitor of ATP generation have on the rate of transport of sucrose into the cell?

d. Name this type of transport mechanism.

2.4 Osmosis and Diffusion Problems

As a group complete the following problems on osmosis and diffusion.

1. Answer the items below using this figure. N = nucleus. Be sure to read the legends below the figure.
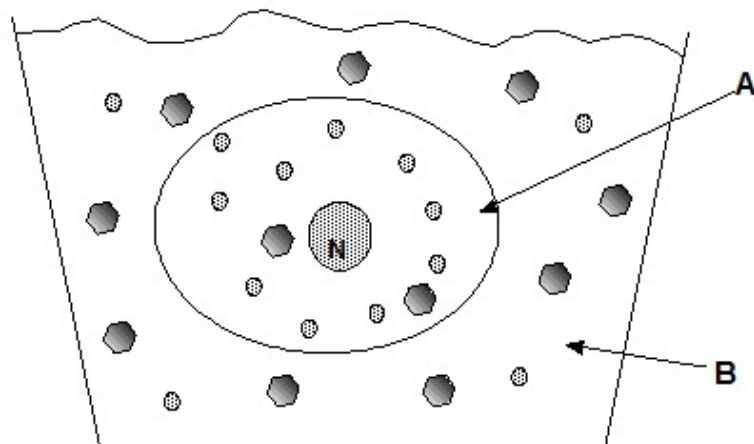
⬡ membrane is impermeable to this ion

⊚ membrane is permeable to this ion

Volume of the cell A is equal to the volume of the container B

N = Nucleus

a. Which is the intracellular compartment and which the extracellular compartment?

b. What will be in each compartment, beyond the solutes shown, in a live cell?

c. Determine the solute and solvent gradients that exist as it is drawn.

d. How does the osmotic pressure of the two compartments compare as it is drawn.

e. Describe what the distribution of solutes would be like after a few hours.

f. Compare the osmotic pressure in the two compartments if only solutes, but not solvents moved between the compartments.

g. Now indicate any solvent movements that might occur and how the shape of the cell might change.

2. Answer the items below using this figure. N = nucleus. Be sure to read the legends below the figure.
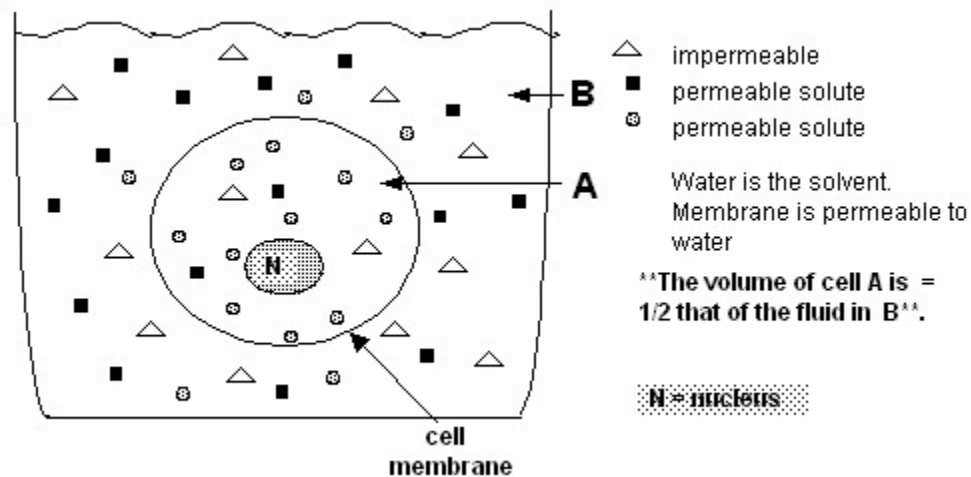
a. Determine the concentrations of each solute in the two compartments assuming each symbol represents a concentration of 0.01M.

b. Determine the solute and solvent gradients that exist as it is drawn.

c. How does the osmotic pressure of the two compartments compare as it is drawn.

d. After 24 hours, which solute(s) have diffused across the membrane into the cell? Which out of the cell?

e. How will the cell appear in size and shape after 24 hr?

f. Describe the relationship between the inside of the cell and the extracellular environment using the terms hypertonic, hypotonic, or isotonic.

g. Suggest a scenario in which the cell could reach equilibrium.

Item 2 describes the process of diffusion. Another way to describe diffusion is using a mathematical model. Mathematical models are able to predict how a cell will react when placed in solutions with higher and lower concentrations of solutes. These models can also identify the rate of diffusion at any given time, identify the equilibrium concentration of a solute for a given cell, and determine how long it will take for a cell to reach equilibrium. Below are two examples of diffusion using mathematical models. You will be able to graphically visualize the rate of diffusion at multiple time points and the time to equilibrium. You can also see how adjusting the permeability of the membrane (diffusion coefficient) or the initial concentration of solutes affects the rate of diffusion and time to equilibrium.

In this section, we will show how mathematics can be used to study the process of diffusion.

2.4.1 Functions of one variable

When you think of a function, you probably think of an equation that relates two quantities. The equation describes precisely how the value of the dependent variable depends on the value of the independent variable. For example, the position of an object traveling along a straight line depends on how long the object has been traveling for. So if s represents the position of an object and t represents the time the object has been traveling for, and we know the equation describing this motion, we could write a function. An example would be $s(t) = t^3 - 6t^2 + 9t$.

Once you begin studying calculus, you can ask answer questions like: How fast is the position of this object changing as time changes (or, what is the object's velocity)? This is the idea of derivative from calculus, which is a central idea in the study of the subject. A related but slightly different question you can ask is: If I know the velocity of the object, what is the function describing the object's motion? This type of question is the basis for the subject of differential equations. In a differential equation, you are given information about the derivative(s) of a function and asked to figure out what the original function was. An example of a differential equation would be $\frac{ds}{dt} = s^2$. This says that the objects velocity is s^2 and you would need to figure out what the position of the object is (or what the original position function is which led to this velocity). For some differential equations, there are techniques for figuring out the solutions to the equation. For others, the equations are too complicated to solve. But even in such cases, we can usually figure out some qualitative information about the solution, even if we cannot figure out the solution itself.

One important qualitative feature of a differential equation that is usually of interest is the equilibrium. The equilibrium is the value which, once attained, the solution

will remain at that value unless some outside force pushes it away from that value. To visualize an equilibrium value, think about a valley between two hills. If you place a ball at the trough of the valley, the ball will remain unchanged (at equilibrium) unless something or someone moves it.

2.4.2   Functions of more than one variable

Though we typically think of the value of the dependent variable depending on just one single independent variable, it is possible for the dependent variable to depend on more than one independent variable. A multivariable function is an equation in which you have multiple independent variable determining the value of the dependent variable. For a simple example, think about temperature on Earth. The temperature depends both on location and time. The temperature in Miami is different than the temperature in Chicago, but even in Miami, the temperature in December is different than it is in June. So, if x represents position, t represents time, T represents temperature, and we knew the equation describing how position and time affected temperature, we could write a multivariable function. An example would be $T(x, t) = xt + x^2$.

The ideas of calculus extend to multivarable functions and this is the idea behind multivariable calculus. With multivariable calculus, we could answer questions like: How fast is the temperature changing as your position changes, for a fixed time? How fast is the temperature changing as time changes, in a fixed position? How fast does temperature change as time changes and as your position changes in a certain direction? And just like with single variable functions, you can ask the related question: If I know how the temperature changes with position and/or time, what was the original

temperature? This leads to partial differential equations. An example of a partial differential equation is $\frac{\partial T}{\partial t} = D\frac{\partial^2 T}{\partial x^2}$. This equation is usually called either the heat equation or diffusion equation. As with differential equations which arise from single variable functions, there are techniques for solving some partial differential equations (such differential equations are usually called ordinary differential equations), although most cannot be solved explicitly (in fact, partial differential equations are usually such harder to solve than ordinary differential equations.

Luckily, the diffusion equation is one which can be solved in simple cases, although that is beyond the scope of this module. Notice that in the equation, there is an extra parameter, D. This parameter is called the diffusion coefficient or diffusivity. The diffusion coefficient is a measure of how effectively the particles disperse from a high concentration to a low concentration and is a characteristic of the solute and the fluid in which it is dissolved. The diffusion coefficient usually depends on things such as the size of the particles, the type of solvent, and the temperature.

When solving the diffusion equation, you usually start with some conditions above and beyond just the equation itself. Usually, you start with certain boundary conditions and certain initial conditions. Usually, we dealing with diffusion, whatever is diffusing (whether it is particles or animals or whatever) does so in a certain region of space, which we call the domain. The domain usually has some sort of boundary (whether it is the borders of a cell in which particles are diffusing or the coast of an island in which a population is diffusing). We can specify condition on this boundary, such as no animals on the boundary, no particles coming in or out of the domain through the boundary, or animals at these locations, this many animals coming in at this location, and this many animals going out at that location. These conditions

constitute the boundary conditions. The boundary conditions can play an important role in the eventual composition of the population within the domain. The other condition, called the initial condition, tells you at each location, how is the population distributed at the very beginning.

The situations we will look will consist of particles inside two infinitely long parallel strips. The boundary conditions we will use are no particles coming in or going out at either of the boundaries (the left side or the right side). We will look at two different initial conditions: one where the particles have a higher initial concentration on the left side of the strip and one where the particles have a higher initial concentration in the center of the strip. These examples are a bit different than particles diffusing across a cell membrane but they are much simpler to handle mathematically and still demonstrate the idea of diffusion pretty well.

2.4.3   Diffusion with Scilab

Download the file diffusionleft.sce, then execute it in Scilab. For certain fixed values of t, you will see how the concentration of particles changes with position, x.

QUESTION: Describe what you see in the graph.

Download the file diffusioncenter.sce, then execute it in Scilab. For certain fixed values of t, you will see how the concentration of particles changes with position, x.

QUESTION: Describe what you see in the graph.

Now open the Scilab editor and open the code for each of the files you downloaded. In each, you will see parameters T, u, a in lines 7 - 9. These parameters represent: T is temperature (in Kelvin), u is cell size (in cm), and a is viscocity of solvent.

Note: For the next few questions, if you want to leave the original graph open in its

original graphics window and open the new graphs in their own graphics windows so you can compare them all side-by-side, you need to change line 17 or 18 (depending on which of the two files you are working with) where it says $scf(1)$;. The 1 indicates that the graph is being opened in graphics window 1. If you change the 1 to 2, that will open the graph in graphics window 2. If you change it to 3, it will open the graph in graphics window 3.

QUESTION: What is the affect of changing the temperature from 298 to 398? From 298 to 198? How does temperature affect diffusion?

QUESTION: What is the affect of changing the viscosity from 0.498 to 0.098? From 0.498 to 0.998? How does viscosity affect diffusion?

QUESTION: What is the affect of changing the cell size from 0.0001 to 0.001? From 0.0001 to 0.00001? How does cell size affect diffusion?

Module 3

Protein Synthesis

3.1 Biological Introduction

The discovery of DNA structure as a double helix and the function of this macro-molecule as the genetic material of the cell was a primary scientific achievement of the 20th century. Countless scientist have contributed to understanding the processes by which the genetic information is replicated prior to cell division and expressed in cell structure and function by the synthesis of RNA and proteins. The goal of this workshop is to master the basics of three processes, DNA replication, the formation of RNA by transcription, and the synthesis of proteins, a process called translation. The three are bound by a universal genetic code that is common to most living things. Prepare for your workshop by reading assignments in your textbook (Campbell and Reece, 6th edition, Chapters 16 and 17) and completing the Pre-Workshop Activities in Module 5 on Blackboard. Show your work on these pages.

3.2 Scholarly definitions

Evaluate the definitions below. Circle any items that are incorrect and change the words to make them correct. Write TRUE if all information is already correct. After completion, go over each item as a large group.

(1) DNA: located in the nucleus; a polymer made of amino acids; contains ribose, phosphate groups, and nitrogen bases; replicates during the S phase of the cell cycle; one strand acts as a template for mRNA replication; strands can be divided into 3-base sequences called codons.

(2) mRNA: m stands for "messenger"; is synthesized in the nucleus; the process of synthesis is called translation; works in polysaccharide synthesis on ribosomes in the cytoplasm; is composed of 3-base units called codons; is single stranded; has T substituted for U in synthesis from DNA.

(3) template: a name given to a DNA strand that serves in mRNA synthesis; has a sequence of triplets which determine the codons of mRNA; works by binding complementary nucleotides which are then linked to form the mRNA strand; binding to free nucleotides is by hydrogen bonding.

(4) codons: an example would be ATC; many occur in sequence on mRNA molecules; sites of attachment for the anticodons of tRNA; determine the order in which amino acids attach to form a polypeptide; are complementary to DNA triplets from which they were formed initially.

(5) tRNA: are short polynucleotide strands; t stands for "target"; carries a sugar at one end for polysaccharide synthesis; at the other end of the molecule is an

anticodon for attachment to codons of mRNA; if the mRNA codon were AUG, the anticodon of tRNA would be UAC; occurs in many varieties to carry different amino acids.

(6) transcription: manufacture of proteins using mRNA and tRNA; occurs on ribosomes in rough endoplasmic reticulum; involves the encoding of a sequence of triplets into a comple-mentary sequence of codons.

(7) translation: the raw materials for the process are free amino acids in the cytoplasm or rough ER; requires enzymes to attach amino acids to one another; occurs on free ribosomes or ribosomes of the rough endoplasmic reticulum; mRNA and tRNA each play an important role; final product is a protein; DNA is only involved if RNA cannot finish the job.

(8) DNA replication: a double DNA strand separates into two single strands; each single strand attracts complementary nucleotides which attach by hydrogen bonding; an enzyme hooks adjacent nucleotides together forming the new double strand; occurs before a cell divides in mitosis.

(9) nucleotides: are the monomers from which DNA and RNA are synthesized; occur in four different varieties in DNA, and three varieties in RNA; each one includes a sugar, nitrogen base and a phosphate group; are synthesized into RNA and DNA in the nucleus; occur only in the nucleus.

(10) ribosome: some of its parts are manufactured in the nucleus; consists of rRNA and proteins; serves as a location for protein synthesis; has two connected parts, one large and one small; occurs free in the cytoplasm and attached to the walls of rough endoplasmic reticulum.

3.3 Short Problems

Organize into pairs and complete two of the following problems. When the second problem assigned to you is presented, your job will be to make any corrections and additions that are appropriate or show an alternative way to represent the problem.

1. A newly formed complementary strand of DNA has the base sequence: AGGTCT-GAG.

   What is the sequence of bases in the template from which it was synthesized?

2. An mRNA strand has the base sequence: AUGACCUUA.

   How many codons are present if only codons are shown?

   What is the sequence of triplets for the DNA strand that acted as a template for its synthesis?

3. A very small gene has the base sequence TAGTAGCAT.

   Describe the molecule it could give rise to which would control protein synthesis in the cytoplasm of the cell.

4. A strand of DNA has the following sequence of bases:

   GCC GAC GAT AGA

   (a) Using the table provided, determine the sequence of bases in the mRNA strand that can be transcribed from the DNA.

   (b) Determine the amino acid sequence in the polypeptide that will be translated from the mRNA.

Second base

First base (5′ end)	U	C	A	G	Third base (3′ end)
U	UUU ⎤ Phe UUC ⎦ UUA ⎤ Leu UUG ⎦	UCU ⎤ UCC ⎥ Ser UCA ⎥ UCG ⎦	UAU ⎤ Tyr UAC ⎦ UAA Stop UAG Stop	UGU ⎤ Cys UGC ⎦ UGA Stop UGG Trp	U C A G
C	CUU ⎤ CUC ⎥ Leu CUA ⎥ CUG ⎦	CCU ⎤ CCC ⎥ Pro CCA ⎥ CCG ⎦	CAU ⎤ His CAC ⎦ CAA ⎤ Gln CAG ⎦	CGU ⎤ CGC ⎥ Arg CGA ⎥ CGG ⎦	U C A G
A	AUU ⎤ AUC ⎥ Ile AUA ⎦ AUG Met or start	ACU ⎤ ACC ⎥ Thr ACA ⎥ ACG ⎦	AAU ⎤ Asn AAC ⎦ AAA ⎤ Lys AAG ⎦	AGU ⎤ Ser AGC ⎦ AGA ⎤ Arg AGG ⎦	U C A G
G	GUU ⎤ GUC ⎥ Val GUA ⎥ GUG ⎦	GCU ⎤ GCC ⎥ Ala GCA ⎥ GCG ⎦	GAU ⎤ Asp GAC ⎦ GAA ⎤ Glu GAG ⎦	GGU ⎤ GGC ⎥ Gly GGA ⎥ GGG ⎦	U C A G

5. For the molecule in question #4, determine what the anticodons are for the tRNAs that attach to them in protein synthesis.

3.4 Diagramming the Processes

Divide the group into three teams. Each team will do one of the problems below and then share their results with the other students. Make the diagrams on the blackboard or large sheets of newsprint.

1. a. Make a rough labeled diagram of how you envision the process of DNA replication including the important molecules in the following list: DNA double helix, DNA polymerase, leading strand, lagging strand, single deoxyribonucleotides, and triplets. Include: Okazaki fragments, DNA ligase, helicase, primase.

   b. Indicate by arrows and numbers the sequence of steps.

   c. Explain the diagram to the other groups, and make any modifications that are needed.

2. a. Make a rough labeled diagram of how you remember the process of RNA transcription including the important elements in the following list: DNA template, single ribonucleotides, RNA polymerase, promoters, initial RNA transcript, RNA splicing, mRNA, rRNA, tRNA, codons.

   b. Indicate by arrows and numbers the sequence of steps.

   c. Explain the diagram to the other groups, and make any modifications that are needed.

3. a. Make a rough labeled diagram of how you envision the process of translation including the important elements in the following list: mRNA, ribosomes, amino acids, tRNA, anticodons, codons, aminoacyl-tRNA synthetase, peptide bond, protein. Include: P site and A site.

   b. Indicate by arrows and numbers the sequence of steps.

   c. Explain the diagram to the other groups, and make any modifications that are needed.

3.5 Mathematical Introduction

One process you have studied during this workshop is DNA replication. DNA replication is a necessary part of the cell cycle. In order for cellular division to occur, the cell must first duplicate its DNA. During the cell cycle, the cell grows and after DNA replication, it divides in two cells containing identical cellular material. DNA replication and cell division are regulated by several key checkpoints during the cell cycle that you will learn about in more detail in lecture. Whether or not replication and cell division occur is dependent on several factors including the mass of the cell and the presence and abundance of a group of substances known as cyclins and cyclin dependant kinases (Cdk).

Thanks to research on this matter, it is possible to determine how frequently cell division occurs as a function of cellular mass or cyclin concentration. Below is a model that described how this occurs.

3.6 Mathematical model

To learn more about cell cycle control and the model, read section 10.1 - 10.3 in *Computational Cell Biology*, edited by Christopher P. Fall, Eric S. Marland, John M. Wagner, and John J. Tyson, 2002. Pay attention to the model equations and the meanings of the variables. The model is a system of four ordinary differential equations (ODEs). A differential equation is an equation that relates the derivative of a function to the function itself. In other words, it describes the rate at which a quantity changes. This system in particular is a coupled system of ODEs, which means that the rates of change of each of the quantities depends on each other. In

this model, the quantities which are changing are the concentration of cyclin/Cdk, the concentration of Cdh1/APC, the concentration of the Cdc20 activator, and the size of the cell.

As you read about the model, do not get hung up on what the terms in the model mean. Just observe that they depend on each other and concentrate on what happens with the biology of the system. Also, don't get wrapped up in any fancy mathematical jargon. For example, when you read the sentence, "Consequently, the S-G2-M steady state is lost by a saddlenode bifurcation, and the control system jumps irreversibly back to the G1 state" you should understand that the cell cycle control system is going from the S-G2-M phase back to the G1 phase as a result of whatever is mentioned in the previous sentence.

3.6.1 Scilab File

Download and execute the file cell_cycle_control.sce. Once the graphics window opens, maximize the window, then export the figure as a JPEG (go to File → Export to... then change the Files of type option from All files to JPEG). Be sure to note where you saved the figure and what name you gave it so you can retrieve it on your computer.

QUESTION: Open the figure you saved from the Scilab file. Using any program which allows you to draw on pictures (MS Paint, MS Word, Photoshop, etc.) draw a vertical line at the Start and Finish of each cell cycle and label each as start or Finish. Then label the G1 and S-G2-M phases.

QUESTION: The text you read on the model claims that APC destroys cyclin molecules. Is this claim supported by the figure? Explain.

QUESTION: The text you read on the model claims that cyclin/Cdk activates Cdc20. Is this claim supported by the figure? Explain.

Module 4

Gene Regulation

4.1 Biological Introduction

Gene expression results in translation into proteins. Genes typically do not express themselves until they are switched on. This is accomplished by the binding of transcription factors to the promoter region of the DNA. Upstream sequences can code for the production of small protein molecules that either induce or repress gene expression. We will explore these concepts in this module.

We will also consider viruses and bacteria. These are two categories of microbes that play a multiplicity of roles in life. Their structure, function and genetics have enabled scientists to gain an ever deeper understanding of the basic operations of life at the cellular/molecular level. This workshop will give you some incite into this microscopic and sub-microscopic world.

Prepare for this workshop by reading your textbook (Campbell and Reece, 7th edition, Chapters 18 and 19) and completing the Pre-Workshop Activities in Module 6 on Blackboard.

4.2 *lac* Operon

In the laboratory, you are given ten strains of E.coli with the following lac operon genotypes, where I = lacI (the repressor gene), P = Plac (the promoter), O = lac O (the operator), and Z = lacZ (the β-galactosidase gene). (Note: In the partial diploid strains (6-10), one copy of the lac operon is in the host chromosome and the other copy is in the extrachromosomal F factor.)

For each strain, predict whether β-galactosidase will be produced (a) if lactose is absent from the growth medium and (b) if lactose is present in the growth medium.

1. I+P+O+Z+

2. I-P+O+Z+

3. I+P+OcZ+

4. I-P+OcZ+

5. I+P+OcZ-

> **QUESTION:** Compare and contrast the lac operon and trp operon with respect to their inducible and repressible features.

> **QUESTION:** What happens when glucose levels are high and lactose levels are low?

4.3 Eukaryotic Gene Regulation

Label the following diagram indicating stages in gene expression that can be regulated in eukaryotic cells.
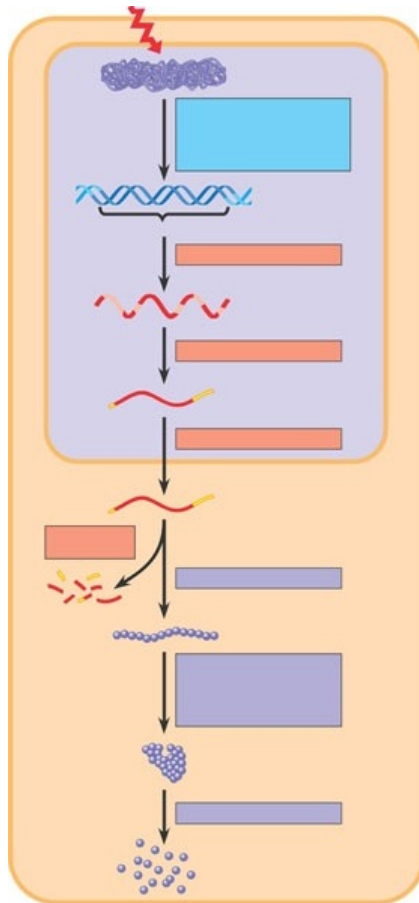
QUESTION: What are the major differences between gene regulation in prokaryotes and eukaryotes?

4.4 Conjugation in Bacteria

QUESTION: In the image below, which process represents an F+ x F- cross and which represent an Hfr x F- cross
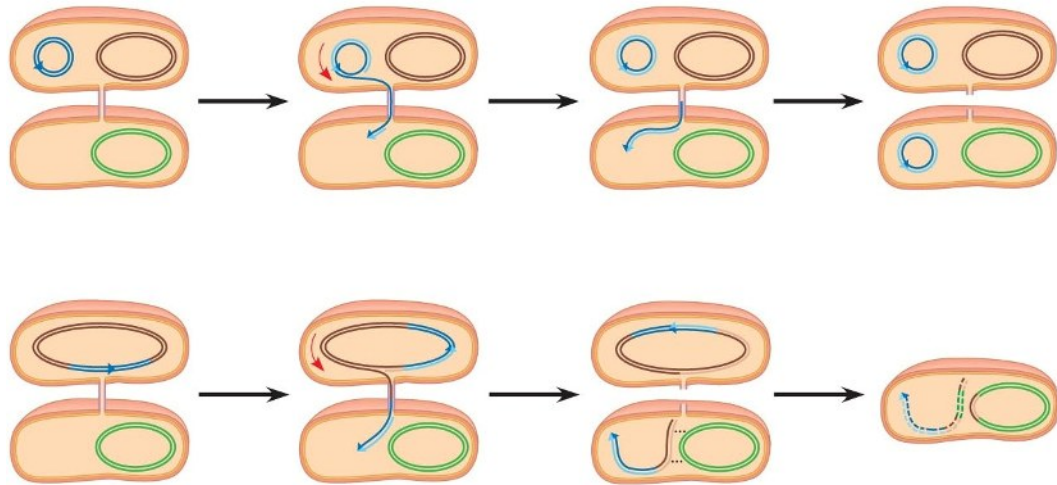
QUESTION: What are the major differences between the F+ x F- and the Hfr x F- bacterial crosses?

4.5   Viral reproduction and Bacteria

Below is an image of a phage infecting a bacterium. Identify which half of the diagram represents the lytic cycle and which represents the lysogenic cycle.
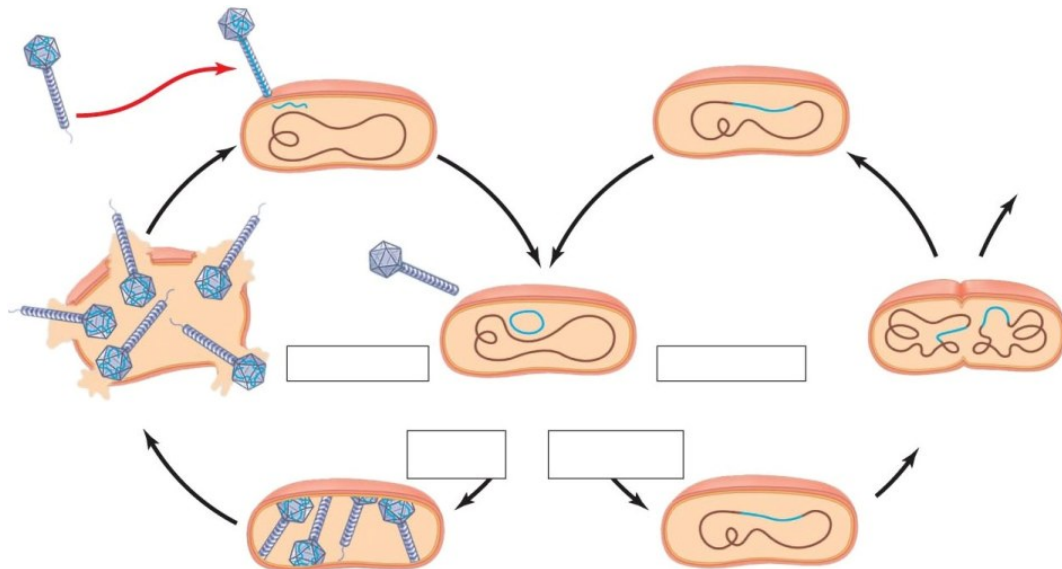
QUESTION: What are the major differences between the lysogenic and lytic phases of a bacteriophage?

4.6   Mathematical Introduction

A specific type of virus, called a retrovirus, uses a similar but much more effective method to transfer its genetic material to its host. Retroviruses do not have DNA but rather have RNA based genomes. Once they infect a cell, they release an enzyme called reverse transcriptase which transcribe the RNA into a double stranded DNA. This is called a provirus. The provirus is then incorporated into the cell's chromosomal DNA and is transcribed into RNA repeatedly along with the rest of the genes in the cell. As you can imagine, this is extremely dangerous to the host organism and can quickly result in the formation of millions of copies of a virus. You will learn more about this process later in the semester.

One example of a retrovirus is HIV. Based on what you know about how HIV reproduces you can understand how dangerous it is to its host and why it is so important to develop effective treatments for this virus. Researchers can utilize mathematical models to determine the effectiveness of different treatment strategies, to best figure out how to treat HIV while they are still trying to find a cure. Below is an example of one such model.

4.6.1   Mathematical Background

In mathematics, it is common to want to try and optimize some quantity, which is usually represented by a function. In application, this function which you are trying to optimize has some practical meaning. For example, if you own a business then

perhaps you have a function $r(x)$ which described how much revenue you make from selling x items, which you want to maximize. Or maybe you have a function $c(w)$ which tells you how much your company's costs are based on hiring w workers, which you want to minimize. In calculus, you are taught to find the maximum or minimum of a function using derivatives. But sometimes the story is more complicated than that. In our previous example, perhaps we are most interested in maximizing the profit. This would involve a combination of maximizing our revenue and minimizing our costs. But there could be a complicated interplay between the two. For instance, the more employees you hire, the higher your costs will be. But on the other hand, the more employees you have, the more sales you can make so the higher your revenue too. On the flip side, the more items you sell, the higher your revenue will be, but you will also need to produce more items and so your costs will be higher too. So now determining the optimal number of employees and items to maximize your profits is a lot more complicated. In fact, it might be the case that instead of having one optimal level of employees and items, there could be a strategy which changes over time. For instance, perhaps it is better to have only a few employees initially then gradually increase for six months, then scale back again. Or maybe it is better to start off with lots of employees and after three months, double your workforce.

The mathematical field of optimal control theory deals with exactly these types of complicated problems. In optimal control theory, there is a variable (or variables) which are controlled by some outside factors and you want to figure out how we should control this variable to produce the "best" outcome, based on some predetermined goal(s).

In this module, you will be using optimal control to determine the best treatment

strategy for treating HIV with chemotherapy.

4.7 HIV Model

One strategy which researchers have studied for treating HIV is the use of chemotherapy of reverse transcription inhibitors, such as AZT, to reduce viral production. These drugs interrupt key stages of the infection process during the life cycle of HIV within a host cell. It is assumed that drug resistance occurs so treatment only acts to reduce the infectivity of the virus until then. The benefit of chemotherapy is increased CD4+T cell count. This model has the following 13 parameters with the following values:

$s = 10$: rate of generation of new CD4+T cells

$m_1 = 0.02$: natural death rate of uninfected CD4+T cells

$m_2 = 0.5$: natural death rate of infected CD4+T cells

$m_3 = 4.4$: natural death rate of free virus particles

$r = 0.03$: growth rate of the T cells per day

$T_{max} = 1500$: maximum level which T cells can grow to

$k = 0.000024$: rate at which free virus cells infect T cells

$N = 300$: average number of virus particles which are produced before the host cell dies, once infection of a T cell occurs and replication is initiated

$T_0 = 800$: initial concentration of uninfected CD4+T cells

$T_{i0} = 0.04$: initial concentration of infected CD4+T cells

$V_0 = 1.5$: initial concentration of free virus particles

$A = 0.05$: "cost" of chemotherapy to the body

$t_{final} = 20$: time frame before drug resistance occurs

For this model, the control variable, $u(t)$, is the strength of the chemotherapy. Here, $u(t) = 1$ represents no chemotherapy and $u(t) = 0$ represents maximum chemotherapy. The goal of this model is to maximize the number of uninfected T cells while minimizing the "cost" of the chemotherapy to the body at the same time.

Download the file HIV_control.sce. When you execute the file, you will notice that in the Scilab console window, the code will stop running and you will see this message:

[Continue display? n (no) to stop, any other key to continue]

As long as this message is in the console window, Scilab won't proceed with the code. In fact, Scilab will freeze until you tell it what to do at this point. Press "n" and Scilab will finish the first part of the code. It will then ask you to enter a value for the source term s, then it will ask you to enter a value for the natural death rate of T cells (m_1), etc. It will ask for values for each of the 13 parameters in the model. For each parameter, enter the value listed above. After you have finished entering the last parameter value, Scilab will continue with the code and eventually, you will see the same message in the console window asking about continuing the display. Again, press n so that Scilab can finish with that part of the code.

Once that is done, Scilab will tell you to type 1 or 2. What Scilab is asking for here is if you would like to input a second value for one of the parameters so that you can see how changing one of the parameters affects the treatment strategy. Press 1. Scilab will then tell you to type 1 - 13. Here Scilab is asking you which of the 13 parameters you want to change so you can see how it affects the treatment strategy. Each of the questions below will tell you which of the 13 parameters you are going

to change and what to change it to. Each time you answer a question, you should close the graphics window and then execute the file using the initial parameter values from above. When you enter your second parameter value, Scilab will again stop in the middle of the code and you will see the same message in the console window about continuing the display. Press "n" so that your graphics window ends up with four graphs. The top graph is T (concentration of uninfected CD4+T cells) vs. t (time). The second graph is T_i (concentration of infected CD4+T cells) vs. t. The third graph is V (concentration of free virus particles) vs. t. The fourth graph is $u(t)$ (strength of chemotherapy) vs. t.

QUESTION:$N = 50$: Which parameter value allows the uninfected T cell count to increase the most? Why is or isn't this what you would expect? Describe the difference in treatment strategies for the two parameter values.

QUESTION:$s = 7$: Which parameter value involves more chemotherapy as part of its strategy? Notice the relationship between the concentration of uninfected T cells & viral particles and chemotherapy strategy for each of the parameter values. How do they compare for the different parameter values?

QUESTION:$k = 0.000032$: Which parameter value involves more chemotherapy? Does the increased chemotherapy result in a lower concentration of infected T cells and viral cells? How do the results of changing this parameter differ from the results in the previous question?

4.8 Notes

The matehmatical model and Scilab file used in this module were adapted from *Optimal Control Applied to Biological Models* by Suzanne Lenhart and John T. Workman,

2007.

Module 5

Control Systems

5.1 Biological Introduction

The most striking feature as the level of complexity increases in living systems is the development of integration and coordination of body functions such as respiration, circulation of blood, and excretion. This integration and coordination ensures homeostasis; the maintenance of a relatively stable internal environment. Homeostasis is accomplished by two systems; the endocrine system and nervous system.

Although both hormone producing cells and nerve cells synthesize specific chemicals, store them in specialized regions of the cell, and release them when they are stimulated, there are major differences between the endocrine system and the nervous system. First, nerve cells usually release their chemicals (neurotransmitters) close to the cells that they influence compared to endocrine cells, which release hormones into the blood to act on distant target cells. Second, this difference in distance affects the degree of control of the two systems. A nerve cell will chemically influence an adjacent nerve cell whereas hormones bathe millions of cells indiscriminately. Third,

since the nervous system is an electrical system, its response is more rapid than the endocrine system in which hormones are released into the blood stream.

In this module we will explore how the endocrine system and nervous system work together to achieve homeostasis. Prepare for this module by completing the pre-workshop activities available on Blackboard.

5.2   Endocrine System

(1) Which of the images below represents the actions of a typical protein hormone and which represents a typical lipid hormone.
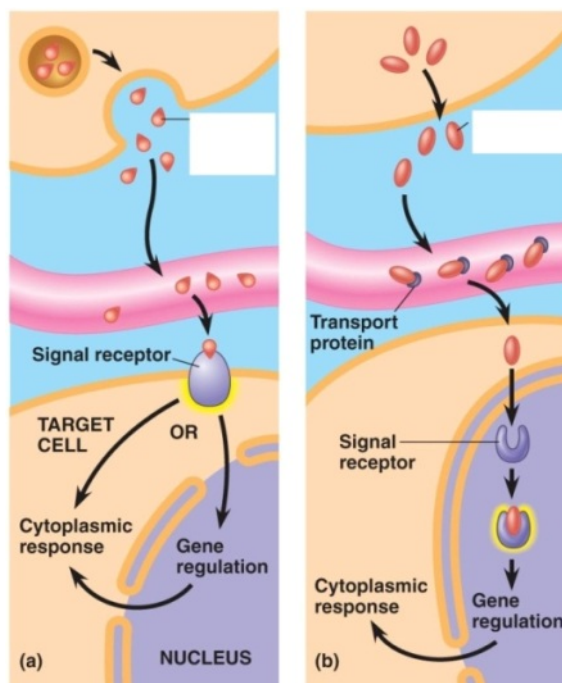
> **QUESTION:** What are the major differences between the actions of lipid and protein hormones?

(2) Suppose that a researcher announces a discovery of a hormone that affects the metabolism of fats in lab rats. Preliminary data indicate that the hormone is a single polypeptide chain 100 amino acids large. Design a protocol for isolating the receptor for the hormone. Using fat cells growing in vitro, how could you test the hypothesis that hormone binding causes a change in a second messenger?

(3) In the image below identify the processes and hormones involved in the regulation of blood glucose levels.
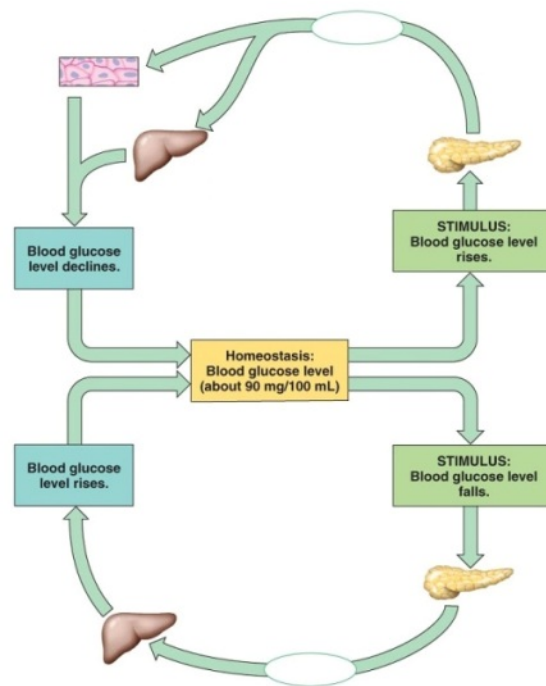
QUESTION:How does the regulation of blood glucose compare to the regulation of blood calcium levels?

5.3 Nervous System

Fill in the blanks in this concept map to help you learn the functional organization of the vertebrate nervous system.

```
                          VERTEBRATE NERVOUS SYSTEM
                              may be separated into
        a.                                              b.

              divisions are                                  includes
        c.          d.                               e.           brain

    carries       carries      divisions are              connects and integrates
 information   information    g.           h.              sensory and motor
 to CNS        from CNS                                    components of PNS

         to        subdivided into    carries    carries    neurotransmitter
 f.          i.          j.           impulses to impulses to   used is
     which              which
                 neurotransmitter  speeds heart,  smooth and  n.
 k.                  used is       metabolism,    cardiac
                                   prepares       muscles,     mostly under
           l.        m.            for action     organs    conscious control   o.
```

QUESTION: Provide some examples where the nervous system and endocrine system interact to maintain homeostasis.

This diagram shows the changes in voltage-gated ion channels during an action potential. Label the channels and gates ions, and five phases of the action potential. Label the axes of the graph and show where each phase occurs. Describe the ion movements associated with each phase.

The figure shows the stages of an action potential with labeled diagrams (numbered 1 through 5) of the plasma membrane and ion channels, along with a graph of membrane potential. Labels include:

- e.
- f.
- b.
- c.
- Outside cell
- Plasma membrane
- Inside cell
- a.
- d.
- h.

Graph labels: +50, 0, −50, −100, Action potential, Threshold potential, Resting potential
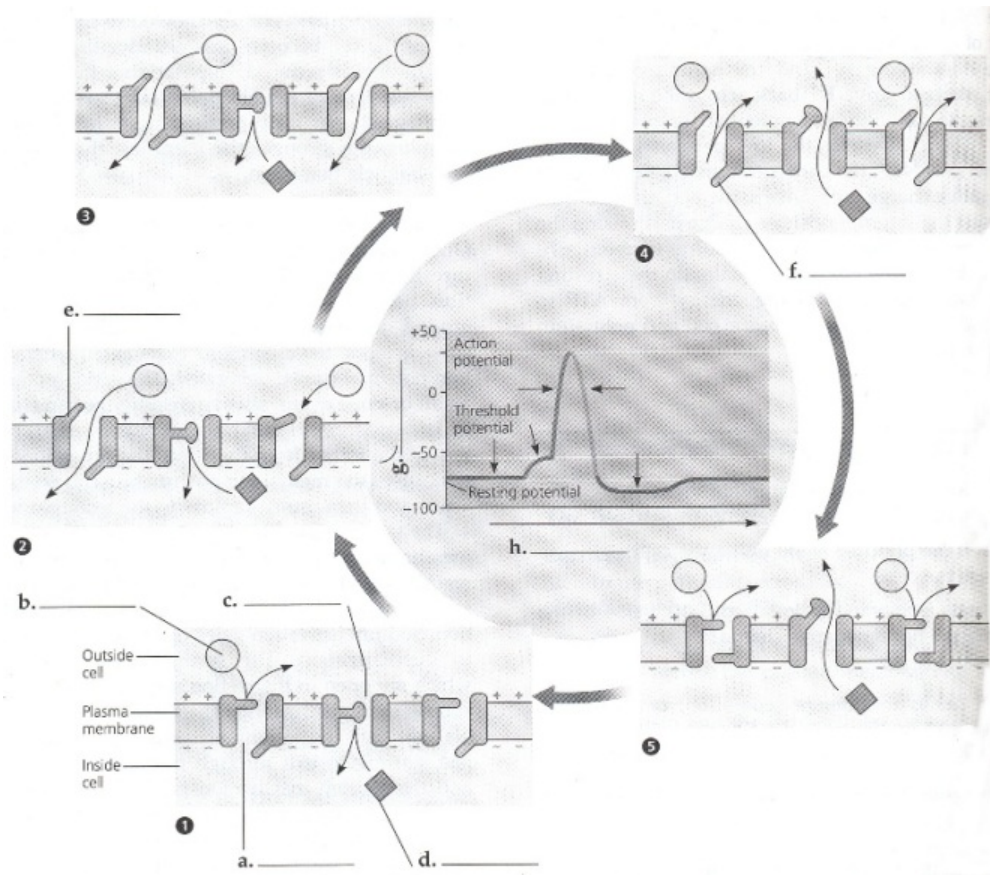
We have just covered the basics of how an action potential is formed. This action potential can then conduct down the entire length of a neuron by depolarizing a neighboring region of the neuron. This is also sometimes called a nerve impulse. We can use mathematical models to see how action potentials conduct down a neuron. We can also see how changing the current will affect an action potential. Using the models below you will be able to explore action potentials in greater detail. While you work with these models, keep in mind what is happening to the sodium and potassium ions during depolarization and repolarization.

5.4   Mathematical Introduction

In 1952, Alan Hodgkin and Andrew Huxley published a mathematical model describing the propagation of an electrical signal along a squid giant axon. Their work earned them the Nobel Prize for Physiology and Medicine in 1963. Their model consists of four coupled differential equations. The first equation describes the potential difference caused primarily by the sodium and potassium ions, although other ions play a part. The second equation describes the potassium activation. The third equation describes the sodium activation and the fourth equation describes the sodium inactivation.

The problem with this system of equations is that it is too complicated to be able to do any qualitative analysis on it. So in the 1960s, Richard FitzHugh (1961) and Jin-Icki Nagumo (1962) independently studied the work of Hodgkin and Huxley. The result was a simplified system of two equations, which was much more conducive for qualitative analysis. The key to the FitzHugh-Nagumo equations is the fact that the change in potential and the sodium activation happen on a much faster time scale than the potassium activation and sodium inactivation (by a factor of 10). So since the potassium activation and sodium inactivation are changing so slowly, they can be thought of as being constant in the equations for the potential and sodium activation, which eliminates two of the equations from the system.

In this module, you will be simulating both the Hodgkin-Huxley equations and the FitzHugh-Nagumo equations. You will notice the qualitative similarities between the two models.

> **QUESTION:**Describe what happens to a nerve cell after it receives a stimulus sufficiently large to trigger an action potential.

5.4.1 Scilab Simulations

Download the files Hodgkin_Huxley.sce and Fitzhugh_Nagumo.sce. First execute the Hodgkin-Huxley system. In this simulation, we start with an applied current of 0, which means that there is no stimulation to the axon after the first action potential. To answer the next couple of questions pertaining to the Hodgkin-Huxley equations, you will need to edit the applied current, which is on line 19 of the code and is labeled as iapp.

> **QUESTION:** What is the effect of changing the applied current to 5? Explain why you think this happens.

> **QUESTION:** What is the effect of changing the applied current to 10? Explain why you think this happens.

Now execute the FitzHugh-Nagumo system. In this simulation, we also start with an applied current of 0. To answer the next couple of questions pertaining to the FitzHugh-Nagumo equations, you will need to edit the applied current, which is on line 8 of the code and is labeled as I.

> **QUESTION:** What is the effect of changing the applied current to 0.1?

> **QUESTION:** What is the effect of changing the applied current to 0.2?

QUESTION: What qualitative similarities do you see between the simulations of the Hodgkin-Huxley equations and the FitzHugh-Nagumo equations?

Module 6

Immune System

6.1 Biological Introduction

In our lifetime we are continually exposed to disease causing bacteria and viruses, as well as a wide variety of parasitic worms, fungi, and protists. Our immune system has evolved to ward off these foreign invaders. There are two types of immunity: innate immunity and acquired immunity. Our innate immunity allows for the recognition of a broad range of pathogens using a small set of receptors. The response is rapid. In this workshop we will discuss one of these responses, the inflammatory response. Acquired immunity allows for the recognition of specific pathogens using a wide variety of receptors. The response is slower than innate immunity. In this workshop you will explore two types of acquired immunity responses: the humoral response and cell mediated response. Prepare for your workshop by reading in your textbook (Campbell and Reece 8th edition, Chapter 43 and completing the Pre-Workshop Activities on the Blackboard site.

6.2   Humoral and Cell Mediated Immunity

Below is a schematic diagram comparing the humoral immune and cell mediated immune responses.
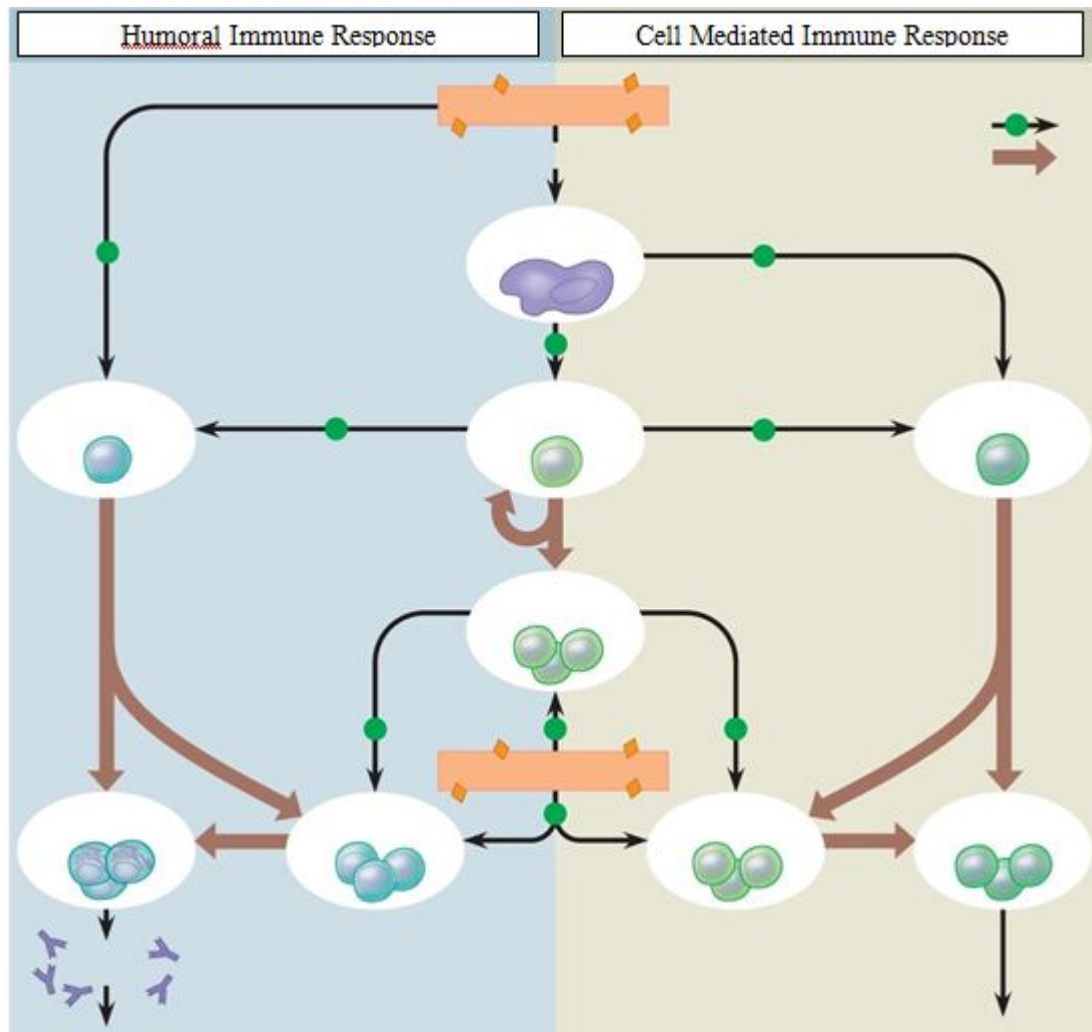
Label everything indicated by an oval or rectangular. As a group compare and contrast humoral and cell mediated immune responses.

6.3 Cytotoxic and Helped T cells

(a) Cytotoxic T cell

(b) Helper T cell
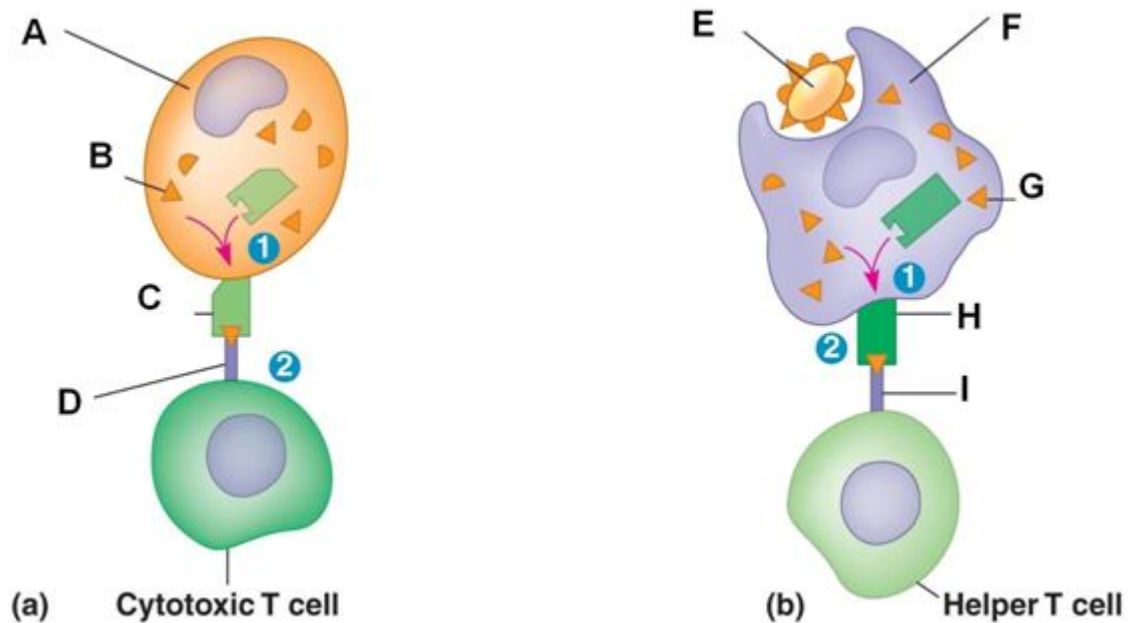
Label all letters in the figures above. Describe the processes indicated by 1 and 2 in Figures A and B.

6.4 Vaccines

QUESTION: What do vaccines need to contain in order to be effective? Why dont we have vaccines for HIV? Why do people need to get a new flu shot every year?

6.5   Life cycle of HIV
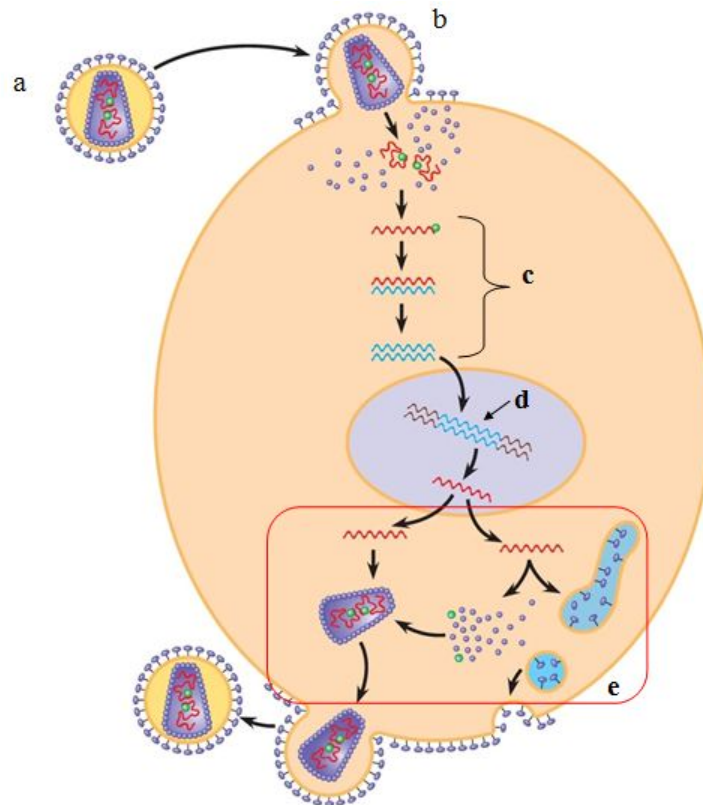
(a) Label all parts of the HIV virus in Figure a.

(b) Describe what is happening in b. Be a specific as possible.

(c) Describe the processes occurring in the three steps in c.

(d) What is the arrow in d pointing to (only the blue part).

(e) Describe the processes occurring in rectangle e.

QUESTION: To test for tuberculosis in AIDS patients why wouldnt you inject purified bacterial antigen and assess signs of immune system reaction several days later?

6.6 Mathematical Introduction

In this module, we will study an SIR epidemiological model. In this model, there are 3 classes of individuals: susceptible, infected, and recovered. The rate at which susceptible individuals become infected is β and the rate at which infected individuals recover is γ.
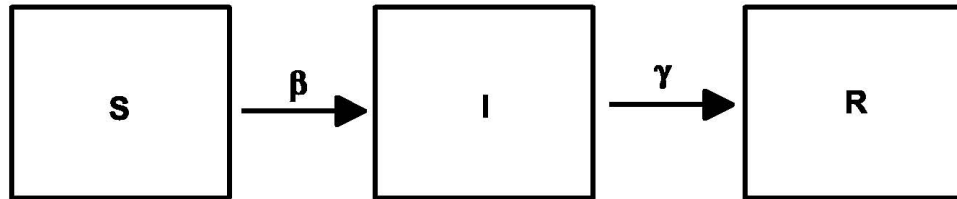
One important piece of information which can be determined from this model is the basic reproductive number, R_0, which tells you how many secondary infections which one primary infection could generate. If $R_0 < 1$ then the disease will die out. If $R_0 > 1$ then there will be an epidemic. In this model, R_0 depends on 3 factors: S_0, which is the number of individuals initially susceptible to the disease, β, which is the transmission rate, and γ, which is the recovery rate.

6.6.1 Model Simulations

Download and execute the file SIR.sce. In this simulation the parameters are $S_0 = 10,000$, $\beta = 0.000007$, and $\gamma = 0.03$, which can be found in lines 14, 11, and 12 of the code, respectively.

QUESTION: For this combination of parameters, does the disease die out or is there an epidemic?

QUESTION: Decrease the value of S_0 from 10,000 to 5,000 and execute the file. Then increase the value of S_0 to 50,000 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to try and increase or decrease S_0? What kind of practical control strategy could be used to achieve this goal?

Change the parameter values back to their original values.

QUESTION: Decrease the value of β from 0.000007 to 0.0000007 and execute the file. Then increase the value of β to 0.00007 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to increase or decrease β? What kind of practical control strategy could be used to achieve this goal?

Change the parameter values back to their original values.

QUESTION: Decrease the value of γ from 0.03 to 0.015 and execute the file. Then increase the value of γ to 0.045 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to increase or decrease γ? What kind of practical control strategy could be used to achieve this goal?

Module 7

Genetics

7.1 Biological Introduction

Patterns of inheritance are often much more complex than those encountered in the first genetics module. Mammals, birds, plants like garden peas, and insects have thousands of different genes in their genomes. Frequently scientists wish to study inheritance patterns for two or more genes simultaneously. When two different genes are involved, dihybrid crosses are made and the distribution of the alleles from parent to filial generations is traced. In some cases, when the genes have loci on different chromosomes, the alleles assort independently. From Mendels work came the Principle of Independent Assortment. However, all alleles are not distributed independently into gametes. If the gene loci are linkedthat is, located on the same chromosome, they move together most of the time. The phenomenon of linkage adds another dimension to the patterns of inheritance.

Most complex organisms have separate sex chromosomes as distinguished from the others which are called autosomes. In mammals the females have two full-sized X

sex chromosomes. Males, in contrast, have one X and one Y chromosome. The Y chromosome is not full sized, and lacks most of the loci on the X chromosome. It follows that, if a gene is located on the X chromosome, a female will get two alleles for that gene while the male gets only one. This creates some potential problems for males related to any gene that is sex-linked. We will study the inheritance of sex-linked genes that result in some diseases and disabilities that occur mainly in males.

Although we will not be covering the subject in this module, you should know that not all phenotypic characters and traits exhibit simple patterns of Mendelian inheritance. These characters result from complex interplays among many genes (epistasis) and their interactions with the environment. Human height and intelligence are among these complex polygenic characters. To prepare for the workshop read your text chapter, review your lecture notes and complete the pre-workshop activities on Blackboard.

7.2   Genetic Problem Solving

Use the genotypes from the following two tables for the questions below.

Garden Pea Plant Table

Genotypes	Phenotypes
PP or Pp	Purple flowers
pp	White flowers
YY or Yy	Yellow seeds
yy	Green Seeds
RR or Rr	smooth seed coat
rr	wrinked seed coat
TT or Tt	Tall plant
tt	Short plants

Human Table	
Genotypes	**Phenotypes**
EE or Ee	Free earlobes
ee	Attached earlobes
RR or Rr	Rh positive
yy	Green Seeds
RR or Rr	smooth seed coat
rr	Rh negative
FF or Ff	freckles
ff	uniform pigment distribution

1. Represent the parent cell and different gametes that come from that cell by the alleles they carry. (In some problems there may be more than one possibility. List all possibilities.)

   a. A dihybrid heterozygous tall pea plant with purple flowers

   b. A short pea plant that is heterozygous for seed coat

   c. A pea plant that produces yellow seeds with a smooth coat

   d. A human who is heterozygous for earlobes and freckles

   e. A human with Rh positive blood type and has attached earlobes

   f. A Rh- person with free earlobes

2. Represent the following crosses. Include all possible genotypes.

   a. Tall pea plant with purple flowers × a short plant with white flowers

b. A short pea plant with a smooth seed coat × a tall plant with a smooth seed coat

c. An Rh+ man with free earlobes (heterozygous) × an Rh-woman with attached earlobes

d. An unfreckled man with attached earlobes × a freckled woman with free earlobes

3. Determine the genotypic ratios for the crosses in #2 (when more than one cross was possible for a given part of the question, you may select to do one of the crosses) and express them with the genotypes written below the numbers.

4. Determine the phenotypic ratios for the crosses in #2. Indicate the phenotypes next to the numbers.

7.3   Genetic Concepts

1. Explain briefly Mendels Law of Independent assortment.

> Give an example of situations in which it applies and doesnt apply to inheritance patterns.

2. Explain the physical basis for linkage or non-linkage between two alleles.

> How could a linkage pattern between genes can be changed?
>
> What type of test cross might you conduct in order to tell if two genes are linked or non-linked? Set it up and show the expected outcomes.

3. Explain the difference between a sex-linked and autosomal gene.

> Why are sex-linked recessives genes are more often expressed in male than female mammals.
>
> In what situation can the recessive alleles be expressed in females?
>
> What type of test cross might you conduct to determine if a gene is sex-linked or not? Set up a specific cross and its outcomes in either case.

7.4 Genetics Problems

For each of the following problems, solve the problem and state whether the cross is a case of simple dominance, sex-linked trait, or linkage

1. In humans, tasters of a bitter substance (PTC) are TT or Tt, while non-tasters are tt. Normally pigmented people are either AA or Aa, while albinos are aa. A normally pigmented woman, who is a nontaster, has an albino taster father. Her albino taster husband has a mother who is a non-taster. Indicate all genotypes and phenotypes possible in their children. T/t and A/a genes occur on different chromosomes.

2. A couple has three girls and one boy. How does this compare with the expected ratio of boys to girls among four offspring? Are their chances of a boy greater now if they have a fifth child than when they had their first child? Explain why or why not.

3. A mating is made between two black, crested birds. The F1 contains 13 offspring in the following proportions: 7 black, crested; 3 red, crested; 2 black, plain; and 1 red, plain. What are the probable genotypes of the parents?

4. Red-green color blindness is a sex-linked recessive trait. A color-blind man marries a woman who is heterozygous for the color vision gene. What are the expected genotypic ratios of their sons? of their daughters? Give the phenotypic ratios.

5. A man with normal color vision marries a heterozygous woman. What are the expected genotypic ratios of their sons? Of their daughters? Give the phenotypic ratios.

6. In fruit flies, body color is normally gray, the expression of a dominant allele (b+), while black color is the expression of a recessive allele (b). Normal long wings result from an allele (vg+) and short vestigial wings are the expression of a recessive allele (vg). A male that is heterozygous for both genes is mated with a black, vestigial winged female. The cross produced 1000 offspring of which 470 had gray bodies and long wings and 480 had black bodies and vestigial wings. 24 had gray bodies and vestigial wings and 26 had black bodies and long wings. Determine if the two genes are linked or not by showing the predicted outcomes with and without linkage. What explains the gray-vestigial and black-long winged flies?

7.5   Linkage

1. Make a drawing of a cell with 2N = 4 with the following genes and loci identified. On a large pair of homologous chromosomes place 3 gene loci. Near one end of the chromosomes, place loci for gene A/a (heterozygous). Near the other end, place loci for gene B/b. Place allele B on the chromosome with allele a, and allele b with A. Between loci A/a and B/b, place loci C/c, but position it close to A/a and more distant from B/b. Make the cell heterozygous for C/c, with C linked to

A and c linked to a.

a. Are genes that are on the same chromosome necessarily linked? Is it possible that there is no linkage detected between two genes on the same chromosome, if they are far enough apart? How is this possible?

b. Explain the mechanism by which the linkage patterns would change, giving an example.

c. Between which pairs is the linkage pattern going to be changed most frequently? Least frequently? Explain why.

d. If the percentage of offspring in which the pattern is changed is 20% between A/a and C/c, predict the approximate percentages between A/a and B/b. Between B/b and C/c.

2. Use the following recombination frequencies to map four genes, A-D.

Genes	Recombination Frequency
A,B	8%
A,C	4%
C,B	4%
A,D	4%
B,D	11%

Consider that there is a fifth gene E that also is linked. If you know that the A-to-E recombination frequency is 4%, can you locate E on the map you constructed above?

As you have seen, a variety of factors affect the inheritance pattern of a trait. Another factor that has to be taken into account is the fitness of a given trait. Often times,

individuals with one genotype are more likely to produce offspring than individuals with another genotype. One example of this would be if the a allele was responsible for a disease in which only half the individuals survived to breed. In this case, individuals with the aa genotype would only be half as fit as individuals with the AA or Aa genotype.

Another example is recessive lethal traits. In recessive lethal traits, any zygote with an aa genotype fails to fully develop. As a result only AA and Aa individuals are represented in the population, and the fitness of the aa genotype is 0. The fitness of a given genotype can sometimes vary depending on the environmental conditions, with some genotypes being beneficial in certain situations and detrimental in others. Luckily, we can apply mathematical models to identify how the frequency of an allele will change in a population, depending on its fitness.

7.6 Mathematical Introductions

In this module you will be simulating a model in which there are two alleles, A & a, at one locus, where the allele A occurs with frequency p and the allele a occurs with frequency q. In this model, the frequencies of each of the alleles depends on the fitness of each genotype. The fitness of the AA genotype is represented by f_{AA}. The fitness of the Aa genotype is represented by f_{Aa} and the fitness of the aa genotype is represented by f_{aa}.

Download and execute the file allele_frequency.sce. Notice that the fitness of the each of genotypes mentioned above occurs in lines 14 - 16 of the code. In this case, the fitness of the AA genotype is $f_{AA} = 1.0$, the fitness of the Aa genotype is $f_{Aa} = 1.0$, and the fitness of the aa genotype is $f_{aa} = 0.5$.

QUESTION: Change the fitness of the aa genotype to $f_{aa} = 0$. In this case the aa genotype is lethal. What are the similarities and differences in this case compared to the original one? Why do you think that is?

QUESTION: Change the fitness of the Aa genotype to $f_{Aa} = 0.75$ and the fitness of the aa genotype back to $f_{aa} = 0.5$. What are the similarities and differences in this case compared to the original one? Why do you think that is?

QUESTION: Change the fitness of the AA genotype to $f_{AA} = 0.75$ and the fitness of the Aa genotype back to $f_{Aa} = 1.0$. This is the case for a person who has sickle cell. What are the similarities and differences in this case compared to the original one? Why do you think that is?

Module 8

Macroevolution vs. Microevolution

8.1 Biological Introduction

In this workshop, we will contrast **macroevolutionary** patterns and processes with **microevolutionary** ones. This will help you gain a better understanding of the similarities and differences between these two broad categories of ecological mechanisms, as well as help you expand your understanding of evolutionary terms and concepts. We will also explore how small genetic changes can result in large phenotypic differences, ultimately resulting in large scale evolutionary change. Finally, we will explore a mathematical model that demonstrates one way that these small genetic changes can occur at the DNA sequence level.

Macroevolution is the category of evolutionary processes and patterns that occur at or above the level of species. Some examples of these include species formation (**speciation**), the formation of novel evolutionary traits (e.g. the evolution of vertebrate jaws from precursor characteristics in jawless ancestors), and patterns of rapid evolutionary diversification (**adaptive radiation**).

Microevolution is the category of evolutionary processes that occur below the level of species acting on populations and groups of populations. Specifically, microevolution is both (1) change the genetic constitution of populations, and (2) the processes that produce such changes (e.g., mutation, migration, genetic drift, non-random mating, natural selection).

QUESTION: Based on these definitions, as a group which of the following statements describe microevolutionary processes and which describe macroevolutionary processes.

1. changes in allele frequencies within a population from one generation to the next

2. evolutionary diversification of flowering plants in the late Cretaceous

3. differential survivorship by phenotypes within a population

4. evolutionary transition from theropod dinosaurs to birds

5. decrease in the allele that causes sickle cell anemia in parts of the world where malaria has been eradicated

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8.2   Modes of Evolutionary Change

8.2.1   Phyletic Gradualism vs. Punctuated Equilibrium

While Darwin's theory of evolution by natural selection is extremely well supported, various modification to this theory have resulted over the years. Some of these have been more controversial than others. Here are two such examples. You be the judge. **Phyletic gradualism** is the idea that evolution is a consequence of the culmination

over many generations of small differences in reproductive success among individuals within populations. This was the concept that Darwin originally put forth in his book On the Origin of Species. Darwin argued that evolutionary forces (especially natural selection, including sexual selection), operating generation after generation on individual variation within populations would, over the immensity of geological time, bring about ancestor-to-descendent evolutionary change. In other words, "descent with modification." While Darwin argued that phyletic gradualism was sufficient to result in macroevolutionary events, many disagreed with him and argued that another process must be at work.

> **QUESTION:** Can the evolution of structures as complex as the photoreceptors of arthropods, cephalopod molluscs, and vertebrates, for example, be properly attributed to the cumulative effects of microevolutionary processes operating over the long term? Think of some other examples of extrememly complex characteristics that are unlikely to have arisen from very gradual genetic changes within populations.

Punctuated equilibrium is the idea that long periods of evolutionary **stasis**–during which a population underwent little or no evolutionary change–were **"punctuated"** by relatively short spans during which a smaller subset of the population underwent relatively rapid evolutionary change. This idea was first proposed by Niles Eldredge and Stephen Jay Gould when they noted that while the fossil record did contain records of what appeared to be "smooth transitions" from one ancestral form to new species, there were also many examples of apparently rapid changes from one form to another, in which transitional fossil forms were lacking. This is an extension of observations first presented by Darwin in Origin of Species.

However, this idea has been seen as highly controversial because of a perceived simi-

larity to the largely debunked idea of **saltational evolution** which suggests that a new species may arise in a single generation via a single **macromutation**. Rather, when Gould and Eldredge referred to "short spans ... of rapid evolutionary change" they were talking on the order of several thousand to millions of years. This time frame is a small blip on a geological time scale. Rather than being a ground breaking refute of Darwin's idea of phyletic gradualism, punctuated equilibrium actually serves as a logical expansion of this theory.

QUESTION: Can you think of some complex characteristics (in any living organisms) that might be good "candidates" for evolution via punctuated equilibrium? Discuss some of these as a group. Propose how they could arise by either phyletic gradualism or punctuated equilibrium.

8.3   Forces of Evolutionary Change

8.3.1   Heterochrony

While humans (*Homo sapiens*) and chimpanzees (*Pan spp.*) share many common traits, and are each other's closest living relatives, they differ in many obvious and important respects. For example, chimps are not fully bipedal, have a smaller cranial capacity than humans, have forward-projecting jaws, heavy brow ridges, and a sagittal crest on the skull that serves as a surface for the attachment of powerful jaw muscles. Despite the close genetic relationship, chimp-human hybrids are unknown, and members of the two species do not normally attempt to breed with one another. Clearly, in the evolutionary divergence between the lineage that led to chimps and the lineage that led to humans, the accumulation of small genetic differences has had

profound phenotypic consequences.

Heterochrony-an evolutionary change in the timing of developmental events-provides a plausible explanation for how this might have happened. Even small genetic changes in the developmental program, when expressed early in development, can have profound and far-reaching effects on the resultant adult phenotype.

Imagine an evolutionary change in the timing of developmental events such that, relative to the development of an ancestral species,

1. development of the reproductive system is accelerated (**PAEDOGENESIS**)

2. development of non-reproductive (**somatic**) tissues is retarded (**NEOTENY**)

The result could be an organism that is a "mosaic" of adult characteristics (e.g., reproductive competence) and juvenile characteristics. Such an organism is said to be paedomorphic (from the Greek paed ("child") and morph ("form")), and its juvenile from generated via one of the two forms of heterochrony described above. More specifically, paedomorphosis describes the appearance of juvenile (or larval)features of an ancestor in the adult of a descendant. The phenomenon of paedomorphosis appears to have been important in the evolution of our own species from the ape-like ancestor we shared with chimpanzees. As an example, depicted are fetal, juvenile and adult skulls of human and chimp.
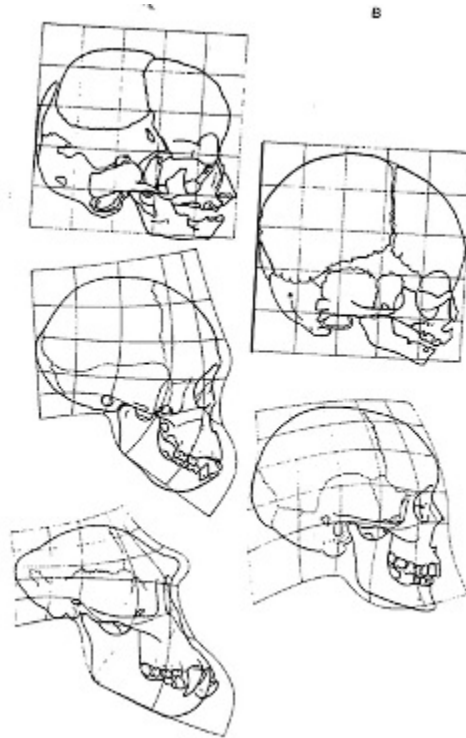
Notice that the fetal skulls of the chimp and human are quite similar in shape, much more so than in the adult. The juvenile skull of the chimp, though already showing more of a protruding jaw than the human skull, is almost more similar to that of the human than it is to that of the adult ape.

QUESTION: In what ways do the fetal skulls of the two species differ? In what ways do the adult skulls differ? Which species, is more "child shaped" as an adult? How do we know that human evolution has involved the suppression of terminal developmental stages rather than the addition of developmental stages in the chimp lineage?

8.3.2 Allometric and Isometric Growth

Differential timing of developmental events may occur within a species, as well as across species over evolutionary time. **Ontogenetic allometry** (analysis of single populations) are estimates obtained for single populations across age groups, with changes reflecting growth of individuals. **Evolutionary allometry** (comparative analysis of populations/species) is a comparison of allometric patterns among different population or species. This relates directly to heterochrony (evolutionary changes in ontogeny).

Ontogenetic Allometry

As an organism grows larger during ontogeny, or as an evolving lineage of organisms increases in size over evolutionary time, the various parts of the organisms also increase in size. Bigger organisms have bigger parts. But not all of the parts necessarily grow at the same rate. Such differential growth of different parts is termed **allometry**, and it results in shape changes as the animal grows. When all parts of an organism grow at the same rate, the organism is said to exhibit **isometric growth**, and this results in a change in size without a change in shape. Although most organisms exhibit allometric growth, some, such as certain salamanders are essentially isometric in their growth.

Note that the various body proportions remain more or less constant as the animal increases in size.

Growth in our own species is decidedly allometric, most obviously with respect to the growth of the head relative to the body. At birth, the head is relatively enormous, and comprises nearly a third of the length of the infant. As we grow larger, our body grows more rapidly than the head such that the body "catches up" eventually to produce the proportions that we recognize as normal in the adult. Maturation in humans thus involves both increase in size and a change in shape.

Years   0.42   0.75   2.75   6.75   12.75   25.75
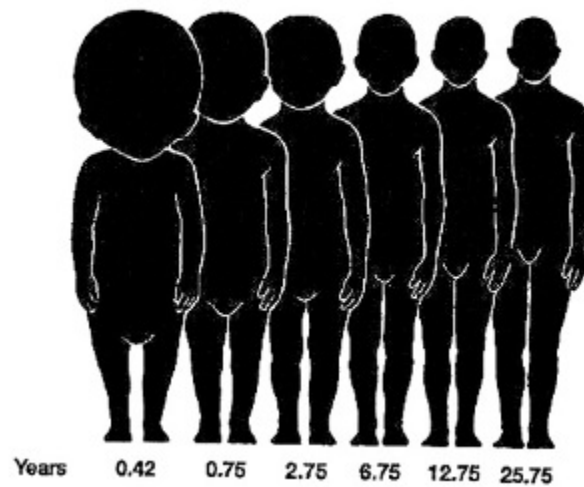
> **QUESTION:** In humans (and in vertebrates in general), the head is large at birth relative to the rest of the body Why is this so?

Evolutionary Allometry

A lineage of organisms can also exhibit allometric growth over evolutionary time, as exemplified by the brontotheres, an extinct group of large mammals.

The brontothere lineage shows a clear trend of increasing size, as seen in the comparison of these four species. From a small, hornless ancestral species, the trend has been for an increase in overall body size, but an even more rapid increase in horn size. Over evolutionary time, the horns have increased in size more rapidly than the head or body, producing a change in shape as well as a change in size.

QUESTION: What might be the adaptive significance of horns in brontotheres? If horns in brontotheres are restricted to males only, what would this suggest concerning the selective agents involved in their evolution?

Regardless of what macorevolutionary processes are at play, all evolution begins below the level of species. Evolution occurs at the level of populations, with selection acting to promote some individuals to produce more offspring then others. Several forces result in evolution at the level of population. These include gene flow, genetic drift, and natural selection. If a population is not experiencing any evolutionary forces it is said to be in Hardy-Weinberg equilibrium. For a population to be in Hardy-Weinberg equilibrium it must meet the following five conditions: no mutation, no selection, no gene flow, random mating, and large population size. While these conditions are often violated in nature, it is not often possible to simply look at a population and tell if it is in hardy Weinberg equilibrium. Luckily we can apply mathematical methods, including models, to populations to see if it is in equilibrium and what will happen if it deviates from equilibrium.

8.4 Mathematical Introduction

8.4.1 Difference Equations

Suppose we want to describe a quantity which changes at discrete time steps. Usually the value of that quantity at one time step depends on the value of the quantity at one or more of the previous time steps. A difference equation is an equation which is used to describe such a quantity based; it relates the quantity at a certain time with the quantity at a previous time. Since a difference equation uses the value of the quantity at a previous time to determine the value of the quantity at a later time, it is necessary to have some information to start with. Usually, a difference equation is accompanied by an initial condition (starting value), which specifies the value of the

quantity at time $t = 0$.

If we use P to represent the number of individuals of a population which changes at discrete time steps, then P_t represents the number of individuals at time t. Likewise, P_{t-1} represents the number of individuals at the previous time, $t - 1$ and P_{t+1} represents the number of individuals in the population at the next time step, $t + 1$. Using this notation, the initial condition (the number of individuals at time $t = 0$ is represented by P_0.

> **QUESTION:** Compute $P_1 \ldots P_5$ (the number of individuals in generations 1 - 5), given that the population grows according to the difference equation $P_{t+1} = 3P_t - 4$ with initial condition $P_0 = 5$.

One important piece of information about a difference equation is its equilibrium value; i.e., the value at which the quantity remains unchanged as time passes. In order for the value to remain the same for each time step, it must satisfy the equation $P_{t+1} = P_t$.

> **QUESTION:** Compute the equilibrium value of the difference equation in the previous problem.

8.4.2 Hardy-Weinberg Law

Suppose we have one locus with two alleles, A_1, which occurs in the population with frequency p, and A_2, which occurs in the population with frequency q. Note that if A_1 and A_2 are the only two alleles, then $p + q = 1$. If mating is by random union of gametes, then the frequency with which the genotype A_1A_1 occurs in the population

is $p \times p = p^2$. Similarly, the frequency with which the genotype $A_2 A_2$ occurs in the population is $q \times q = q^2$. The frequency of $A_1 A_2$ is $p \times q = pq$ and the frequency of $A_2 A_1$ is $q \times p = qp$. But these are the same genotype, so the frequency of the $A_1 A_2$ genotype is $pq + qp = 2pq$. Note that every individual must be one of either the $A_1 A_1$, $A_1 A_2$ or $A_2 A_2$ genotypes, so $p^2 + 2pq + q^2 = 1$.

> **QUESTION:** Suppose there are 2,000 individuals (so 4,000 alleles in the gene pool at locus A) in a population, of which 1 in 400 individuals possesses a recessive trait. How many heterozygotic and how many homozygotic dominant individuals are in the population?

A population in which the Hardy-Weinberg frequencies are not changing with time is said to be in Hardy-Weinberg equilibrium.

8.4.3   Model of Natural Selection

The following model describes how genes spread because of natural selection. We assume that all organisms reproduce only once and then die, so all generations are nonoverlapping. We also assume that each time step corresponds to one generation and zygotes are made random unions of gametes. We let p represent the fraction of the population with the A_1 allele and q represent the fraction of the population with the A_2 allele (so the frequency of the $A_1 A_1$ genotype is p^2, the frequency of the $A_1 A_2$ genotype is $2pq$, and the frequency of the $A_2 A_2$ genotype is q^2. Let ℓ_{ij} represent the probability that genotype $A_i A_j$ survives to adulthood. Let m_{ij} represent half of the number of gametes than an individual of genotype $A_i A_j$ makes that are actually incorporated into zygotes that start the next generation. Then the fraction of the

gene pool with the A_1 allele in the $t + 1$ generation is given by

$$p_{t+1} = \frac{m_{11}\ell_{11}p_t + m_{12}\ell_{12}q_t}{m_{11}\ell_{11}p_t^2 + m_{12}\ell_{12}2p_tq_t + m_{22}\ell_{22}q_t^2}p_t$$

Let's see where this equation came from. To get the fraction of the gene pool with the A_1 allele at time $t + 1$, we need to know two things: the total number A_1 alleles at time $t + 1$ and the total number of alleles at time $t + 1$. Once we know these two, we will have

$$p_{t+1} = \frac{\text{total number of } A_1 \text{ alleles at time } t + 1}{\text{total number of alleles at time } t + 1}$$

To get the total number of A_1 alleles at time $t + 1$, we need to take all the gametes made from the parents of genotype A_1A_1 plus half of the gametes from the parents of genotype A_1A_2. Let N represent the total population size. Then the start of the $t + 1$ generation, when all of the organisms are zygotes, there are $p_t^2N_t$ zygotes from the A_1A_1 allele from the end of the time t generation. Hence, there are $\ell_{11}p_t^2N_t$ adults at the end of the generation from the A_1A_1 allele. Therefore, there are $2m_{11}\ell_{11}p_t^2N_t$ gametes from the A_1A_1 allele. Similarly, there are $2p_tq_tN_t$ zygotes at the beginning of the $t+1$ generation from the A_1A_2 allele from the time t generation, of which $\ell_{12}2p_tq_tN_t$ survive to become adults at the end of the generation, producing $2m_{12}\ell_{12}2p_tq_tN_t$ gametes.

$$\text{total number of } A_1 \text{ alleles at time } t + 1 = 2m_{11}\ell_{11}p_t^2N_t + \left(\frac{1}{2}\right)2m_{12}\ell_{12}2p_tq_tN_t$$

For the total number of alleles at time $t + 1$, we need to add the total number of A_2 alleles to the total number of A_1 alleles (which we just figured out). For the total number of A_2 alleles, take all the gametes made from the parents of genotype

A_2A_2 plus half of the gametes from the parents of genotype A_1A_2. Luckily, we just computed half of the gametes from the genotype A_1A_2, so all we need is the number of gametes from the A_2A_2 genotype. But, as we stated above, we only take half of the gametes made from the parents of genotype A_1A_2, so the number of alleles from the A_1A_2 genotype is $\left(\frac{1}{2}\right)2m_{12}\ell_{12}2p_tq_tN_t$. Thus, as before, at the start of the $t+1$ generation, there are $q_t^2N_t$ zygotes from the t generation before. Of these, $\ell_{22}q_tN_t$ survive to adulthood, and $2m_{22}\ell_{22}q_t^2N_t$ gametes from the A_2A_2 allele. Hence, we have

total number of alleles at time $t+1 = 2m_{11}\ell_{11}p_t^2N_t + 2m_{12}\ell_{12}2p_tq_tN_t + 2m_{22}\ell_{22}q_t^2N_t$

Therefore,

$$p_{t+1} = \frac{2m_{11}\ell_{11}p_t^2N_t + \left(\frac{1}{2}\right)2m_{12}\ell_{12}2p_tq_tN_t}{2m_{11}\ell_{11}p_t^2N_t + 2m_{12}\ell_{12}2p_tq_tN_t + 2m_{22}\ell_{22}q_t^2N_t}$$
$$= \frac{m_{11}\ell_{11}p_t^2 + \left(\frac{1}{2}\right)m_{12}\ell_{12}2p_tq_t}{m_{11}\ell_{11}p_t^2 + m_{12}\ell_{12}2p_tq_t + m_{22}\ell_{22}q_t^2}$$
$$= \frac{m_{11}\ell_{11}p_t + m_{12}\ell_{12}q_t}{m_{11}\ell_{11}p_t^2 + m_{12}\ell_{12}2p_tq_t + m_{22}\ell_{22}q_t^2}p_t$$

It is a common practice in evolutionary biology models to combine survival and reproduction into a single quantity. In this case, that means we define $w_{ij} = m_{ij}\ell_{ij}$. We call w_{ij} selective value or "fitness" of an individual. Making this combination here gives us the final form of our equation, which is

$$p_{t+1} = \frac{w_{11}p_t + w_{12}q_t}{w_{11}p_t^2 + w_{12}2p_tq_t + w_{22}q_t^2}p_t$$

QUESTION: Write an equation analogous to the one above but for q_{t+1}, the frequency of the A_2 allele at time $t+1$.

QUESTION: Using the equations for p_{t+1} (given above) and q_{t+1} (which you derived in the previous problem), determine the equilibria of the system. *Hint:* It will be easier to utilize the fact that $p + q = 1$ to rewrite each equation as an equation with one variable instead of two. There will be three equilibria and you will need the quadratic formula for two of them.

QUESTION: What conditions are necessary for the third equilibrium to be biologically relevant? What does this mean for the chances of an allele to survive?

8.5 Notes

This module was adapted from *Primer of Theoretical Ecology* by Joan Roughgarden, 1998.

Module 9

Alternation of Generations

9.1 Biological Introduction

For students new to the study of Kingdom Plantae, the life cycle of plants–in which a diploid generation alternates with a haploid generation–can be difficult to understand. The purpose of this workshop is to allow the student to better relate to the phenomenon of Alternation of Generations by (1) examining the details of plant gametophyte and sporophyte structure and function, and (2) creating an animal analog to this type of life history.

In today's workshop, your goals will be to

1. Understand the alternation of haploid and diploid individuals in the plant life cycle.

2. Understand the terminology used to describe parts of the life cycle, and recognize what each life cycle stage looks like in the major plant taxa.

3. Acquire a more "personal" understanding of how the alternation of generations works by designing an imaginary animal that goes through this type of life cycle.

9.2 Overview

The plant life cycle, unlike that of animals, consists of alternating generations of individual organisms that are haploid (the **gametophyte**) and diploid (the **sporophyte**). Specialized diploid cells in the sporophyte undergo meiosis to produce haploid spores (hence the name "sporophyte"). Each spore grows mitotically to become the new gametophyte, which then produces gametes (hence, the name "gametophyte") which fuse to form a **zygote**. This grows into the sporophyte, and the cycle continues, as shown in the diagram below.
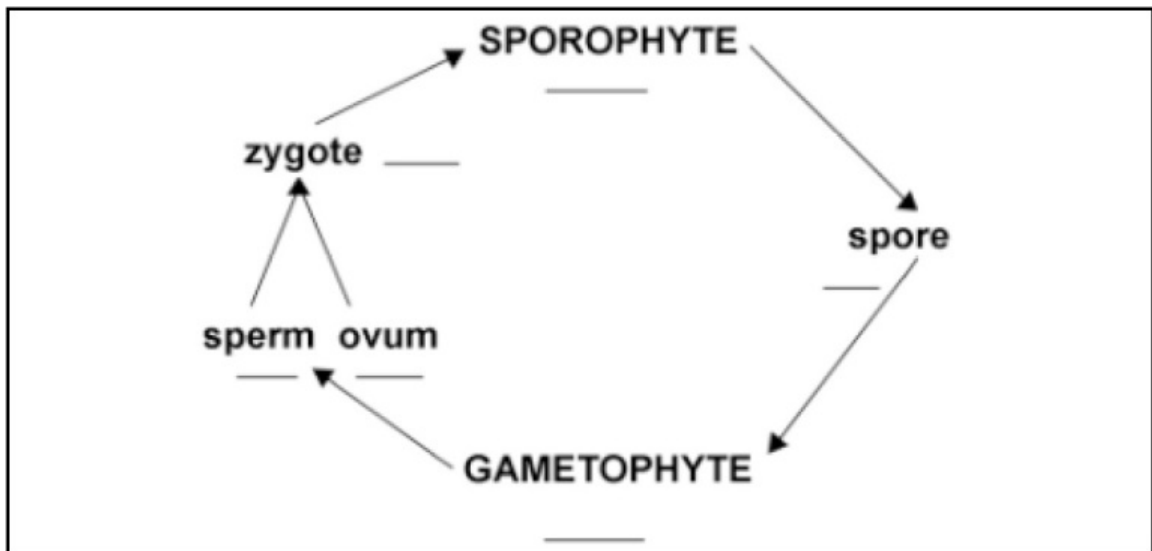
In the diagram

1. Indicate the ploidy (n for haploid, 2n for diploid) of each life cycle stage or struc-

ture.

2. Over each of the five arrows, indicate which of the following processes is taking place: mitosis, meiosis, or fertilization.

In the sporophyte, the structure within which diploid cells undergo meiosis to become haploid spores is the **sporangia**.

QUESTION: Where is this structure found in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

If the spore-producing structures you just named are found on a leaf specialized to bear those structures, that leaf is called a **sporophyll**.

QUESTION: What does this structure look like in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

A spore that develops into a female gametophyte is called a **megaspore**.

QUESTION: Where is this structure found in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

A spore that develops into a male gametophyte is called a **microspore**.

QUESTION: Where is this structure found in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

A sporophyll that bears megaspores is called a **megasporophyll**.

QUESTION: What does this structure look like in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

A sporophyll that bears microspores is called a **microsporophyll**.

QUESTION: What does this structure look like in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

QUESTION: Describe the appearance of the mature male and female gametophyte in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

In the female gametophyte, the structure within which haploid cells develop into ova is called the **archegonium**.

QUESTION: Describe what this structure looks like in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

In the male gametophyte, the structure within which haploid cells develop is called the **antheridium**.

QUESTION: Describe what this structure looks like in:

a. a moss (or other bryophyte)

b. a fern (or other seedless tracheophyte)

c. a pine (or other gymnosperm)

d. a flowering plant (any of the angiosperms)

QUESTION: What do the terms monoecious and dioecious mean?

9.3   An Animal Analogy

Don't get your hopes up too high. We are merely going to mimic the life cycle stages as one typically sees them in a SEEDLESS TRACHEOPHYTE. The sporophyte produces spores in sporangia on sporophylls, then releases the spores to the environment. A spore germinates into a free-living gametophyte that produces gametes in gametangia (analogous to testes and ovaries). Fertilization occurs when sperm travel from the male gametophyte to the female, enter her gametangium and fertilize her ovum to produce a zygote. The zygote grows into the new sporophyte, obliterating the female gametophyte. The male withers and dies shortly after the sperm are released. Keep this cycle in mind when you design your animal model.

1. As a group, create an animal (it can be an existing animal, or something similar to a species with which you are already familiar) that is diploid. This animal will be your sporophyte generation, and you should decide in advance whether it will be dioecious or monoecious. Does this animal have gonads (ovaries or testes)? Explain. Briefly describe your animal sporophyte.

2. Next, choose an area on the animal where specialized diploid cells will undergo meiosis to produce spores. Remember that this should be an external area, since the spores will be released to the environment. Also remember to create the areas on your animal as appropriate to dioecy or monoecy, whichever you have chosen your animal to be.

3. Release the spores! What happens to the spores that land in an area appropriate to germination? Describe the resulting organism (the gametophyte generation of this species), and again note whether it is monoecious or dioecious, since this will

be important in the next few steps. Be sure to note this animal's ploidy, and whether it has gonads (testes and/or ovaries).

4. If your gametophyte is bisexual, describe how and in what anatomical locations it will produce sperm and ova. How will sperm reach the ova? Describe the process.

5. If your gametophyte animal is male, describe how and in what anatomical location it will produce sperm. How will these gametes reach the female gametophyte's ova? Describe the process.

6. If your gametophyte animal is female, describe how it will produce ova, and where. Will these gametes be released into the environment, or will they remain inside the female? If they remain inside the female, describe where they will be found.

7. Describe fertilization between the male and female gametophytes of your species (if the species is monoecious) or how fertilization takes place in your individual bi-sexual gametophyte (if the species is dioecious). What is the result of fertilization? Where would you find it if you were to dissect your gametophyte animal?

8. What will now happen to the fertilized ovum (zygote)? Describe how it grows, and where. What happens to the gametophytes once fertilization is complete?

9. Describe the mature result of growth of the zygote. What will be the next step in this life cycle?

9.4   Mathematical Introduction

In this module, we will consider a metapopulation model with five species sharing a patchy environment. Each habitat patch (site) in this environment can be occupied

by only one species at a time. All five species compete not only for sites to occupy, but also for other natural resources. We will assume that there is a trade-off between a species' dispersal and colonization abilities and their competitive abilities; that is, species that are better at dispersing and colonizing are worse competitors and vice-versa. What we will be investigating is how habitat destruction affects the fraction of sites occupied by each species.

We will start with Colonizer #1/ Competitor #5 occupying 8.2% of the sites, Colonizer #2/ Competitor #4 occupying 10.24% of the sites, Colonizer #3/ Competitor #3 occupying 12.8% of the sites, Colonizer #4/ Competitor #2 occupying 16% of the sites, and Colonizer #5/ Competitor #1 occupying 20% of the sites (the rest of the sites are unoccupied).

QUESTION: Given that we start with dispersal/colonization abilities (and hence competition abilities) suitable for all five species to coexist and no habitat destruction, state the order in which you think the species will occupy the largest fraction of sites down to the smallest fraction of sites.

Download and execute the file dispersal.sce.

QUESTION: Were your predictions correct?

On line 20 of the Scilab code, you will see a quantity q. This quantity represents habitat destruction. Change 0 to 0.3 for all five species, **but do not execute the file yet**. (**Note:** If you want the new graph to open in a new graphics window so that you can keep the original graphics window intact, change line 23 of the code from $scf(1)$; to $scf(2)$;.)

> **QUESTION:** What affect do you think increasing the habitat destruction will have on the fraction of sites occupied by each species?

Now execute the file with the habitat destruction of 0.3 for all five species.

> **QUESTION:** Was your prediction correct? Why do you think the results of the simulation were the way they were?

Now change the habitat destruction from 0.3 to 0.63 for all five species, **but do not execute the fil** You can change the graphics window from 2 to 3 if you think it will help to keep the previous window open for comparison.

> **QUESTION:** What do you think will happen in this case?

Now execute the file with the habitat destruction of 0.63 for all five species.

> **QUESTION:** Was your prediction correct?

Now change the habitat destruction from 0.63 to 0.73 for all five species, **but do not execute the f**

> **QUESTION:** What affect do you think this will have?

Now execute the file with the habitat destruction of 0.73 for all five species.

> **QUESTION:** Was your prediction correct?

Now change the habitat destruction from 0.73 to 0.93 for all five species. This will cause all five species to go extinct. Also change the final time in line 15 of the code from 2000 to 500, **but do not execute the file yet**.

QUESTION: In what order do you expect the species to go extinct in? Why?

Now execute the file with the habitat destruction of 0.93 for all five species and with the ending time of 200.

QUESTION: Was your prediction correct? Why do you think the results of the simulation were the way they were?

In all of these simulations, Colonizer #1/ Competitor #5 started off with the smallest fraction of sites occupied. Change the habitat destruction back to 0 for all five species and change the final time back to 2000. On line 21 of the code, you will see the quantity $p0$. This represents the fraction of sites each species initially occupies, starting with Colonizer #1/ Competitor #5. Change the first one (for Colonizer #1/ Competitor #5) from .082 (8.2%) to .382 (38.2%), **but do not execute the file yet**.

QUESTION: What affect do you think this change will have on the results?

Now execute the file.

QUESTION: Was your prediction correct?

QUESTION: If you were to repeat all of the previous simulations, how do you think the outcomes of each would differ? Why?

Now repeat each of the previous simulations but with Colonizer #1/ Competitor #5 now occupying 38.2% of the sites initially.

QUESTION: Were your predictions correct?

9.5 Notes

This module was adapted from *Primer of Theoretical Ecology* by Joan Roughgarden, 1998.

Module 10

Speciation

10.1   Introduction

Speciation is the process by which new species arise. In order for speciation to occur, two populations must become reproductively isolated, and as a result incapable of producing fertile offspring. Reproductive isolation may evolve due to changes in genotype and phenotype frequencies in a population as a result of:

1. Mutation

2. Gene flow

3. Genetic Drift

4. Non-random mating

5. Natural selection

Each of these processes can result in reproductive isolation, but more commonly several processes combine to produce this isolation.

> **QUESTION:** Discuss with your peers how gene flow and genetic drift might act to enhance or eliminate the effects of mutation?

There are four recognized geographic modes of speciation: allopatric, peripatric, parapatric, and sympatric. Allopatric speciation results when a population is separated into two geographically isolated populations, followed by genotypic or phenotypic divergence. This can occur following mountain formation, island formation, or habitat fragmentation, among other things. One example of allopatric speciation is the formation of the Isthmus of Panama which has resulted in the formation of several reproductively isolated species.

Peripatric speciation results when a small portion of a population becomes geographically isolated from the larger population. As a result, this speciation is a special case of allopatric speciation. The isolated population then experiences genetic drift, or different selective pressures than the larger population, resulting in reproductive isolation. This is typically the result of a founder effect. One example is the Pacific robin, Petroica multicolor.

Parapatric speciation occurs in the absence of a geographic barrier to gene flow. In this case organisms are more likely to mate with those geographically close to them, producing a gradient of genetic variation. This may result when the environment variers greatly throughout the species range. This may occur along a mountain where some organisms are better capable of inhabiting areas with reduced oxygen at higher elevations. The grass Anthoxanthum appears to be undergoing parapatric speciation due to varying concentrations heavy metals in the soil surrounding mines.

Sympatric speciation occurs in the absence of any geographically isolating barriers to gene flow. As a result, speciation occurs in a completely interbreeding population. This type of speciation can result from sexual selection, niche exploitation, or ploidy shifts. Sexual selection is believed to have resulted in the formation of several species of African cichlids. Over time cichlids developed a preference for mating with similarly colored fish, which eventually led to the formation of separate species. Niche exploitation is indicated in the speciation of the apple and hawthorn flies. After the introduction of apples to the US, hawthorn flies began colonizing both types of trees which fruit at different times. Over time this led to the formation of separate species. Finally, ploidy shifts, duplications of partial or entire genomes, can result in reproductive isolation. As such, this type of speciation is typically spontaneous. This is hypothesized to have occurred several times in the evolutionary history of plants.

> **QUESTION:** Discuss with your peers a hypothetical example of each type of geo-geographic mode of speciation?

The reproductive isolation associated with speciation can take two forms: prezygotic (prevents the formation of viable zygotes) or postzygotic (a zygote forms but cannot pass on its genes).

Types of prezygotic isolation

1. Environmental/spatial isolation occurs when two species either never come into contact, or breed in different habitats within the same environment. An example of this is the red-legged frog which occurs in the same habitat as the bullfrog, but breeds in different bodies of water.

2. Temporal isolation occurs when two species share a common habitat but have different breeding seasons. A good example of this is the hawthorn and apple flies which were previously mentioned.

3. Behavioral isolation results when species develop courtship rituals or calls that only attract members of the same species. Two similar species with different calls are the wood and leopard frogs.

4. Mechanical isolation occurs when two species are physically incapable of inter-breeding due to differences due to morphological incompatibility. Bush babies are divided into several species due to unique differences in their genitalia which prevent interspecies breeding.

5. Gametic isolation results when the sperm and ova of two species cannot combine to form a zygote. This is common in aquatic environments where sperm and ova are released into the environment and then fuse.

Types of posyzygotic isolation

1. Hybrid inviability results when a zygote forms but is incapable of developing to maturity. This type of isolation occurs between water buffalo and cattle as well as between roof rats and Norway rats.

2. Hybrid sterility occurs when a mating produces a zygote which develops to maturity but the resulting offspring is incapable of producing offspring. Examples this include mules (horse-donkey), leopons (lion-leopard), and goat-sheep hybrids.

3. Hybrid breakdown occurs when hybrids are viable but have a reduced fitness compared with either species. This reduced fitness continues to reduce over successive

generations. This has been identified in pocket gophers, and is also common in plant hybrids developed by horticulturists.

QUESTION: As a a group identify one additional example of prezygotic and postzygotic isolation and identify what category each fits into?

10.2   Example

As you can see, many factors are involved in the process of speciation. Sometimes these factors work together to promote speciation, other times they work against each other. Mathematical modeling can be used to identify the processes involved in speciation in nature. One example of this is the rough periwinkle, Littorina saxatilis. It was hypothesized that this Swedish snail underwent nonallopatric speciation. In order to test this, researchers developed a mathematical model that took into account ecological and spatial data, and incorporated experimental data on mate selection preferences. Using this model, they were able to identify naturally occurring parapatric speciation. They were also able to identify the necessary conditions for this speciation to occur. Finally, researchers found that ecotype formation which was believed to promote speciation, can actually inhibit speciation in some cases. As such, they identified that a complex system of factors and interactions were involved. Below we will explore the model they developed, and how changing parameters of this model affects the speciation process.

10.2.1 Mathematical Background

A probability distribution tells you the probability of the value of a random variable being within a certain range. One of the most common probability distributions is the normal or Gaussian distribution. The normal distribution is bell-shaped and is used to describe data that clusters around a mean. A few examples of normal distributions are given in Figure 10.1.
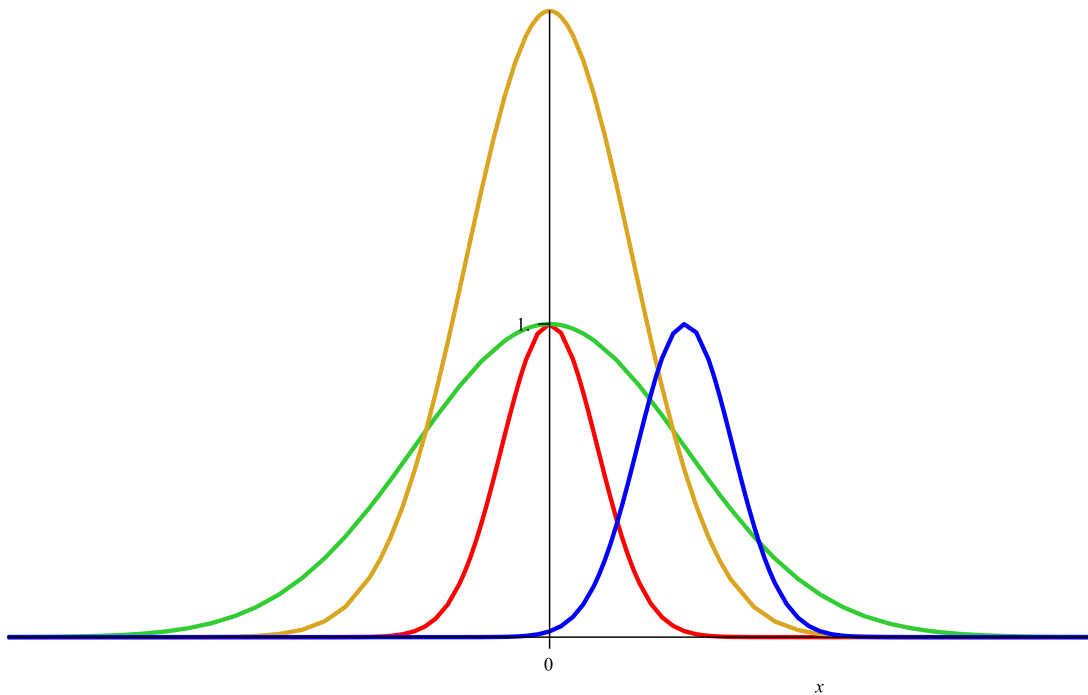

Figure 10.1: A few examples of normal distributions

The probability density function for the random variable x with mean μ and variance σ^2 is given by

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

> **QUESTION:** Write a Scilab program and graph (all on the same plot) the normal
> distribution for:
>
> (a) $\mu = 0$, $\sigma^2 = \frac{1}{2}$,
>
> (b) $\mu = 1$, $\sigma^2 = 4$, and
>
> (c) $\mu = -2$, $\sigma^2 = \frac{1}{8}$ for $-8 \leq x \leq 8$.
>
> Use a different color for each graph and be sure to put a title and legend on the graph.
> Discuss with your peers how μ and σ^2 effect the graph of the normal distribution.

10.2.2 Littorina saxatilis

Littorina saxatilis form ecotypes that are adapted to cliff and bolder habitats interspersed along the coast of the Swedish North Sea. There are three habitats which Littorina saxatilis inhabit:

- Exposed cliffs where wave action is a major cause of mortality (exposed)

- Boulder shores where predatory crabs exist in large quantities (sheltered)

- Intermediate habitat

The exposed phenotype is small, thin-shelled snails with large apertures and feet providing strong adhesion, while the sheltered phenotype is large, thick-shelled snails with small apertures. Littorina saxatilis who ecotype is locally adapted to their optimal habitat survive three times better.

Let x be a trait that determines a certain ecological phenotype which influences mating behavior. Let f be a trait of females for a certain ecological phenotype

preferred by males. Let c be a trait that determines the strength and direction of mating preference (mating discrimination). Then the fitness, w of an individual with ecological phenotype x is given by

$$w = e^{-\frac{(x-\theta)^2}{2\sigma_s^2}}$$

where θ is the optimum phenotype and σ_s controls the strength of the mating preference.

The relative probability of mating between a male with traits f and c and a female with trait x is given by

$$\psi(x,f,c) = \begin{cases} e^{-(2c-1)^2 \frac{(f-x)^2}{2\sigma_a^2}}, & \text{if } c < 0.5 \\ 1, & \text{if } c = 0.5 \\ e^{-(2c-1)^2 \frac{(f-(1-x))^2}{2\sigma_a^2}}, & \text{if } c < 0.5 \end{cases}$$

where σ_a controls the strength of the male mating preference.

Module 11

Animal Body Plan

11.1   Biological Introduction

Perhaps even more than the other Eukarya, Animalia is characterized by a distinct progression of complexity in form and function as one moves from the more primitive to the more derived taxa. Early in animal evolution, major changes in **body symmetry**, **embryonic germ layers**, and **ontogenetic origins** of major anatomical structures diverge in the nascent monophyletic groups. Over the course of this workshop, you will review the major changes that occurred during the evolution of Kingdom Animalia. By the end of the workshop, you should be able to

1. List the synapomorphies that distinguish animals from other eukaryotes

2. Understand the meanings of asymmetry, radial symmetry and bilateral symmetry

3. Be able to recognize the major animal phyla on the basis of

   a. body symmetry

b. embryonic germ layers

c. presence or absence of an internal body cavity

d. ontogeny and morphology of the internal body cavity

e. ontogenetic differences between protostomes and deuterostomes

4. Be able to recognize acoelomate, pseudocoelomate and coelomate body plans

5. Distinguish between

a. spiral and radial cleavage

b. determinate and indeterminate cleavage

c. schizocoely and enterocoely

> **QUESTION:** What are some characteristics that set animals apart from other types of organisms?

11.2   Body Plan

11.2.1   Germ Layers

Information about the development of organisms can sometimes be useful to identify evolutionary relationships among those organisms.

> **QUESTION:** At what stage in an embryo's development are germ layers first present? Which germ layers form first and where are they located?

For each of the following phyla identify how many germ layers it contains and what the name of the middle layer is called?

1. **Porifera**

2. **Cnidarian**

3. **Platyhelminthes**

4. **Nematoda**

5. **Annelida**

6. **Echinodermata**

> **QUESTION:** For each of these groups is the middle layer derivated from the endoderm, ectoderm, or mesoderm?

> **QUESTION:** Look at the similarities in germ layer development. Do these similarities identify monophyletic groups. Why or why not?

11.2.2 Symmetry
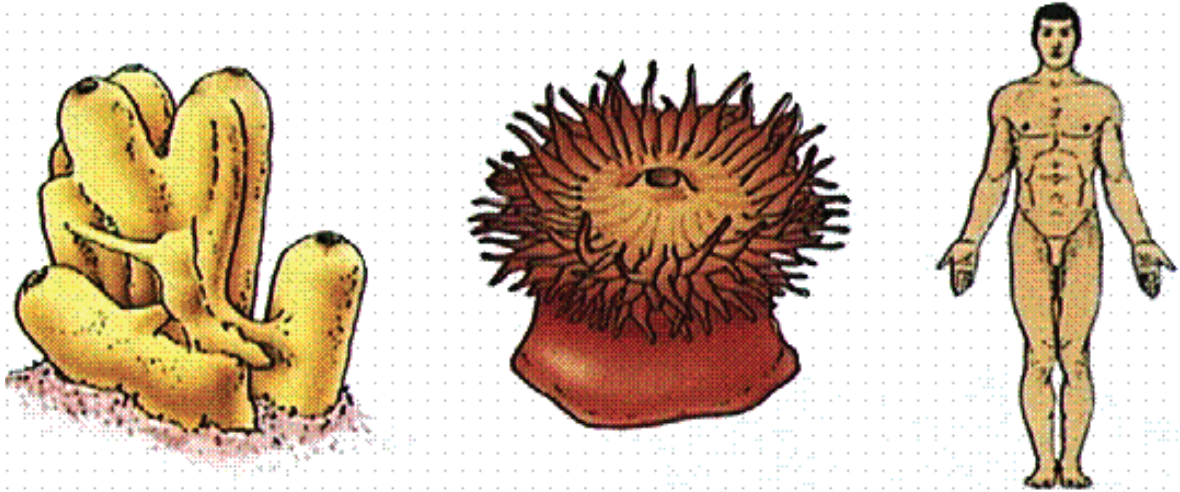
> **QUESTION:** Identify which organism in the picture exhibits each of the following types of body plan: asymmetry, radial symmetry, bilateral symmetry? What do each of those terms mean?

QUESTION: What type of symmetry does this organism have? What other types of organisms is this true of? Are these organisms monophyletic?

QUESTION: What type of symmetry does this organism have? What other phyla are characterized by these type of symmetry? Is this type of symmetry homologous among these phyla? Why or why not?

QUESTION: What type of symmetry does this organism have? Why do most animals possess this type of symmetry?

11.2.3 Body Cavities

Your textbook, course notes and other resources often provide you with a crosssectional view of the three animal body plans. On a separate piece of paper sketchan acoelomate, pseudocoelomate, and coelomate body plan in LONGITUDINAL section. Label ectoderm, endoderm, and mesoderm/mesenchyme, intestinal lumen, parietal and visceral surfaces.

QUESTION: What is the function of a pseudocoelem? Why is it considered a persistent blastocoel?

11.2.4 Protostome vs. Deuterostome

The most derived lineages of eumetazoans have an internal body cavity (**coelom**) lined on both the parietal and visceral surfaces with **mesoderm**. However, the two major (putatively) monophyletic groups of coelomates achieve this adult anatomy in different ways. Other ontogenetic features also suggest that although the **protostomes** and **deuterostomes** share a common ancestor, the taxa within each lineage are distinct unto themselves. Consider the following and discuss.

QUESTION: Describe some possible ontogenetic origins of the following in a hypo-
thetical common ancestor of protostomes and deuterostomes:

a. origin of mesoderm (i.e., from ectoderm or endoderm?)

b. fate of the blastopore (mouth or anus?)

c. cleavage at the 4- to 8-cell stage (i.e., spiral or radial?)

d. determinate or indeterminate cleavage?

e. embryonic location of the circulatory system

f. embryonic location of the nervous system

11.3 Diversification and Progression of Complexity

You should now have a good grasp of the progression of complexity in ontogeny
and anatomy of the animals. Using the phylogenetic tree below, place each of the
characters listed at the proper place where it originated in an ancestral lineage, giving
rise to today's extant animal phyla. At the root of the tree, begin with a hypothetical
ancestral colonial flagellate. (Note that this phylogenetic tree does not include all
animal phyla, and it's only the most recent hypothesis. It could change as new data
become available.)

a. diversification of cell types

b. gastrulation

c. ectoderm & endoderm (diploblasty)

d. mesenchyme (mesogloea with cellular components)

e. true mesoderm (triploblasty)

f. pseudocoelom

g. coelom derived via schizocoely

h. coelom derivedc via enterocoely

i. blastopore becomes the mouth

j. blastopore becomes the anus

k. circulatory system dorsal in the embryo

l. circulatory system ventral in the embryo

m. nervous system ventral in the embryo

n. nervous system dorsal in the embryo

o. spiral, determinate cleavage

p. radial, indeterminate cleavage

QUESTION: The tree above is based on molecular data. Are the morphological characters you placed on the tree consistent with a most parsimonious explanation for the evolutionary relationships shown? How is it possible that morphological data and molecular data might not produce trees that are congruent with each other?

The truth is that similarities in morphological characters frequently disagree with molecular data. However, molecular data is the most effective and honest data we

have to identify the evolutionary relationships among organisms, Remember, all evolution begins at the DNA sequence level. **Mutation** is a microevolutionary process that involves changes in the DNA sequence of an cell. Regardless of how evolution proceeds, observed phenotypic changes are the result of changes in the DNA sequence of an organism. In order to accurately assess the evolutionary relationships among organisms using molecular data, we must have an understanding of how mutation and the evolution of DNA sequences occurs. By combining biological knowledge with mathematics, we can use mathematical models to identify how changes occur in a DNA sequence, how they accumulate over time, and what types of changes occur.

11.4 Mathematical Introduction

11.4.1 Conditional Probabilities

A conditional probability describes the probability that an event will occur, given that another event has already occurred. For example, suppose a bag contains 3 orange marbles and 7 green marbles. The probability of pulling an orange marble out of the bag at random is $\frac{3}{10} = 0.3$. But if we know that a green marble has already been pulled out of the bag, then the conditional probability of pulling an orange marble out of the bag, given that a green marble has already been pulled out is now $\frac{3}{9} = 0.333$. So the probability of pulling an orange marble out of the bag has increased based on the previous event of a green marble having been pulled out of the bag.

11.4.2 Markov Models

Suppose that we have an ancestral DNA sequence, where each site in the sequence can be occupied by one of the four bases: A, G, C, or T. Suppose that we want to model the mutation process over one time step, assuming that only base substitutions occur; i.e., there are no deletions, insertions, or inversions. Such a process is an example of a Markov process, which means the state of the system (the DNA sequence in this case) changes over time, transitioning between one of a finite number of states to another, and where the state of the system at the next time step depends only on the state of the system at the current time step. In other words, the system has no memory of the past time steps because it does not matter how the system got to the current state. Let $\mathcal{P}_A$, $\mathcal{P}_G$, $\mathcal{P}_C$, and $\mathcal{P}_T$ represent the probabilities that each base will occur at any given site in the sequence. Note that one of the four bases must occur at each site, so $\mathcal{P}_A, +\mathcal{P}_G + \mathcal{P}_C + \mathcal{P}_T = 1$. In order to see how these probabilities change from one time step to the next, we need to know the probability of each base changing into each of the other bases. In other words, we need to know the conditional probabilities of having any base in any site in the sequence, given that that site was previously occupied by any of the bases. If we represent the conditional probability of a site being occupied by base i, given that it was occupied by base j (where $i, j = A, G, C, T$) in the previous time step by $\mathcal{P}_{i|j}$, then we can form a matrix called the transitional matrix, M with all these conditional probabilities by allowing all the columns to share the same ancestral base and all the rows to share the same

descendant base. In other words,

$$
M = \begin{pmatrix} \mathcal{P}_{A|A} & \mathcal{P}_{A|G} & \mathcal{P}_{A|C} & \mathcal{P}_{A|T} \\ \mathcal{P}_{G|A} & \mathcal{P}_{G|G} & \mathcal{P}_{G|C} & \mathcal{P}_{G|T} \\ \mathcal{P}_{C|A} & \mathcal{P}_{C|G} & \mathcal{P}_{C|C} & \mathcal{P}_{C|T} \\ \mathcal{P}_{T|A} & \mathcal{P}_{T|G} & \mathcal{P}_{T|C} & \mathcal{P}_{T|T} \end{pmatrix}
$$

It turns out that all the entries of M are ≥ 0 since they all represent probabilities, and each column of M adds up to 1, since every site in the sequence must be occupied by one of the four bases in the descendant sequence, regardless of what base that site was occupied by in the ancestral sequence. Any matrix satisfying these conditions is called a Markov matrix. If we represent the ancestral base distribution (i.e., we can represent the fraction of sites that we would expect to be occupied by each of the four bases) by the vector $\mathbf{p}_0 = (\mathcal{P}_A,\ \mathcal{P}_G,\ \mathcal{P}_C,\ \mathcal{P}_T)$, then the descendant base distribution after the first time step, $\mathbf{p}_1$ is found by multiplying $\mathbf{p}_1 = M\mathbf{p}_0$. Similarly, the descendent base distribution after the second time step, $\mathbf{p}_2$ is found by multiplying $\mathbf{p}_2 = M\mathbf{p}_1 = M^2\mathbf{p}_0$.

11.4.3   Exercise

Suppose a 40-base ancestral DNA sequence is

$$
S_0 :\ ACTTGTCGGATGATCAGCGGTCCATGCACCTGACAACGGT
$$

and its descendent aligned sequence is

$$S_1: \ ACATGTTGCTTGACGACAGGTCCATGCGCCTGAGAACGGC$$

QUESTION: What is $\mathbf{p}_0$ in this case? Round to three decimal places.

The frequencies of $S_1 = i$ and $S_0 = j$ for $i, j = $ A,G,C,T are summarized in the following table.

$S_1 \backslash S_0$	A	G	C	T
A	7	0	1	1
G	1	9	2	0
C	0	2	7	2
T	1	0	1	6
Total	9	11	11	9

QUESTION: Compute the transitional matrix, M, of conditional probabilities of having any base in any site in the sequence, given that that site was previously occupied by any of the bases. Round to three decimal places.

In the Scilab console, define the vector $\mathbf{p}_0$ and the transitional matrix M by typing

$$\mathbf{p}_0 = [\mathcal{P}_A; \mathcal{P}_G; \mathcal{P}_C; \mathcal{P}_T]$$

and

$$M = \begin{bmatrix} \mathcal{P}_{A|A}, \mathcal{P}_{A|G}, \mathcal{P}_{A|C}, \mathcal{P}_{A|T}; \mathcal{P}_{G|A}, \mathcal{P}_{G|G}, \mathcal{P}_{G|C}, \mathcal{P}_{G|T}; \mathcal{P}_{C|A}, \mathcal{P}_{C|G}, \mathcal{P}_{C|C}, \mathcal{P}_{C|T}; \mathcal{P}_{T|A}, \\ \mathcal{P}_{T|G}, \mathcal{P}_{T|C}, \mathcal{P}_{T|T} \end{bmatrix}.$$

(**Note:** You should type the actual values for the probabilities and not $\mathcal{P}_i$ or $\mathcal{P}_{i|j}$. Additionally, all the values should be entered on one line in the brackets, not two.

Finally, be careful to type the commas and semicolons exactly as you see them above.)

> **QUESTION:** What are the descendent base sequences $\mathbf{p}_1$ and $\mathbf{p}_2$?

To determine the equilibrium base distribution; i.e., the final DNA sequence in which all mutations have stopped, we need to compute $\mathbf{p}_\infty = \lim_{t\to\infty} M^t\mathbf{p}_0$.

> **QUESTION:** What is the equilibrium base distribution for this example? *Hint: To do this limit, you will need to make a table of values.*

11.4.4 Jukes-Cantor Model

The simplest Markov model of molecular evolution is called the Jukes-Cantor model. The Jukes-Cantor model makes two simplifying assumptions:

(1) All bases occur with equal probability in the ancestral sequence; i.e., $\mathbf{p}_0 = \left(\frac{1}{4},\ \frac{1}{4},\ \frac{1}{4},\ \frac{1}{4}\right)$.

(2) The conditional probability describing an observable base substitution from any base to any other base are all the same. In other words, if α is the probability that a given site in the sequence will change from its current base to any of the three other bases, then $\mathcal{P}_{i|j} = \frac{\alpha}{3}$ for $i \neq j$. Therefore, in the Jukes-Cantor model, the transitional matrix is

$$
M = \begin{pmatrix}
1-\alpha & \frac{\alpha}{3} & \frac{\alpha}{3} & \frac{\alpha}{3} \\[6pt]
\frac{\alpha}{3} & 1-\alpha & \frac{\alpha}{3} & \frac{\alpha}{3} \\[6pt]
\frac{\alpha}{3} & \frac{\alpha}{3} & 1-\alpha & \frac{\alpha}{3} \\[6pt]
\frac{\alpha}{3} & \frac{\alpha}{3} & \frac{\alpha}{3} & 1-\alpha
\end{pmatrix}
$$

The value of α will depend on the time step used and the features of the particular DNA sequence being modeled. Although α is a probability, we can interpret it as the rate at which observable base substitutions occur over one time step, measured in units of (substitutions per sites)/(time step).

Download and execute the file Jukes-Cantor.sce. Notice that the sequence starts at its equilibrium distribution.

QUESTION: In line 4 of the code, change $\mathbf{p}_0$ to $[.2; .3; .4; .1]$. In this case, what is the equilibrium base distribution?

In the previous problem, the graph opened in graphics window 2. Leave this graphics window when you do the next problem so that you can compare the graphs.

QUESTION: In line 1 of the code, reduce the value of α (represented by a in the Scilab code) from .06 to .03 and change line 10 of the code from 2 to 1. This will open the new graph in graphics window 1. Before closing the graphics windows, increase α to 0.9 and change line 10 to 3 so that this new graph opens in graphics window 3. What affect does changing α have on the equilibrium base distribution? Does this support the alternate interpretation we gave of α above?

Module 12

Animal Form and Function

12.1   Biological Introduction

This is the currently accepted phylogeny of the Kingdom Animalia. There are several characters unique to particular groups of animals, many of which identify monophyletic groups of organisms.
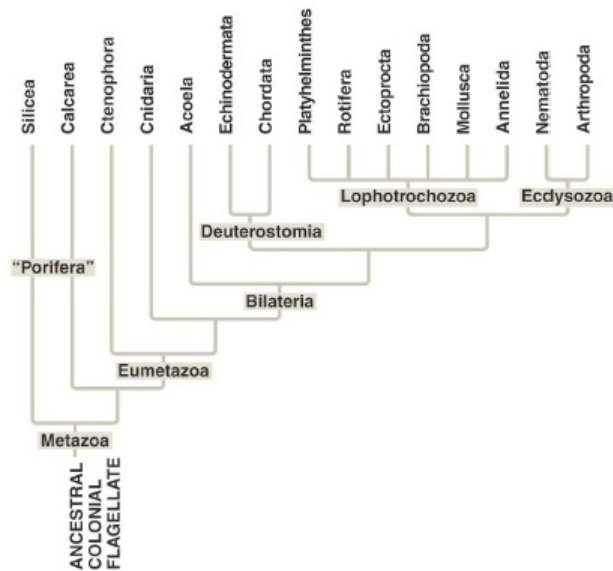
12.2   Synapomorphies defining animal taxa

Place each of the following characters on the phylogenetic tree above, indicating where it first evolved (making it a synapomorphy uniting all the taxa above it on the tree).

a. lophophore feeding apparatus coelom formed via schizocoely

b. mesoderm lines parietal side of body wall

c. body cavity contains non-cellular mesogloea

d. coelom formed via enterocoely

e. mesoderm derived from endoderm

f. body cavity contains cellular mesenchyme

g. cellular division of labor

h. complete digestive system

i. diploblasty

j. triploblasty

k. coelom formed via schizocoely

l. bilateral symmetry

m. radial symmetry

n. cnidoblast stinging cells

o. true tissues

p. nervous system embryonically dorsal

q. secondary opening becomes the anus

r. secondary opening becomes the mouth

s. trochophore larva

t. pseudocoelom a persistent blastocoel

> **QUESTION:** What does this tree imply about evolutionary relationships among the Lophotrochozoa?

12.3 Ancestry, Form, and Function

For each of the following taxa indicate what their most recent common ancestor likely looked like and what characters it had.

Protostomes and Deuterostomes

Ecdyzoans

Lophotrochozoans

QUESTION: What synapomorphies set nematodes and arthropods apart from the ancestral Ecdyzoan? How does the main body cavity of a nematode differ from that of an arthropod?

QUESTION: What synapomorphies set molluscs and annelids apart from the ancestral Lophotrocozoan? How does the main body cavity of a nematode differ from that of an arthropod?

Both Mollusks and Arthropods have (1) an open circulatory system and (2) a reduced coelom that functions as the **pericardium** and **gonocoel**.

QUESTION: What is a pericardium? A Gonocoel? What defines a true coelom? What does this suggest about these two characters in these two phyla?

> For each of the following taxa indicate what their most recent common ancestor likely looked like and what characters it had.
>
> Deuterostomes
>
> Echinodermata
>
> Hemichordata
>
> Chordata
>
> What characters set each of these groups apart from the ancestral deuterostome?

12.4   Practical Applications

A drug called **lufenuron** interferes with the activity of an enzyme known as chitinase, which is involved in the normal formation of chitin. Lufenuron prevents normal maturation of animals that use chitin as structural support.

Animal phyla have long been classified into putatively monophyletic assemblages on the basis of their body plans. Unfortunately, as we are now discovering with more sophisticated identification techniques such as DNA sequencing and metabolic studies, this can sometimes create artificial taxa that are para- or polyphyletic. Consider the following phylogenetic trees. The one on the left shows a classification based upon molecular (DNA sequencing) data. The one on the right shows a "traditional" classification based upon body plans and morphology.

(a) Tree based on molecular comparisons

(b) Tree based on body-plan grades
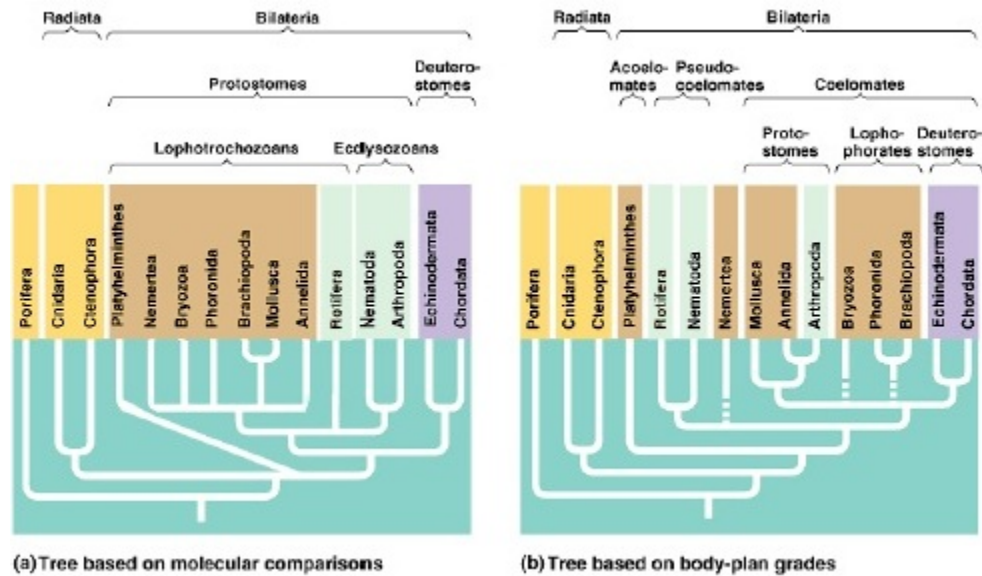
In the previous module you learned about the application of molecular sequence data to develop phylogenies. As you can see here, molecular data and morphological data frequently disagree. However, as we said before, molecular data provides the most accurate information about the evolutionary history of organisms.

You also learned that we can apply mathematical models to identify how DNA sequences evolve. In particular we discussed the Jukes-Cantor model of sequence evolution. We can apply this model of DNA evolution in a different way to identify how genetically different species are from each other. To do this we measure the **genetic distance** between sequences, which is a measure of how different sequences are based on the types of substitutions between them and the likelihood of multiple changes at a single site.

12.5   Mathematical Introduction

12.5.1   Review

In the previous module Animal Body Plan, we studied Markov models and in partic-
ular, we looked at the Jukes-Cantor model. There, we said that in order to describe
the mutation process for a given DNA sequence, we need the transitional matrix, M
which describes the conditional probabilities, $\mathcal{P}_{i|j}$, of any site in the sequence changing
to base i given that it was previously occupied by base j $(i, j = A, G, C, T)$.

$$M = \begin{pmatrix} \mathcal{P}_{A|A} & \mathcal{P}_{A|G} & \mathcal{P}_{A|C} & \mathcal{P}_{A|T} \\ \mathcal{P}_{G|A} & \mathcal{P}_{G|G} & \mathcal{P}_{G|C} & \mathcal{P}_{G|T} \\ \mathcal{P}_{C|A} & \mathcal{P}_{C|G} & \mathcal{P}_{C|C} & \mathcal{P}_{C|T} \\ \mathcal{P}_{T|A} & \mathcal{P}_{T|G} & \mathcal{P}_{T|C} & \mathcal{P}_{T|T} \end{pmatrix}.$$

For the Jukes-Cantor model in particular, the transitional matrix is

$$M = \begin{pmatrix} 1-\alpha & \frac{\alpha}{3} & \frac{\alpha}{3} & \frac{\alpha}{3} \\ \frac{\alpha}{3} & 1-\alpha & \frac{\alpha}{3} & \frac{\alpha}{3} \\ \frac{\alpha}{3} & \frac{\alpha}{3} & 1-\alpha & \frac{\alpha}{3} \\ \frac{\alpha}{3} & \frac{\alpha}{3} & \frac{\alpha}{3} & 1-\alpha \end{pmatrix}.$$

Using the transitional matrix, M, we were able to determine the descendant base
distribution after one time step, $\mathbf{p}_1$, from the ancestral base distribution, $\mathbf{p}_0$ by mul-
tiplying $\mathbf{p}_1 = Mp\mathbf{p}_0$. Similarly, the descendant base distribution after two time steps,
$\mathbf{p}_2$ was $\mathbf{p}_2 = M\mathbf{p}_1 = M^2\mathbf{p}_0$.

12.5.2 More on the Jukes-Cantor Model

If we want the descendant base distribution after t time steps, it is $\mathbf{p}_t = M^t \mathbf{p}_0$. If you calculate M^t, it turns out to be

$$M^t = \begin{pmatrix} \frac{1}{4} + \frac{3}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t \\ \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} + \frac{3}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t \\ \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} + \frac{3}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t \\ \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} - \frac{1}{4}\left(1 - \frac{4}{3}\alpha\right)^t & \frac{1}{4} + \frac{3}{4}\left(1 - \frac{4}{3}\alpha\right)^t \end{pmatrix}.$$

From this, we see that the fraction of the sites we would expect to observe no change in, between time 0 and time t, is $q(t) = \frac{1}{4} + \frac{3}{4}\left(1 - \frac{4\alpha}{3}\right)^t$ (from the diagonal entries). And the fraction of the sites that we expect to be different from time 0 to time t is $p(t) = 1 - q(t) = \frac{3}{4} - \frac{3}{4}\left(1 - \frac{4\alpha}{3}\right)^t$.

Download and execute the file Jukes-Cantor_differences.sce.

> **QUESTION:** How does increasing the value of α affect $p(t)$? What does the maximum value of $p(t)$ appear to be?

12.5.3 Jukes-Cantor Distances

Suppose we have two DNA sequences - an ancestral sequence and a mutated sequence from some later time. By comparing the number of sites which are different after the mutations with the total number of sites, we can estimate $p(t)$. But from $p(t)$, we usually cannot recover α and t. So instead we use their product, $t\alpha$, which can still tell us something useful based on $p(t)$. By approximating this product, we get the

Jukes-Cantor distance between the DNA sequences S_0 and S_1, which is

$$d_{JC}(S_0, S_1) = -\frac{3}{4} \ln \left(1 - \frac{4}{3}p \right).$$

This Jukes-Cantor distances tells us the total number of expected substitutions per site during the elapsed time. In other words, distance refers to how different the sequences are due to mutations.

In Scilab, the command

$$\rightarrow log(x)$$

is used to compute $\ln x$.

Consider the two 40-base DNA sequences from the previous module:

S_0 : $ACTTGTCGGATGATCAGCGGTCCATGCACCTGACAACGGT$

and its descendent aligned sequence is

S_1 : $ACATGTTGCTTGACGACAGGTCCATGCGCCTGAGAACGGC$

QUESTION: Compute $d_{JC}(S_0, S_1)$ for these two sequences. Why do you think the average number of observed base substitutions per site (given by p) is different from the estimated number of substitutions per site that occurred in the course of evolution (given by d_{JC})?

QUESTION: Do you think the Jukes-Cantor distance will increase or decrease as p increases? Why?

Download and execute the file Jukes-Cantor_distance.sce.

QUESTION: Was your answer to the previous question confirmed? If not, why do you think you were wrong?

Module 13

Predation

13.1 Biological Introduction

Predation is the process by which one organism feeds on and kills another organism. This process requires two components: the predator (the one feeding) and the prey (the one being consumed). Predatory-prey interactions commonly refer to one animal (a carnivore) hunting and killing another animal (an herbivore), but they can also refer to several other types of interactions.

QUESTION: Describe at least two predator prey interactions that do not involve carnivores consuming herbivores. How do predator prey interactions differ from host-parasite interaction?

Since predator-prey interactions are not limited to one animal feeding on another, predator prey interactions can be illustrated as webs or pyramids of interactions. These are commonly referred to as food webs or trophic cascades. These cascades describe all of the predator prey interactions within an ecosystem, and are valuable

for looking at the transfer of energy in a particular system. This is of particular importance because only about 10% of the energy consumed from prey is converted to biomass for the predator. In turn, 90% of energy consumed is lost to cellular and homeostatic processes of the predator, or excreted as waste. As a result, a great deal of energy is lost in a trophic cascade. For instance, plants commonly serve as prey for herbivores, which serve as prey for carnivores, which then may serve as prey for secondary and tertiary carnivores. One example of this is as follows, a rabbit consumes a flowering plant in the Everglades, the rabbit is then consumed by a rattlesnake, the rattlesnake is then consumed by an eagle. In each prey event energy is transferred from the prey to the predator, and a large portion is lost.

> **QUESTION:**In the previous example, how much of the energy of the plant is eventually transferred to the eagle? What implications does this have for food consumption by predators? Identify another example by which energy is transferred from a plant to at least a tertiary consumer.

As you can see, predatory-prey relationships involve a complex series of interactions. These interactions occur across a wide range of species and in nearly every environment on Earth. As a result these interactions can have a variety of consequences for both the predator and the prey. One such consequence is the evolution of antipredatory adaptations. In these cases, individuals that by chance have developed certain behaviors or morphological characteristics are less likely to be preyed upon that those that do not exhibit these characteristics. As a result, those individuals survive, and their traits are passed on to the next generation eventually becoming widespread throughout the population. Examples of such adaptations include schooling behavior in fish, herding in zebras, and aposematic coloration in a variety of species. Apose-

matism is the use of bright coloration to deter potential predators. It is commonly referred to as warning coloration because it is typically associated with animals that pose a physical or chemical threat to predators.

> **QUESTION:**Give another example of an antipredatory adapatation and hypothesize how it may have developed.

13.2   Example

On a more simple level predatory prey interactions result in fluctuations in populations for both groups of organisms involved. An increase in prey items, provides more food predators, allowing their populations to increase. As predatory populations increase, they exert a greater pressure on prey and the prey population decreases. Once the prey population decreases predators have less food and begin to starve, resulting in a decrease in number of predators, and the cycle begins again. This is just one example of possible population dynamics associated with predator prey interactions. However, it is probably the most well documented type of interaction, largely due to the case of the Canadian lynx and the snowshoe hare. In 1937, MacLulich published a paper analyzing data collected by fur trappers selling pelts to The Hudson Bay Company over a period of nearly 100 years. From these data, a "classic" Lynx vs. Snowshoe Hare population fluctuation phenomenon emerged, as shown below. MacLulich noted that the "boom" and "bust" of hare and lynx population seem to mirror each other, with the lynx peaks and valleys coming slightly after those of the hares.
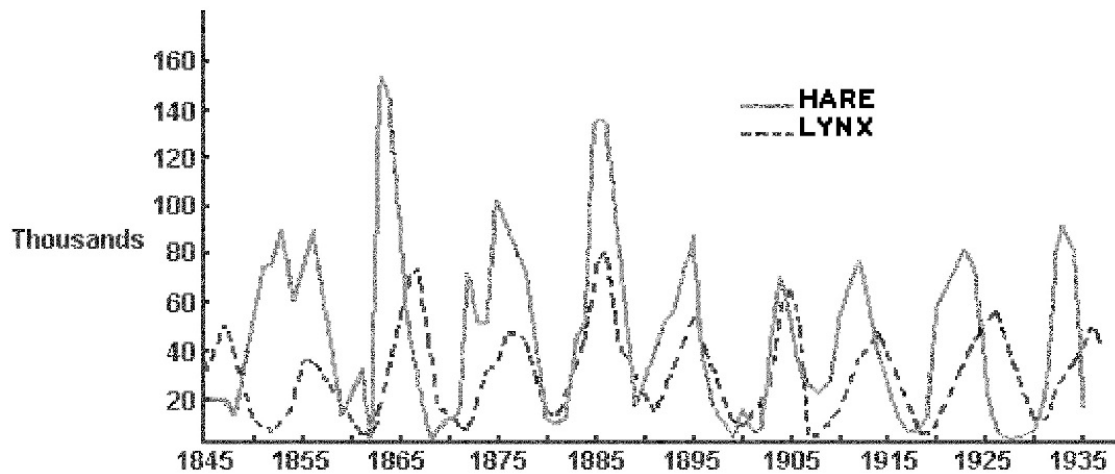
There are a variety of responses that predator and prey populations can have as a result of pressures. Many if not all potential outcomes of predator prey interactions can be predicted and model by combining experimental and field data with some simple mathematical models.

13.3   Mathematical Models

In this module, we studied a discrete-time single species population model, called the Discrete Logistic Model. Here, we will study models which involve two species, where the presence of each species affects the other population. In this case, the model equations are called coupled equations because both must be considered together as one system of equations. The way in which a predator-prey system is modeled depends on what is being assumed about the populations being modeled. In the models we consider, we will use x_t to denote the prey population at time t and y_t to

denote the predator population at time t.

In the first model, we make the following assumptions:

1. The fraction of the prey population that survives from one generation to the next is given by

$$\frac{1}{1 + ay_t}$$

   So, the fraction of prey that survive is inversely related to the number of predators.

2. The prey have a net reproductive rate of r.

3. The only source growth for the predator population is the prey.

4. Each consumed prey gives rise to b new predators.

The form of the first model is:

$$x_{t+1} = \frac{rx_t}{1 + ay_t}$$

$$y_{t+1} = b\left(1 - \frac{1}{1 + ay_t}\right)x_t$$

Download the file predator_prey1.sce and execute it in Scilab.

QUESTION: What are the similarities and differences between the behavior of this model and the behavior of the Lynx vs. Snowshoe Hare populations? What do you think the model is lacking to account for this difference? Explain why the qualitative behavior of the predator vs. prey graph on the right should be expected from the dynamics of the population vs. time graph on the left.

In the next model we consider, we make the following assumptions:

1. The fraction of the prey population that survives declines exponentially with the number of predators.

2. There is a limit to the predators' appetite, so as the number of prey increase, the number of predator-prey interactions does not grow unbounded.

3. The prey have a net reproductive rate of r.

4. The only source of growth for the predator population is the prey.

The form of the second model is:

$$x_{t+1} = x_t e^{r\left(1 - \frac{x_t}{K}\right) - ay_t}$$

$$y_{t+1} = x_t \left(1 - e^{-ay_t}\right)$$

Download the file predator_prey2.sce and execute it in Scilab.

QUESTION: What are the similarities and differences between the behavior of this model and the behavior of the previous model? Explain the qualitative behavior of the predator vs. prey graph on the right from the dynamics of the population vs. time graph on the left.

The last model we consider has the form:

$$x_{t+1} = r \left(1 - \frac{x_t}{K}\right) x_t - ay_t$$

$$y_{t+1} = by_t + x_t$$

Download the file predator_prey3.sce and execute it in Scilab.

QUESTION: What modeling assumptions were used in constructing this model? What are the similarities and differences between the behavior of this model and the behavior of the previous models? Explain why the qualitative behavior of the predator vs. prey graph on the right should be expected from the dynamics of the population vs. time graph on the left.

Module 14

Population Ecology

14.1   Biological Introduction

Ecology is the scientific study of the interactions that determine the distribution and abundance of organisms. More generally, it is the study of how organisms interact with each other and their environments. Population ecology is the study of changes in growth and composition in a single group of organisms.

As the name implies, this can be an extremely daunting task. An, infinitely large number of factors can affect how populations change. These factors can be divided into two groups: abiotic and biotic.

Abiotic factors are non-living environmental factors that can affect populations (temperature, radiation, amount of light, etc.).

Biotic factors are living factors and interactions that can affect populations (predators, prey, etc.).

> **QUESTION:**Give two additional abiotic and two biotic factors that may affect a population.

Abiotic and biotic factors combine to change population demographics and distributions over time. There are a great many factors that researchers study in order to gain insight into populations and how they are changing. In this module we will explore four:

1. Age Structure of Populations

2. Population Growth Rate

3. Beneficial Species Interactions (Symbioses)

4. Intra- and Interspecific Competition

> **QUESTION:**Describe two other factors that may affect a populations demographics and distribution. HINT: We have already had a module on one of them this semester.

14.1.1 Age Structure of Populations

Many factors influence the age structure of a population of organisms. These are commonly broke down into three categories: fecundity, morbidity, and survivorship. While these are not the only factors involved, they give us a good place to start. **Fecundity** can be expressed as the number of offspring produced per female per unit time (i.e. 0.5 children per female per year, this indicates that half of females in a population have one offspring each year). This can also be described as the birth rate for the population. **Mortality** can be expressed as the number of individuals

dying per unit time. This is also commonly known as the death rate of the population. **Survivorship** is the proportion of individuals in a population which survive to a given age. Other factors which may affect the age distribution of a population include age at sexual maturity, immigration, and emigration.

QUESTION: What would you expect the survivorship curve to look like for a fish that produces large clutches of really small live offspring? What would the corresponding age distribution pyramid look like? See pg. 1154 in Campbell for an example of an age pyramid.

QUESTION: What do you expect the age pyramid to look like for each of the following population scenarios: rapid growth, rapid decline, stable? What would the ratio of birth rate to death rate be for each of the above cases?

14.1.2   Population Growth Rate

Closely tied to age structure is the concept of population growth rate. This is the rate at which a population increases or decreases and depends on many of the same factors previously described. Fecundity, morbidity, survivorship, age at sexual maturity, immigration, and emigration all have an impact on how a population grows. Other important factors that can impact how a population grows are whether generations are overlapping or discrete, and availability of resources. Much of this was covered in the module on population growth from earlier this semester.

From this module and your class material, you know that there are two types of growth: exponential and logistic.

QUESTION: What are the equations for logistic growth and exponential growth? What do each of the variable represent (see p.1143-1147 in Campbell)

In exponential growth models, populations continue to grow at a rate that is dependent exclusively on the birth rate of the population.

QUESTION: Why is this an unrealistic model for most populations? Give an example when this model may prove accurate? In your example will this model always apply or will the population switch to a logistic growth? Why?

In logistic growth models, populations cannot grow infinitely, but are limited by a populations carrying capacity, the maximal population size that can be sustained in the given environment.

QUESTION: What factors may influence a populations carrying capacity? Which of these models will produce a J shaped curve? Which will produce an S shaped curve? What is the difference between an r selected population and a K selected population?

14.1.3   Beneficial Species Interactions

Beneficial species interaction can also be described as symbiosis. A symbiosis is a relationship between two organisms where both organisms receive a benefit. These interactions are common throughout nature and can have a great impact on the demographics and distribution of a population. However, not all interactions are this clear cut. Oftentimes, a relationship that is a symbiosis in one situation can actually become a commensalism in another situation. A commensalism is a relationship between two organisms in which one benefits and the other is not significantly harmed or helped. The following example provides just such a case.

Example

Mycorrhizae are plant root-fungus symbioses. They can have a profound impact on the growth and survival of individual plants and therefore plant populations. This can then lead to influencing plant community composition and succession of an area. Look at the following graph (modified from Maffia 1997). By final harvest, Sunflower plants grown at high density without mycorrhizas are twice the size of those grown with mycorrhizas. The total number of Sunflower plants grown without mycorrhizas are, however, only half that of the Sunflowers grown with mycorrhizas.
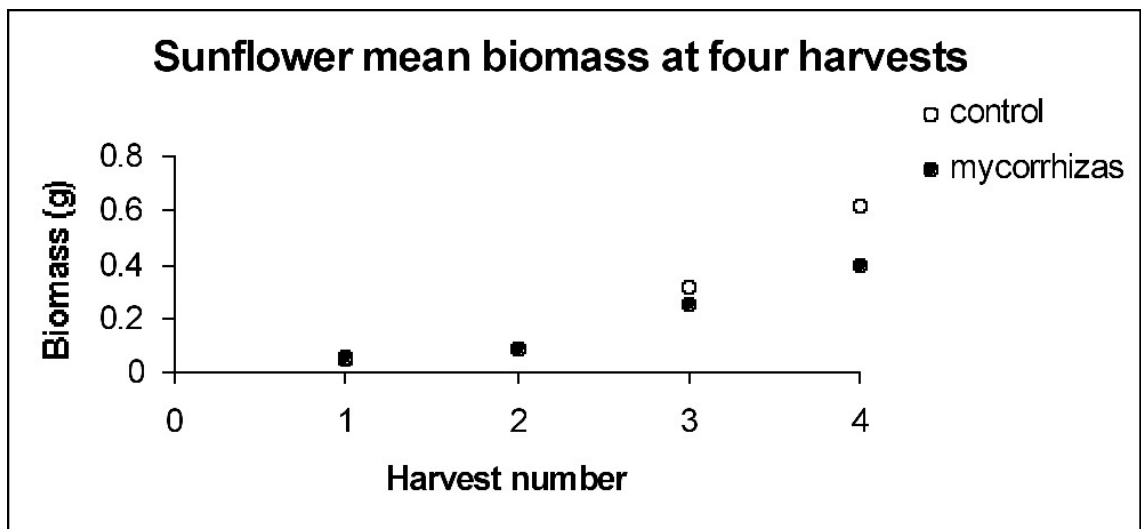
QUESTION: Based on these data, describe a scenario where it is advantageous to have mycorrhizas; disadvantageous to have mycorrhizas. Speculate as to why Sunflowers continue to associate with mycorrhizas.

14.1.4 Competition

Competition is an interaction between two that use or seek the same set of limited resources. This is interaction is detrimental to both species. In this case each species

is competing with the other for these resources. These resources can include a specific habitat, a particular breeding ground, a certain food source, etc. In addition, it is important to note that competition can be either intraspecific or interspecific.

QUESTION: Why is competition detrimental to both groups of organisms involved?

Intraspecific competition occurs when two populations of the same organism seek to utilize the same resource at the same time. This commonly occurs when organisms are seeking specific breeding grounds. Established populations must often exhibit considerable energy to maintain their breeding grounds from other members of the same species.

Interspecific competition occurs when the organisms competing for a particular resource are members of different species. While this type of competition may be more difficult to understand, it is still quite common. Additionally, it can have a strong impact on the population demographics of both species involved. An example of this would be when two populations of rodents inhabit the same area and eat the same food. These populations are in constant competition for habitat, breeding area, and available food. As a result, the population demographics of both species are impacted. If one species has an advantage over the other, then the competition may eventually result in the loss of one species from the environment while the other thrives. More commonly, the two species continue to coexist in a state of flux in a given habitat. This commonly results in variation in the population demographics of both species.

> **QUESTION:**Describe a situation whereby two species continuously compete in a particular habitat? Include in your description an explanation of why one species does not outcompete the other?

In an increasingly urbanized world, these situations become all the more common as available habitat and food sources continue to shrink. In response to this we can use mathematical modeling to explore the effects of competition in a variety of different scenarios.

14.2   Mathematical Model

In this module, we will consider a discrete-time model for two species, x (Species 1) and y (Species 2), which exhibit both interspecific competition with each other, and intraspecific competition among themselves. The form of the model we will use is:

$$x_{t+1} = \frac{b_1 x_t}{1 + c_{11}x_t + c_{12}y_t}$$
$$y_{t+1} = \frac{b_2 y_t}{1 + c_{21}x_t + c_{22}y_t}$$

Here, b_1 and b_2 represent growth rates for Species 1 and Species 2, respectively. The constants c_{ij} for $i, j = 1, 2$ represent the strength of the competition on Species i by Species j.

> **QUESTION:** Give a specific interpretation for c_{11}, c_{12}, c_{21}, c_{22}. Which ones represent interspecific competition and which ones represent intraspecific competition?

Download the file competition.sce and execute it in Scilab. You will notice four identical graphs, labeled Model #1, Model #2, Model #3, and Model #4. They show Species 1, which starts with an initial population of $x(1) = 1.6$ and Species 2, which starts with an initial population of $y(1) = 1.1$ coexisting and coming to equilibrium at the same population level.

> **QUESTION:** Find a set of parameter values which allows both species to coexist, but come to equilibrium at different population levels. *Hint*: Use the four graphs to make various changes and simultaneously compare the changes.

> **QUESTION:** Find two sets of parameter values which allows Species 1 to exclude Species 2 (Species 1 exists but Species 2 becomes extinct). First do it by changing only the growth rates then do it by changing only the interspecific competition.

> **QUESTION:** Can changing the strength of the intraspecific competition save Species 2 in either set of parameter values in the previous problem?

> **QUESTION:** What, if any, interesting, unexpected, or different phenomena did you discover while searching for the sets of parameter values you were asked to find?

Appendix A

Scilab Code

A.1 Introduction to Scilab

A.1.1 oracle.sce

```
t = 0:0.5:10;
y = 0.5*t + sin(t)/2;
// best linear fit; general case is datafit or leastsq
[m b] = reglin(t,y);
z = m*t + b;
scf(0);
clf;
plot(t,y,'rx',t,z,'b:');
// Scilab also has xtitle command
xlabel('t'); ylabel('y');
title('Data points in red x; Blue dotted line is best
linear fit');
xs2eps(0,'oracle.eps')
xs2pdf(0,'oracle.pdf')
xs2png(0,'oracle.png')
```

A.1.2   introduction_lab.sce

```
lines(0);

function y=sum1(n)
// sum1(n) computes the sum of 1 + 2 + ... + n
total =  0;
for  i= 1:n,
        total=  total+ i;
end;
y = total;
endfunction;

function  out=firstRowDown(in)
row1 = in(1,:);
n = size(in,2);
for  i= 1:n,
        out(i,1) = row1(i);
end;
endfunction

function  out=firstRowDownSecondColumn(in)
row1 = in(1,:);
n = size(in,2);
for  i= 1:n,
        out(i,2) = row1(i);
end;
endfunction

function  out=countDownNumberOfColumns(in)
n = size(in,2);
for  i= 1:n,
        out(i,1) = i;
end;
endfunction
```

A.2   The Cell and Biomolecules

A.2.1   diffusionleft.sce

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .0001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(0);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

A.2.2 diffusioncenter.sce

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .0001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(10);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```

A.3   Protein Synthesis

A.3.1   cell_cycle_control.sce

```
function  dx=cdkapc(t,x)
dx(1) = k1-(k2p+k2pp*x(2))*x(1)
dx(2) =
((k3p+k3pp*x(3))*(1-x(2)))/(J3+1-x(2))-(k4*x(4)*x(1)*x(2))
/(J4+x(2))
dx(3) =
k5p+k5pp*((x(4)*x(1))^n)/(J5^n+(x(4)*x(1))^n)-k6*x(3)
dx(4) = u*x(4)*(1-x(4)/Ms)
endfunction

scf(0);
clf;
k1 = 0.04
k2p = 0.04
k2pp = 1
k3p = 1
k3pp = 10
J3 = 0.04
k4 = 35
J4 = 0.04
k5p = 0.005
k5pp = 0.2
k6 = 0.1
n = 4
J5 = 0.3
u = 0.01
Ms = 1
t =0:0.01:400;
x0 = [0.05 ;0.04; 0.0; 0.6];
x = ode(x0,0,t,cdkapc);

plot2d(t,x(1,:),style= 1)
```

```
plot2d(t,x(2,:),style= 2)
plot2d(t,x(3,:),style= 3)
legends(['[cyclin/Cdk]','Cdh1/APC','[Cdc20]'],[1 2
3],"ur")
xlabel('Time')
ylabel('Concentration')
```

A.4 Gene Regulation

A.4.1 HIV_control.sce

```
//close

function  y=
code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A,tfinal)

test = -1;

delta = 0.001;
M = 1000;
t=linspace(0,tfinal,M+1);
h=tfinal/M;
h2 = h/2;

T=zeros(1,M+1);
Ti=zeros(1,M+1);
V=zeros(1,M+1);
T(1)=T0;
Ti(1)=Ti0;
V(1)=V0;

lambda1=zeros(1,M+1);
lambda2=zeros(1,M+1);
lambda3=zeros(1,M+1);

u=zeros(1,M+1);

while(test < 0)

    oldu= u;
    oldT= T;
    oldTi= Ti;
    oldV= V;
```

```
    oldlambda1= lambda1;
    oldlambda2= lambda2;
    oldlambda3= lambda3;

  for i=1:M
        k11= s/(1 +  V(i))+ T(i)*(-m1 + r*(1 -  (T(i)+
Ti(i))/Tmax) - u(i)*k*V(i));
        k12= u(i)*k*V(i)*T(i) - m2*Ti(i);
        k13= N*m2*Ti(i) - m3*V(i);

        k21= s/(1 + (V(i)+h2*k13)) + (T(i)+h2*k11)*(-m1
+ r*(1 - ((T(i)+h2*k11) + (Ti(i)+h2*k12))/Tmax) -
0.5*(u(i)+u(i+1))*k*(V(i)+h2*k13));
        k22=
0.5*(u(i)+u(i+1))*k*(V(i)+h2*k13)*(T(i)+h2*k11) -
m2*(Ti(i)+h2*k12);
        k23= N*m2*(Ti(i)+h2*k12) - m3*(V(i)+h2*k13);

        k31= s/(1 + (V(i)+h2*k23)) + (T(i)+h2*k21)*(-m1
+ r*(1 - ((T(i)+h2*k21) + (Ti(i)+h2*k22))/Tmax) -
0.5*(u(i)+u(i+1))*k*(V(i)+h2*k23));
        k32=
0.5*(u(i)+u(i+1))*k*(V(i)+h2*k23)*(T(i)+h2*k21) -
m2*(Ti(i)+h2*k22);
        k33= N*m2*(Ti(i)+h2*k22) - m3*(V(i)+h2*k23);

        k41= s/(1 + (V(i)+h*k33)) + (T(i)+h*k31)*(-m1 +
r*(1 - ((T(i)+h*k31) + (Ti(i)+h*k32))/Tmax) -
u(i+1)*k*(V(i)+h*k33));
        k42= u(i+1)*k*(V(i)+h*k33)*(T(i)+h*k31) -
m2*(Ti(i)+h*k32);
        k43= N*m2*(Ti(i)+h*k32) - m3*(V(i)+h*k33);
```

```
        T(i+1) =  T(i)+ (h/6)*(k11 + 2*k21 + 2*k31 + k41);
        Ti(i+1) =  Ti(i)+ (h/6)*(k12 + 2*k22 + 2*k32 +
k42);
        V(i+1) =  V(i)+ (h/6)*(k13 + 2*k23 + 2*k33 + k43);
    end

    for  i= 1:M
        j=  M+  2- i;
        k11= -(A + lambda1(j)*(-m1 + r*(1 - (2*T(j) +
Ti(j))/Tmax) - u(j)*k*V(j)) + lambda2(j)*(u(j)*k*V(j)));
        k12= -(lambda1(j)*(-r*T(j)/Tmax) +
lambda2(j)*(-m2) + lambda3(j)*(N*m2));
        k13= -(lambda1(j)*(-s/((1+V(j))^2) -
u(j)*k*T(j)) + lambda2(j)*(u(j)*k*T(j)) +
lambda3(j)*(-m3));


        k21= -(A + (lambda1(j)-h2*k11)*(-m1 + r*(1 -
(2*0.5*(T(j)+T(j-1)) + 0.5*(Ti(j)+Ti(j-1)))/Tmax) -
0.5*(u(j)+u(j-1))*k*0.5*(V(j)+V(j-1))) +
(lambda2(j)-h2*k12)*(0.5*(u(j)+u(j-1))*k*0.5*(V(j)+V(j-1))
));
        k22=
-((lambda1(j)-h2*k11)*(-r*0.5*(T(j)+T(j-1))/Tmax) +
(lambda2(j)-h2*k12)*(-m2) + (lambda3(j)-h2*k13)*(N*m2));
        k23=
-((lambda1(j)-h2*k11)*(-s/((1+0.5*(V(j)+V(j-1)))^2) -
0.5*(u(j)+u(j-1))*k*0.5*(T(j)+T(j-1))) +
(lambda2(j)-h2*k12)*(0.5*(u(j)+u(j-1))*k*0.5*(T(j)+T(j-1))
) + (lambda3(j)-h2*k13)*(-m3));

        k31= -(A + (lambda1(j)-h2*k21)*(-m1 + r*(1 -
```

```
(2*0.5*(T(j)+T(j-1)) + 0.5*(Ti(j)+Ti(j-1)))/Tmax) -
0.5*(u(j)+u(j-1))*k*0.5*(V(j)+V(j-1))) +
(lambda2(j)-h2*k22)*(0.5*(u(j)+u(j-1))*k*0.5*(V(j)+V(j-1))
));
        k32=
-((lambda1(j)-h2*k21)*(-r*0.5*(T(j)+T(j-1))/Tmax) +
(lambda2(j)-h2*k22)*(-m2) + (lambda3(j)-h2*k23)*(N*m2));
        k33=
-((lambda1(j)-h2*k21)*(-s/((1+0.5*(V(j)+V(j-1)))^2) -
0.5*(u(j)+u(j-1))*k*0.5*(T(j)+T(j-1))) +
(lambda2(j)-h2*k22)*(0.5*(u(j)+u(j-1))*k*0.5*(T(j)+T(j-1))
) + (lambda3(j)-h2*k23)*(-m3));

        k41= -(A + (lambda1(j)-h*k31)*(-m1 + r*(1 -
(2*T(j-1) + Ti(j-1))/Tmax) - u(j-1)*k*V(j-1)) +
(lambda2(j)-h*k32)*(u(j-1)*k*V(j-1)));
        k42= -((lambda1(j)-h*k31)*(-r*T(j-1)/Tmax) +
(lambda2(j)-h*k32)*(-m2) + (lambda3(j)-h*k33)*(N*m2));
        k43= -((lambda1(j)-h*k31)*(-s/((1+V(j-1))^2) -
u(j-1)*k*T(j-1)) + (lambda2(j)-h*k32)*(u(j-1)*k*T(j-1)) +
(lambda3(j)-h*k33)*(-m3));

     lambda1(j-1) = lambda1(j)- (h/6)*(k11 + 2*k21 +
2*k31 + k41);
     lambda2(j-1) = lambda2(j)- (h/6)*(k12 + 2*k22 +
2*k32 + k42);
     lambda3(j-1) = lambda3(j)- (h/6)*(k13 + 2*k23 +
2*k33 + k43);
   end

   temp= ((lambda2- lambda1).*k.*V.*T + 2)./2;
   u1=  min(1, max(0, temp));
```

```
    u=  0.5*(u1 + oldu);

    temp1= delta*sum(abs(u)) - sum(abs(oldu - u));
    temp2= delta*sum(abs(T)) - sum(abs(oldT - T));
    temp3= delta*sum(abs(Ti)) - sum(abs(oldTi - Ti));
    temp4= delta*sum(abs(V)) - sum(abs(oldV - V));
    temp5= delta*sum(abs(lambda1)) - sum(abs(oldlambda1
- lambda1));
    temp6= delta*sum(abs(lambda2)) - sum(abs(oldlambda2
- lambda2));
    temp7= delta*sum(abs(lambda3)) - sum(abs(oldlambda3
- lambda3));
    test= min(temp1, min(temp2, min(temp3, min(temp4,
min(temp5, min(temp6,temp7))))));
end

y(1,:) = t;
y(2,:) = T;
y(3,:) = Ti;
y(4,:) = V;
y(5,:) = u;

endfunction

flag1=0;
flag2=0;
flag3=0;
flag4=0;
var1=0;
var2=0;
var3=0;
var4=0;
```

```matlab
while(flag1==0)
    var1= input('Enter a value for the source term s: ');
    if(var1>0)
        s=var1;
        flag1=1;
    else
        disp('            ')
        disp('ERROR: s must be positive.')
        disp('            ')
    end
end
flag1=0;
disp('            ')
while(flag1==0)
    var1= input('Enter a value for natural death rate of
T cells (m_1): ');
    if(var1>0)
        m1=var1;
        flag1=1;
    else
        disp('            ')
        disp('ERROR: m_1 must be positive.')
        disp('            ')
    end
end
flag1=0;
disp('            ')
while(flag1==0)
    var1= input('Enter a value for death rate of
infected T cells (m_2): ');
    if(var1>0)
```

```
            m2=var1;
            flag1=1;
        else
            disp('          ')
            disp('ERROR: m_2 must be positive.')
            disp('          ')
        end
    end
    flag1=0;
    disp('          ')
    while(flag1==0)
        var1= input('Enter a value for viral death rate
(m_3): ');
        if(var1>0)
            m3=var1;
            flag1=1;
        else
            disp('          ')
            disp('ERROR: m_3 must be positive.')
            disp('          ')
        end
    end
    flag1=0;
    disp('          ')
    while(flag1==0)
        var1= input('Enter a value for the T cell growth
rate (r): ');
        if(var1>0)
            r=var1;
            flag1=1;
        else
            disp('          ')
```

```matlab
        disp('ERROR: r must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter a maximum T cell level (T_max):
');
    if(var1>0)
        Tmax= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: T_max must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter a value for infection rate (k):
');
    if(var1>0)
        k= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: k must be positive.')
        disp('          ')
    end
end
```

```matlab
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter the average number of virus cells
produced (N): ');
    if(var1>0)
         N= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: N must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter an initial uninfected T cell
concentration (T_0): ');
    if(var1>0)
         T0= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: T_0 must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter an initial infected T cell
```

```matlab
concentration (T_i0): ');
    if(var1>0)
        Ti0= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: T_i0 must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter an initial free virus
concentration (V_0): ');
    if(var1>0)
        V0= var1;
        flag1=1;
    else
        disp('          ')
        disp('ERROR: V_0 must be positive.')
        disp('          ')
    end
end
flag1=0;
disp('          ')
while(flag1==0)
    var1= input('Enter a value for the weight parameter
A: ');
    if(var1>=0)
        A= var1;
        flag1=1;
```

```matlab
    else
        disp('           ')
        disp('ERROR: A must be non-negative.')
        disp('           ')
    end
end
flag1=0;
disp('              ')
while(flag1==0)
     var1= input('Enter the number of days you would like
to run this model (t_final): ');
    if(0<var1);
        time=var1;
        flag1=1;
    else
        disp('               ')
        disp('ERROR: t_final must be positive.')
        disp('               ')
    end
end
disp('             ')
disp('One moment please...')
y1=code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A,time);

disp('                ')

while(flag2==0)
    disp('Would you like to vary any parameters?')
    disp('1. Yes')
    disp('2. No')
    var2=input('Type 1 or 2: ');
```

```
    if(var2==1)
        disp('            ')
        flag2=1;
        while(flag3==0)
            disp('Which parameter would you like to
vary?')
            disp('1. s')
            disp('2. m_1')
            disp('3. m_2')
            disp('4. m_3')
            disp('5. r')
            disp('6. T_max')
            disp('7. k')
            disp('8. N')
            disp('9. T_0')
            disp('10. T_i0')
            disp('11. V_0')
            disp('12. A')
            disp('13. t_final')
            var3=input('Type 1 - 13: ');
            if(var3==1)
                disp('          ')
                while(flag4==0)
                    var4= input('Enter a second s value:
');
                    if(var4 > 0)
                        s2= var4;
                        flag4= 1;
                    else
                        disp('              ')
                        disp('ERROR: s must be positive.')
                        disp('          ')
```

```matlab
                        end
                    end
                    disp('       ')
                    disp('One moment please...')

y2=code8(s2,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A,time);
                    flag3=1;
                elseif(var3==2)
                    disp('          ')
                    while(flag4==0)
                        var4=input('Enter a second m_1 value:
');

                        if(var4 > 0)
                            m12= var4;
                            flag4= 1;
                        else
                            disp('        ')
                            disp('ERROR: m_1 must be
positive.')
                            disp('          ')
                        end
                    end
                    disp('             ')
                    disp('One moment please...')

y2=code8(s,m12,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A,time);
                    flag3=1;
                elseif(var3==3)
                    disp('          ')
                    while(flag4==0)
                        var4= input('Enter a second m_2
value: ');
```

```matlab
                        if(var4 > 0)
                            m22= var4;
                            flag4= 1;
                        else
                            disp('        ')
                            disp('ERROR: m_2 must be
positive.')
                            disp('          ')
                        end
                    end
                disp('                ')
                disp('One moment please...')

y2=code8(s,m1,m22,m3,r,Tmax,k,N,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==4)
                disp('          ')
                while(flag4==0)
                    var4=input('Enter a second m_3 value:
');
                    if(var4 > 0)
                        m32= var4;
                        flag4= 1;
                    else
                        disp('        ')
                        disp('ERROR: m_3 must be
positive.')
                        disp('          ')
                    end
                end
                disp('              ')
                disp('One moment please...')
```

```matlab
y2=code8(s,m1,m2,m32,r,Tmax,k,N,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==5)
                disp('          ')
                while(flag4==0)
                    var4=input('Enter a second r value:
');
                    if(var4 > 0)
                        r2= var4;
                        flag4= 1;
                    else
                        disp('        ')
                        disp('ERROR: r must be positive.')
                        disp('            ')
                    end
                end
                disp('                ')
                disp('One moment please...')

y2=code8(s,m1,m2,m3,r2,Tmax,k,N,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==6)
                disp('            ')
                while(flag4==0)
                    var4=input('Enter a second T_max
value: ');
                    if(var4 > 0)
                        Tmax2= var4;
                        flag4= 1;
                    else
                        disp('        ')
```

```matlab
                        disp('ERROR: T_max must be
positive.')
                        disp('            ')
                    end
                end
                disp('                ')
                disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax2,k,N,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==7)
                disp('                ')
                while(flag4==0)
                    var4=input('Enter a second k value:
');

                    if(var4 > 0)
                        k2= var4;
                        flag4= 1;
                    else
                        disp('        ')
                        disp('ERROR: k must be positive.')
                        disp('            ')
                    end
                end
                disp('                 ')
                disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k2,N,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==8)
                disp('                 ')
                while(flag4==0)
```

```matlab
                    var4=input('Enter a second N value:
');

                    if(var4 > 0)
                        N2= var4;
                        flag4= 1;
                    else
                        disp('        ')
                        disp('ERROR: N must be positive.')
                        disp('          ')
                    end
                end
                disp('                ')
                disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N2,T0,Ti0,V0,A,time);
                flag3=1;
            elseif(var3==9)
                disp('              ')
                while(flag4==0)
                    var4=input('Enter a second T_0 value:
');

                    if(var4 > 0)
                        T02= var4;
                        flag4= 1;
                    else
                        disp('       ')
                        disp('ERROR: T_0 must be
positive.')
                        disp('          ')
                    end
                end
                disp('               ')
```

```matlab
                    disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N,T02,Ti0,V0,A,time);
                    flag3=1;
                elseif(var3==10)
                    disp('              ')
                    while(flag4==0)
                        var4=input('Enter a second T_i0
value: ');
                        if(var4 > 0)
                            Ti02= var4;
                            flag4= 1;
                        else
                            disp('      ')
                            disp('ERROR: T_i0 must be
positive.')
                            disp('          ')
                        end
                    end
                    disp('                ')
                    disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti02,V0,A,time);
                    flag3=1;
                elseif(var3==11)
                    disp('               ')
                    while(flag4==0)
                        var4=input('Enter a second V_0 value:
');
                        if(var4 > 0)
                            V02= var4;
                            flag4= 1;
```

```matlab
                        else
                            disp('          ')
                            disp('ERROR: V_0 must be
positive.')
                            disp('          ')
                        end
                    end
                    disp('              ')
                    disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V02,A,time);
                    flag3=1;
                elseif(var3==12)
                    disp('              ')
                    while(flag4==0)
                        var4=input('Enter a second A value:
');

                        if(var4 >= 0)
                            A2= var4;
                            flag4= 1;
                        else
                            disp('          ')
                            disp('ERROR: A must be
non-negative.')
                            disp('          ')
                        end
                    end
                    disp('              ')
                    disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A2,time);
                    flag3=1;
```

```
        elseif(var3==13)
            disp('              ')
            while(flag4==0)
                var4=input('Enter a second t_final
value: ');

                if(var4 > 0)
                    time2= var4;
                    flag4= 1;
                else
                    disp('      ')
                    disp('ERROR: t_final must be
positive.')
                    disp('            ')
                end
            end
            disp('              ')
            disp('One moment please...')

y2=code8(s,m1,m2,m3,r,Tmax,k,N,T0,Ti0,V0,A,time2);
            flag3=1;
        else
            disp('           ')
            disp('Pardon?')
            disp('            ')
        end
    end

  elseif(var2==2)
        disp('            ')
        flag2=1;
        scf(1)
        subplot(4,1,1);plot(y1(1,:),y1(2,:))
```

```matlab
            subplot(4,1,1);xlabel('Days')
            subplot(4,1,1);ylabel('T')
            subplot(4,1,2);plot(y1(1,:),y1(3,:))
            subplot(4,1,2);xlabel('Days')
            subplot(4,1,2);ylabel('T_i')
            subplot(4,1,3);plot(y1(1,:),y1(4,:))
            subplot(4,1,3);xlabel('Days')
            subplot(4,1,3);ylabel('V')
            subplot(4,1,4);plot(y1(1,:),y1(5,:))
            subplot(4,1,4);xlabel('Days')
            subplot(4,1,4);ylabel('u^*')
            subplot(4,1,4);axis([0 time-0.1 1.1])
    else
        disp('      ')
        disp('Pardon?')
        disp('            ')
    end
end

if(var2==1)

subplot(4,1,1);plot(y1(1,:),y1(2,:),'b',y2(1,:),y2(2,:),'g
')
    subplot(4,1,1);xlabel('Days')
    subplot(4,1,1);ylabel('T')
    subplot(4,1,1);legend('First value','Second value')

subplot(4,1,2);plot(y1(1,:),y1(3,:),'b',y2(1,:),y2(3,:),'g
')
    subplot(4,1,2);xlabel('Days')
    subplot(4,1,2);ylabel('T_i')
    subplot(4,1,2);legend('First value','Second value')
```

```
subplot(4,1,3);plot(y1(1,:),y1(4,:),'b',y2(1,:),y2(4,:),'g
')
    subplot(4,1,3);xlabel('Days')
    subplot(4,1,3);ylabel('V')
    subplot(4,1,3);legend('First value','Second value')

subplot(4,1,4);plot(y1(1,:),y1(5,:),'b',y2(1,:),y2(5,:),'g
')
    subplot(4,1,4);xlabel('Days')
    subplot(4,1,4);ylabel('u^*')
    subplot(4,1,4);legend('First value','Second value')
    if(var3==13)
        subplot(4,1,4);mtlb_axis([0 max(time,time2) -0.1
1.1])
    else
        subplot(4,1,4);mtlb_axis([0  time-0.1 1.1])
    end
end
```

A.5 Control Systems

A.5.1 Hodgkin_Huxley.sce

```
function  dx=hodgkinhuxley(t,x)
alpham = 0.1*(25-x(1))/(exp((25-x(1))/10)-1)
betam = 4*exp(-x(1)/18)
alphah = 0.07*exp(-x(1)/20)
betah = 1/(exp((30-x(1))/10)+1)
alphan = 0.01*(10-x(1))/(exp((10-x(1))/10)-1)
betan = 0.125*exp(-x(1)/80)
dx(1) =
(-gk*x(3)^4*(x(1)-vk)-gna*x(2)^3*x(4)*(x(1)-vna)-gl*(x(1)-
vl)+iapp)/cm
dx(2) = alpham*(1-x(2))-betam*x(2)
dx(3) = alphan*(1-x(3))-betan*x(3)
dx(4) = alphah*(1-x(4))-betah*x(4)
endfunction

scf(0);
clf;
cm = 1
gk = 36
vk = -12
iapp = 0
gna = 120
vna = 115
gl = 0.3
vl = 10.6
t = 0:0.001:55;
x0 = [0 ;0; 0; 1];
x = ode(x0,0,t,hodgkinhuxley);

//xbasc()
plot2d(t,x(1,:),style=1)
//legends(['Voltage'],[1],"ur")
```

```
                  xtitle('Action Potential')
                  xlabel('Time')
                  ylabel('Potential')
```

A.5.2 Fitzhugh_Nagumo.sce

```
        function dx=actionpotential(t,x)
        dx(1) = x(1)*(x(1)-0.1)*(1-x(1))-x(2)+I
        dx(2) = 0.01*(x(1)-0.5*x(2))
        endfunction

        scf(1);
        clf;
        I = 0
        t = 0:0.001:550;
        x0 = [0.22 ;0;];
        x = ode(x0,0,t,actionpotential);

        //xbasc()
        plot2d(t,x(1,:),style=1)
        //legends(['A','B'],[1 2],"ur")
        xtitle('Action Potential')
        xlabel('Time')
        ylabel('Potential')
```

A.6 Immune System

A.6.1 SIR.sce

```
clear
function dx= SIR(t,x)
dx(1) =-r*x(1)*x(2)
dx(2) = r*x(1)*x(2)-a*x(2)
dx(3) = a*x(2)
dx(4) = 0
endfunction

scf(1);
clf;
r = .000007;
a = .03
t = 0:0.001:600;
S0 = 10000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

A.7 Genetics

A.7.1 allele_frequency.sce

```
function  dx=genetics(t,x)
fA = x(1)*fAA+(1-x(1))*fAa
fa = x(1)*fAa+(1-x(1))*faa
f = x(1)*fA+(1-x(1))*fa
dx(1) = x(1)*(1-x(1))*(fA-fa)
dx(2) = x(2)*f
dx(3) = -x(1)*(1-x(1))*(fA-fa)
endfunction

fAA = 1.0
fAa = 1.0
faa = 0.5
t = 0:0.001:100;
x0 = [0.5 ;100000; 0.5];
x = ode(x0,0,t,genetics);

//xbasc()
scf(0);
plot2d(t,x(1,:),style=1)
plot2d(t,x(3,:),style=2)
legends(['A', 'a'],[1 2],"ur")
xlabel('Time')
ylabel('AlleleFrequency')
```

A.8 Alternation of Generations

A.8.1 dispersal.sce

```
function dx=dispersal(t,p)
  global m c q n;
  for  i= 1:n
     sum1= 0.0
     sum2= 0.0
    for  j= 1:i ;
       sum1=  sum1+p(j);
    end
    for  j= 1:(i-1)
       sum2=  sum2+c(j)*p(i)*p(j)
    end
     dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:2000;
  global c m n q
   m= [.02; .02; .02; .02; .02];
   c= [.025; .039; .061; .095; .149];
   n= 5;
   q= [0; 0; 0; 0; 0];
   p0= [.082; .1024; .128; .16; .2]
   p= ode(p0,0,t,dispersal);
  scf(1);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

A.9   Speciation

A.9.1   fitness.sce

```
//exposed
  theta= 0;
  x= 0:.1:1;
  sigma(1)= .02;
  for  i= 1:3
    sigma(i)= .02+.06*(i-1)
  end
  w1= exp(-(x-theta).^2/(2.*sigma(1)));
  w2= exp(-(x-theta).^2/(2.*sigma(2)));
  w3= exp(-(x-theta).^2/(2.*sigma(3)));
  scf(1); clf;
  subplot(3,1,1)
  plot(x,w1,'b:',x,w2,'r-',x,w3,'k--')
  title('Exposed (theta = 0)')
  xlabel('x');
  ylabel('Fitness, w');
  legend('sigma_s = 0.02','sigma_s = 0.08', 'sigma_s =
0.14');

//intermediate
  theta= 0.5;
  x= 0:.1:1;
  sigma(1)= .02;
  for  i= 1:3
    sigma(i)= .02+.06*(i-1)
  end
  w1= exp(-(x-theta).^2/(2.*sigma(1)));
  w2= exp(-(x-theta).^2/(2.*sigma(2)));
  w3= exp(-(x-theta).^2/(2.*sigma(3)));
  scf(1);
  subplot(3,1,2)
  plot(x,w1,'b:',x,w2,'r-',x,w3,'k--')
```

```
title('Intermediate (theta = 0.5))'
xlabel('x');
ylabel('Fitness, w');
legend('sigma_s = 0.02','sigma_s = 0.08', 'sigma_s =
0.14');

//sheltered
  theta= 1.0;
  x= 0:.1:1;
  sigma(1)= .02;
  for  i= 1:3
    sigma(i)= .02+.06*(i-1)
  end
  w1= exp(-(x-theta).^2/(2.*sigma(1)));
  w2= exp(-(x-theta).^2/(2.*sigma(2)));
  w3= exp(-(x-theta).^2/(2.*sigma(3)));
  scf(1);
  subplot(3,1,3)
  plot(x,w1,'b:',x,w2,'r-',x,w3,'k--')
  title('Sheltered (theta = 1.0)')
  xlabel('x');
  ylabel('Fitness, w');
  legend('sigma_s = 0.02','sigma_s = 0.08', 'sigma_s =
0.14',2);
```

A.9.2 mating_probability.sce

```
//f = 0.000
  sigma_a= 0.05
   x= 0:.05:1;
   f= 0.000;
   c(1)= 0.000;
  for  i= 1:9
     c(i)= 0.125.*(i-1);
  end
   psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
   psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
   psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
   psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
   psi5= 1;
   psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
   psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
   psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
   psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  scf(1); clf;
  subplot(3,1,1)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
  title('f = 0.000')
  xlabel('x');
  ylabel('Psi');
  legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

  //f = 0.125
  sigma_a= 0.05
```

```
x= 0:.05:1;
f= 0.125;
c(1)= 0.000;
for  i= 1:9
    c(i)= 0.125.*(i-1);
end
psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi5= 1;
psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
scf(1);
subplot(3,1,2)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
title('f = 0.125')
xlabel('x');
ylabel('Psi');
legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

//f = 0.250
    sigma_a= 0.05
x= 0:.05:1;
f= 0.250;
```

```
 c(1)= 0.000;
 for  i= 1:9
   c(i)= 0.125.*(i-1);
 end
 psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
 psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
 psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
 psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
 psi5= 1;
 psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
 psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
 psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
 psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
 scf(1);
 subplot(3,1,3)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
 title('f = 0.250')
 xlabel('x');
 ylabel('Psi');
 legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

 //f = 0.375
   sigma_a= 0.05
 x= 0:.05:1;
 f= 0.375;
 c(1)= 0.000;
 for  i= 1:9
```

```
    c(i)= 0.125.*(i-1);
  end
  psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi5= 1;
  psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  scf(2);
  subplot(3,1,1)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
  title('f = 0.375')
  xlabel('x');
  ylabel('Psi');
  legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');



  //f = 0.500
    sigma_a= 0.05
  x= 0:.05:1;
  f= 0.500;
  c(1)= 0.000;
  for  i= 1:9
```

```
    c(i)= 0.125.*(i-1);
  end
  psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi5= 1;
  psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  scf(2);
  subplot(3,1,2)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
  title('f = 0.500')
  xlabel('x');
  ylabel('Psi');
  legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

  //f = 0.625
    sigma_a= 0.05
  x= 0:.05:1;
  f= 0.625;
  c(1)= 0.000;
  for  i= 1:9
    c(i)= 0.125.*(i-1);
  end
```

```
  psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi5= 1;
  psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
 scf(2);
 subplot(3,1,3)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
 title('f = 0.625')
 xlabel('x');
 ylabel('Psi');
 legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

 //f = 0.750
   sigma_a= 0.05
 x= 0:.05:1;
 f= 0.750;
 c(1)= 0.000;
 for  i= 1:9
   c(i)= 0.125.*(i-1);
 end
 psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
 psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
```

```
psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi5= 1;
psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
scf(3);
subplot(3,1,1)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
title('f = 0.750')
xlabel('x');
ylabel('Psi');
legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

//f = 0.875
sigma_a= 0.05
x= 0:.05:1;
f= 0.875;
c(1)= 0.000;
for  i= 1:9
c(i)= 0.125.*(i-1);
end
psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
```

```
  psi5= 1;
  psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
  scf(3);
  subplot(3,1,2)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
  title('f = 0.875')
  xlabel('x');
  ylabel('Psi');
  legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');

  //f = 1.000
    sigma_a= 0.05
  x= 0:.05:1;
  f= 1.000;
  c(1)= 0.000;
  for  i= 1:9
    c(i)= 0.125.*(i-1);
  end
  psi9= exp(-(2.*c(1)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi8= exp(-(2.*c(2)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi7= exp(-(2.*c(3)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi6= exp(-(2.*c(4)-1).^2.*(f-x).^2/(2.*sigma_a).^2);
  psi5= 1;
  psi4= exp(-(2.*c(6)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
```

```
psi3= exp(-(2.*c(7)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi2= exp(-(2.*c(8)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
psi1= exp(-(2.*c(9)-1).^2.*(f-1+x).^2/(2.*sigma_a).^2);
scf(3);
subplot(3,1,3)

plot(x,psi1,'r-',x,psi2,'b-',x,psi3,'k-',x,psi4,'m-',x,psi
5,'r:.',x,psi6,'r-.',x,psi7,'b-.',x,psi8,'k-.',x,psi9,'m-.
')
title('f = 1.000')
xlabel('x');
ylabel('Psi');
legend('c = 0.000','c = 0.125','c = 0.250','c =
0.375','c = 0.500','c = 0.625','c = 0.750','c = 0.875','c
= 1.000');
```

A.10   Animal Body Plan

A.10.1   Jukes-Cantor.sce

```
a=.06;
b=a/3;
M=[1-a,b,b,b;b,1-a,b,b;b,b,1-a,b;b,b,b,1-a];
p=[.25;.25;.25;.25];
P=p;
for i=1:100
  p=M*p;
  P=[P p];
end;
scf(2);
plot(P')
legend('A','G','C','T');
```

A.11   Animal Form and Function

A.11.1   Jukes-Cantor_differences.sce

```
alpha = 0.01;
t = 0:.1:400;
p1 = (3/4)-(3/4)*(1-((4*alpha)/3)).^t;
p2 = (3/4)-(3/4)*(1-((40*alpha)/3)).^t;
p3 = (3/4)-(3/4)*(1-((100*alpha)/3)).^t;
plot(t,p1,'b:',t,p2,'r-',t,p3,'k--')
title('p(t) for different values of alpha')
xlabel('t');
ylabel('p(t)');
legend('alpha = 0.01','alpha = 0.1', 'alpha = 0.25',  opt= 4);
```

A.11.2   Jukes-Cantor_distance.sce

```
p =0:.00001:0.7499999999;
djc = -(3/4)*log(1-((4.*p)/3));
plot(p,djc)
title('Jukes-Cantor Distances)
xlabel('p');
ylabel('Jukes-Cantor distance);
```

A.12 Predation

A.12.1 predator_prey1.sce

```
//Model #1
t = 1:1:152;
r = 2.5;
w(1) = 0.6;
z(1) = 0.1;
for  i= 1:151
  w(i+1)=r.*w(i)./(1+z(i));
  z(i+1)=w(i).*z(i)./(1+z(i));
end
scf(1);
subplot(1,2,2)
plot(w,z);
xlabel('prey');
ylabel('predator');
subplot(1,2,1);
plot(t,w,'r-',t,z,'k--');
xlabel('generation');
ylabel('population size');
legend('prey','predator');
```

A.12.2   predator_prey2.sce

```
//Model #2
t = 1:1:152;
l = 2.1;//(r)
m = .6;//(a)
k = 5;
a(1) = 0.1;
b(1) = 0.6;
for  i= 1:151
  a(i+1)=a(i).*exp(l.*(1-a(i)./k)-m.*b(i));
  b(i+1)=a(i).*(1-exp(-m.*b(i)));
end
scf(2);
subplot(1,2,2);
plot(a,b);
xlabel('prey');
ylabel('predator');
subplot(1,2,1);
plot(t,a,'r-',t,b,'k--');
xlabel('generation');
ylabel('population size');
legend('prey','predator');
```

A.12.3   predator_prey3.sce

```
//Model #3
t = 1:1:152;
g = .35;
c(1) = .1;
d(1) = 0.01;
for  i= 1:151
  c(i+1)=(1-c(i)).*c(i)-g.*d(i);
  d(i+1)=.5.*d(i)+c(i);
end
scf(3);
subplot(1,2,2);
plot(c,d);
xlabel('prey');
ylabel('predator');
subplot(1,2,1);
plot(t,c,'r-',t,d,'k--');
xlabel('generation');
ylabel('population size');
legend('prey','predator');
```

A.13 Population Ecology

A.13.1 competition.sce

```
//Model #1
t = 1:1:252;
b1 = 1.5;
b2 = 1.5;
c11 = 1;
c12 = .25;
c21 = .25;
c22 = 1;
x(1) = 1.6;
y(1) = 1.1;
for  i= 1:251
  x(i+1)=b1.*x(i)./(1+c11.*x(i)+c12.*y(i));
  y(i+1)=b2.*y(i)./(1+c21.*x(i)+c22.*y(i));
end
scf(1); clf;
subplot(2,2,1)
plot(t,x,'k-',t,y,'r--');
title('Model #1')
xlabel('time');
ylabel('population size);
legend('x','y');

//Model #2
t = 1:1:252;
b1 = 1.5;
b2 = 1.5;
c11 = 1;
c12 = .25;
c21 = .25;
c22 = 1;
x(1) = 1.6;
y(1) = 1.1;
```

```
for  i= 1:251
  x(i+1)=b1.*x(i)./(1+c11.*x(i)+c12.*y(i));
  y(i+1)=b2.*y(i)./(1+c21.*x(i)+c22.*y(i));
end
scf(1);
subplot(2,2,2);
plot(t,x,'k-',t,y,'r--');
title('Model #2')
xlabel('time');
ylabel('population size);
legend('x','y');

//Model #3
t = 1:1:252;
b1 = 1.5;
b2 = 1.5;
c11 = 1;
c12 = .25;
c21 = .25;
c22 = 1;
x(1) = 1.6;
y(1) = 1.1;
for  i= 1:251
  x(i+1)=b1.*x(i)./(1+c11.*x(i)+c12.*y(i));
  y(i+1)=b2.*y(i)./(1+c21.*x(i)+c22.*y(i));
end
scf(1);
subplot(2,2,3);
plot(t,x,'k-',t,y,'r--');
title('Model #3')
xlabel('time');
ylabel('population size);
```

```
legend('x','y');

//Model #4
t = 1:1:252;
b1 = 1.5;
b2 = 1.5;
c11 = 1;
c12 = .25;
c21 = .25;
c22 = 1;
x(1) = 1.6;
y(1) = 1.1;
for  i= 1:251
  x(i+1)=b1.*x(i)./(1+c11.*x(i)+c12.*y(i));
  y(i+1)=b2.*y(i)./(1+c21.*x(i)+c22.*y(i));
end
scf(1);
subplot(2,2,4);
plot(t,x,'k-',t,y,'r--');
title('Model #4')
xlabel('time');
ylabel('population size);
legend('x','y');
```

Appendix B

Workshop Leader Guides

B.1 Introduction to Scilab

QUESTION: Download the file oracle.sce. What is the result of executing the file oracle.sce? Discuss the correct answer with your peers.

Solution: Executing the file oracle.sce produces the following graph:

Data points in red x; Blue dotted line is best linear fit
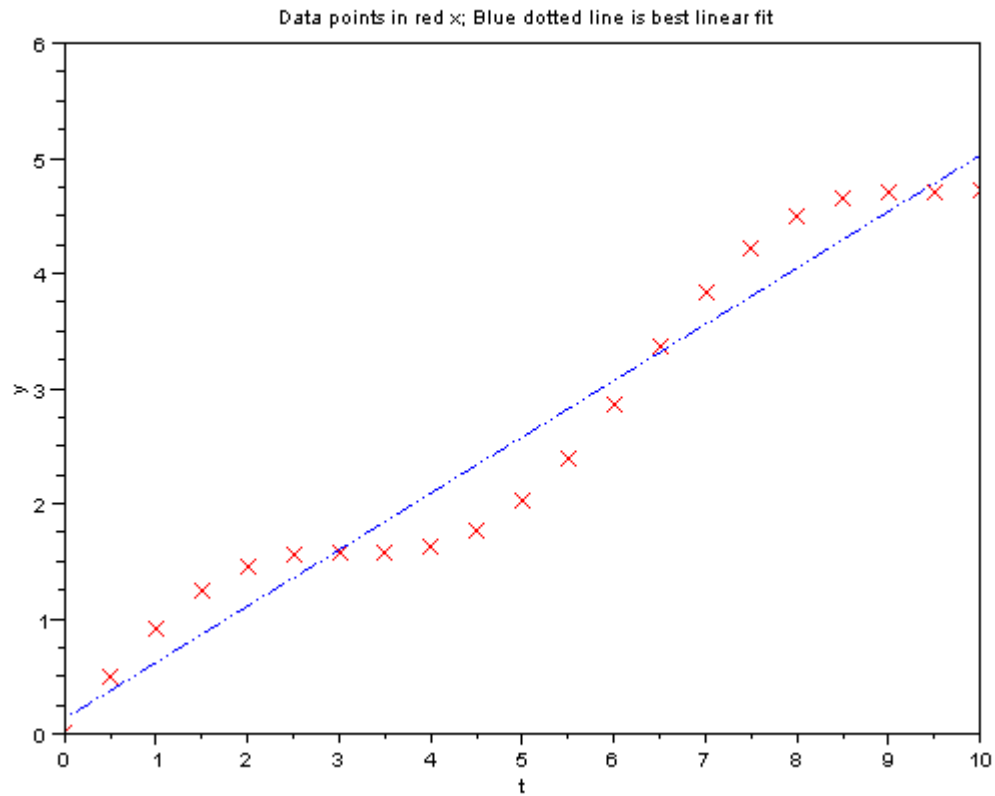
Note: Executing the file introduction_lab.sce does not produce a graph. The list of commands from the .sce files will be displayed in the Scilab console but otherwise, Scilab won't do anything.

QUESTION: What is the value of $sum1(8)$?

Solution: If you type $sum1(8)$ into the Scilab console, it will give you the answer:

$$\boxed{sum1(8) = 36}$$

Note: The Scilab code for the file introduction_lab2.sce that the students will be creating should look as follows:

```
lines(0);

function y=sum2(n)
// sum2(n) computes the sum of 1^2 + 2^2 + ... + n^2
total =  0;
for  i= 1:n,
        total=  total+ i^2;
end;
y = total;
endfunction;

function  out=firstRowDown(in)
row1 = in(1,:);
n = size(in,2);
for  i= 1:n,
        out(i,1) = row1(i);
end;
endfunction

function  out=firstRowDownSecondColumn(in)
row1 = in(1,:);
n = size(in,2);
for  i= 1:n,
        out(i,2) = row1(i);
end;
endfunction

function  out=countDownNumberOfColumns(in)
n = size(in,2);
for  i= 1:n,
        out(i,1) = i;
end;
endfunction
```

QUESTION: What is the value of $sum2(8)$?

Solution: Executing the file introduction_lab2.sce again does not produce a graph.

But now if you type $sum2(8)$ into Scilab, you get the answer:

$$sum2(8) = 204$$

B.2 The Cell and Biomolecules

Note: Executing the file **diffusionleft.sce** produces the following graph:
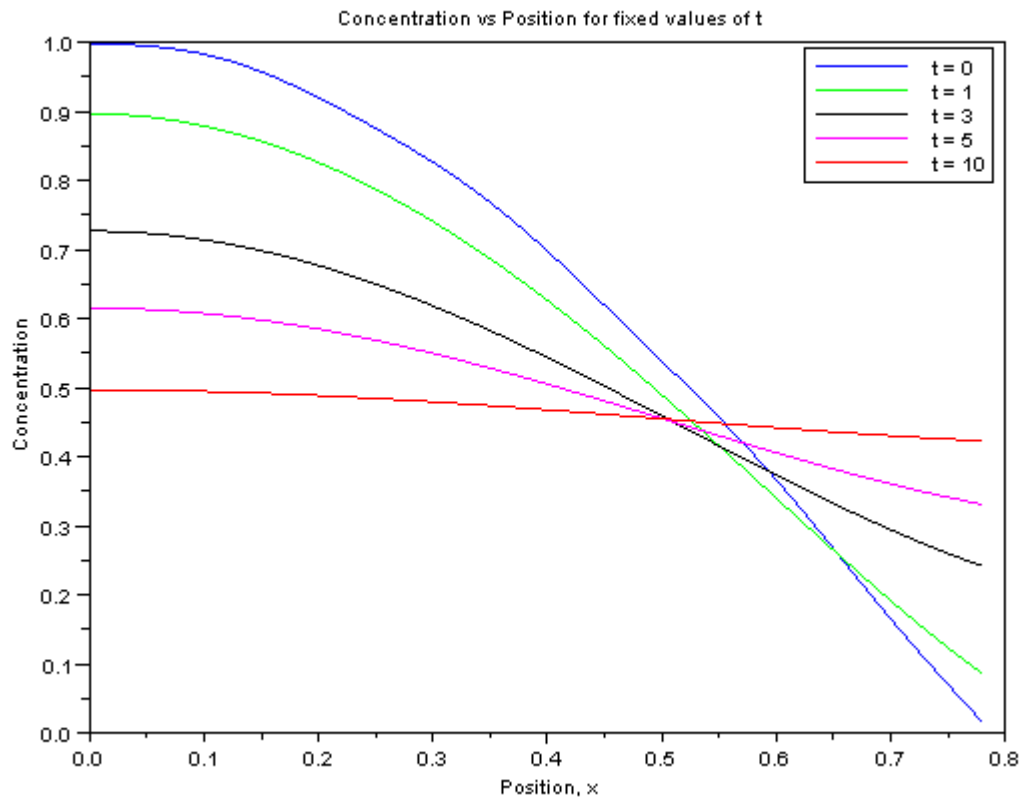
QUESTION: Describe what you see in the graph.

Solution: Initially (time $t = 0$), the concentration is high on the left side and low on the left side, but as time passes, the concentration on the left side decreases and the concentration on the right side increases until the concentration on the two sides nearly evens out at time $t = 10$.

Note: Executing the file **diffusioncenter.sce** produces the following graph:
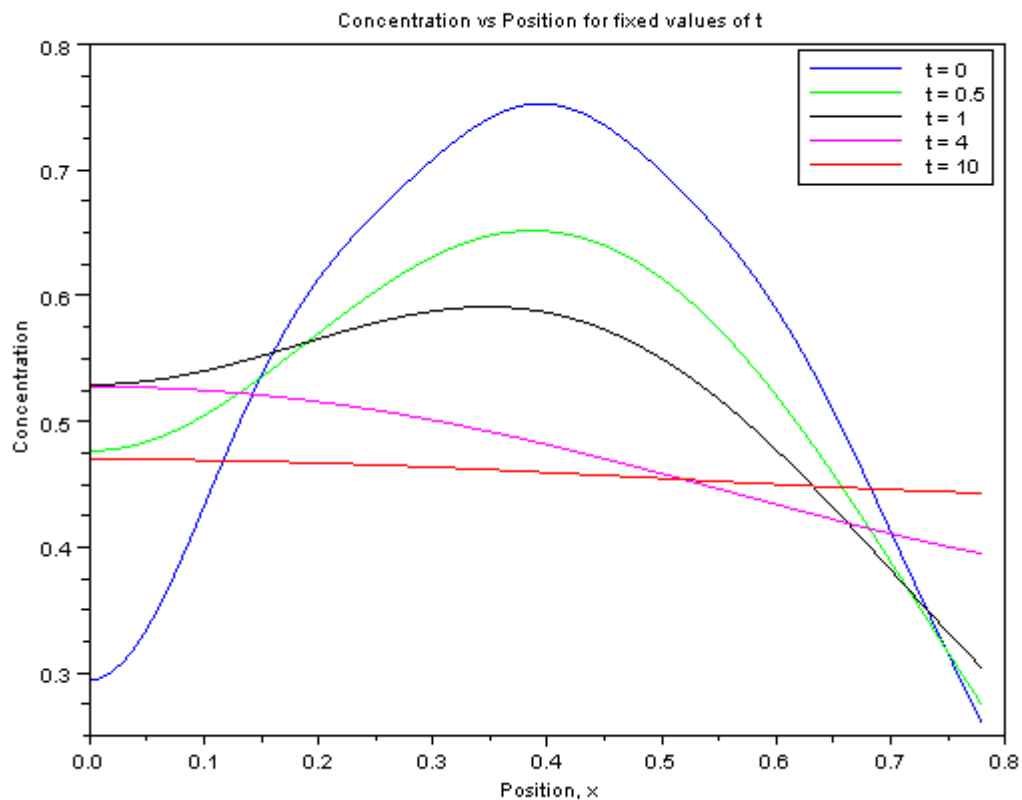
Concentration vs Position for fixed values of t

QUESTION: Describe what you see in the graph.

Solution: Initially (time $t = 0$), the concentration is high in the center and it decreases as you move away from the center, either to the left or to the right. As time

passes, the concentration evens out a bit, more on the left than the right initially, until at time $t = 10$ when the concentration is nearly even at all positions.

QUESTION: What is the affect of changing the temperature from 298 to 398? From 298 to 198? How does temperature affect diffusion?

Solution: After changing the temperature from 298 to 398 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 398;
u = 0.498;
a = .0001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(1);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 398;
u = 0.498;
a = .0001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(11);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```
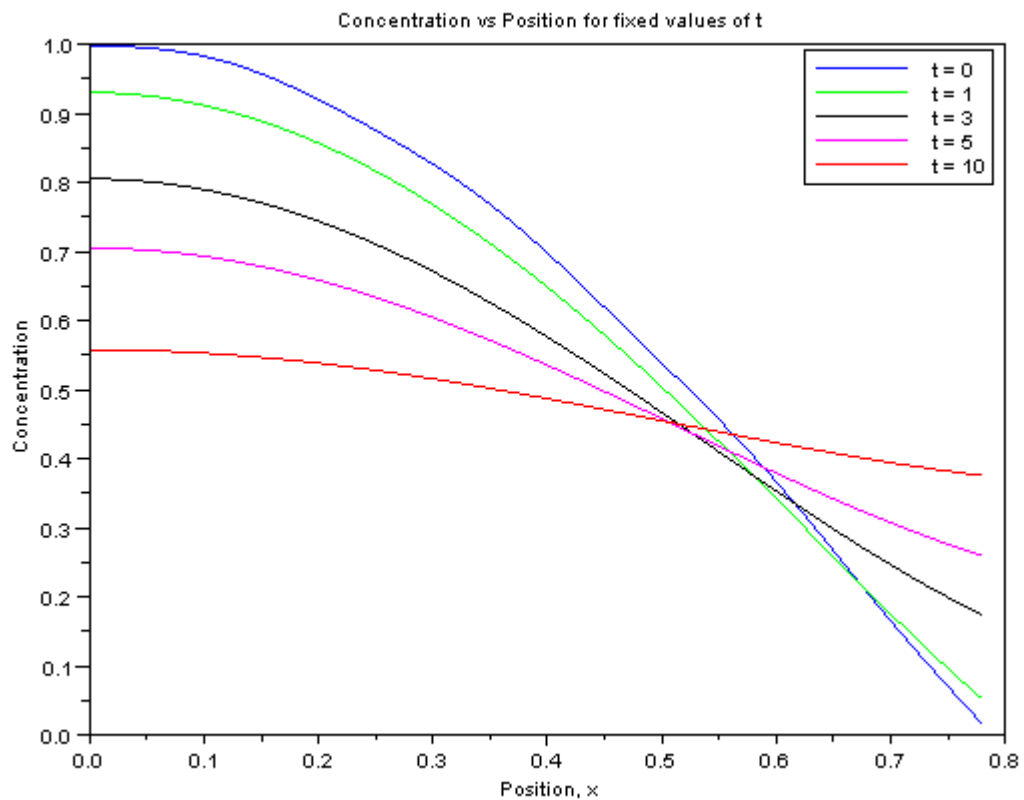
Executing this code produces the following graph:

Concentration vs Position for fixed values of t
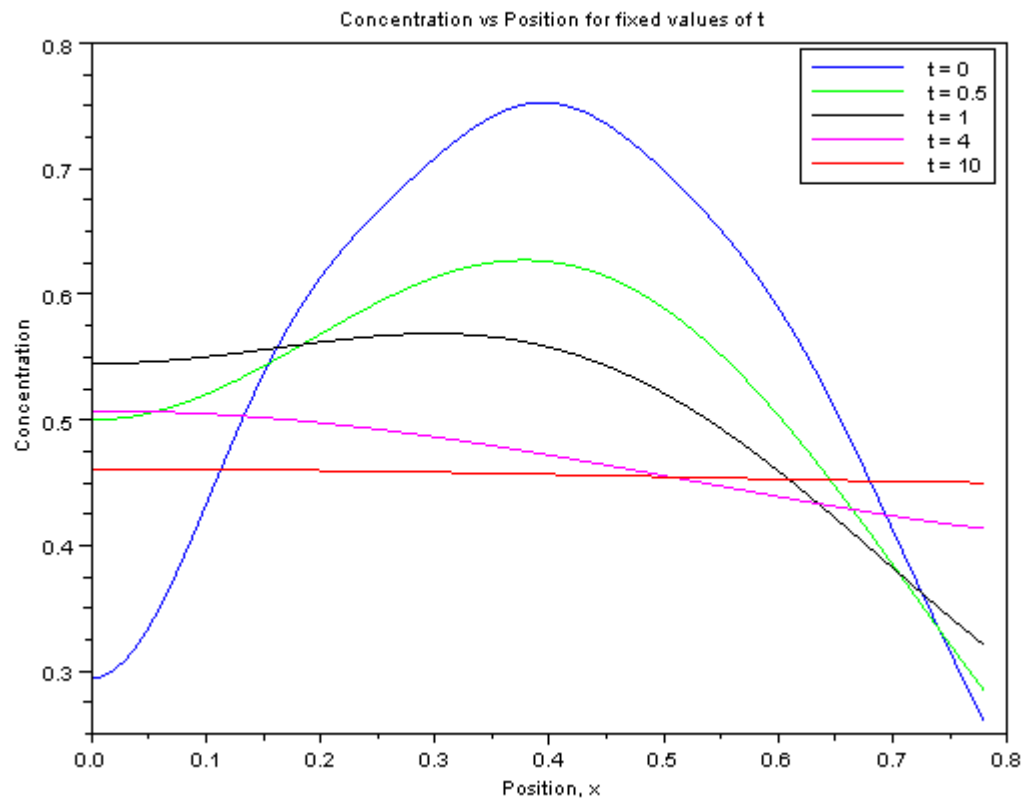
After changing the temperature to 198 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 198;
u = 0.498;
a = .0001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(2);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 198;
u = 0.498;
a = .0001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(12);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```
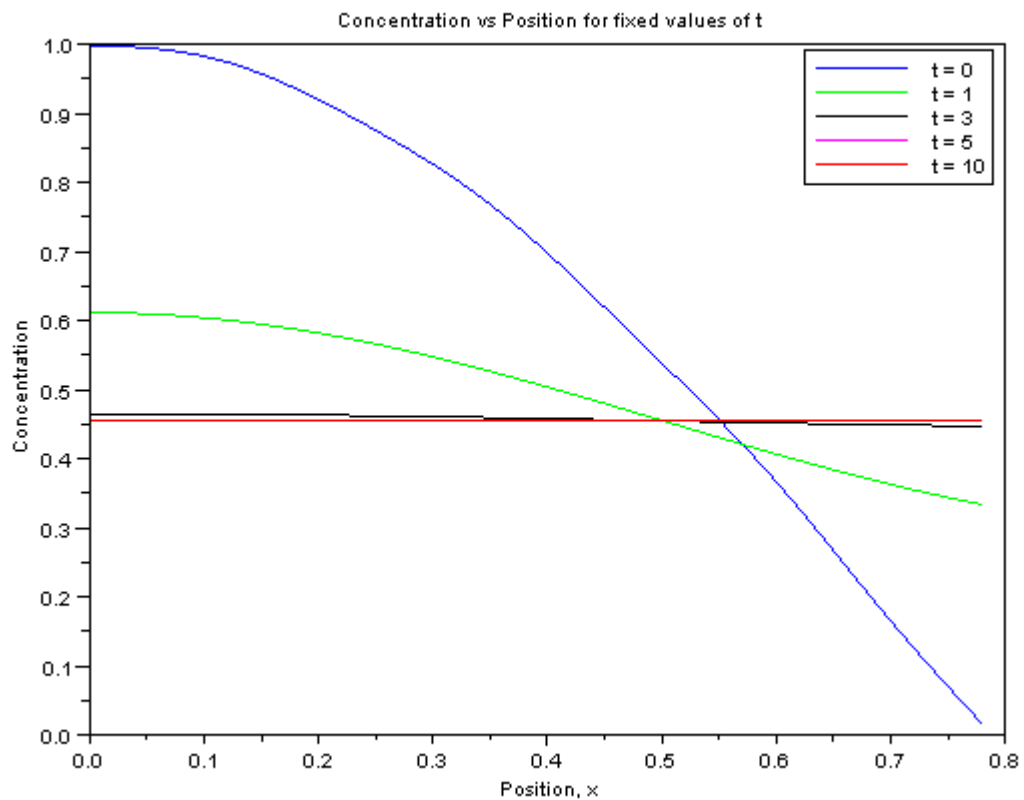
Executing this code produces the following graph:

Concentration vs Position for fixed values of t
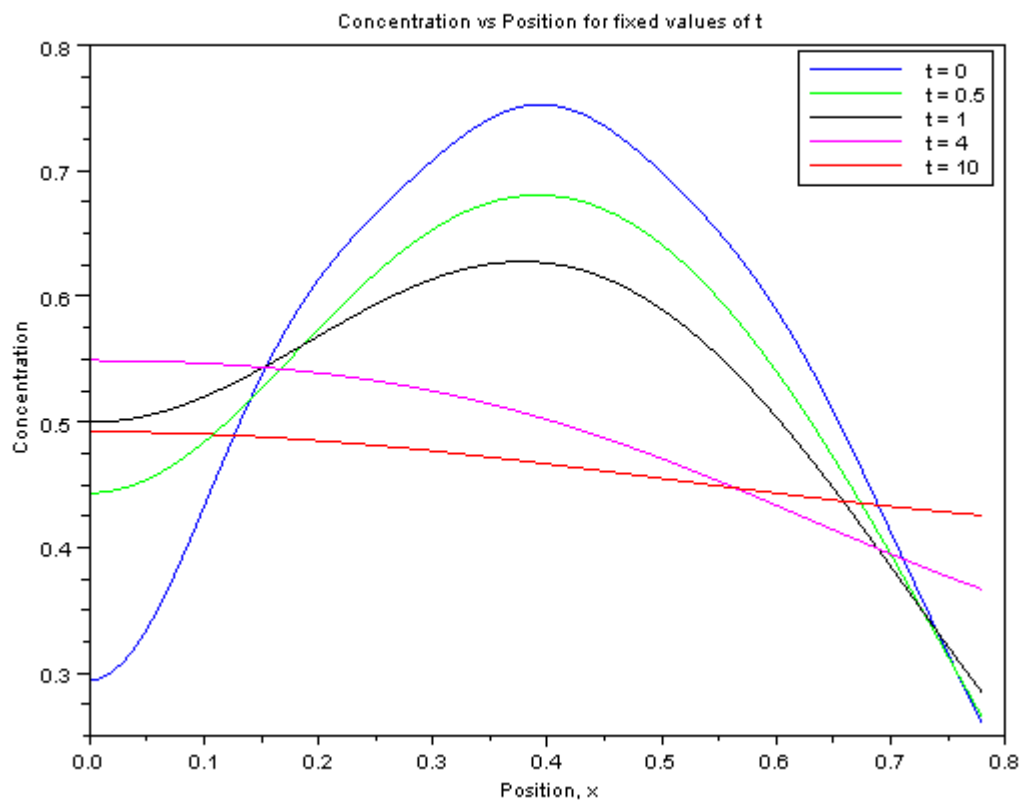
From these graphs we see that the higher the temperature, the faster the concentrations even out. The differences between the graphs is kind of subtle, but if you look at say the diffusionleft file and compare the concentrations at position 0 (you could use the other file or look at any other position but these seem like they are the easiest to see), you will see that for $T = 198$ (graphics window 2), the concentration at time $t = 1$ is around 0.93, at time $t = 3$ the concentration is around 0.81, and at time $t = 5$ the concentration is around 0.71. For $T = 298$ (graphics window 0), the concentration at position 0 at time $t = 1$ is around 0.9, at time $t = 3$ the concentration is around 0.73, and at time $t = 5$ the concentration is around 0.62, so the concentrations are getting close to 0.5 faster with the higher temperature. And for

$T = 398$ (graphics window 1), the concentration at position 0 at time $t = 1$ is about 0.87, the concentration at time $t = 3$ is around 0.67, and the concentration at time $t = 5$ is around 0.56, so the concentration is getting closer to 0.5 even faster now that the temperature is even higher.

QUESTION: What is the affect of changing the viscosity from 0.498 to 0.098? From 0.498 to 0.998? How does viscosity affect diffusion?

Solution: After changing the viscosity from 0.498 to 0.098 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.098;
a = .0001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(3);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.098;
a = .0001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(13);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```
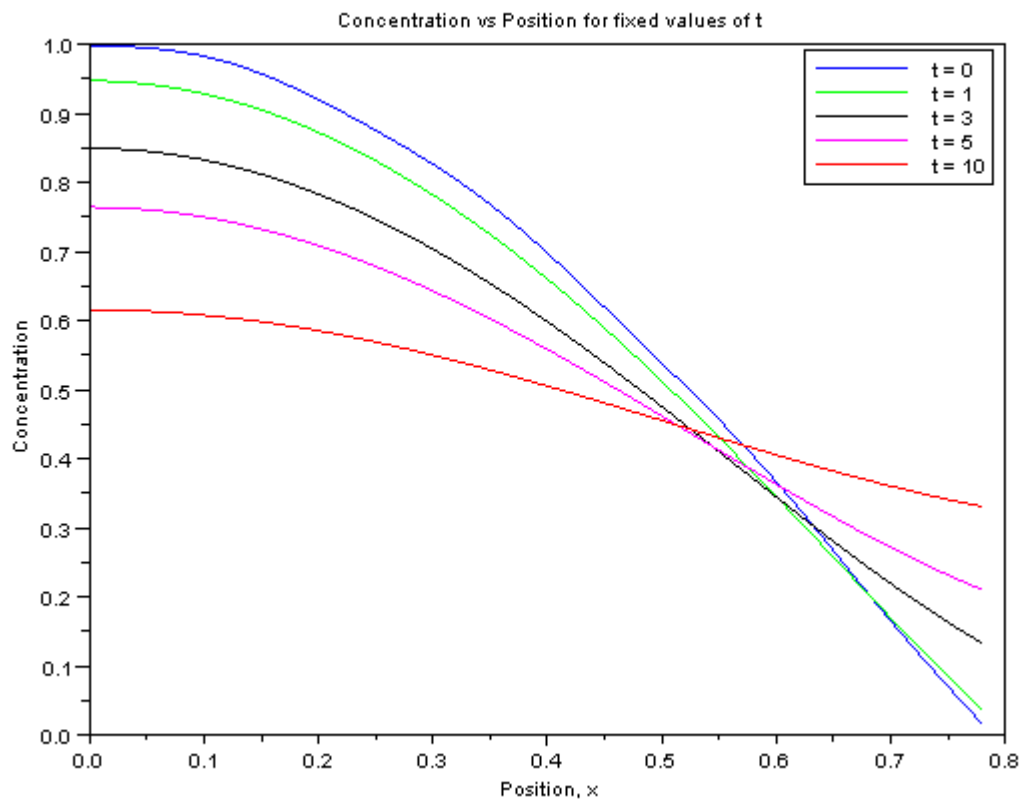
Executing this code produces the following graph:

Concentration vs Position for fixed values of t
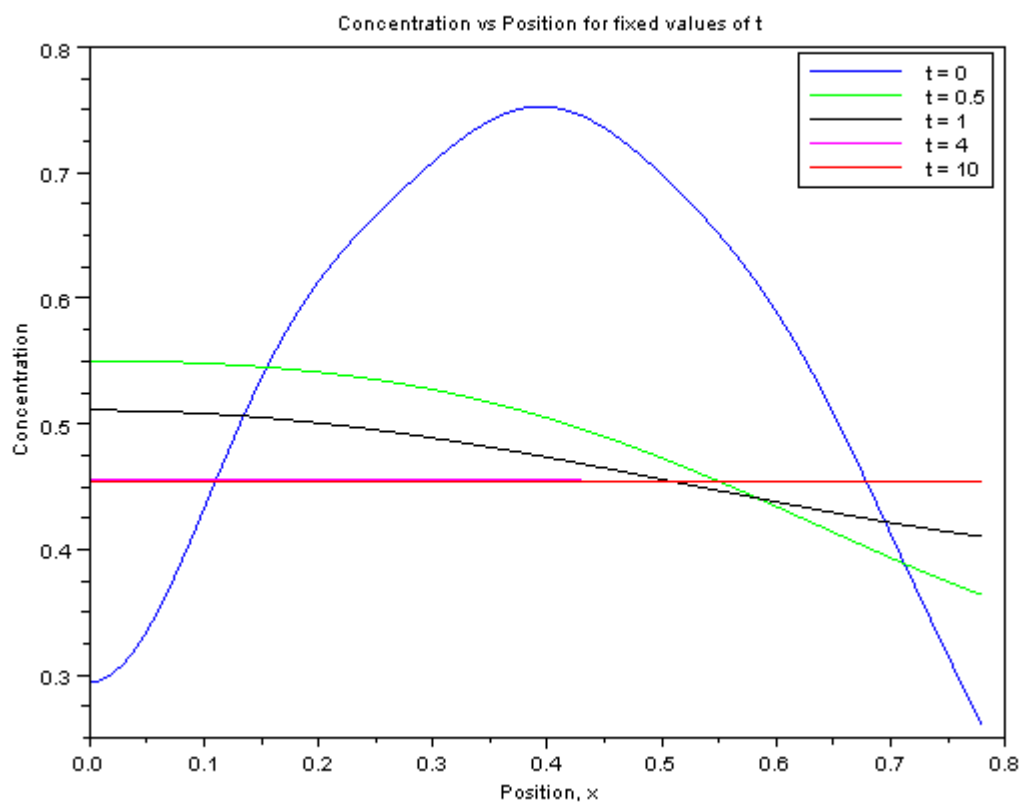
After changing the viscosity to 0.998 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.998;
a = .0001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(4);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.998;
a = .0001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(14);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```
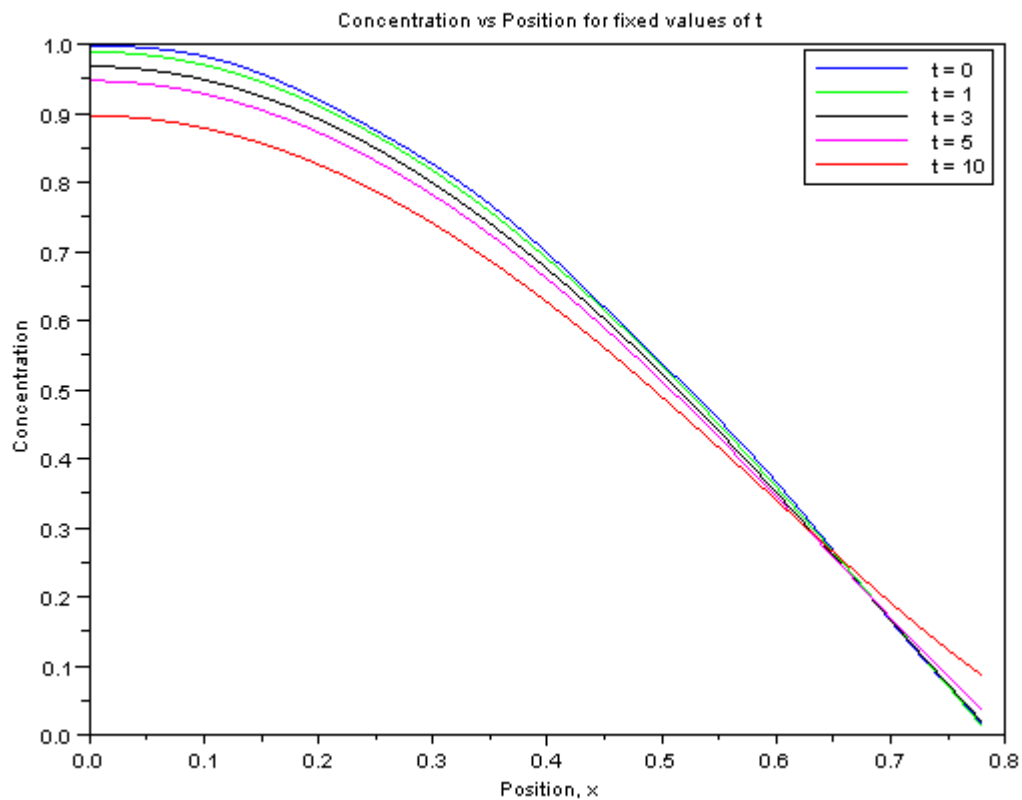
Executing this code produces the following graph:

Concentration vs Position for fixed values of t
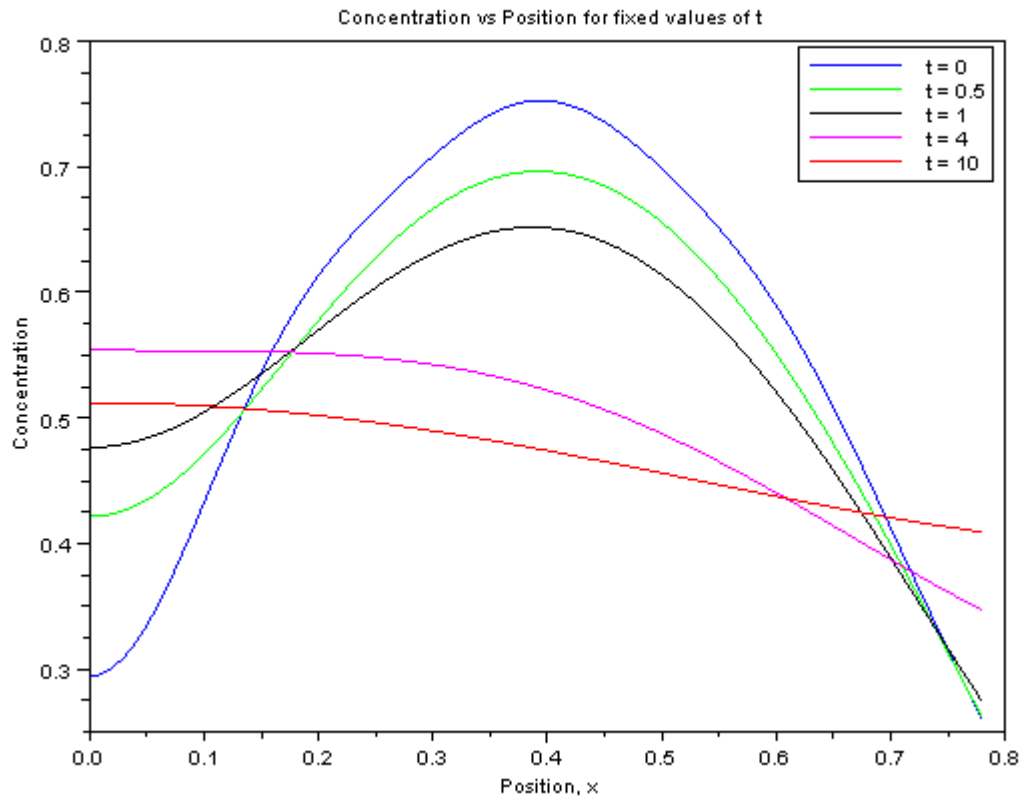
From these graphs we see that the lower the viscosity, the faster the concentrations even out. The differences here are a bit easier to see. If you look at say the diffusioncenter file you see that when the viscosity is 0.098 (graphics window 13), then by time $t = 4$, the concentrations are evened out. When the viscosity is 0.498 (graphics window 10), the concentration is nearly evened out by time $t = 10$. And when the viscosity is 0.998 (graphics window 14), even by time $t = 10$, the concentration on the left is a bit higher than the concentration on the right so even more time would be needed for the concentration to even out.

QUESTION: What is the affect of changing the cell size from 0.0001 to 0.001? From 0.0001 to 0.00001? How does cell size affect diffusion?

Solution: After changing the cell size from 0.0001 to 0.001 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .001;
D = 0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(5);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(15);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```
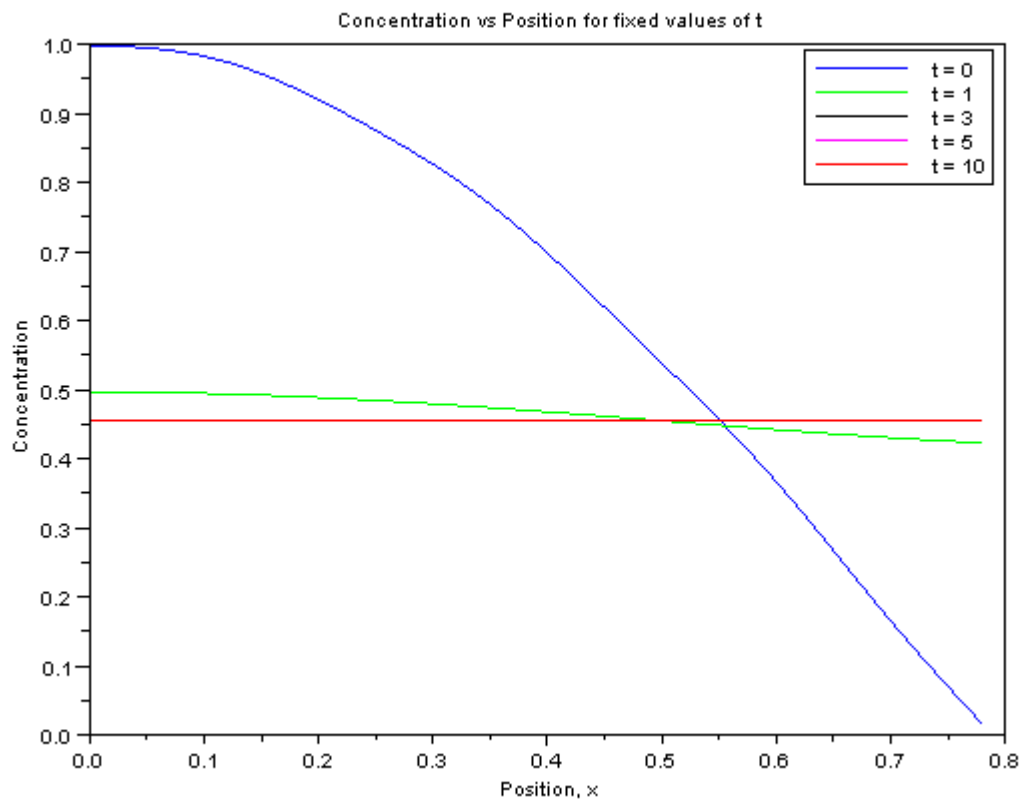
Executing this code produces the following graph:
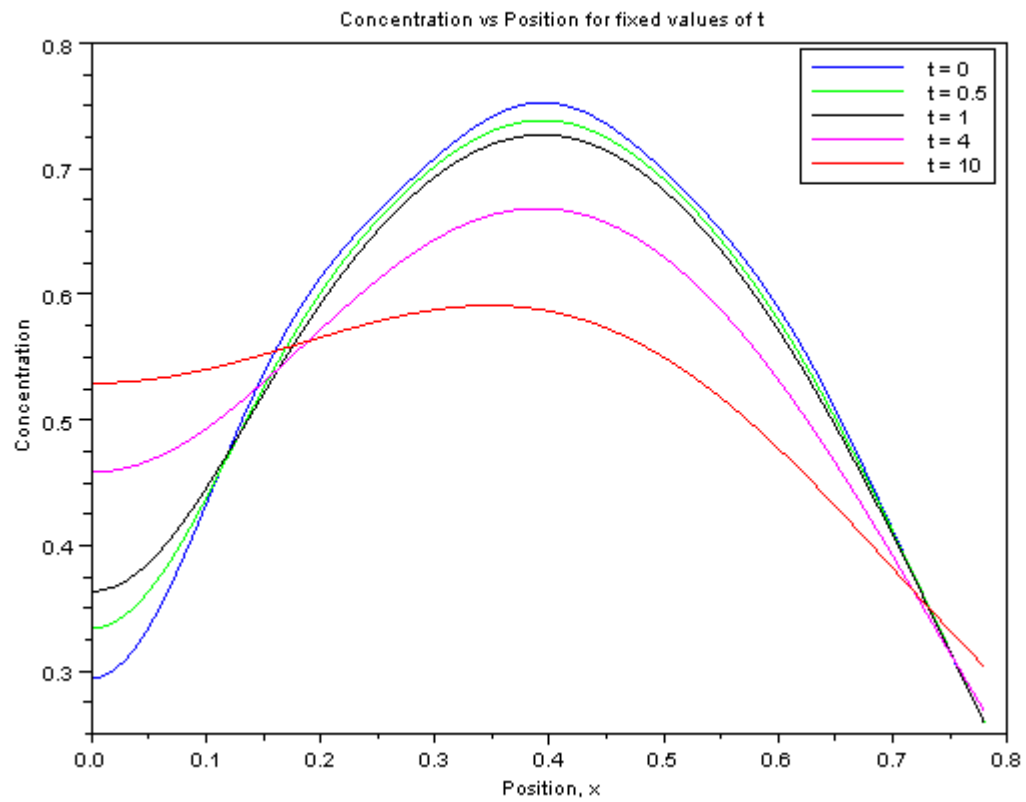
After changing the cell size to 0.00001 in diffusionleft.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 1.0;
t3 = 3.0;
t4 = 5.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .00001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t1)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t1)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t1)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t1)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t1)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t1)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t1);
y2 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t2)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t2)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t2)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t2)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t2)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t2)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
```

```
*%pi*x)*exp(-D*8^2*%pi*%pi*t2);
y3 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t3)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t3)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t3)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t3)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t3)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t3)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t3);
y4 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t4)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t4)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t4)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t4)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t4)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
p(-D*7^2*%pi*%pi*t4)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t4);
y5 =
sin(2)/2-(-1)^1*4*sin(2)/(1^2*%pi*%pi-4)*cos(1*%pi*x)*exp(
-D*1^2*%pi*%pi*t5)-(-1)^2*4*sin(2)/(2^2*%pi*%pi-4)*cos(2*%
pi*x)*exp(-D*2^2*%pi*%pi*t5)-(-1)^3*4*sin(2)/(3^2*%pi*%pi-
4)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)-(-1)^4*4*sin(2)/(4^
2*%pi*%pi-4)*cos(4*%pi*x)*exp(-D*4^2*%pi*%pi*t5)-(-1)^5*4*
sin(2)/(5^2*%pi*%pi-4)*cos(5*%pi*x)*exp(-D*5^2*%pi*%pi*t5)
-(-1)^6*4*sin(2)/(6^2*%pi*%pi-4)*cos(6*%pi*x)*exp(-D*6^2*%
pi*%pi*t5)-(-1)^7*4*sin(2)/(7^2*%pi*%pi-4)*cos(7*%pi*x)*ex
```

```
p(-D*7^2*%pi*%pi*t5)-(-1)^8*4*sin(2)/(8^2*%pi*%pi-4)*cos(8
*%pi*x)*exp(-D*8^2*%pi*%pi*t5);
scf(6);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 1','t = 3','t = 5','t = 10');
```

Executing this code produces the following graph:

After making the same changes to the file diffusioncenter.sce, the Scilab code should look as follows:

```
resethistory()
t1 =  0.0;
t2 = 0.5;
t3 = 1.0;
t4 = 4.0;
t5 = 10.0;
x = 0:0.01:%pi/4;
T = 298;
u = 0.498;
a = .00001;
D =0.00000000457*T/(u*a);
y1 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t1)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t1)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t1)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t1)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t1)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t1)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t1)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t1);
y2 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t2)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t2)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t2)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t2)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t2)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t2)+((-1)^7*4*cos(4)-
```

```
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t2)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t2);
y3 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t3)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t3)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t3)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t3)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t3)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t3)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t3)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t3);
y4 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t4)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t4)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t4)+((-1
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t4)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t4)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t4)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t4)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t4);
y5 =
sin(2)/2+((-1)^1*4*cos(4)-4)/(1^2*%pi*%pi-16)*cos(1*%pi*x)
*exp(-D*1^2*%pi*%pi*t5)+((-1)^2*4*cos(4)-4)/(2^2*%pi*%pi-1
6)*cos(2*%pi*x)*exp(-D*2^2*%pi*%pi*t5)+((-1)^3*4*cos(4)-4)
/(3^2*%pi*%pi-16)*cos(3*%pi*x)*exp(-D*3^2*%pi*%pi*t5)+((-1
```

```
)^4*4*cos(4)-4)/(4^2*%pi*%pi-16)*cos(4*%pi*x)*exp(-D*4^2*%
pi*%pi*t5)+((-1)^5*4*cos(4)-4)/(5^2*%pi*%pi-16)*cos(5*%pi*
x)*exp(-D*5^2*%pi*%pi*t5)+((-1)^6*4*cos(4)-4)/(6^2*%pi*%pi
-16)*cos(6*%pi*x)*exp(-D*6^2*%pi*%pi*t5)+((-1)^7*4*cos(4)-
4)/(7^2*%pi*%pi-16)*cos(7*%pi*x)*exp(-D*7^2*%pi*%pi*t5)+((
-1)^8*4*cos(4)-4)/(8^2*%pi*%pi-16)*cos(8*%pi*x)*exp(-D*8^2
*%pi*%pi*t5);
scf(16);
plot(x,y1,'b',x,y2,'g',x,y3,'k',x,y4,'m',x,y5,'r');
title('Concentration vs Position for fixed values of t');
xlabel('Position, x');
ylabel('Concentration');
legend('t = 0','t = 0.5','t = 1','t = 4','t = 10');
```

Executing this code produces the following graph:

Concentration vs Position for fixed values of t
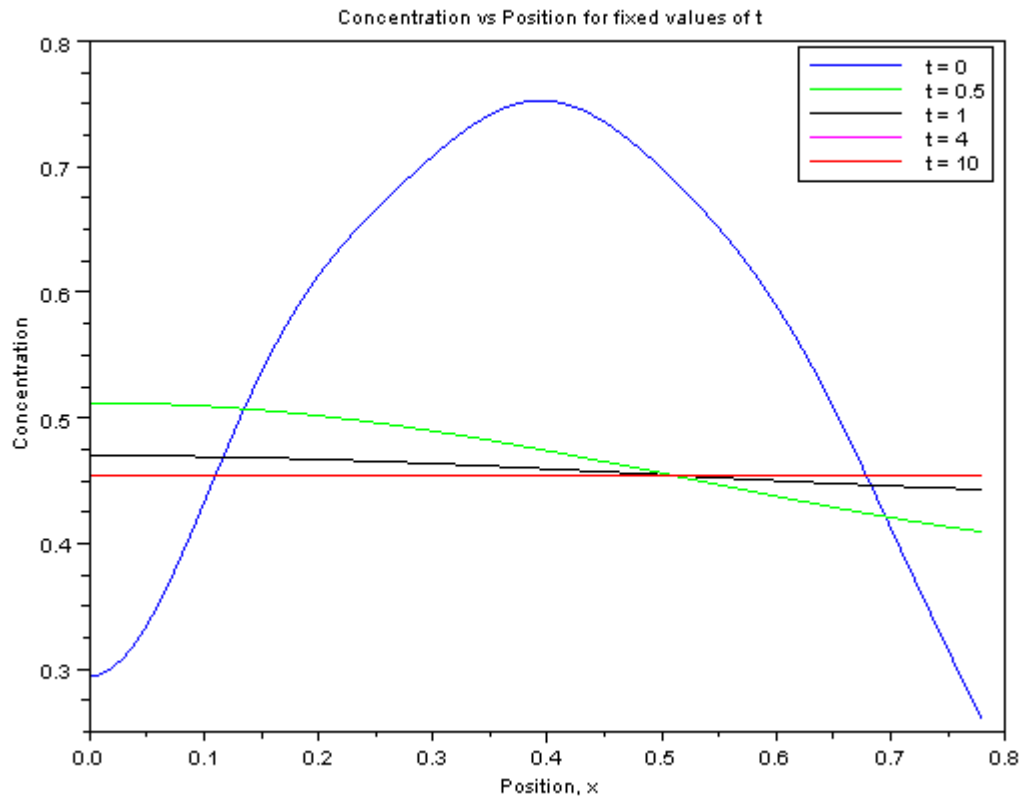
From these graphs we see that the smaller the cell size, the faster the concentrations even out. The differences here are also bit easy to see. If you look at say the diffusioncenter file you see that when the cell size is 0.00001 (graphics window 16), then by time $t = 1$, the concentrations are nearly evened out. When the cell size is 0.0001 (graphics window 10), the concentration is nearly evened out by time $t = 10$. And when the cell size is 0.001 (graphics window 15), even by time $t = 10$, the concentration on the left is much higher than the concentration on the right so a lot more time would be needed for the concentration to even out.

B.3 Protein Synthesis

Note: After executing the file Cell cycle control.sce, the following graph should appear:
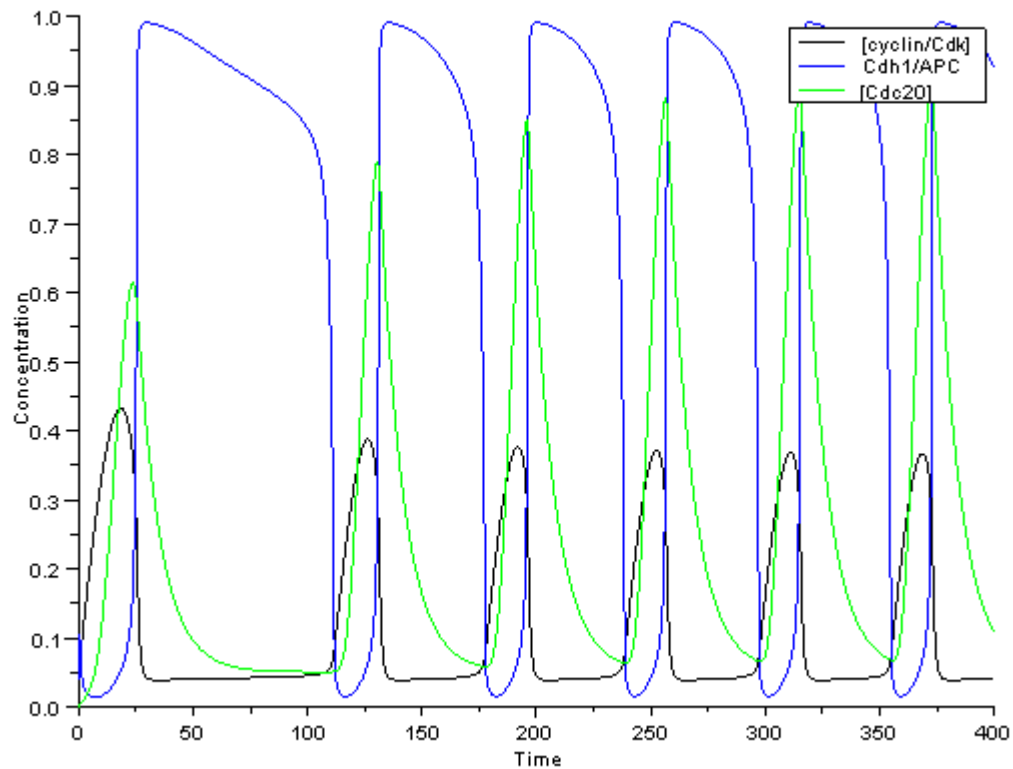
QUESTION: Open the figure you saved from the Scilab file. Using any program which allows you to draw on pictures (MS Paint, MS Word, Photoshop, etc.) draw a vertical line at the Start and Finish of each cell cycle and label each as start or Finish. Then label the G1 and S-G2-M phases.

Solution:
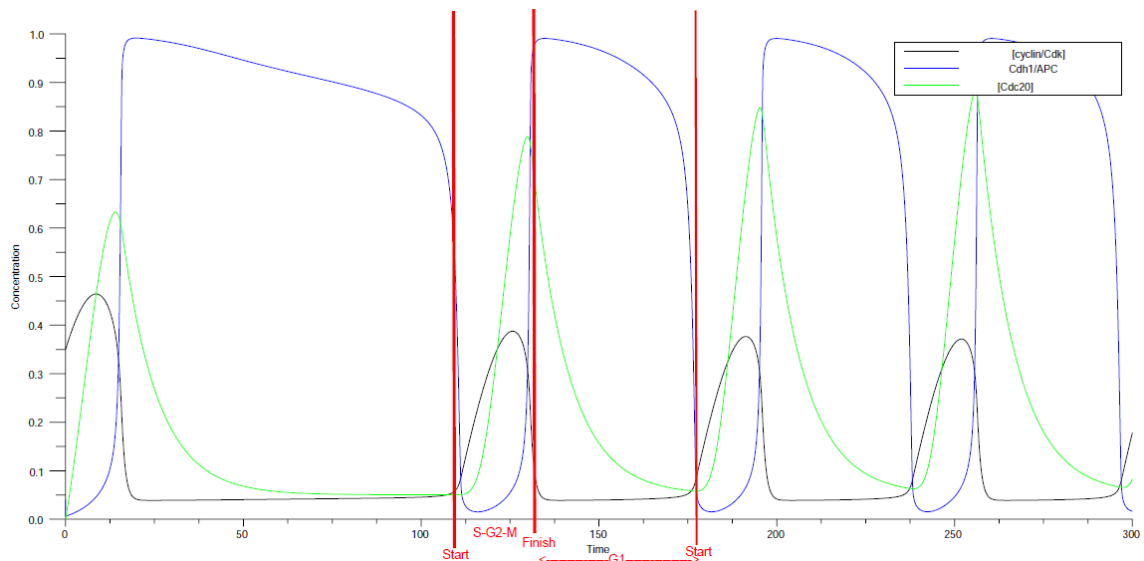
QUESTION: The text you read on the model claims that APC destroys cyclin molecules. Is this claim supported by the figure? Explain.

Solution: Yes, the claim is supported by the figure because in the figure, when the concentration of APC (blue curve in the graph) is at its lowest (just after start), cyclin (black curve in the graph) is increasing. Then as APC begins to rise in the S-G2-M phase, cyclin reaches its maximum concentration then begins to decrease. Then when APC concentration is high (during the G1 phase), cyclin concentration is at its minimum. And as APC concentration declines again near start, cyclin concentration begins to increase again.

QUESTION: The text you read on the model claims that cyclin/Cdk activates Cdc20. Is this claim supported by the figure? Explain.

Solution: Yes, the claim is supported by the figure because in the figure, when as concentration of cyclin/Cdk (black curve in the graph) starts increasing, the concen-

tration of Cdc20 (green curve in the graph) also starts to increase a short period of time later. Then as the concentration of cyclin/Cdk starts to decrease, the concentration of Cdc20 also starts to decrease a short period of time later. The increases and decreases in Cdc20 concentration follow the increases and decreases in cyclin/Cdk concentration, but on a short time lag.

B.4   Gene Regulation

Note: When you execute the file HIV_control.sce, initially no graph will appear and it will seem that Scilab hasn't done anything. If you look at the Scilab console, you will see the following message:

[Continue display? n (no) to stop, any other key to continue]

As long as that message appears in the Scilab console, Scilab won't do anything else. Press "n" and Scilab will proceed. At this point, a graph still will not appear. But in the Scilab console you will be prompted to enter a value for s. Enter 10 as is indicated in the module. You will then be prompted for each of the other parameter values in turn. Enter the values given in the module for each parameter until you reach the value of t_{final}, which is the last parameter value. After entering 20 as the value of t_{final}, Scilab will display the same message as before, asking to continue display. Again, Scilab will not do anything until you press "n." Scilab will then tell you to "Type 1 or 2." Press 1. Scilab will then tell you to "Type 1 - 13." What Scilab is asking for here is which of the 13 parameters do you want to change from its original value. The number you press at this point will change with each of the next three

questions. The first question tells you to change the value of N to 50. In the module, N is parameter #8, so you would type 8 and enter the new value for N. To do the second question, you will have to execute the file HIV_control.sce again and reenter all the parameter values. But this time the question wants you to change the value of s, which is parameter #1, to 7, so when Scilab prompts you to "Type 1 - 13" you will type 1 and enter the new value for s. Likewise, in order to do the third question, you will need to execute the file one more time and reenter all the parameter values one more time. But this time the questions wants you to change the value of k, which is parameter #7, to 0.000032. Each time you enter the new value for the variable, Scilab will think for a minute and then a graph will appear. But there should be 4 graphs. If you look at the Scilab console, you will see the same message asking to continue display. Scilab won't display all the graphs until you press "n." The top graph is T (concentration of uninfected CD4+T cells) vs. t (time). The second graph is T_i (concentration of infected CD4+T cell) vs. t. The third graph is V (concentration of free virus particles) vs. t. And the bottom graph is $u(t)$ (strength of chemotherapy where 1 represents no chemotherapy and 0 represents maximum chemotherapy) vs. t.

QUESTION:$N = 50$: Which parameter value allows the uninfected T cell count to increase the most? Why is or isn't this what you would expect? Describe the difference in treatment strategies for the two parameter values.

Solution: After executing the file, entering all the parameter values, and entering 50 as the new value of N, the following graph will appear:
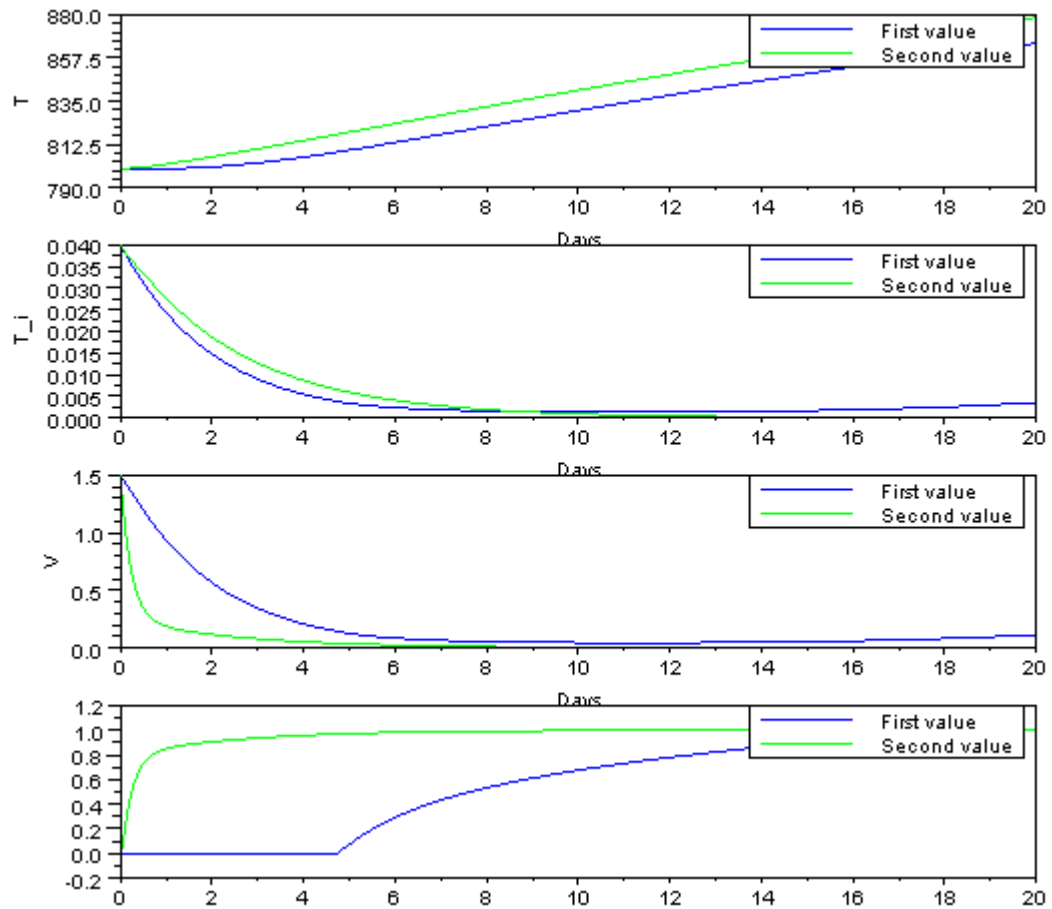
The top graph shows the concentration of uninfected CD4+T cells versus time. From that graph, we see that the second value (of N, which is 50) allows the uninfected T cell count to increase the most. Since N represents the average number of virus particles which are produced before the host cell dies, once infection of a T cell occurs and replication is initiated, then the smaller the value of N, then the fewer number of virus particles are produced on average, so there should be more uninfected T cells. The treatment strategy is shown in the bottom graph. For the first value (of N, which is 300), we start with maximum chemotherapy (remember that 0 is maximum chemotherapy and 1 is no chemotherapy) for close to 5 days then gradually decrease

the chemotherapy until there is no chemotherapy around day 17 - 20.

> **QUESTION:**$s = 7$: Which parameter value involves more chemotherapy as part of its strategy? Notice the relationship between the concentration of uninfected T cells & viral particles and chemotherapy strategy for each of the parameter values. How do they compare for the different parameter values?

Solution: After executing the file again, entering all the parameter values, and now entering 7 as the new value of s, the following graph will appear:
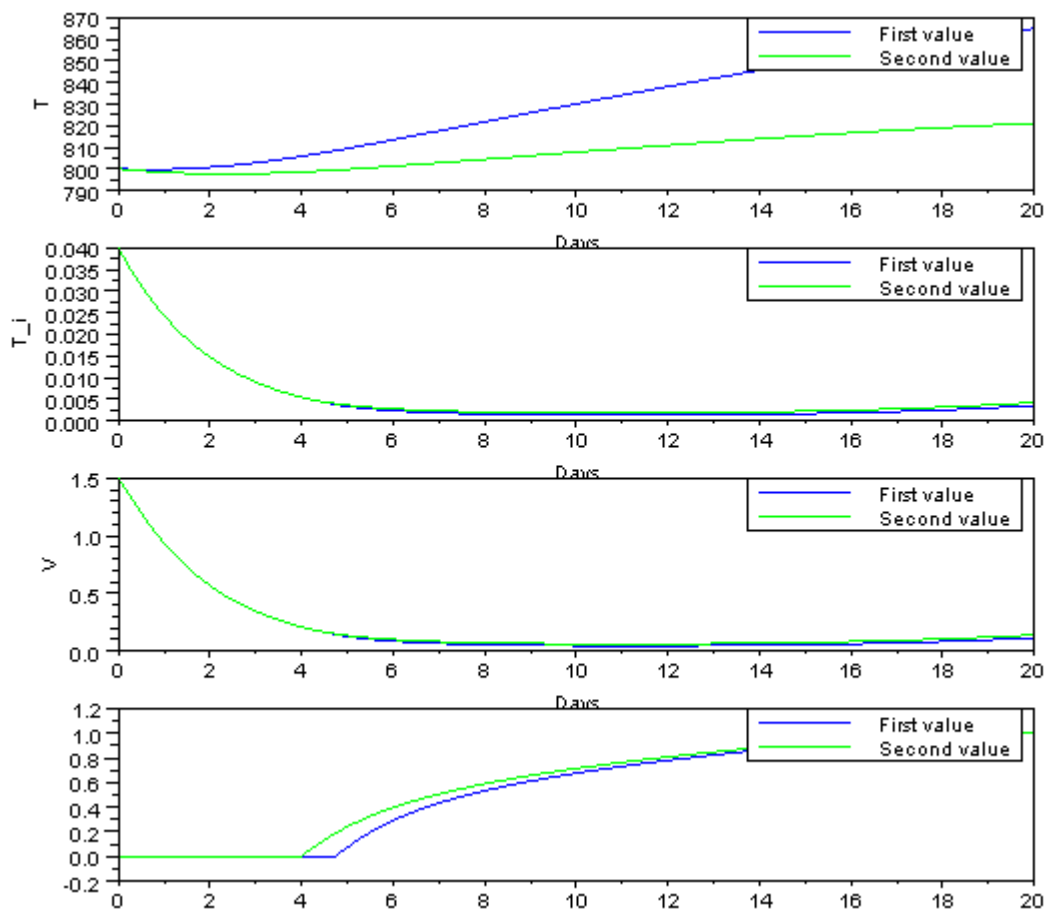
As before, the bottom graph shows the chemotherapy strategy. Both strategies look

almost identical (they differ only slightly and only for about a week before the strate-gies become the same again) but for the first value (of s), we stick with the maximum chemotherapy (remember that 0 is maximum chemotherapy) for about $\frac{1}{2}$ - 1 day longer, so $s = 10$ involves more chemotherapy as part of its strategy. Even though the chemotherapy strategy is nearly identical for both parameter values, the concen-tration of uninfected T cells (top graph) is quite different. Even initially when the chemotherapy strategies are identical the concentration of uninfected T cells is differ-ent. For $s = 10$ (the first value), there is a little more chemotherapy and a lot more uninfected T cells. With the viral particles (third graph from the top) the concen-trations remain virtually identical, even when the chemotherapy strategies begin to diverge from each other. In this case, for the higher value of s (the first value when $s = 10$) more chemotherapy is needed to attain the same low level of viral particles. Since S represents the rate of generation of new CD4+T cells, it seems plausible that if the cells are being generated quicker then more chemotherapy would be needed to achieve the same level of viral cells as when the rate of generation is lower.

QUESTION:$k = 0.000032$: Which parameter value involves more chemotherapy? Does the increased chemotherapy result in a lower concentration of infected T cells and viral cells? How do the results of changing this parameter differ from the results in the previous question?

Solution: After executing the file again, entering all the parameter values, and now entering 7 as the new value of s, the following graph will appear:
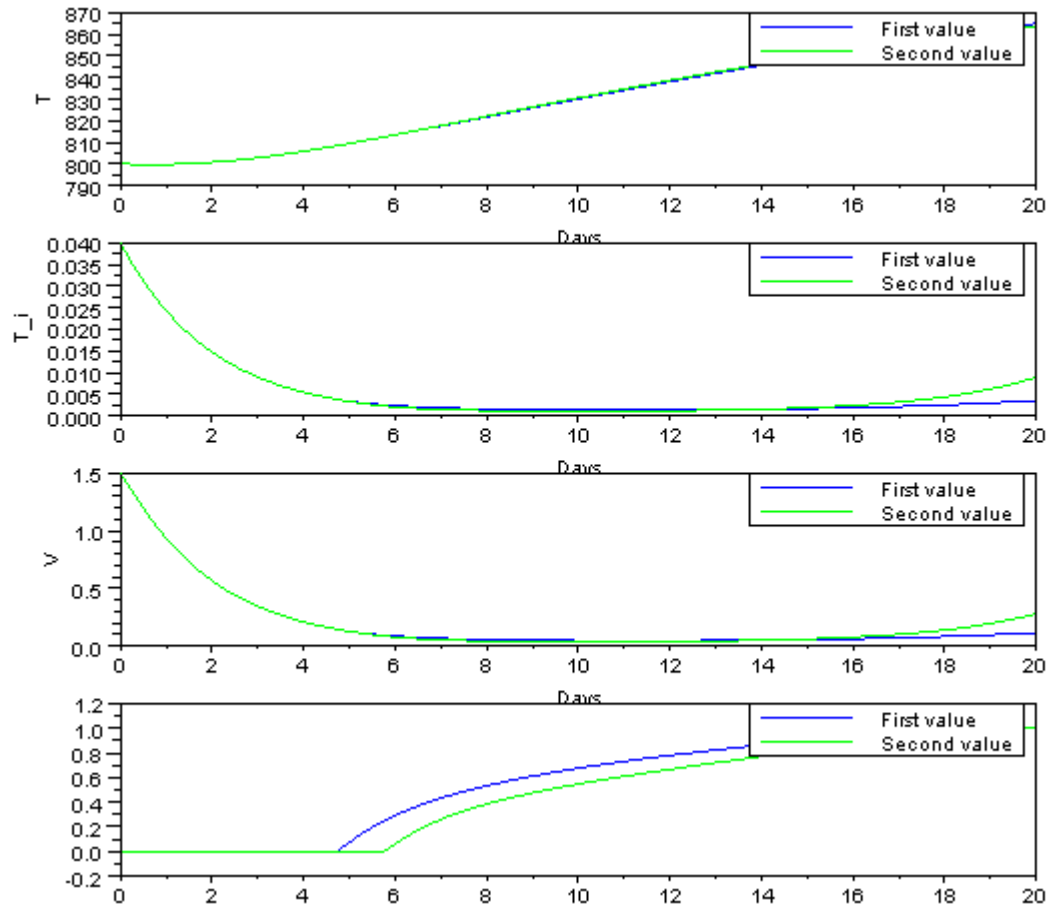
As before, the bottom graph shows the chemotherapy strategy. Both strategies are virtually the same (one strategy mirrors the other one except in the amount of time before the amount of chemotherapy is reduced) but this time for the second value (of k), we stick with the maximum chemotherapy for about 1 - $1\frac{1}{2}$ days longer and the chemotherapy strategies never become the same again. So $k = 0.000032$ involves more chemotherapy. In this case, more chemotherapy (second value) results in the same concentration of uninfected T cells (top graph) and the same concentration of viral cells (third graph from the bottom) until around day 17 when the second value has a higher concentration of viral cells, despite also having more chemotherapy. In

the previous question, more chemotherapy was able to result in the same level of infected T cells and viral cells for both parameter values whereas in this case, even with more chemotherapy, we cannot achieve the same level of infected T cells and viral cells at the end of treatment.

B.5 Control Systems

Note: Executing the file Hodgkin_Huxley.sce produces the following graph:
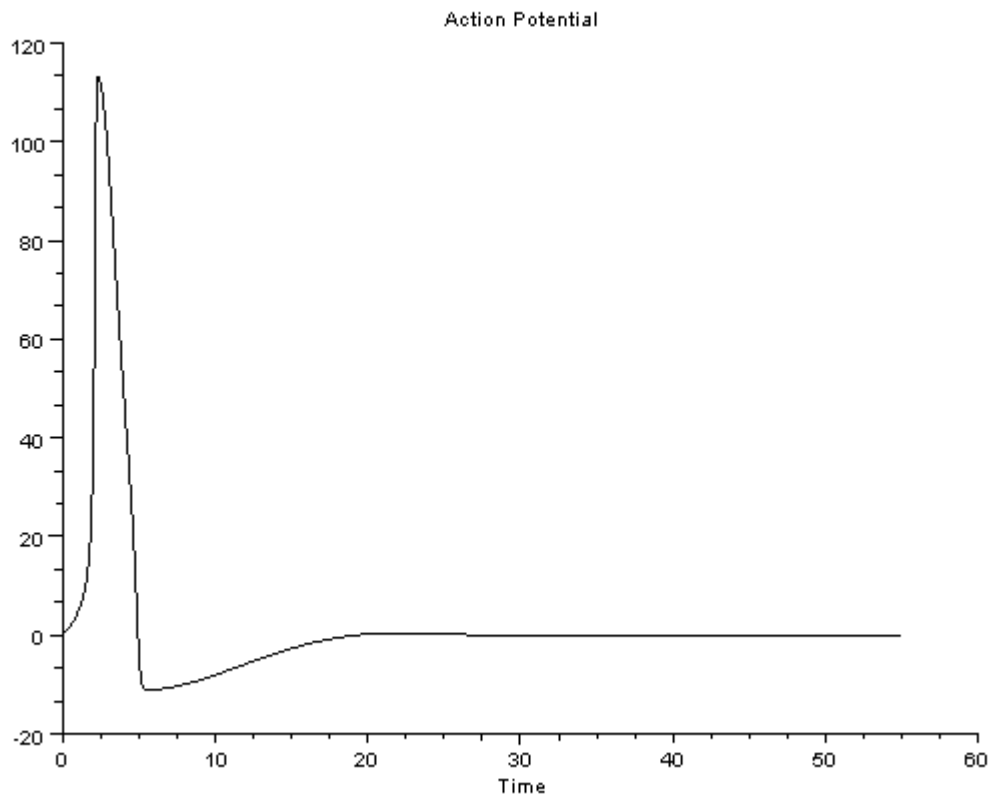
QUESTION: What is the effect of changing the applied current to 5? Explain why you think this happens.

Solution: After changing the applied current to 5, the Scilab code should look as follows:

```
function dx=hodgkinhuxley(t,x)
alpham = 0.1*(25-x(1))/(exp((25-x(1))/10)-1)
betam = 4*exp(-x(1)/18)
alphah = 0.07*exp(-x(1)/20)
betah = 1/(exp((30-x(1))/10)+1)
alphan = 0.01*(10-x(1))/(exp((10-x(1))/10)-1)
betan = 0.125*exp(-x(1)/80)
dx(1) =
(-gk*x(3)^4*(x(1)-vk)-gna*x(2)^3*x(4)*(x(1)-vna)-gl*(x(1)-vl)+iapp)/cm
dx(2) = alpham*(1-x(2))-betam*x(2)
dx(3) = alphan*(1-x(3))-betan*x(3)
dx(4) = alphah*(1-x(4))-betah*x(4)
endfunction

scf(1);
clf;
cm = 1
gk = 36
vk = -12
iapp = 5
gna = 120
vna = 115
gl = 0.3
vl = 10.6
t = 0:0.001:55;
x0 = [0 ;0; 0; 1];
x = ode(x0,0,t,hodgkinhuxley);

//xbasc()
plot2d(t,x(1,:),style-1)
//legends(['Voltage'],[1],"ur")
xtitle('ActionPotential')
xlabel('Time')
ylabel('Potential')
```

Executing the file produces the following graph:

Action Potential
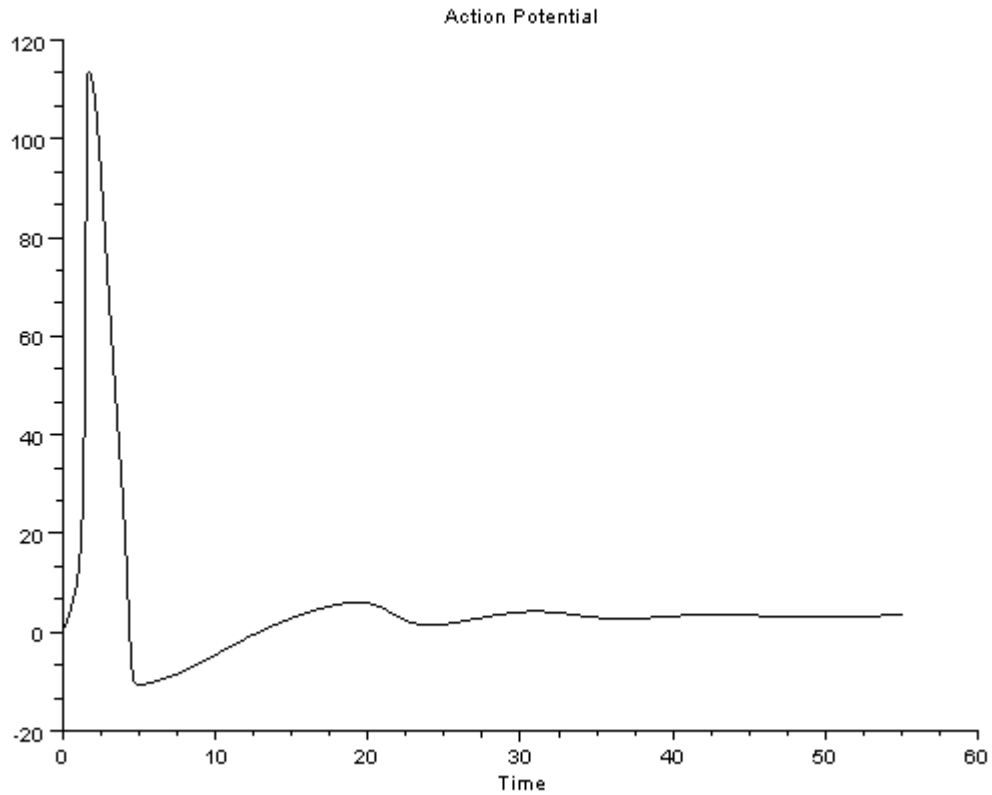
Increasing the applied current to 5 causes repeated spikes in potential after the nerve returns to its resting potential, but the spikes decrease in size as time goes on. This is because the stimulus is not strong enough to raise the potential sufficiently to induce another action potential.

QUESTION: What is the effect of changing the applied current to 10? Explain why you think this happens.

Solution: After changing the applied current to 10, the Scilab code should look as follows:

```
function dx=hodgkinhuxley(t,x)
alpham = 0.1*(25-x(1))/(exp((25-x(1))/10)-1)
betam = 4*exp(-x(1)/18)
alphah = 0.07*exp(-x(1)/20)
betah = 1/(exp((30-x(1))/10)+1)
alphan = 0.01*(10-x(1))/(exp((10-x(1))/10)-1)
betan = 0.125*exp(-x(1)/80)
dx(1) =
(-gk*x(3)^4*(x(1)-vk)-gna*x(2)^3*x(4)*(x(1)-vna)-gl*(x(1)-vl)+iapp)/cm
dx(2) = alpham*(1-x(2))-betam*x(2)
dx(3) = alphan*(1-x(3))-betan*x(3)
dx(4) = alphah*(1-x(4))-betah*x(4)
endfunction

scf(2);
clf;
cm = 1
gk = 36
vk = -12
iapp = 10
gna = 120
vna = 115
gl = 0.3
vl = 10.6
t = 0:0.001:55;
x0 = [0 ;0; 0; 1];
x = ode(x0,0,t,hodgkinhuxley);

//xbasc()
plot2d(t,x(1,:),style=1)
//legends(['Voltage'],[1],"ur")
xtitle('ActionPotential')
xlabel('Time')
ylabel('Potential')
```

Executing the file produces the following graph:
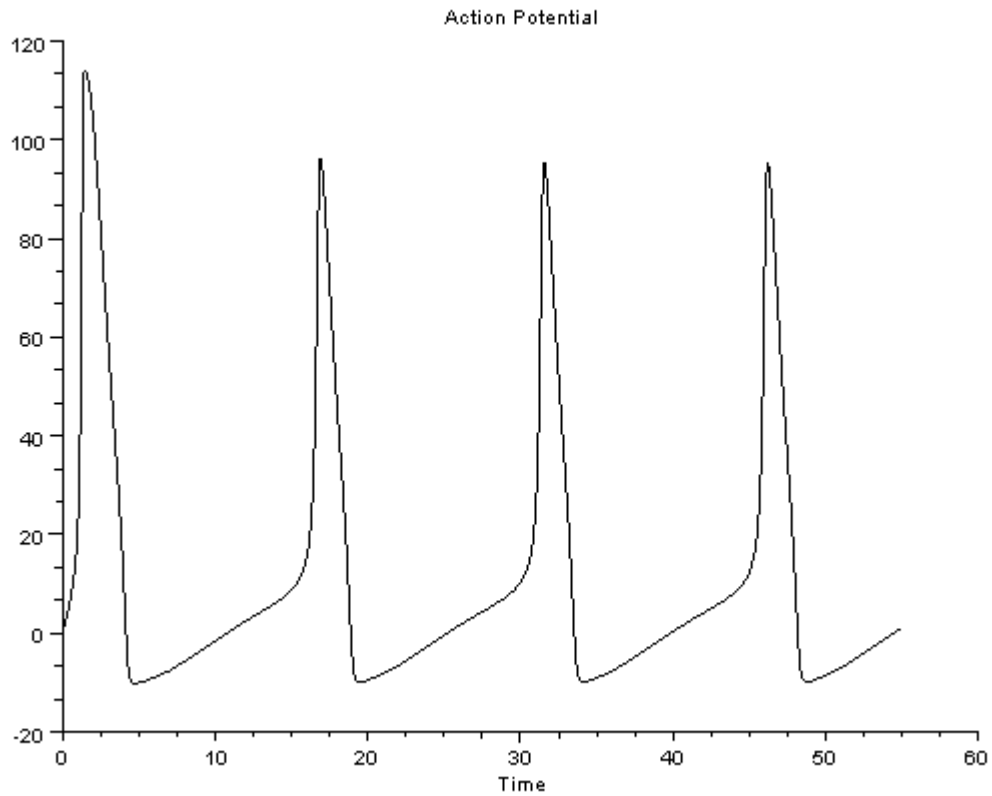
By increasing the applied current to 10 the nerve undergoes repeated action potentials. This is because the stimulus is now strong enough to increase the potential to a level necessary to elicit an action potential after the nerve has returned to its resting potential.

Note: Executing the file FitzHugh-Nagumo.sce produces the following graph:
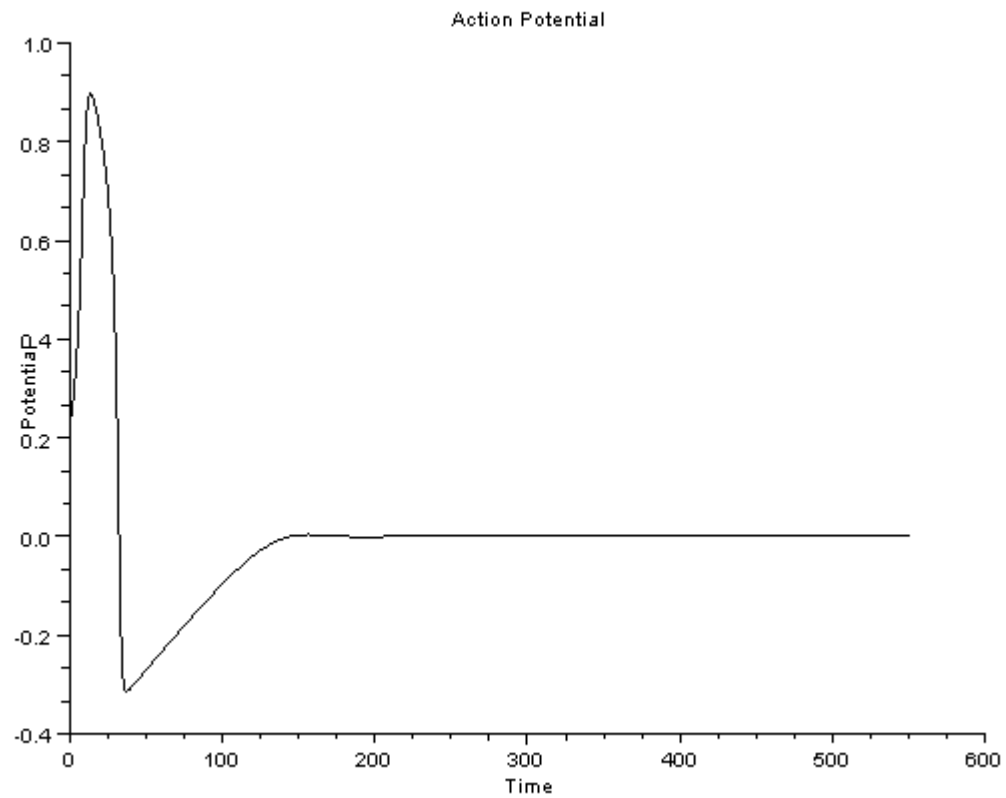
Action Potential

QUESTION: What is the effect of changing the applied current to 0.1?

Solution: After changing the applied current to 0.1, the Scilab code should look as follows:

```
function  dx=actionpotential(t,x)
dx(1) = x(1)*(x(1)-0.1)*(1-x(1))-x(2)+I
dx(2) = 0.01*(x(1)-0.5*x(2))
endfunction

scf(2);
clf;
I = 0.1
t = 0:0.001:550;
x0 = [0.22 ;0;];
x = ode(x0,0,t,actionpotential);

//xbasc()
plot2d(t,x(1,:),style=1)
//legends(['A','B'],[1 2],"ur")
xtitle('ActionPotential')
xlabel('Time')
ylabel('Potential')
```

Executing the file produces the following graph:

Action Potential
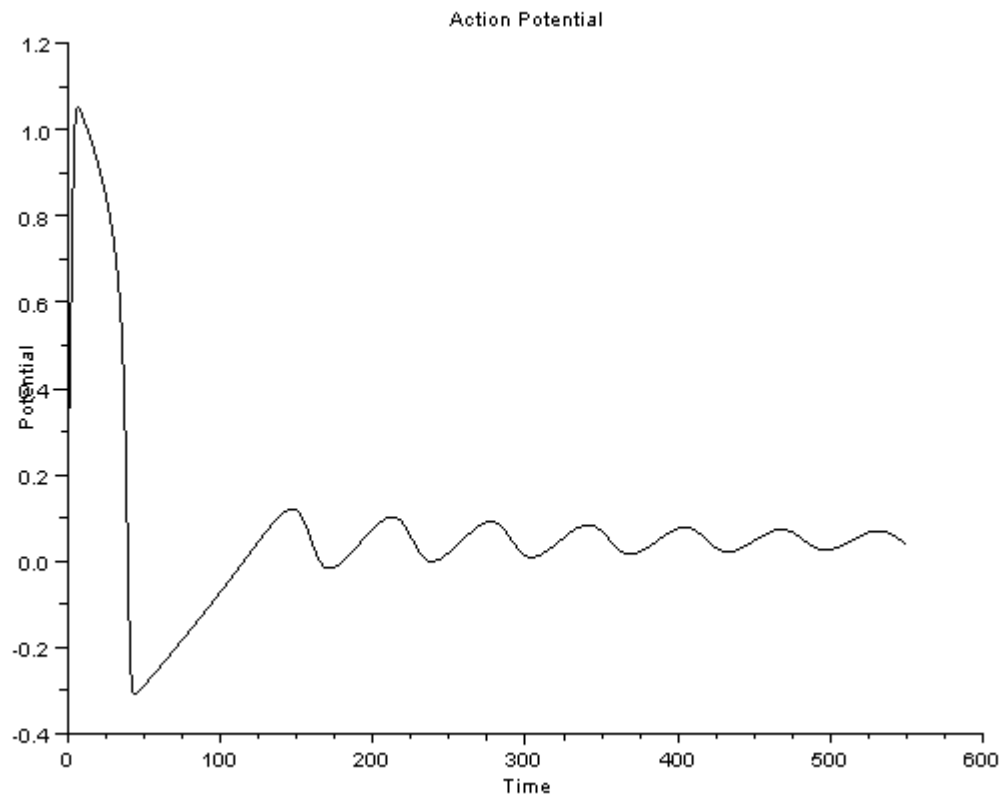
Increasing the applied current to 0.1 causes repeated spikes in potential after the nerve returns to its resting potential, but this time spikes remain constant in size as time goes on. This is because the stimulus is not strong enough to raise the potential sufficiently to induce another action potential.

QUESTION: What is the effect of changing the applied current to 0.2?

Solution: After changing the applied current to 0.2, the Scilab code should look as follows:

```
function dx=actionpotential(t,x)
dx(1) = x(1)*(x(1)-0.1)*(1-x(1))-x(2)+I
dx(2) = 0.01*(x(1)-0.5*x(2))
endfunction

scf(3);
clf;
I = 0.2
t = 0:0.001:550;
x0 = [0.22 ;0;];
x = ode(x0,0,t,actionpotential);

//xbasc()
plot2d(t,x(1,:),style=1)
//legends(['A','B'],[1 2],"ur")
xtitle('ActionPotential')
xlabel('Time')
ylabel('Potential')
```

Executing the file produces the following graph:
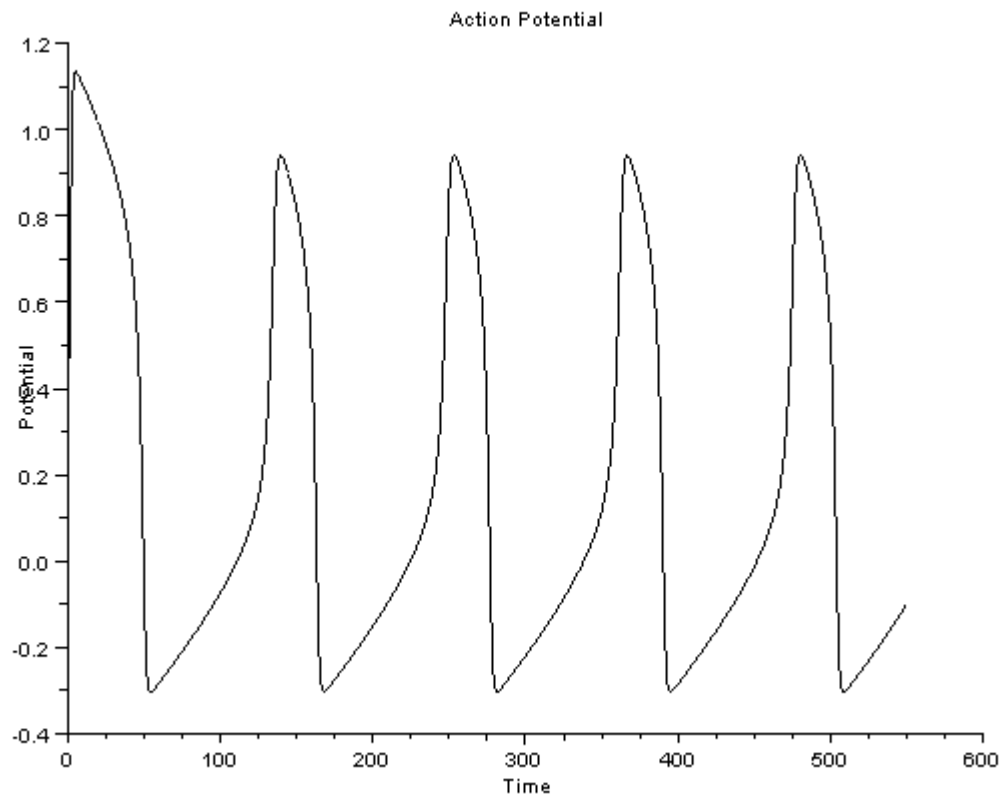
By increasing the applied current to 0.2 the nerve undergoes repeated action potentials. This is because the stimulus is now strong enough to increase the potential to a level necessary to elicit an action potential after the nerve has returned to its resting potential.

> **QUESTION:** What qualitative similarities do you see between the simulations of the Hodgkin-Huxley equations and the FitzHugh-Nagumo equations?

In both cases, when there is no applied current then the nerve returns to its resting potential after the initial action potential. In both cases, when there is a sufficiently small stimulus (applied current), the potential has small, repeated spikes after re-

turning to its resting potential but no further action potentials are produced. And in both cases, when there is a sufficiently large stimulus, the potential increases causes repeated action potentials.

B.6   Immune System

Note: Executing the file SIR.sce produces the following graph:
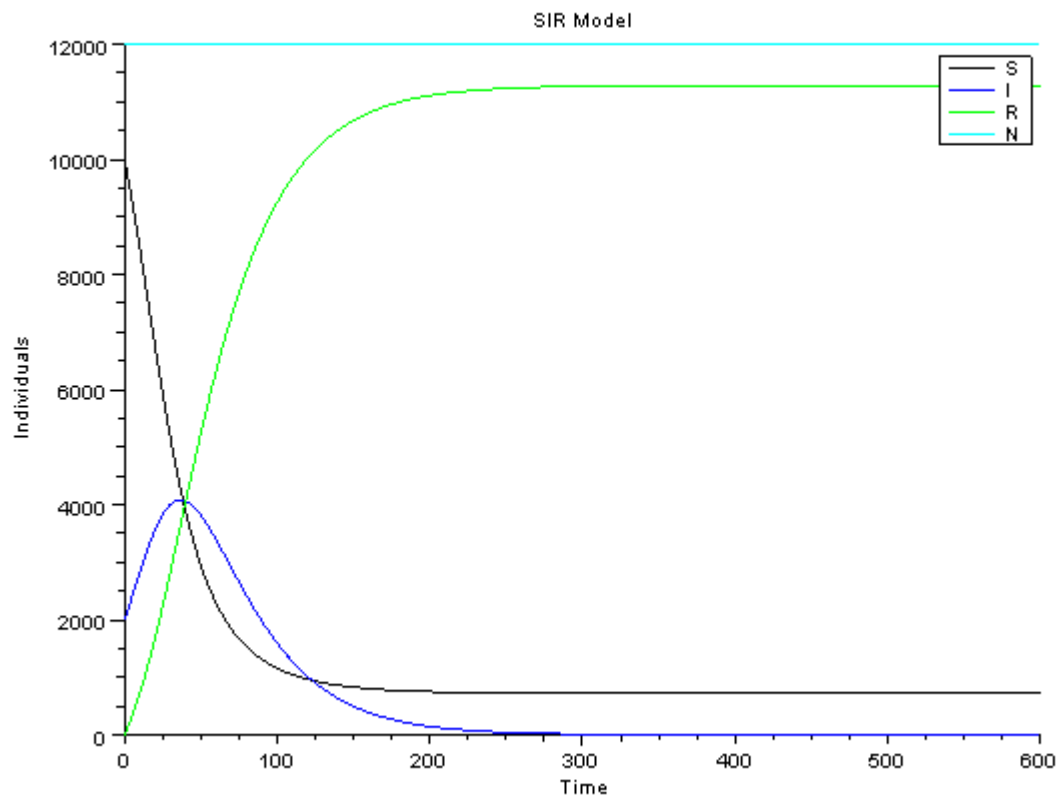
> **QUESTION:** For this combination of parameters, does the disease die out or is there an epidemic?

Solution: Since the number of individuals susceptible to the disease doesn't become

zero, then that means the disease dies out before everyone becomes infected.

> **QUESTION:** Decrease the value of S_0 from 10,000 to 5,000 and execute the file. Then increase the value of S_0 to 50,000 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to try and increase or decrease S_0? What kind of practical control strategy could be used to achieve this goal?

Solution: After making the first change, namely decreasing the value of S_0 from 10,000 to 5,000, the Scilab code should look as follows:
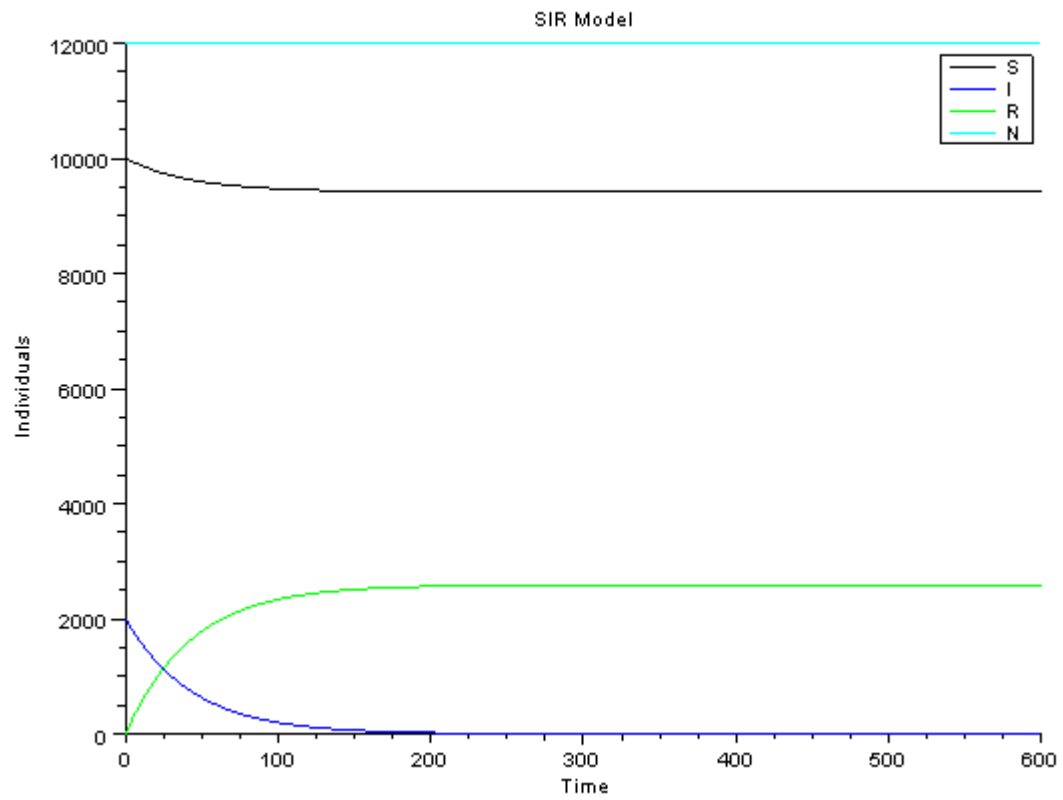
```
clear
function dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(1);
clf;
Beta = .000007;
Gamma = .03
t = 0:0.001:600;
S0 = 5000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the code produces the following figure:
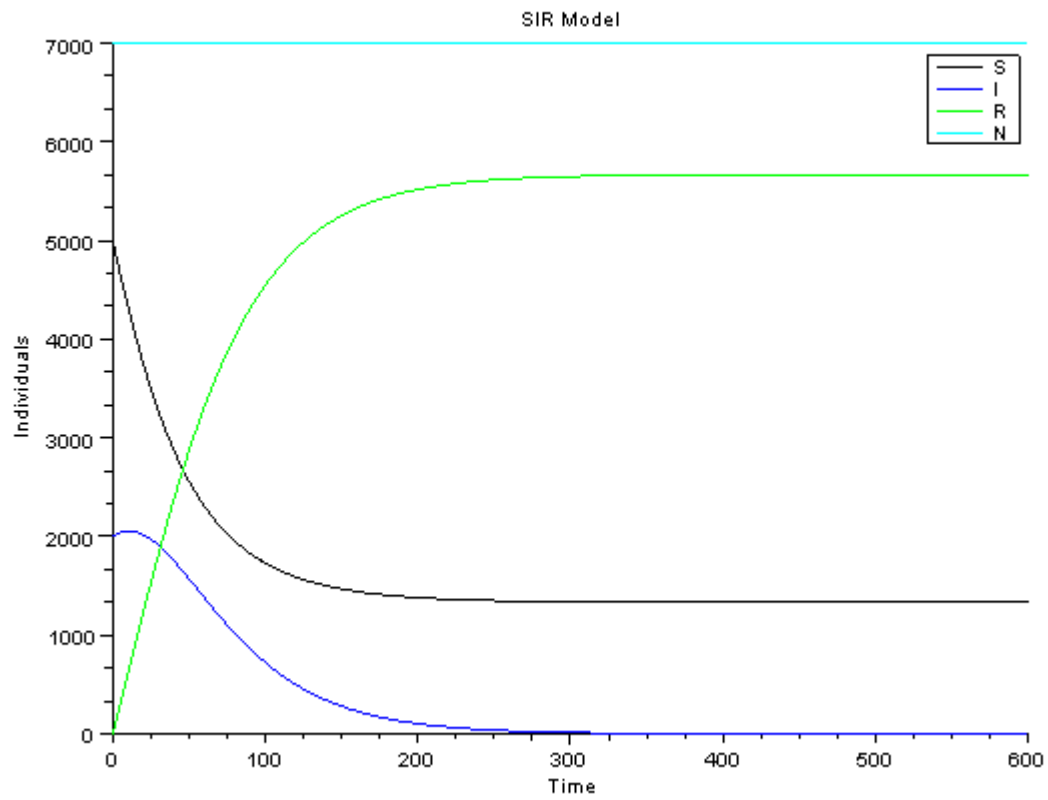
After making the second change, namely increasing the value of S_0 to 50,000, the Scilab code should look as follows:
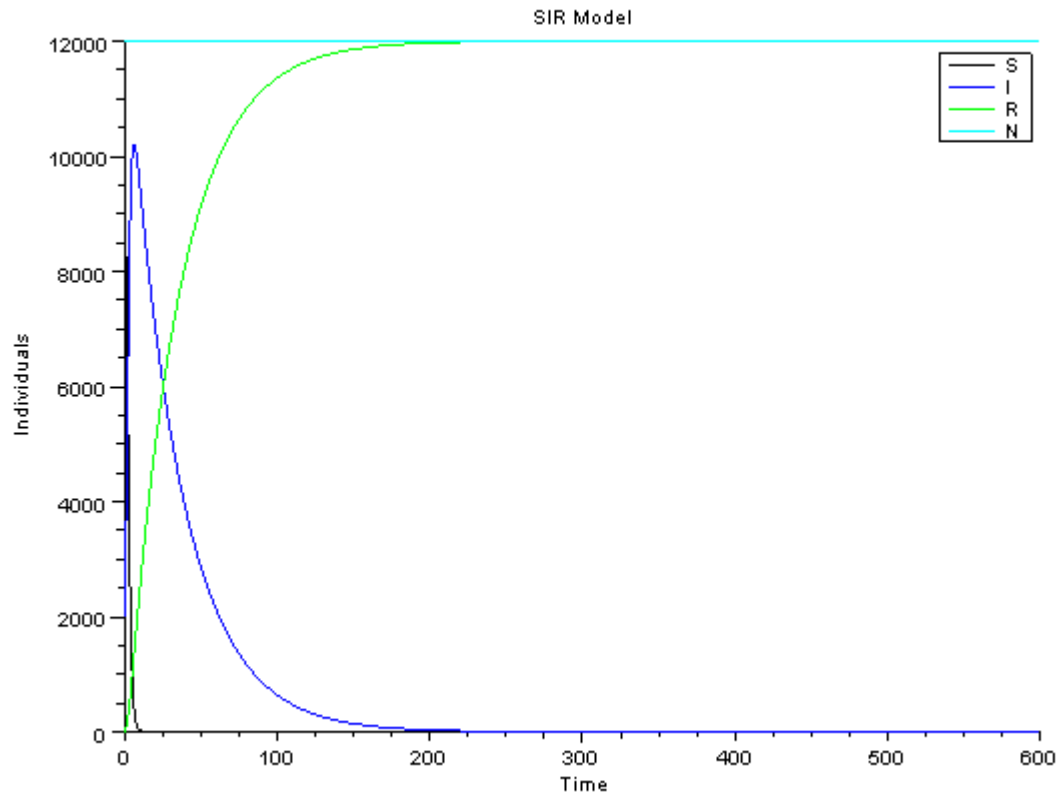
```
clear
function dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(2);
clf;
Beta = .000007;
Gamma = .03
t = 0:0.001:600;
S0 = 50000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the code produces the following figure:

In the first graph, notice that some of the susceptible individuals remain susceptible, while in the second graph, none of the susceptible individuals remain susceptible. So in the second graph, all the individuals in the population have become infected with the disease. So if you were trying to prevent the disease from becoming an epidemic, you would want to decrease the value of S_0 rather than increase it. One control strategy that could be used to decrease S_0; i.e., to decrease the number of individuals initially susceptible to the disease, would be the use of vaccines.

QUESTION: Decrease the value of β from 0.000007 to 0.0000007 and execute the file. Then increase the value of β to 0.00007 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to increase or decrease β? What kind of practical control strategy could be used to achieve this goal?

Solution: After changing S_0 back to 10,000 and decreasing *beta* from 0.000007 to 0.0000007, the Scilab code should look as follows:

```
clear
function  dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(1);
clf;
Beta = .0000007;
Gamma = .03
t = 0:0.001:600;
S0 = 10000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the file produces the following graph:

After increasing β to 0.00007, the Scilab code should look as follows:

```
clear
function  dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(2);
clf;
Beta = .00007;
Gamma = .03
t = 0:0.001:600;
S0 = 10000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the file produces the following graph:

In the first graph, notice that some of the susceptible individuals remain susceptible, while in the second graph, none of the susceptible individuals remain susceptible. So in the second graph, all the individuals in the population have become infected with the disease. So if you were trying to prevent the disease from becoming an epidemic, you would want to decrease the value of β rather than increase it. One control strategy that could be used to decrease β; i.e., to decrease the transmission rate, would be to quarantine or isolate infected individuals.

QUESTION: Decrease the value of γ from 0.03 to 0.015 and execute the file. Then increase the value of γ to 0.045 and execute the file again. If you are trying to prevent the disease from becoming an epidemic, would you want to increase or decrease γ? What kind of practical control strategy could be used to achieve this goal?

Solution: After changing β back to 0.00007 and decreasing γ to 0.015, the Scilab code should look as follows:

```
clear
function dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(1);
clf;
Beta = .000007;
Gamma = .015
t = 0:0.001:600;
S0 = 10000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the file produces the following graph:
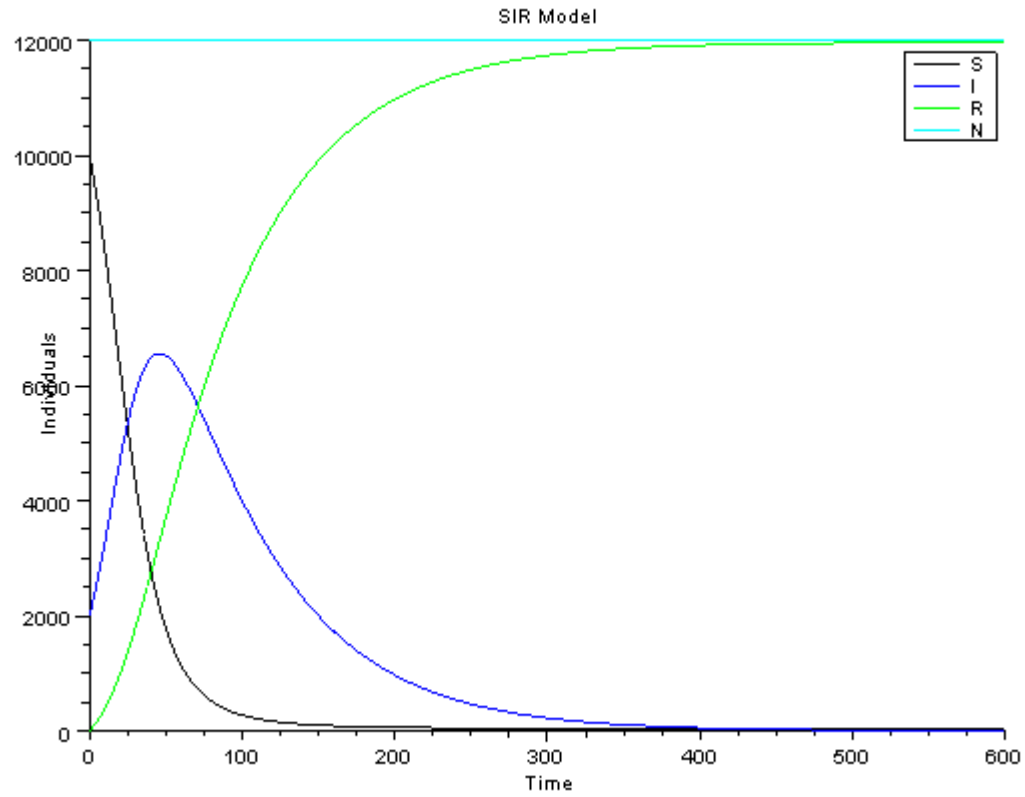
After increasing γ to 0.045, the Scilab code should look as follows:

```
clear
function dx= SIR(t,x)
dx(1) =-Beta*x(1)*x(2)
dx(2) = Beta*x(1)*x(2)-Gamma*x(2)
dx(3) = Gamma*x(2)
dx(4) = 0
endfunction

scf(2);
clf;
Beta = .000007;
Gamma = .045
t = 0:0.001:600;
S0 = 10000;
I0 = 2000;
R0 = 0;
N =  S0+  I0+ R0
x0 = [S0 ; I0 ; R0; N];
x = ode(x0,0,t,SIR);

//xbasc()
plot2d(t,x(1,:),style=1)
plot2d(t,x(2,:),style=2)
plot2d(t,x(3,:),style=3)
plot2d(t,x(4,:),style=4)
legends(['S', 'I', 'R','N'],[1, 2, 3, 4],"ur")
xtitle('SIR Model')
xlabel('Time')
ylabel('Individuals')
```

Executing the file produces the following graph:
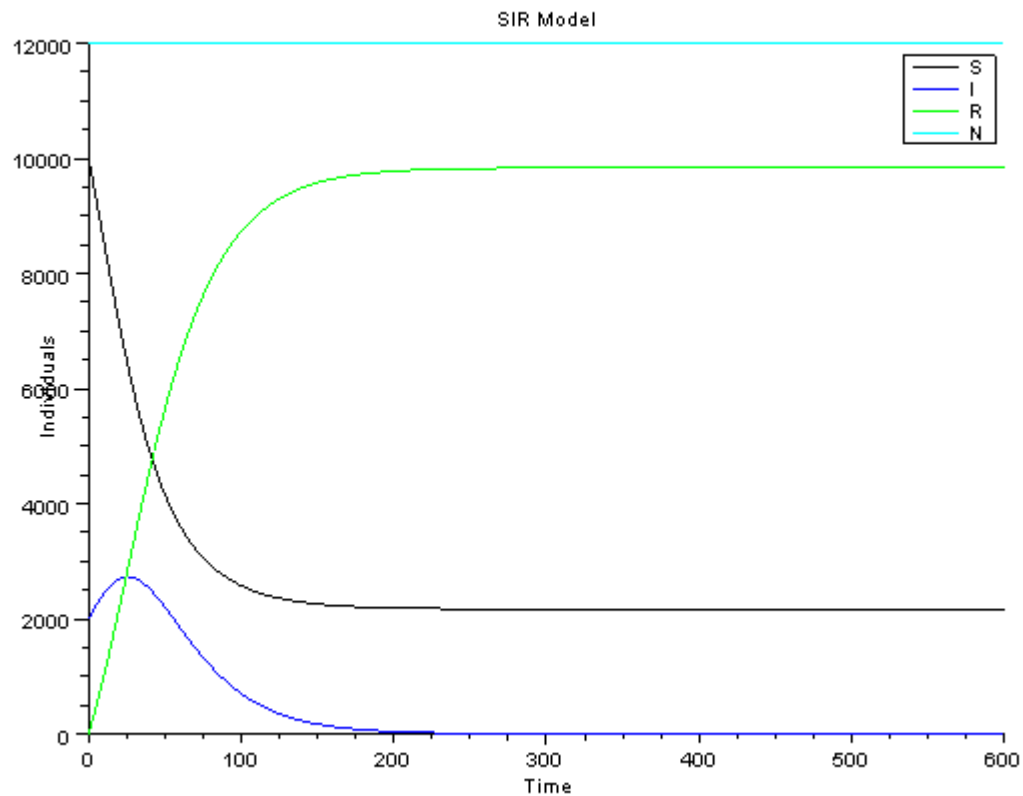
In the first graph, notice that none of the susceptible individuals remain susceptible, while in the second graph, some of the susceptible individuals remain susceptible. So in the first graph, all the individuals in the population have become infected with the disease. So if you were trying to prevent the disease from becoming an epidemic, you would want to increase the value of γ rather than increase it. One control strategy that could be used to increase γ; i.e., to increase the recovery rate, would be through medical intervention, such as the use of medications.

B.7 Genetics

Note: After executing the file allele_frequency.sce, the following graph will appear:
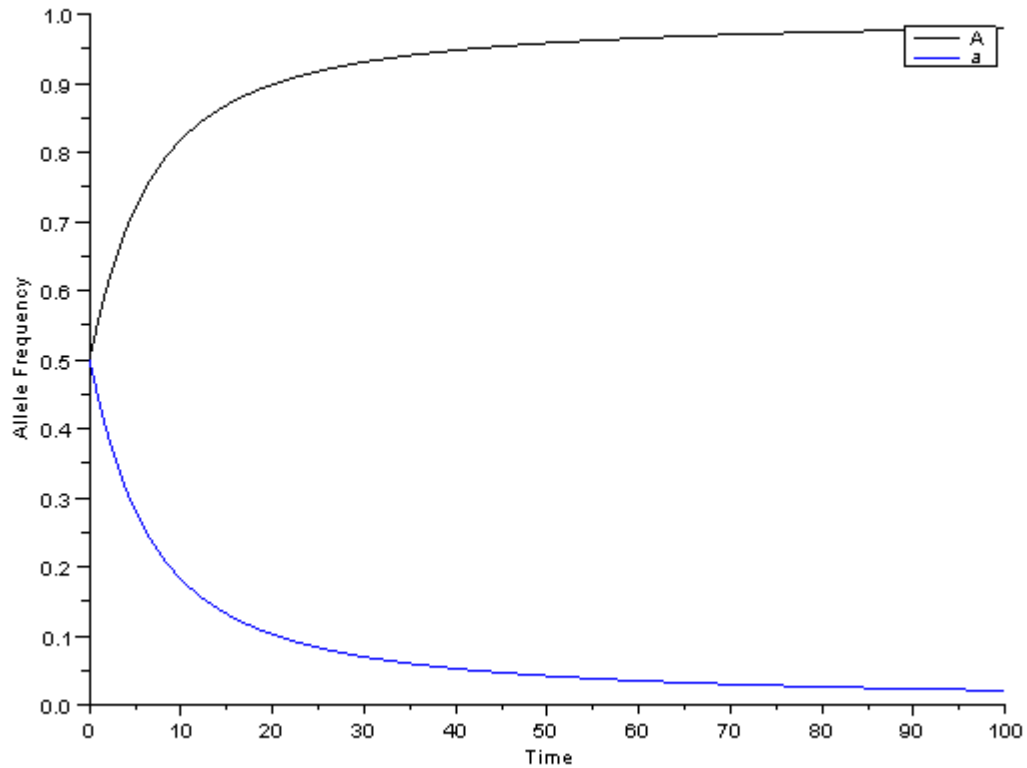
QUESTION: Change the fitness of the aa genotype to $f_{aa} = 0$. In this case the aa genotype is lethal. What are the similarities and differences in this case compared to the original one? Why do you think that is?

Solution: After changing the fitness of genotype aa to $f_{aa} = 0$, the Scilab code should look as follows:

```
function dx=genetics(t,x)
fA = x(1)*fAA+(1-x(1))*fAa
fa = x(1)*fAa+(1-x(1))*faa
f = x(1)*fA+(1-x(1))*fa
dx(1) = x(1)*(1-x(1))*(fA-fa)
dx(2) = x(2)*f
dx(3) = -x(1)*(1-x(1))*(fA-fa)
endfunction

fAA = 1.0
fAa = 1.0
faa = 0
t = 0:0.001:100;
x0 = [0.5 ;100000; 0.5];
x = ode(x0,0,t,genetics);

//xbasc()
scf(1);
plot2d(t,x(1,:),style=1)
plot2d(t,x(3,:),style=2)
legends(['A', 'a'],[1 2],"ur")
xlabel('Time')
ylabel('AlleleFrequency')
```

After executing the code, we get the following graph:
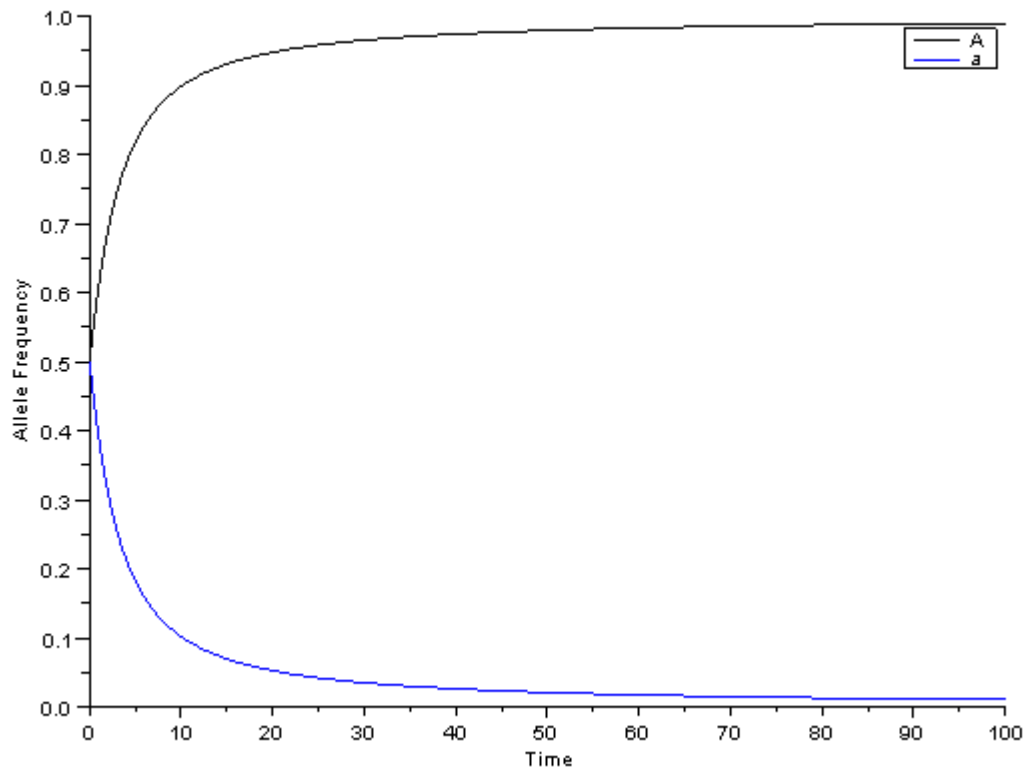
We see that in both the original graph and in this graph, the a allele approaches extinction while the A allele nears a frequency of 1 within the population. But in this graph, the frequency of the a allele decrease faster and the frequency of the A allele increases more rapidly compared to the original graph. (The difference is very subtle and may be hard to see but if you look at a specific time, say 10, and compare the height of each graph at that time, you will see that the frequency of the a allele is slightly lower in the new graph compared to the original graph.) The reason for this is because the aa genotype is lethal so some of the a alleles are removed from the population faster.

QUESTION: Change the fitness of the Aa genotype to $f_{Aa} = 0.75$ and the fitness of the aa genotype back to $f_{aa} = 0.5$. What are the similarities and differences in this case compared to the original one? Why do you think that is?

**Solution:** After changing the fitness of the aa genotype back to 0.5 and changing the fitness of the Aa genotype to 0.75, the Scilab code should look as follows:

```
function dx=genetics(t,x)
fA = x(1)*fAA+(1-x(1))*fAa
fa = x(1)*fAa+(1-x(1))*faa
f = x(1)*fA+(1-x(1))*fa
dx(1) = x(1)*(1-x(1))*(fA-fa)
dx(2) = x(2)*f
dx(3) = -x(1)*(1-x(1))*(fA-fa)
endfunction

fAA = 1.0
fAa = 0.75
faa = 0.5
t = 0:0.001:100;
x0 = [0.5 ;100000; 0.5];
x = ode(x0,0,t,genetics);

//xbasc()
scf(2);
plot2d(t,x(1,:),style=1)
plot2d(t,x(3,:),style=2)
legends(['A', 'a'],[1 2],"ur")
xlabel('Time')
ylabel('AlleleFrequency')
```

Executing the code produces the following graph:
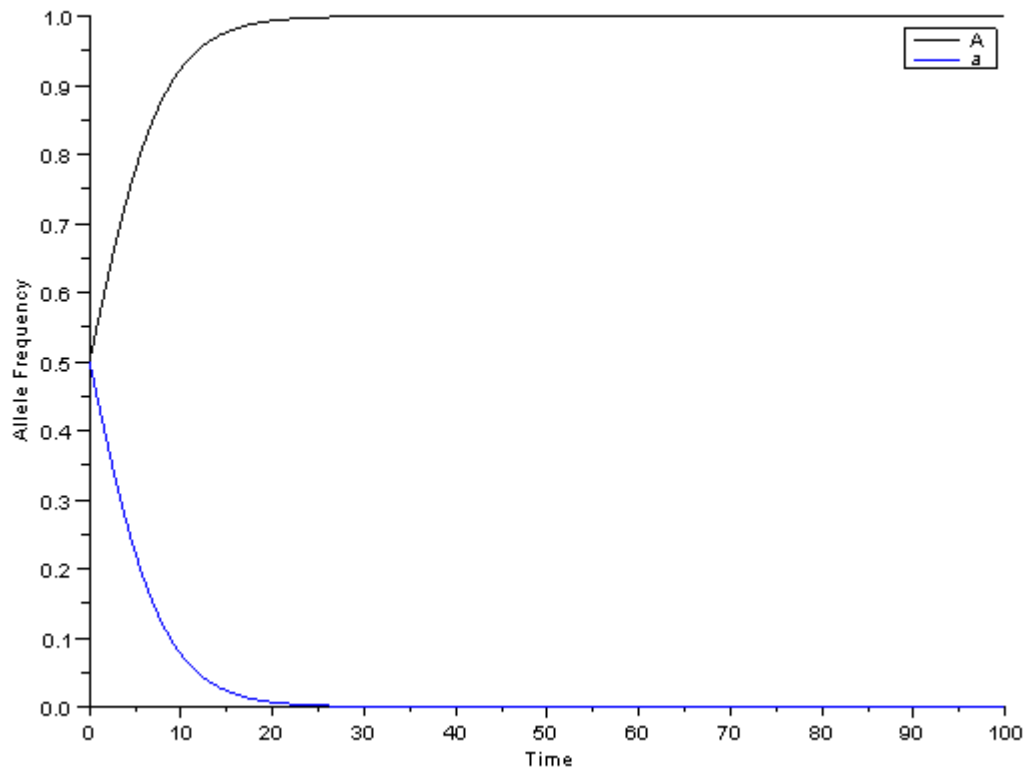
We see that in this case, just as in the original, the frequency of the A allele increases while the frequency of the a allele decreases. But in this case, the a allele decreases must faster than in the original, reaching extinction within the first 100 time steps. This is because the frequency of the aa allele is so small and the frequency of the Aa allele can no cannot sustain the a allele because it too is diminished.

QUESTION: Change the fitness of the AA genotype to $f_{AA} = 0.75$ and the fitness of the Aa genotype back to $f_{Aa} = 1.0$. This is the case for a person who has sickle cell. What are the similarities and differences in this case compared to the original one? Why do you think that is?

Solution: After changing the frequency of the Aa allele back to 1.0 and the frequency

of the AA allele to 0.75, the Scilab code should look as follows:

```
function dx=genetics(t,x)
fA = x(1)*fAA+(1-x(1))*fAa
fa = x(1)*fAa+(1-x(1))*faa
f = x(1)*fA+(1-x(1))*fa
dx(1) = x(1)*(1-x(1))*(fA-fa)
dx(2) = x(2)*f
dx(3) = -x(1)*(1-x(1))*(fA-fa)
endfunction

fAA = 0.75
fAa = 1.0
faa = 0.5
t = 0:0.001:100;
x0 = [0.5 ;100000; 0.5];
x = ode(x0,0,t,genetics);

//xbasc()
scf(3);
plot2d(t,x(1,:),style=1)
plot2d(t,x(3,:),style=2)
legends(['A', 'a'],[1 2],"ur")
xlabel('Time')
ylabel('AlleleFrequency')
```

Executing the code produces the following graph:
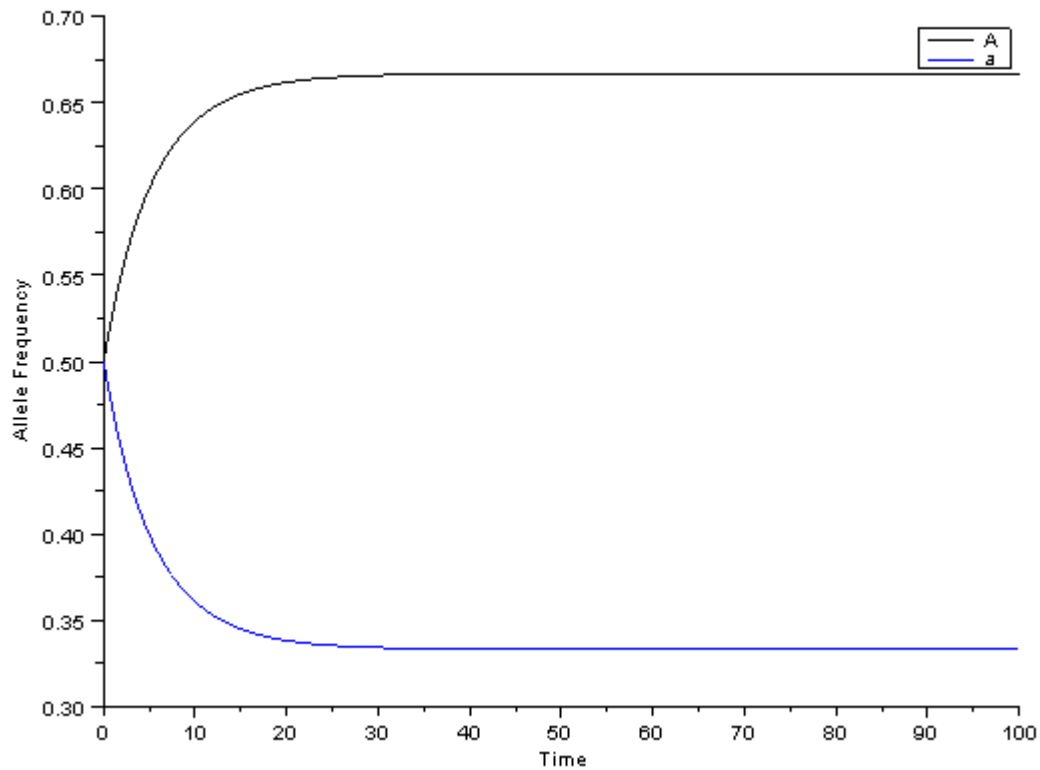
As in the original, the frequency of the a allele decreases and the frequency of the A allele increases. But this time, the a allele reaches an equilibrium value around 0.35 instead of going extinct. Similarly, the A allele reaches an equilibrium value around 0.65 instead of 1.0. This is because the Aa genotype has the highest fitness so it supports the survival of both alleles.

B.8 Macroevolution vs. Microevolution

QUESTION: Compute $P_1 \ldots P_5$ (the number of individuals in generations 1 - 5), given that the population grows according to the difference equation $P_{t+1} = 3P_t - 4$ with initial condition $P_0 = 5$.

Solution: The equation we are given is for P_{t+1}, so to get P_1, we plug in 0 for t, since $P_{0+1} = P_1$. Doing the same thing on the right side of the equation gives us $3P_0 - 4$. But we are given that $P_0 = 5$, so we plug this in to get $3P_0 - 4 = 3(5) - 4 = 15 - 4 = 11$. So we get:

$$\boxed{P_1 = 11}$$

To get P_2, we plug in 1 for t, since $P_{1+1} = P_2$. Doing the same thing on the right side of the equation gives $3P_1 - 4$. But we just computed P_1 and figured out that $P_1 = 11$, so we plug this in to get $3P_1 - 4 = 3(11) - 4 = 33 - 4 = 29$. So we get:

$$\boxed{P_2 = 29}$$

To get P_3, we plug in 2 for t on both sides of the equation to get $P_3 = 3P_2 - 4 = 3(29) - 4 = 87 - 4 = 83$. So we have:

$$\boxed{P_3 = 83}$$

To get P_4, we plug in 3 for t on both sides of the equation to get $P_4 = 3P_3 - 4 = 3(83) - 4 = 249 - 4 = 245$. So we have:

$$\boxed{P_4 = 245}$$

And to get P_5, we plug in 4 for t on both sides of the equation to get $P_5 = 3P_4 - 4 = 3(245) - 4 = 735 - 4 = 731$. So we have:

$$\boxed{P_5 = 731}$$

QUESTION: Compute the equilibrium value of the difference equation in the previous problem.

Solution: To get the equilibrium value of the equation, we set $P_{t+1} = P_t$. In other words, we need to solve the equation

$$\underbrace{3P_t - 4}_{P_{t+1}} = P_t.$$

To do that, we first need to get P_t on one side of the equation, which we accomplish by subtracting $3P_t$ from both sides of the equation to get

$$-4 = -2P_t.$$

Now to get P_t by itself, divide both sides of the equation by -2 to get the equilibrium value of

$$\boxed{P_t = 2}$$

QUESTION: Suppose there are 2,000 individuals (so 4,000 alleles in the gene pool at locus A) in a population, of which 1 in 400 individuals possesses a recessive trait. How many heterozygotic and how many homozygotic dominant individuals are in the population?

Solution: If we suppose that A_1 is the dominant allele and has frequency p, and A_2 is the recessive allele and has frequency q, then individuals who possess a recessive trait have the A_2A_2 genotype and their frequency within the population is q^2. If the frequency of this recessive trait is 1 out of 400, then we know that $q^2 = 1/400$. To get q, we square root both sides of this equation. This gives us $q = 1/20 = 0.05$. So the frequency of the A_2 allele is $1/20$. To get the frequency of the A_1 allele, we use the fact that $p + q = 1$. So we have that $p + 0.05 = 1 \Rightarrow p = 0.95 = \frac{19}{20}$. This tells us that the

frequency of the $A_1 A_2$ genotype is $2pq = (2)(0.05)(0.95) = 0.095 = \frac{38}{400} = \frac{19}{200}$ and the frequency of the $A_1 A_1$ genotype is $p^2 = 0.9025 = \frac{361}{400}$. So, if there are 1,000 individuals and $\frac{19}{200}$ have the $A_1 A_2$ genotype, then the number of heterozygotic individuals is $2000 \times \frac{19}{200} = \boxed{180}$. Similarly, the number of homozygotic dominant individuals is $2000 * \frac{361}{400} = \boxed{1805}$.

QUESTION: Write an equation analogous to the one above but for q_{t+1}, the frequency of the A_2 allele at time $t + 1$.

Solution: To get the fraction of the gene pool with the A_2 allele at time $t + 1$, we need to know two things: the total number A_2 alleles at time $t + 1$ and the total number of alleles at time $t + 1$. Once we know these two, we will have

$$q_{t+1} = \frac{\text{total number of } A_2 \text{ alleles at time } t + 1}{\text{total number of alleles at time } t + 1}$$

To get the total number of A_2 alleles at time $t + 1$, we need to take all the gametes made from the parents of genotype $A_2 A_2$ plus half of the gametes from the parents of genotype $A_1 A_2$. Since N represents the total population size, then the start of the $t + 1$ generation, when all of the organisms are zygotes, there are $q_t^2 N_t$ zygotes from the $A_2 A_2$ allele from the end of the time t generation. Hence, there are $\ell_{22} q_t^2 N_t$ adults at the end of the generation from the $A_2 A_2$ allele. Therefore, there are $2 m_{22} \ell_{22} q_t^2 N_t$ gametes from the $A_2 A_2$ allele. Similarly, there are $2 p_t q_t N_t$ zygotes at the beginning of the $t+1$ generation from the $A_1 A_2$ allele from the time t generation, of which $\ell_{12} 2 p_t q_t N_t$ survive to become adults at the end of the generation, producing $2 m_{12} \ell_{12} 2 p_t q_t N_t$

gametes.

total number of A_2 alleles at time $t + 1 = 2m_{22}\ell_{22}p_t^2 N_t + \left(\dfrac{1}{2}\right) 2m_{12}\ell_{12}2p_tq_t N_t$

For the total number of alleles at time $t + 1$, we can use the expression calculated in the module, which is

total number of alleles at time $t + 1 = 2m_{11}\ell_{11}p_t^2 N_t + 2m_{12}\ell_{12}2p_tq_t N_t + 2m_{22}\ell_{22}q_t^2 N_t$

Therefore,

$$
\begin{aligned}
q_{t+1} &= \frac{2m_{22}\ell_{22}q_t^2 N_t + \left(\frac{1}{2}\right) 2m_{12}\ell_{12}2p_tq_t N_t}{2m_{11}\ell_{11}p_t^2 N_t + 2m_{12}\ell_{12}2p_tq_t N_t + 2m_{22}\ell_{22}q_t^2 N_t} \\
&= \frac{m_2\ell_2q_t^2 + \left(\frac{1}{2}\right) m_{12}\ell_{12}2p_tq_t}{m_{11}\ell_{11}p_t^2 + m_{12}\ell_{12}2p_tq_t + m_{22}\ell_{22}q_t^2} \\
&= \frac{m_{22}\ell_{22}q_t + m_{12}\ell_{12}p_t}{m_{11}\ell_{11}p_t^2 + m_{12}\ell_{12}2p_tq_t + m_{22}\ell_{22}q_t^2}q_t
\end{aligned}
$$

Using the same convention as mentioned in the module of combining survival and reproduction into a single quantity, and using the same notation of letting $w_{ij} = m_{ij}\ell_{ij}$ represent selective value or "fitness" of an individual, then we get the final form of our equation, which is

$$
q_{t+1} = \frac{w_{22}q_t + w_{12}p_t}{w_{11}p_t^2 + w_{12}2p_tq_t + w_{22}q_t^2}q_t
$$

QUESTION: Using the equations for p_{t+1} (given above) and q_{t+1} (which you derived in the previous problem), determine the equilibria of the system. *Hint:* It will be easier to utilize the fact that $p + q = 1$ to rewrite each equation as an equation with one variable instead of two. There will be three equilibria and you will need the quadratic formula for two of them.

Solution: Let's start with the equilibrium for p. The equation for p was

$$p_{t+1} = \frac{w_{11}p_t + w_{12}q_t}{w_{11}p_t^2 + w_{12}2p_tq_t + w_{22}q_t^2}p_t.$$

To get the equilibrium, we need to solve the equation $p_{t+1} = p_t$. In this case, that becomes

$$p_t = \underbrace{\frac{w_{11}p_t + w_{12}q_t}{w_{11}p_t^2 + w_{12}2p_tq_t + w_{22}q_t^2}p_t}_{p_{t+1}}.$$

In order to simplify this, we can get rid of the q's by utilizing the fact that $p_t + q_t = 1$. If we solve for q_t, we get $q_t = 1 - p_t$. If we plug this into the equation then we get

$$p_t = \frac{w_{11}p_t + w_{12}(1 - p_t)}{w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2}p_t.$$

The first thing we can do to begin solving this is to move p_t from the left to the right side of the equation so that the equation equals zero. Doing this gives us

$$0 = \frac{w_{11}p_t + w_{12}(1 - p_t)}{w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2}p_t - p_t.$$

Now, since both terms on the right side have p_t in common, we can factor it out as

a common factor, giving us gives us

$$0 = p_t \left(\frac{w_{11}p_t + w_{12}(1 - p_t)}{w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2} - 1 \right).$$

Setting each factor equal to zero gives us

$$0 = p_t \text{ or } 0 = \frac{w_{11}p_t + w_{12}(1 - p_t)}{w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2} - 1.$$

So we know that one equilibrium value of p is $p_t = 0$. To get the other equilibrium value, we will need to solve the second equation above. We can get rid of the fraction by multiplying both sides of the equation by the denominator. That will give us

$$0 = w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2 - \left(w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2 \right)$$

$$= w_{11}p_t^2 + w_{12}2p_t(1 - p_t) + w_{22}(1 - p_t)^2 - w_{11}p_t^2 - w_{12}2p_t(1 - p_t) - w_{22}(1 - p_t)^2$$

You will notice that this equation is a quadratic equation because we have p_t^2. So in order to solve it, we will need to use the quadratic formula. Recall that the quadratic formula says that if $ax^2 + bx + c = 0$ then $x = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$. So we need to get the equation into standard form. In order to do this, we first distribute and FOIL as needed on both sides of the equation.

$$0 = w_{11}p_t^2 + \overbrace{w_{12}2p_t(1 - p_t)}^{2w_{12}p_t - 2w_{12}p_t^2} + \overbrace{w_{22}(1 - p_t)^2}^{w_{22}\left(1 - 2p_t + p_t^2\right) = w_{22} - 2w_{22}p_t + w_{22}p_t^2} - w_{11}p_t - \overbrace{w_{12}(1 - p_t)}^{w_{12} - w_{12}p_t}.$$

So we have

$$0 = w_{11}p_t^2 + 2w_{12}p_t - 2w_{12}p_t^2 + w_{22} - 2w_{22}p_t + w_{22}p_t^2 - w_{11}p_t - w_{12} + w_{12}p_t.$$

Now we combine like terms and arrange the terms in decreasing order of their exponents.

$$0 = (w_{11} - 2w_{12} + w_{22})p_t^2 - (w_{11} - 3w_{12} + 2w_{22})p_t + (w_{22} - w_{12}).$$

Plugging into the quadratic equation gives us the following (*Note*: The numerator didn't fit on one line, but the denominator is under the whole thing and not just the term in the second line.):

$$p_t = -\Bigg(-(w_{11} - 3w_{12} + 2w_{22}) \Bigg)$$

$$\frac{\pm\sqrt{\Big(-(w_{11} - 3w_{12} + 2w_{22})\Big)^2 - 4(w_{11} - 2w_{12} + w_{22})(w_{22} - w_{12})}}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= (w_{11} - 3w_{12} + 2w_{22})$$

$$\frac{\pm\sqrt{(w_{11} - 3w_{12} + 2w_{22})^2 - 4(w_{11} - 2w_{12} + w_{22})(w_{22} - w_{12})}}{2(w_{11} - 2w_{12} + w_{22})}$$

To simplify this further, we need to square and distribute the terms in the parenthesis, then combine like terms.

$$(w_{11} - 3w_{12} + 2w_{22})^2 = w_{11}^2 - 6w_{11}w_{12} + 4w_{11}w_{22} + 9w_{12}^2 - 12w_{12}w_{22} + 4w_{22}^2$$

$$4(w_{11} - 2w_{12} + w_{22})(w_{22} - w_{12}) = 4\Big(w_{11}w_{22} - w_{11}w_{12} - 3w_{12}w_{22} + 2w_{12}^2 + w_{22}^2\Big)$$

$$= 4w_{11}w_{22} - 4w_{11}w_{12} - 12w_{12}w_{22} + 8w_{12}^2 + 4w_{22}^2$$

If we subtract these, then the term inside the parenthesis becomes

$$w_{11}^2 - 6w_{11}w_{12} + 4w_{11}w_{22} + 9w_{12}^2 - 12w_{12}w_{22} + 4w_{22}^2$$

$$- \left(4w_{11}w_{22} - 4w_{11}w_{12} - 12w_{12}w_{22} + 8w_{12}^2 + 4w_{22}^2\right)$$

$$= w_{11}^2 - 2w_{11}w_{12} + w_{12}^2.$$

So what we have is

$$p_t = (w_{11} - 3w_{12} + 2w_{22})$$

$$\frac{\pm\sqrt{(w_{11} - 3w_{12} + 2w_{22})^2 - 4(w_{11} - 2w_{12} + w_{22})(w_{22} - w_{12})}}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= \frac{(w_{11} - 3w_{12} + 2w_{22}) \pm \sqrt{w_{11}^2 - 2w_{11}w_{12} + w_{12}^2}}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= \frac{(w_{11} - 3w_{12} + 2w_{22}) \pm \sqrt{(w_{11} - w_{12})^2}}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= \frac{(w_{11} - 3w_{12} + 2w_{22}) \pm (w_{11} - w_{12})}{2(w_{11} - 2w_{12} + w_{22})}$$

So we have two possibilities:

$$p_t = \frac{(w_{11} - 3w_{12} + 2w_{22}) + (w_{11} - w_{12})}{2(w_{11} - 2w_{12} + w_{22})} \quad \text{or} \quad p_t = \frac{(w_{11} - 3w_{12} + 2w_{22}) - (w_{11} - w_{12})}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= \frac{2w_{11} - 4w_{12} + 2w_{22}}{2(w_{11} - 2w_{12} + w_{22})} \qquad\qquad = \frac{-2w_{12} + 2w_{22}}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= \frac{2(w_{11} - 2w_{12} + w_{22})}{2(w_{11} - 2w_{12} + w_{22})} \qquad\qquad = \frac{2(-w_{12} + w_{22})}{2(w_{11} - 2w_{12} + w_{22})}$$

$$= 1 \qquad\qquad\qquad\qquad\qquad = \frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}}$$

So for the equilibrium of the q equation, we have two options. One would be to solve the equation $q_{t+1} = q_t$, which would require us to go through similar calculations to

what we just did. The other option is to again utilize the fact that $p + q = 1$, which tells us that $q = 1 - p$. If we plug in each of our three equilibrium values for p (the two that we just determined and one that we found at the beginning of this calculation which was $p_t = 0$), we get

$$
\begin{aligned}
q_t \quad = 1 - 0 \quad \text{or} \quad q_t \quad = 1 - 1 \quad \text{or} \quad q_t \quad &= 1 - \frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}} \\
= 1 \qquad\qquad\qquad = 0 \qquad\qquad\qquad &= \frac{w_{11} - 2w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}} - \frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}} \\
&= \frac{w_{11} - 2w_{12} + w_{22} - (-w_{12} + w_{22})}{w_{11} - 2w_{12} + w_{22}} \\
&= \frac{w_{11} - w_{12}}{w_{11} - 2w_{12} + w_{22}}
\end{aligned}
$$

So we have three equilibria:

$$
(p_t, q_t) = (0, 1) \text{ and } (p_t, q_t) = (1, 0) \text{ and } (p_t, q_t) = \left(\frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}}, \frac{w_{11} - w_{12}}{w_{11} - 2w_{12} + w_{22}} \right)
$$

QUESTION: What conditions are necessary for the third equilibrium to be biologically relevant? What does this mean for the chances of an allele to survive?

Solution: Notice that depending on the values of w_{11}, w_{12}, and w_{22}, the third equilibrium could have coordinates which are either positive or negative. But since p_t and q_t represent the frequency with which an allele is present in a population, we are only interested in the cases when they are positive. In other words, we need to know when

$$
\frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}} > 0 \text{ and } \frac{w_{11} - w_{12}}{w_{11} - 2w_{12} + w_{22}} > 0.
$$

In order for $\frac{-w_{12} + w_{22}}{w_{11} - 2w_{12} + w_{22}} > 0$, either the numerator and denominator must both be

positive (since a positive divided by a positive is positive) or both must be negative (since a negative divided by a negative is positive). The same is true in order to have $\frac{w_{11}-w_{12}}{w_{11}-2w_{12}+w_{22}} > 0$. Since both fractions have the same denominator, then if one fraction's numerator is positive, then the other one will have to also be positive at the same time. And if one fraction's numerator is negative, then the other one will also have to be negative at the same time.

In order for both numerators to be positive at the same time, we must have $-w_{12} + w_{22} > 0$ and $w_{11} - w_{12} > 0$ which is the same as $w_{22} > w_{12}$ and $w_{11} > w_{12}$. Notice that if both of these occur at the same time, then the denominator is also positive. To see this, note that the denominator being positive means $w_{11} - 2w_{12} + w_{22} > 0$. But this is the same as $w_{11} + w_{12} > 2w_{12}$. But if $w_{11} > w_{12}$ and $w_{22} > w_{12}$, then when you add the two sides of the inequalities which are bigger, namely $w_{11} + w_{22}$, that will be bigger than if you add the two sides of the inequalities which are smaller, namely $w_{12} + w_{12} = 2w_{12}$. So one way in which the the third equilibrium could be biologically relevant is if both $w_{11} > w_{12}$ and $w_{22} > w_{12}$; in other words, if both homozygotic genotypes have a higher fitness than the heterozygotic genotype.

In order for both denominators to be negative at the same time, we must have $-w_{12} + w_{22} < 0$ and $w_{11} - w_{12} < 0$ which is the same as $w_{22} < w_{12}$ and $w_{11} < w_{12}$. Notice that if both of these occur at the same time, then the denominator is also negative. To see this, note that the denominator being negative means $w_{11} - 2w_{12} + w_{22} < 0$. But this is the same as $w_{11} + w_{12} < 2w_{12}$. But if $w_{11} < w_{12}$ and $w_{22} < w_{12}$, then when you add the two sides of the inequalities that are smaller, namely $w_{11} + w_{12}$, that will be smaller than if you add the two sides of the inequalities which are bigger, namely $w_{12} + w_{12} = 2w_{12}$. So the other way in which the third equilibrium could

be biologically relevant is if both $w_{11} < w_{12}$ and $w_{22} < w_{12}$; in other words, if the heterozygotic genotype has a higher fitness than both of the homozygotic genotypes.

B.9   Alternation of Generations

QUESTION: Given that we start with dispersal/colonization abilities (and hence competition abilities) suitable for all five species to coexist and no habitat destruction, state the order in which you think the species will occupy the largest fraction of sites down to the smallest fraction of sites.

Solution: Answers will vary by student.

Note: When you execute the file dispersal.sce, the graph should look as follows:
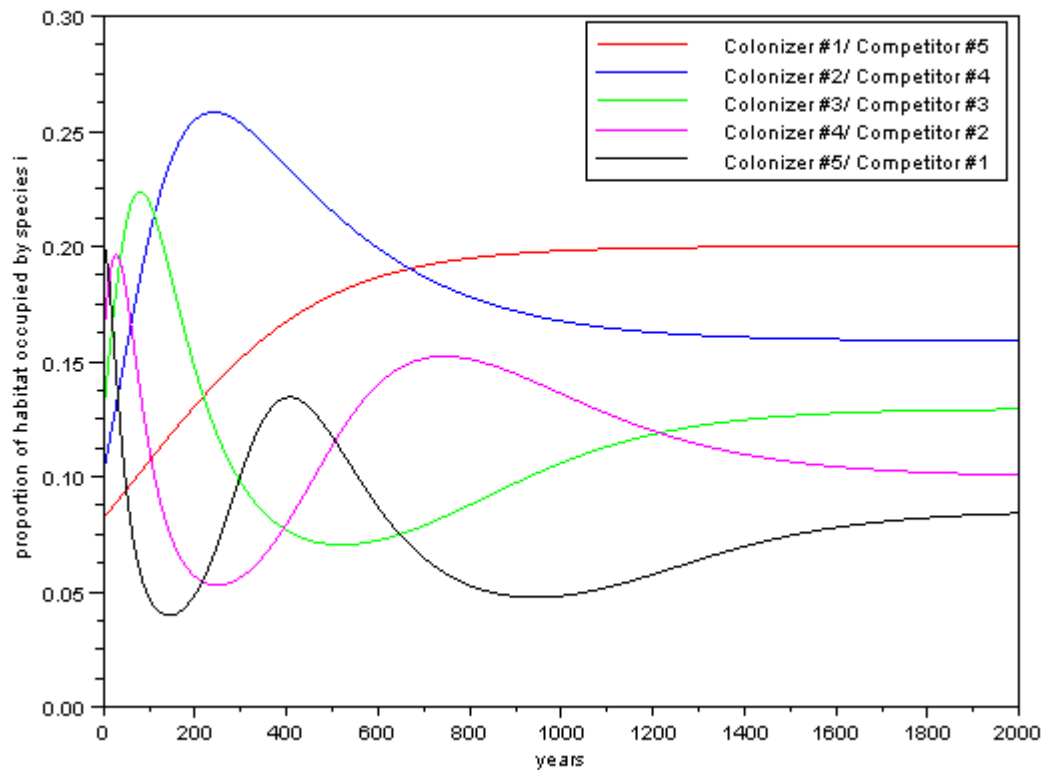
QUESTION: Were your predictions correct?

Solution: Answers will vary depending on student responses to the previous question. But students should notice the better the species is at dispersing and colonizing, the larger the fraction of sites they occupy; in other words, Colonizer #1/ Competitor #5 occupies the largest fraction of sites, followed by Colonizer #2/ Competitor #4, Colonizer #3/ Competitor #3, Colonizer #2/ Competitor #4, with Colonizer #5/ Competitor #1 occupying the fewest fraction of sites. And this is despite the fact that the number of sites they all initially occupied was reverse what they ended up being.

Note: After making the changes to the Scilab code, namely changing the value of q

from 0 to 0.3 and changing the graphics window from 1 to 2, the Scilab code should look like this:

```
function dx=dispersal(t,p)
  global m c q n;
  for i= 1:n
     sum1= 0.0
     sum2= 0.0
    for j= 1:i ;
       sum1=  sum1+p(j);
    end
    for j= 1:(i-1)
       sum2=  sum2+c(j)*p(i)*p(j)
    end
     dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:2000;
  global c m n q
   m= [.02; .02; .02; .02; .02];
   c= [.025; .039; .061; .095; .149];
   n= 5;
   q= [0.3; 0.3; 0.3; 0.3; 0.3];
   p0= [.082; .1024; .128; .16; .2]
   p= ode(p0,0,t,dispersal);
  scf(2);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

QUESTION: What affect do you think increasing the habitat destruction will have on the fraction of sites occupied by each species?

Solution: Answers will vary by student.

Note: After executing the file with the value of q changed from 0 to 0.3, graphics window 2 will open with the following graph:
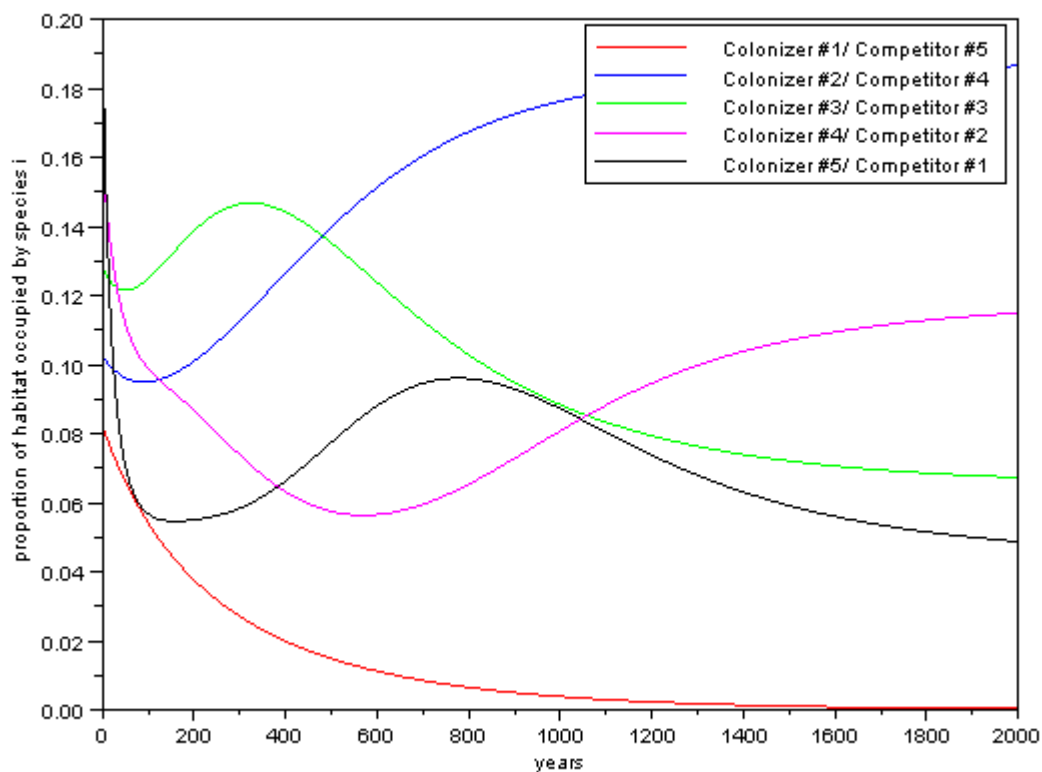
QUESTION: Was your prediction correct? Why do you think the results of the simulation were the way they were?

Solution: Answers will vary by student, depending on their response to the previous question. But students should notice that habitat destruction leads to a loss of resources, which gives better competitors a survival advantage. In fact, Colonizer

#1/ Competitor #5 had previously occupied the largest fraction of sites but now they went extinct because they weren't good enough at competing for resources.

Note: After making the changes to the Scilab code, namely changing the value of q from 0.3 to 0.63 and changing the graphics window from 2 to 3, the Scilab code should look like this:

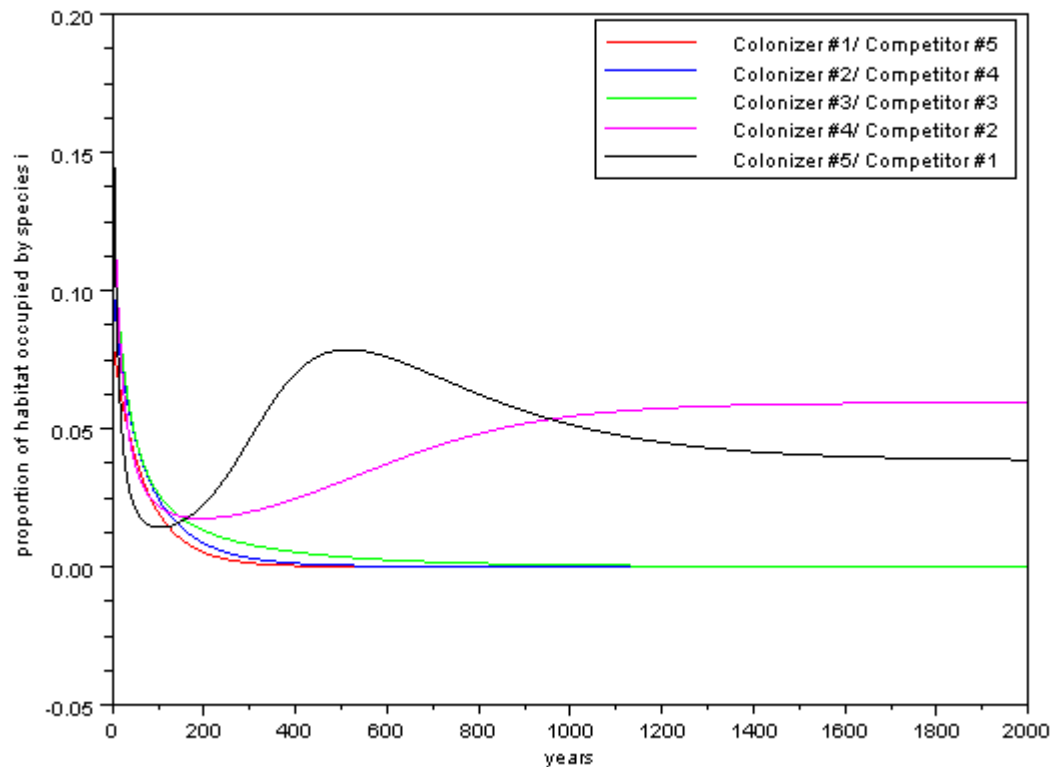```
function dx=dispersal(t,p)
  global m c q n;
  for i= 1:n
     sum1= 0.0
     sum2= 0.0
    for j= 1:i ;
       sum1= sum1+p(j);
    end
    for j= 1:(i-1)
       sum2= sum2+c(j)*p(i)*p(j)
    end
    dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:2000;
  global c m n q
  m= [.02; .02; .02; .02; .02];
  c= [.025; .039; .061; .095; .149];
  n= 5;
  q= [0.63; 0.63; 0.63; 0.63; 0.63];
  p0= [.082; .1024; .128; .16; .2]
  p= ode(p0,0,t,dispersal);
  scf(3);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

QUESTION: What do you think will happen in this case?

**Solution:** Answers will vary by student.

**Note:** After executing the file, graphics window 3 will open with the following graph:
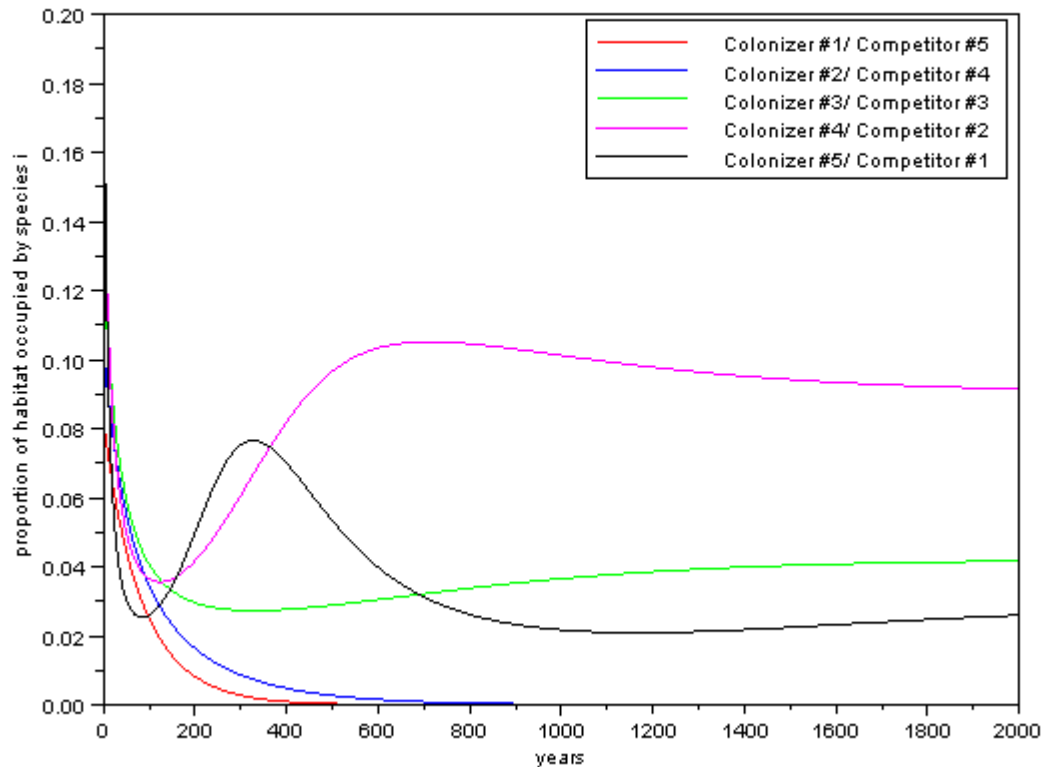


QUESTION: Was your prediction correct?

**Solution:** Answers will vary depending on student responses to the previous question. But students should notice that again, the worse competitor was driven to extinction, despite previously occupying the largest fraction of sites.

**Note:** After making the changes to the Scilab code, namely changing the value of $q$ from 0.63 to 0.73 and changing the graphics window from 3 to 4, the Scilab code

should look like this:

```
function  dx=dispersal(t,p)
  global m c q n;
  for  i= 1:n
     sum1= 0.0
     sum2= 0.0
    for  j= 1:i ;
       sum1=  sum1+p(j);
    end
    for  j= 1:(i-1)
       sum2=  sum2+c(j)*p(i)*p(j)
    end
     dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:2000;
  global c m n q
   m= [.02; .02; .02; .02; .02];
   c= [.025; .039; .061; .095; .149];
   n= 5;
   q= [0.73; 0.73; 0.73; 0.73; 0.73];
   p0= [.082; .1024; .128; .16; .2]
   p= ode(p0,0,t,dispersal);
  scf(4);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

Solution: Answers will vary by student.

Note: After executing the file, graphics window 4 will open with the following graph:

Solution: Answers will vary depending on responses to the previous question. But students should notice that again, the worse competitor was driven to extinction, despite previously occupying the largest fraction of sites.

Note: After making the changes to the Scilab code, namely changing the value of q from 0.73 to 0.93, changing the graphics window from 4 to 5, and changing the final

time from 2000 to 200, the Scilab code should look like this:

```
function dx=dispersal(t,p)
  global m c q n;
  for i= 1:n
    sum1= 0.0
    sum2= 0.0
    for j= 1:i ;
      sum1= sum1+p(j);
    end
    for j= 1:(i-1)
      sum2= sum2+c(j)*p(i)*p(j)
    end
    dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:500;
  global c m n q
  m= [.02; .02; .02; .02; .02];
  c= [.025; .039; .061; .095; .149];
  n= 5;
  q= [0.93; 0.93; 0.93; 0.93; 0.93];
  p0= [.082; .1024; .128; .16; .2]
  p= ode(p0,0,t,dispersal);
  scf(5);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

QUESTION: In what order do you expect the species to go extinct in? Why?

Solution: Answers will vary by student.

Note: After executing the file, graphics window 5 will open with the following graph:
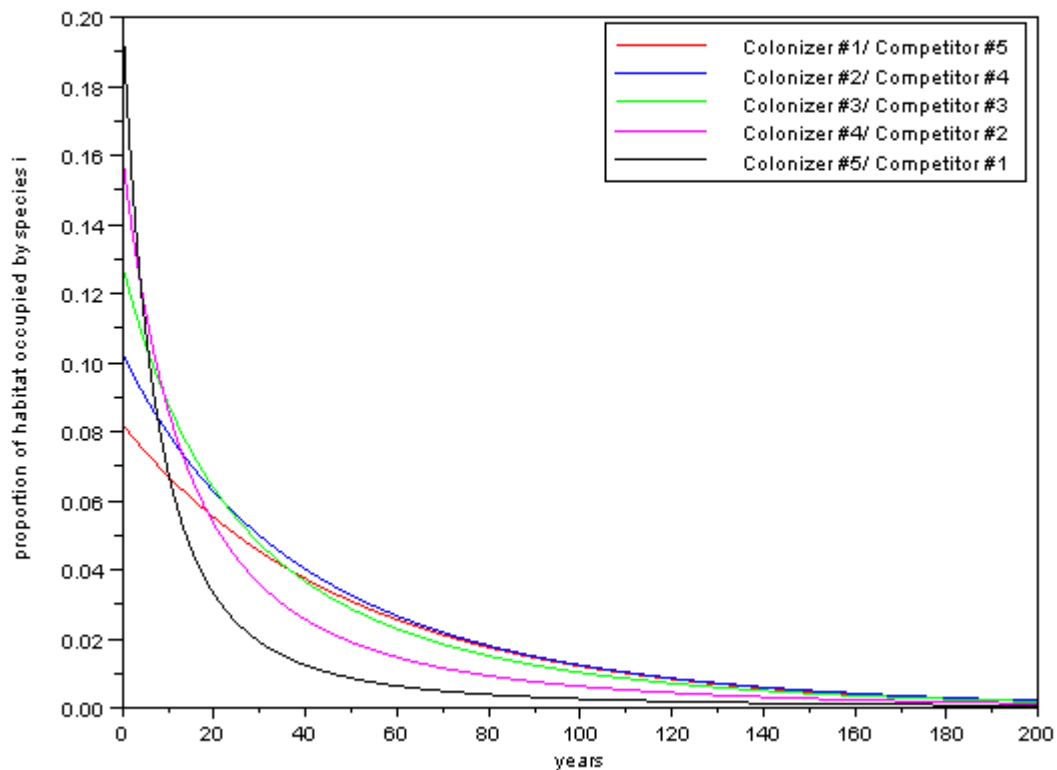
QUESTION: Was your prediction correct? Why do you think the results of the simulation were the way they were?

Solution: Answers will vary depending on student responses to the previous question. But students should notice that when habitat loss is high and resources are insufficient to sustain any of the populations then competition is no longer an issue. And when this happens, dispersal and colonization abilities become the important factor again

and so the worse colonizers go extinct first and the better colonizers take longer to go extinct.

Note: After changing the habitat destruction back to 0, the ending time back to 2000, the graphics window back to 1, and the initial fraction of sites that colonizer #1/ Competitor #5 occupies from .082 to .382, the Scilab code should look like this:

```
function dx=dispersal(t,p)
  global m c q n;
  for  i= 1:n
     sum1= 0.0
     sum2= 0.0
    for  j= 1:i ;
       sum1=  sum1+p(j);
    end
    for  j= 1:(i-1)
       sum2=  sum2+c(j)*p(i)*p(j)
    end
     dx(i,1)= c(i)*p(i)*(1-q(1)-sum1)-m(i)*p(i)-sum2;
  end
endfunction
t = 0:1:2000;
  global c m n q
   m= [.02; .02; .02; .02; .02];
   c= [.025; .039; .061; .095; .149];
   n= 5;
   q= [0; 0; 0; 0; ];
   p0= [.382; .1024; .128; .16; .2]
   p= ode(p0,0,t,dispersal);
  scf(1);
  plot(t,p(1,:),'r')
  plot(t,p(2,:),'b')
  plot(t,p(3,:),'g')
  plot(t,p(4,:),'m')
  plot(t,p(5,:),'k')
  legend('Colonizer #1/ Competitor #5','Colonizer #2/
Competitor #4','Colonizer #3/ Competitor #3','Colonizer
#4/ Competitor #2','Colonizer #5/ Competitor #1');
  xlabel('years');
  ylabel('proportion of habitat occupied by species i');
```

QUESTION: What affect do you think this change will have on the results?

Solution: Answers will vary by student.

Note: After executing the file, graphics 1 will open with the following graph:
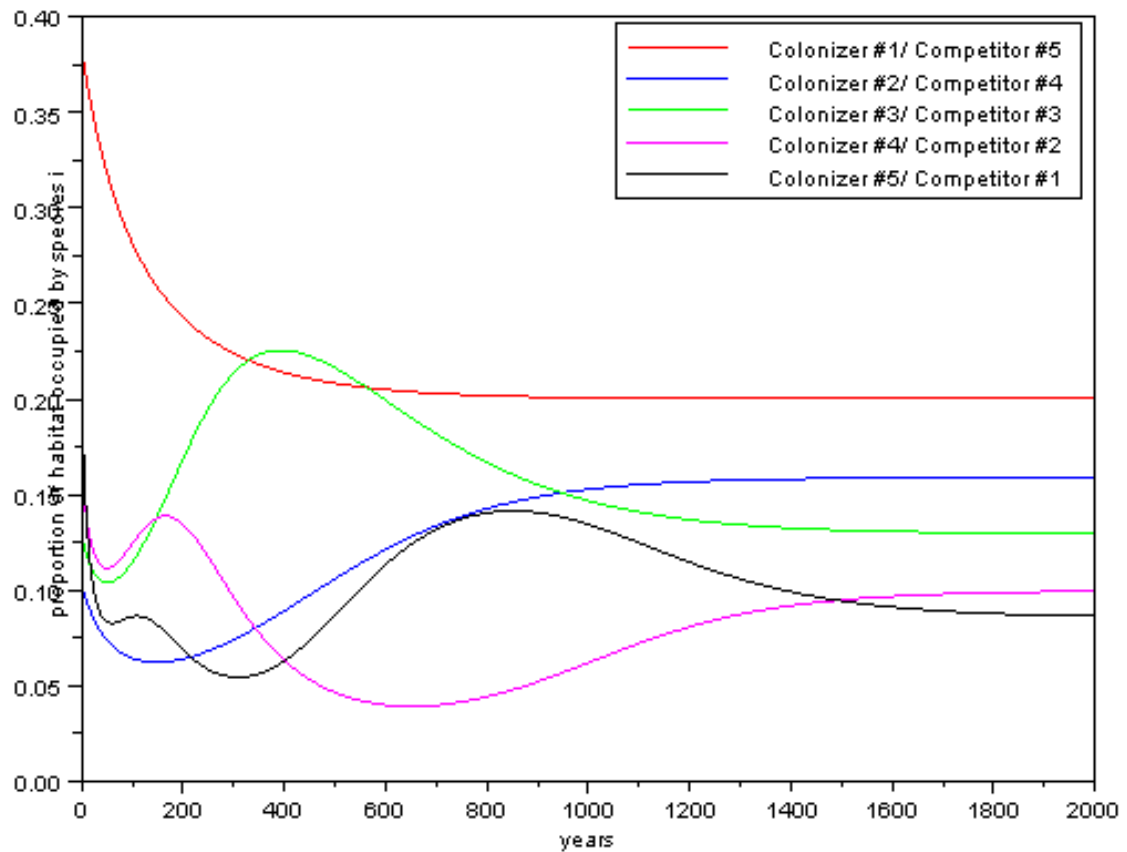
QUESTION: Was your prediction correct?

Solution: Answers will vary depending on student responses to the previous question. But students should notice that, as before, when there is no habitat destruction, the better a species is at colonizing, the larger the fraction of sites they will occupy. Of

course, given that we are now considering the case where the best colonizer begins occupying the largest fraction of sites (as opposed to before when the best colonizer began by occupying the smallest fraction of sites), this should probably be what the students predicted would happen.

QUESTION: If you were to repeat all of the previous simulations, how do you think the outcomes of each would differ? Why?

Solution: Answers will vary by student.

Note: Repeating the simulations but with the the best colonizer starting off occupying a the largest fraction of sites produces the exact same results. So even by starting off occupying the largest fraction of sites, habitat destruction cannot save the worst competitor (best colonizer) from going extinct first.

QUESTION: Were your predictions correct?

Solution: Answers will vary by student.

B.10   Speciation

QUESTION: Write a Scilab program and graph (all on the same plot) the normal distribution for:

(a) $\mu = 0$, $\sigma^2 = \frac{1}{2}$,

(b) $\mu = 1$, $\sigma^2 = 4$, and

(c) $\mu = -2$, $\sigma^2 = \frac{1}{8}$ for $-8 \leq x \leq 8$.

Use a different color for each graph and be sure to put a title and legend on the graph. Discuss with your peers how μ and σ^2 effect the graph of the normal distribution.

Solution: The Scilab code will vary from student to student, but here is one example which will work.

```
x = -8:.1:8;
mu_a = 0;
sigmasquared_a = 1/2;
y =
1/(2*%pi*sigmasquared_a)*exp(-(x-mu_a).*(x-mu_a)/(2*sigma
squared_a));
mu_b = 1;
sigmasquared_b = 4;
w =
1/(2*%pi*sigmasquared_b)*exp(-(x-mu_b).*(x-mu_b)/(2*sigma
squared_b));
mu_c = -2;
sigmasquared_c = 1/8;
z =
1/(2*%pi*sigmasquared_c)*exp(-(x-mu_c).*(x-mu_c)/(2*sigma
squared_c));

scf(1);
plot(x,y,'r',x,w,'b',x,z,'k')
title('Normal distributionfor different values of mu
and sigma^2');
legend('mu = 0 & sigma^2 = 1/2','mu = 1 & sigma^2 =
4','mu = -2 & sigma^2 = 1/8');
```

Executing this code will produce the following graph:

Normal distribution for different values of mu and sigma^2
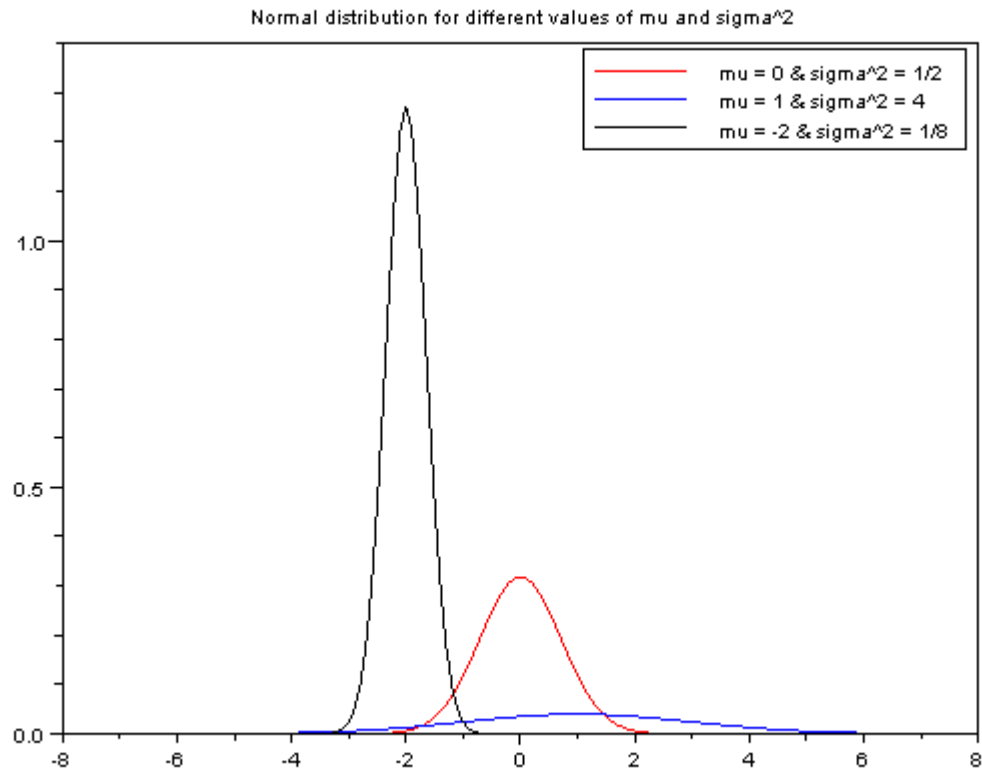
This graph shows that μ determines the center of the distribution, while σ^2 controls the width and height of the distribution, with larger values of σ^2 producing shorter but wider distributions and smaller values of σ^2 producing taller but more narrow distributions.

QUESTION: Download and execute the file fitness.sce. Discuss with your peers the relationship between trait x and fitness within each habitat.

Solution: Executing the file produces the following graphs:

Exposed (theta = 0), Intermediate (theta = 0.5), Sheltered (theta = 1.0)
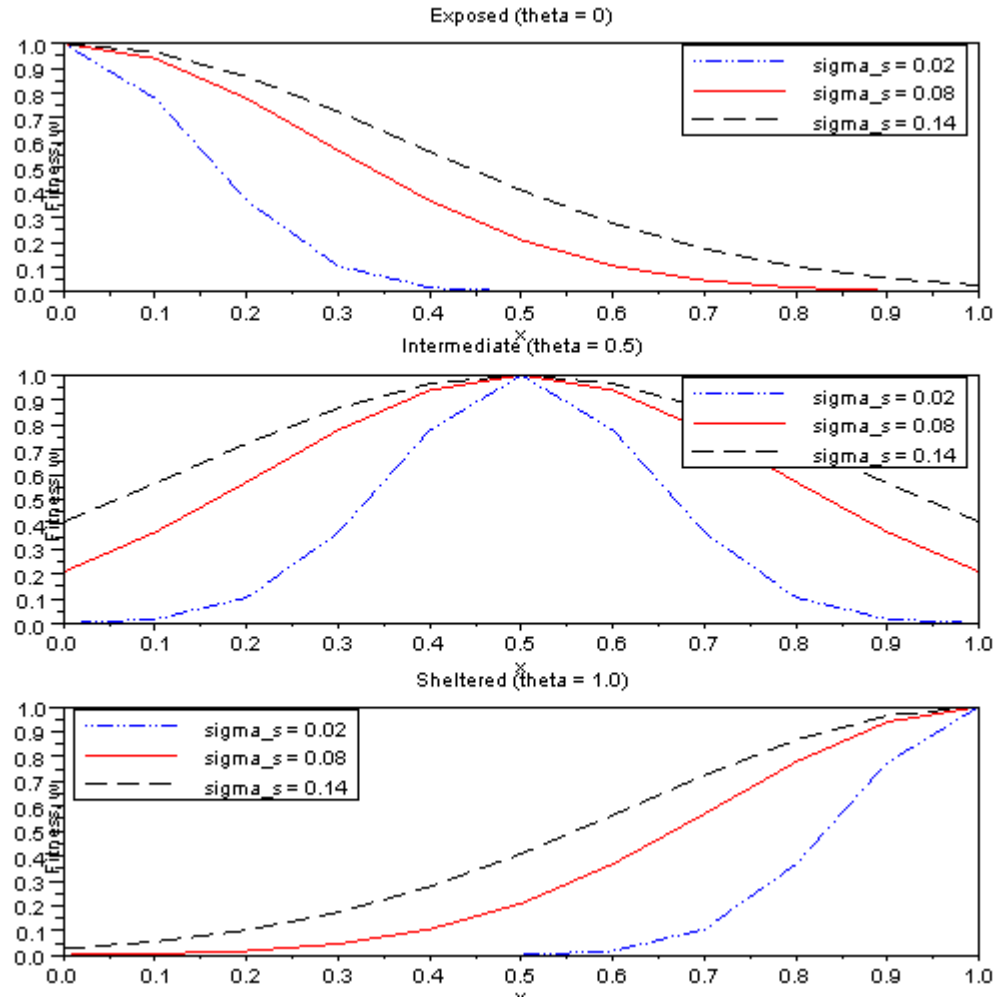
To determine the relationship between trait x and the fitness within each habitat, notice that above each figure, the optimal phenotype is given by the value of θ (theta). In the top graph (exposed habitat), $\theta = 0$. And in the graph, the fitness is highest when x is close to 0 and the fitness decreases as x increases away from 0. In the middle graph (intermediate habitat), $\theta = 0.5$. And in that graph, the fitness is highest when x is close to 0.5 and the fitness decreases as x moves away from 0.5. In the bottom graph (sheltered habitat), $\theta = 1.0$. In that graph, the fitness is highest when x is close

to 1 and the fitness decreases as x decreases away from 1. So within each habitat, the closer an individual's x trait value is to the optimum phenotype for that habitat, the higher their fitness.

QUESTION: Download and execute the file mating_probability.sce. Discuss with your peers the relationship between trait c and the mating probability of a male with trait f with a female with trait x.
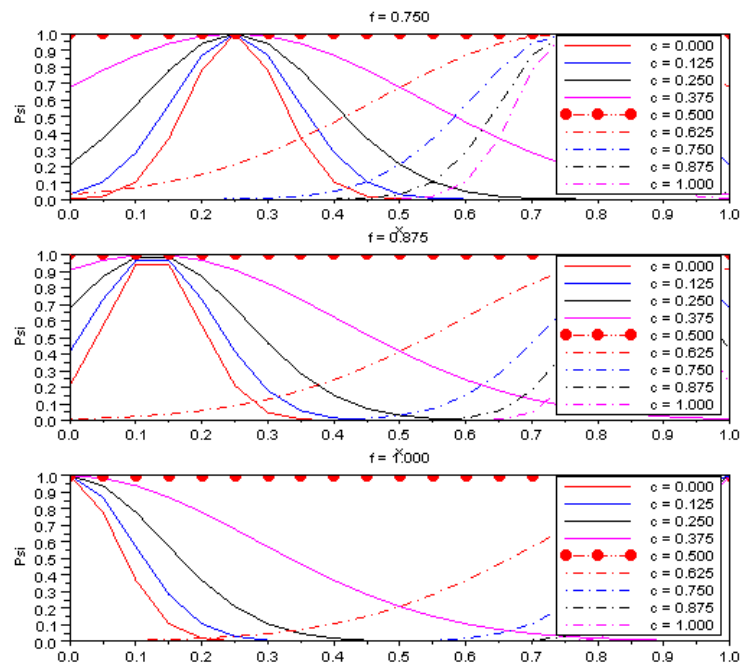
Solution: Executing the file produces the following graphs:
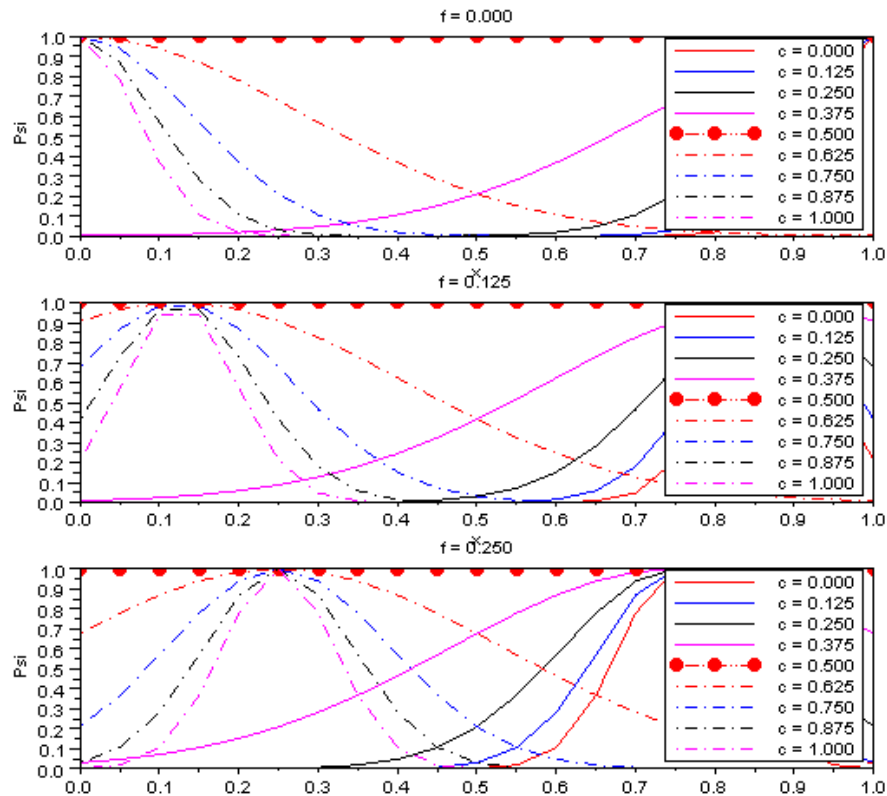
(a) graphics window 1
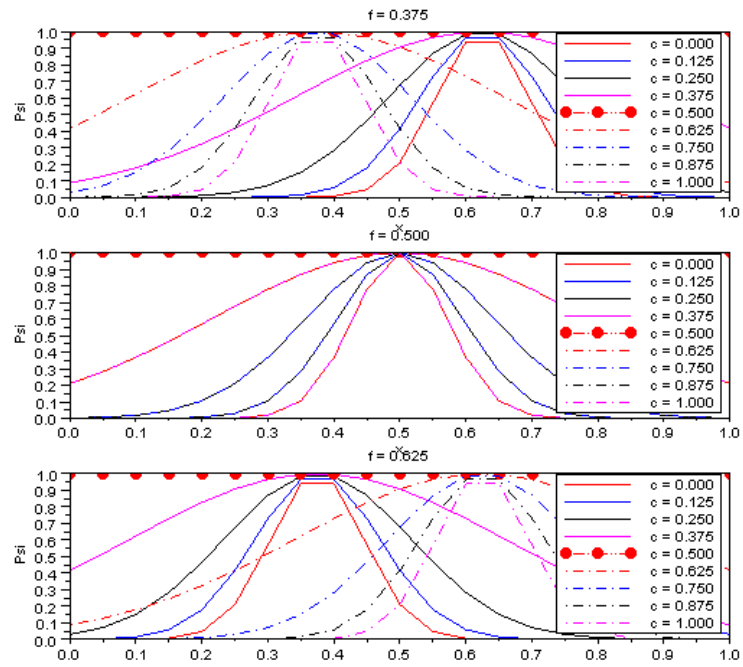
(**b**) graphics window 2

(**c**) graphics window 3

In all the cases, if a male has $c = 0.5$, the mating probability is flat, meaning there is an equal likelihood that the male will mate with any female, regardless of the male's f trait value or female's x trait value. The farther c gets from $c = 0.5$, the pickier the male gets. For $c < 0.5$, males prefer to mate with females whose x trait values are as different to their f trait value as possible. The male's f trait value is given above each graph, so when $c < 0.5$ (the solid lines in each graph), the mating probability, ψ (psi), will be highest when the value of x is most different from the value of f and ψ will be lowest when the value of x is closest to the value of f. For $c > 0.5$, males prefer to mate with females whose x trait values are as close to their f trait value as possible. So when $c > 0.5$ (the dashed/dotted lines in each graph), the mating probability, ψ will be highest when the value of x is closest to the value of f and ψ will be lowest when the value of x is most different from the value of f.

B.11   Animal Body Plan

QUESTION: What is $\mathbf{p}_0$ in this case? Round to three decimal places.

Solution: The ancestral base sequence is

$$S_0 : \ ACTTGTCGGATGATCAGCGGTCCATGCACCTGACAACGGT$$

so if we count the number of sites occupied by each base, we see that there are 9 A's, 11 C's, 11 G's, and 9 T's. Since there are 40 sites, we have $\mathcal{P}_A = \frac{9}{40} = .225$, $\mathcal{P}_C = \frac{11}{40} = .275$, $\mathcal{P}_G = \frac{11}{40} = .275$, and $\mathcal{P}_t = \frac{9}{40} = .225$. So the ancestral base distribution is

$$\boxed{\mathbf{p}_0 = (.225, .275, .275, .225)}$$

> **QUESTION:** Compute the transitional matrix, M, of conditional probabilities of having any base in any site in the sequence, given that that site was previously occupied by any of the bases. Round to three decimal places.

Solution: The following table (from the module) summarizes the number of transitions from each base into each other base.

$S_1 \backslash S_0$	A	G	C	T
A	7	0	1	1
G	1	9	2	0
C	0	2	7	2
T	1	0	1	6
Total	9	11	11	9

So we see that of the 9 sites that were initially occupied by A, 7 of them remained A, 1 changed to G, 0 changed to C, and 1 changed to T. Similarly, of the 11 sites which were initially occupied by G, 0 changed to A, 9 remained G, 2 changed to C, and 0 changed to T. Going down the columns, the same can be determine for sites initially occupied by C and sites initially occupied by T. For the first column of M, we start with the fact that initially, 9 sites were occupied by A. Of those, 7 remained occupied by A, so $\mathcal{P}_{A|A} = \frac{7}{9} = .778$. And of those 9 initially occupied by A, 1 changed to G, so $\mathcal{P}_{G|A} = \frac{1}{9} = .111$. Similarly, $\mathcal{P}_{C|A} = \frac{0}{9} = 0$ and $\mathcal{P}_{T|A} = \frac{1}{9} = .111$. For the second column of M, we start with the fact that 11 sites were initially occupied by G. Given those 11 sites, 0 changed to A, so $\mathcal{P}_{A|G} = \frac{0}{9} = 0$. Similarly, of the 11 sites initially occupied by G, 9 remain occupied by G so $\mathcal{P}_{G|G} = \frac{9}{11} = .818$. Likewise, $\mathcal{P}_{C|G} = \frac{2}{11} = .182$ and $\mathcal{P}_{T|G} = \frac{0}{11} = 0$. For the third column of M, we start with the fact that 11 sites were initially occupied by C. Of those 11 sites, 1 changed to

A so $\mathcal{P}_{A|C} = \frac{1}{11} = .091$. Of the 11 sites initially occupied by C, 2 changed to G so $\mathcal{P}_{G|C} = \frac{2}{11} = .182$. Similarly, $\mathcal{P}_{C|C} = \frac{7}{11} = .636$ and $\mathcal{P}_{T|C} = \frac{1}{11} = .091$. And for the fourth column of M, we start with the fact that 9 sites were initially occupied by T. Of those 9 sites, 1 changed to A so $\mathcal{P}_{A|T} = \frac{1}{9} = .111$. Of the 9 sites initially occupied by T, 0 changed to G so $\mathcal{P}_{G|T} = \frac{0}{9} = 0$. Similarly, $\mathcal{P}_{C|T} = \frac{2}{9} = .222$ and $\mathcal{P}_{T|T} = \frac{6}{9} = .667$. So the transitional matrix is

$$
M = \begin{pmatrix} \mathcal{P}_{A|A} & \mathcal{P}_{A|G} & \mathcal{P}_{A|C} & \mathcal{P}_{A|T} \\ \mathcal{P}_{G|A} & \mathcal{P}_{G|G} & \mathcal{P}_{G|C} & \mathcal{P}_{G|T} \\ \mathcal{P}_{C|A} & \mathcal{P}_{C|G} & \mathcal{P}_{C|C} & \mathcal{P}_{C|T} \\ \mathcal{P}_{T|A} & \mathcal{P}_{T|G} & \mathcal{P}_{T|C} & \mathcal{P}_{T|T} \end{pmatrix} = \begin{pmatrix} .778 & 0 & .091 & .111 \\ .111 & .818 & .182 & 0 \\ 0 & .182 & .636 & .222 \\ .111 & 0 & .091 & .667 \end{pmatrix}
$$

Note: In the module, you are told to type $\mathbf{p}_0$ and M into Scilab. When you do so, it should look as follows:

```
-->p0 = [.225; .275; .275; .225]
p0  =

    0.225
    0.275
    0.275
    0.225

-->M=[.778, 0, .091, .111; .111, .818, .182, 0; 0, .182, .636, .222; .111, 0, .091, .667]
M =

    0.778   0.     0.091   0.111
    0.111   0.818  0.182   0.
    0.      0.182  0.636   0.222
    0.111   0.     0.091   0.667
```

QUESTION: What are the descendent base sequences $\mathbf{p}_1$ and $\mathbf{p}_2$?

Solution: $\mathbf{p}_1 = M\mathbf{p}_0$, so we type this into Scilab, which gives us

```
-->M*p0
 ans  =

     0.22505
     0.299975
     0.2749
     0.200075
```

If we round to three decimal places then that gives us

$$\mathbf{p}_1 = \begin{pmatrix} .225 \\ .300 \\ .275 \\ .200 \end{pmatrix}$$

$\mathbf{p}_2 = M\mathbf{p}_1 = M^2\mathbf{p}_0$, so we have two options for the way we enter this into Scilab. We can either define $\mathbf{p}_1$ in Scilab the same way we defined $\mathbf{p}_0$ in Scilab or we can just use M and $\mathbf{p}_0$ which are already defined in Scilab. Either way we would get the same answer. Doing these would look as follows:

```
-->p1=[.225; .300; .275; .200]
 p1  =

    0.225
     0.3
    0.275
     0.2

-->M*p1
 ans  =

    0.222275
    0.320425
     0.2739
     0.1834

-->M^2*p0
 ans  =

    0.2223131
    0.3203919
    0.2738485
    0.1834465
```

Rounding to three decimal places gives us

$$\mathbf{p}_2 = \begin{pmatrix} .222 \\ .320 \\ .274 \\ .183 \end{pmatrix}$$

QUESTION: What is the equilibrium base distribution for this example? *Hint: To do this limit, you will need to make a table of values.*

Solution: The equilibrium base distribution is given by $\mathbf{p}_\infty = \lim_{t \to \infty} M^t \mathbf{p}_0$. As the hint in the problem says, we need to make a table of values in order to determine this limit. So in Scilab, we will compute $M^{10}\mathbf{p}_0$, $M^{100}\mathbf{p}_0$, $M^{1000}\mathbf{p}_0$, $M^{10000}\mathbf{p}_0, \ldots$ until we can see what the limit is. Doing this gives us

-->M^10*p0	-->M^100*p0	-->M^1000*p0	-->M^10000*p0
ans =	ans =	ans =	ans =
0.1939358	0.1848654	0.1848654	0.1848654
0.3839634	0.3946166	0.3946166	0.3946166
0.2779849	0.2818690	0.2818690	0.2818690
0.1441159	0.1386491	0.1386491	0.1386491

If we round to three decimal places then the equilibrium base distribution is

$$\boxed{\mathbf{p}_\infty = (.185, .395, .282, .139)}$$

Note: When you execute the file Jukes-Cantor.sce, you will get the following figure:

QUESTION: In line 4 of the code, change $\mathbf{p}_0$ to $[.2; .3; .4; .1]$. In this case, what is the equilibrium base distribution?

Solution: The Scilab code should now look like this:

```
a=.06;
b=a/3;
M=[1-a,b,b,b;b,1-a,b,b;b,b,1-a,b;b,b,b,1-a];
p=[.2;.3;.4;.1];
P=p;
for i=1:100
  p=M*p;
  P=[P p];
end;
scf(2);
plot(P')
legend('A','G','C','T');
```
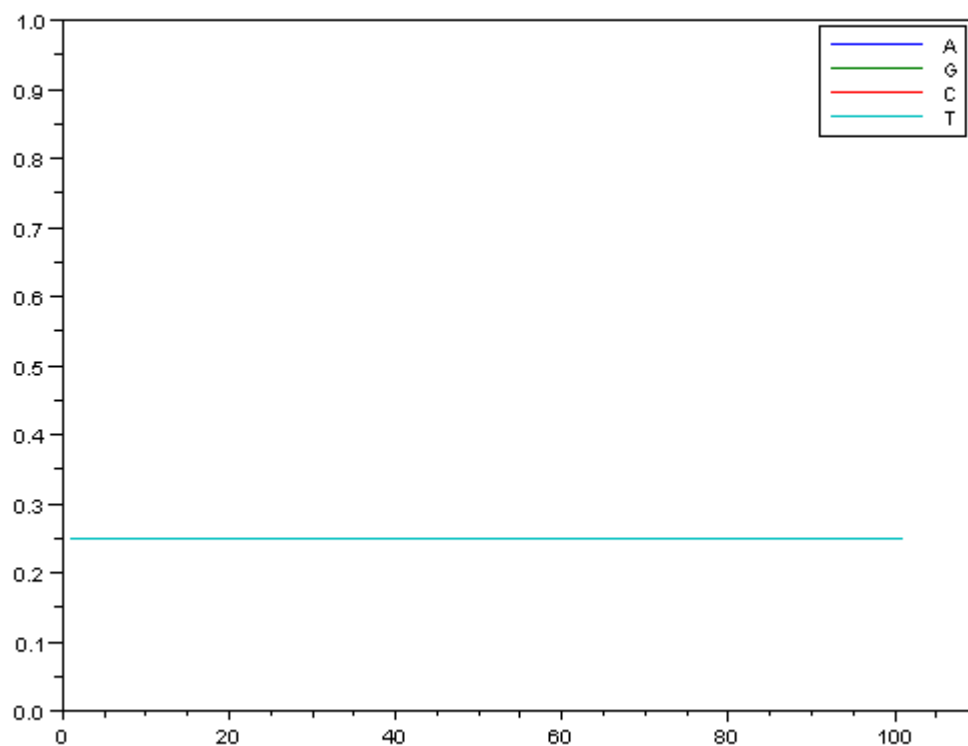
When the file is executed, the new graph should look like this:
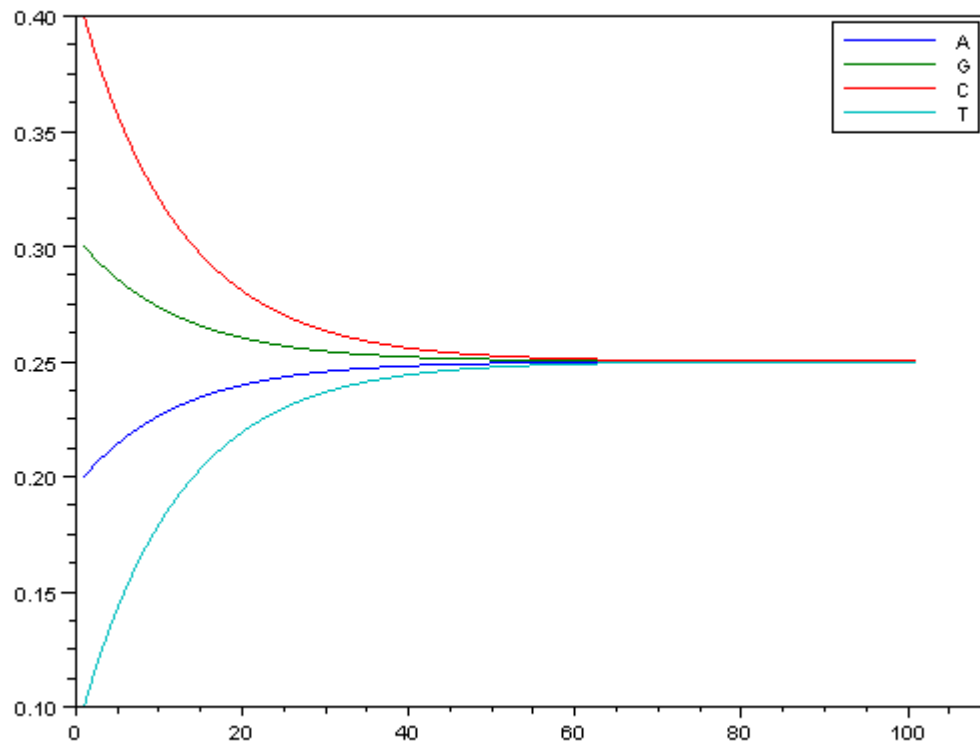
So we can see that in this case, the equilibrium base distribution is

$$\mathbf{p}_\infty = (.25,\ .25,\ .25,\ .25)$$

QUESTION: In line 1 of the code, reduce the value of α (represented by a in the Scilab code) from .06 to .03 and change line 10 of the code from 2 to 1. This will open the new graph in graphics window 1. Before closing the graphics windows, increase α to 0.9 and change line 10 to 3 so that this new graph opens in graphics window 3. What affect does changing α have on the equilibrium base distribution? Does this support the alternate interpretation we gave of α above?

Solution: If we make the changes mentioned in the first part of the question, namely

changing the value of α from .06 to .03 and changing the graphics window from 2 to 1, the new Scilab code and graph look as follows:

```
a=.03;
b=a/3;
M=[1-a,b,b,b;b,1-a,b,b;b,b,1-a,b;b,b,b,1-a];
p=[.2;.3;.4;.1];
P=p;
for i=1:100
  p=M*p;
  P=[P p];
end;
scf(1);
plot(P')
legend('A','G','C','T');
```
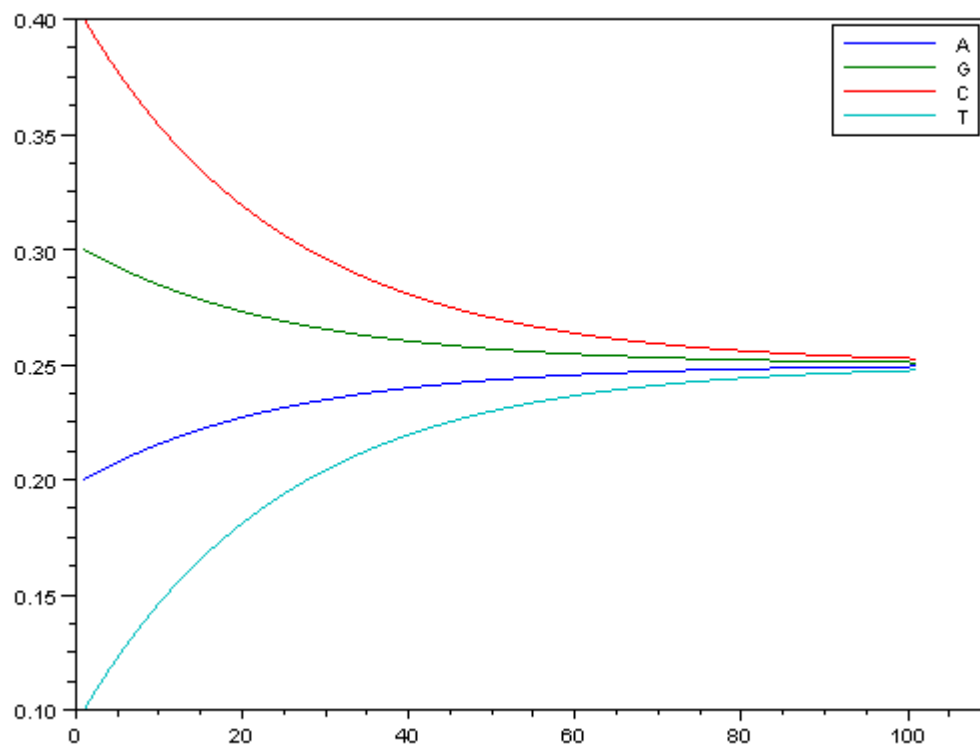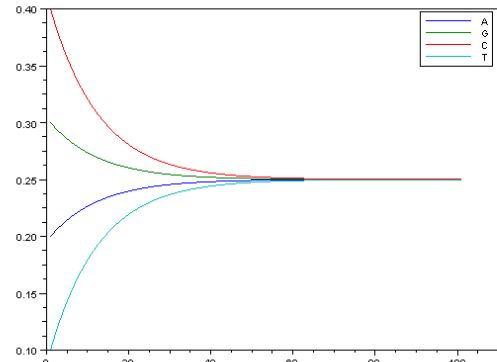
If we make the next set of changes mentioned in the question, namely changing the value of α from .03 to .09 and changing the graphics window from 1 to 3, the new Scilab code and graph look as follows:

```
a=.09;
b=a/3;
M=[1-a,b,b,b;b,1-a,b,b;b,b,1-a,b;b,b,b,1-a];
p=[.2;.3;.4;.1];
P=p;
for i=1:100
  p=M*p;
  P=[P p];
end;
scf(3);
plot(P')
legend('A','G','C','T');
```
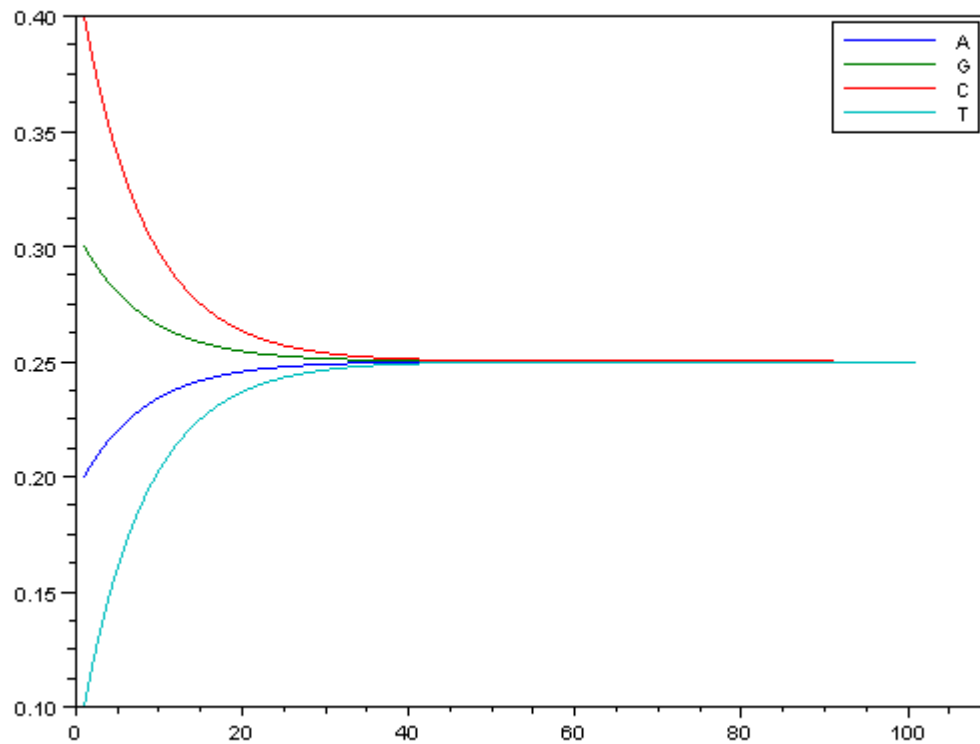
So if we compare all three graphs, we see the following:
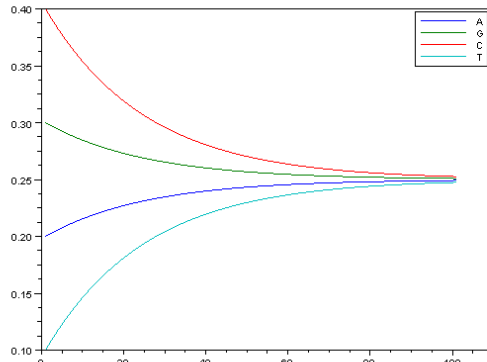
(a) Graphics window 1 with $\alpha = .03$

**(b)** Graphics window 2 with $\alpha = .06$
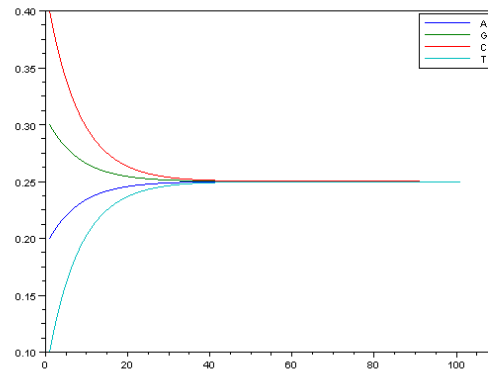
(c) Graphics window 3 with $\alpha = .09$

So the value of α does not affect the equilibrium base distribution, as the equilibrium base distribution is $\mathbf{p}_\infty = (.25, \ .25, \ .25, \ .25)$ is all three cases, just as it was before the changed $\mathbf{p}_0$ in the previous question. But notice that the smaller the value of α, the longer it takes to reach equilibrium and the larger the value of α, the faster it reaches equilibrium. So the graphs do support the interpretation of α as the rate at which observable base substitutions occur over one time step.

B.12 Animal Form and Function

Note: When you execute the file Jukes-Cantor_differences.sce, the following graph will appear:
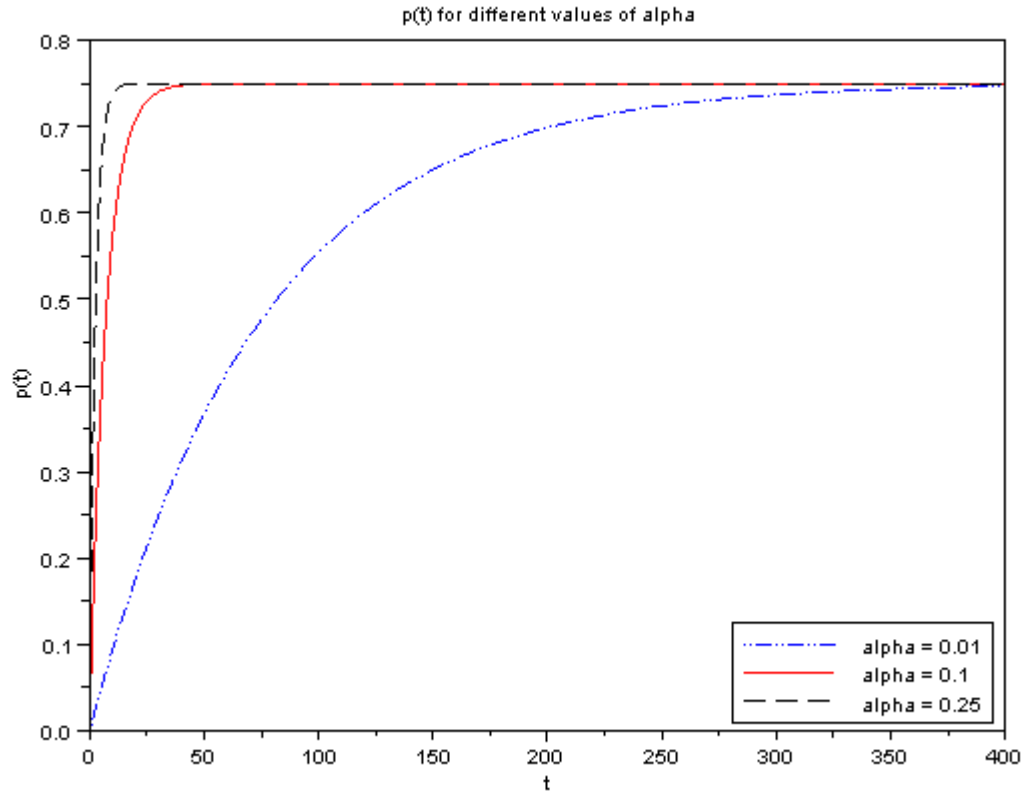
p(t) for different values of alpha

QUESTION: How does increasing the value of α affect $p(t)$? What does the maximum value of $p(t)$ appear to be?

Solution: From the figure, we see that as α increases, the fraction of site that we expect to be different increases and reaches its maximum faster. We see that the maximum value of $p(t)$ is 0.75.

QUESTION: Compute $d_{JC}(S_0, S_1)$ for these two sequences. Why do you think the average number of observed base substitutions per site (given by p) is different from the estimated number of substitutions per site that occurred in the course of evolution (given by d_{JC})?

Solution: Comparing the sequence

$$S_0 : \ ACTTGTCGGATGATCAGCGGTCCATGCACCTGACAACGGT$$

to the sequence

$$S_1 : \ ACATGTTGCTTGACGACAGGTCCATGCGCCTGAGAACGGC$$

we see that substitutions have occurred in 11 of the 40 sites, so in this case $p = \frac{11}{40}$. If we plug this into the formula for $d_{JC}(S_0, S_1)$ and plug that into a calculator, we get

$$\boxed{d_{JC}(S_0, S_1) = -\tfrac{3}{4} \ln \left(1 - \tfrac{4}{3} \cdot \tfrac{11}{40} \right) \approx 0.343}$$

The reason that the average number of **observed** base substitutions per site is $\frac{11}{40} = 0.275$, while the **estimated** number of substitutions per site that occurred in the course of evolution is 0.343, is because we do not observe changes that leave the site with the same base as it start with. For example, if site #1 is initially occupied by base A but then changes to C, T, C, and back to A, then we do not observe the intermediate mutations when we compare the initial and final sequences.

QUESTION: Do you think the Jukes-Cantor distance will increase or decrease as p increases? Why?

Solution: Answers will vary by student.

**Note:** After executing the file Jukes-Cantor_distance.sce, the following graph will appear:
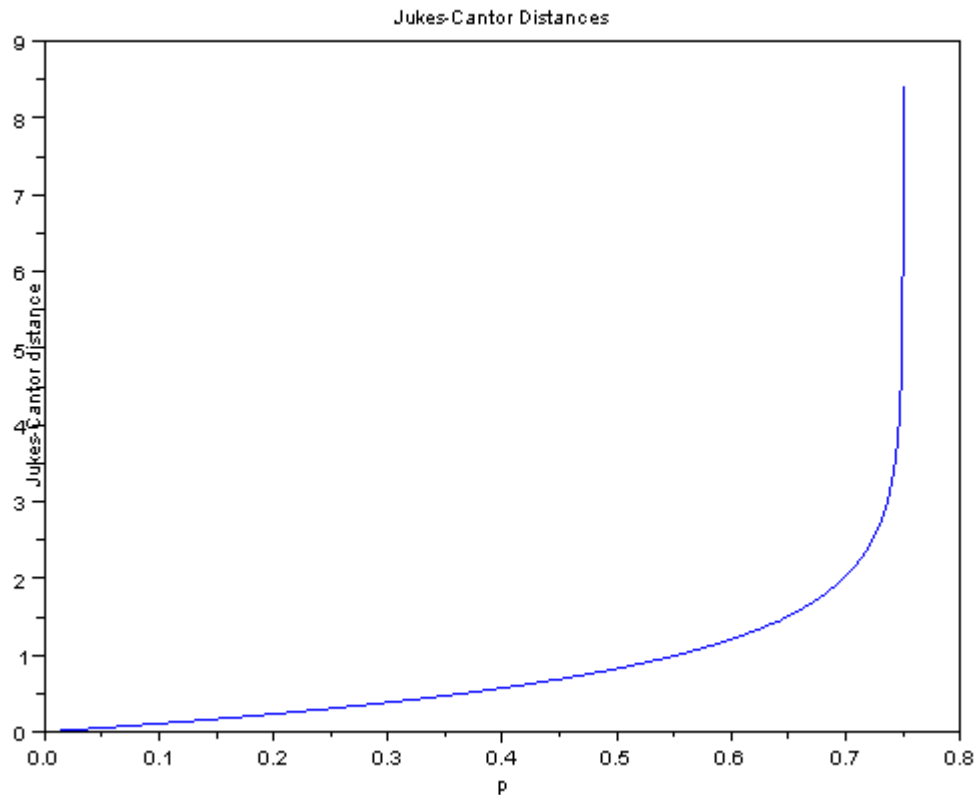
QUESTION: Was your answer to the previous question confirmed? If not, why do you think you were wrong?

Solution: Answers will depending on student responses to the previous question. But students should notice that as p increases, the Jukes-Cantor distance also increases. And as p, the fraction of sites that are different in the descendant sequence from the ancestral sequence, approaches its maximum value of 0.75, the Jukes-Cantor distance,

the number of expected substitutions per site during the elapsed time, increases more rapidly than when p is small.
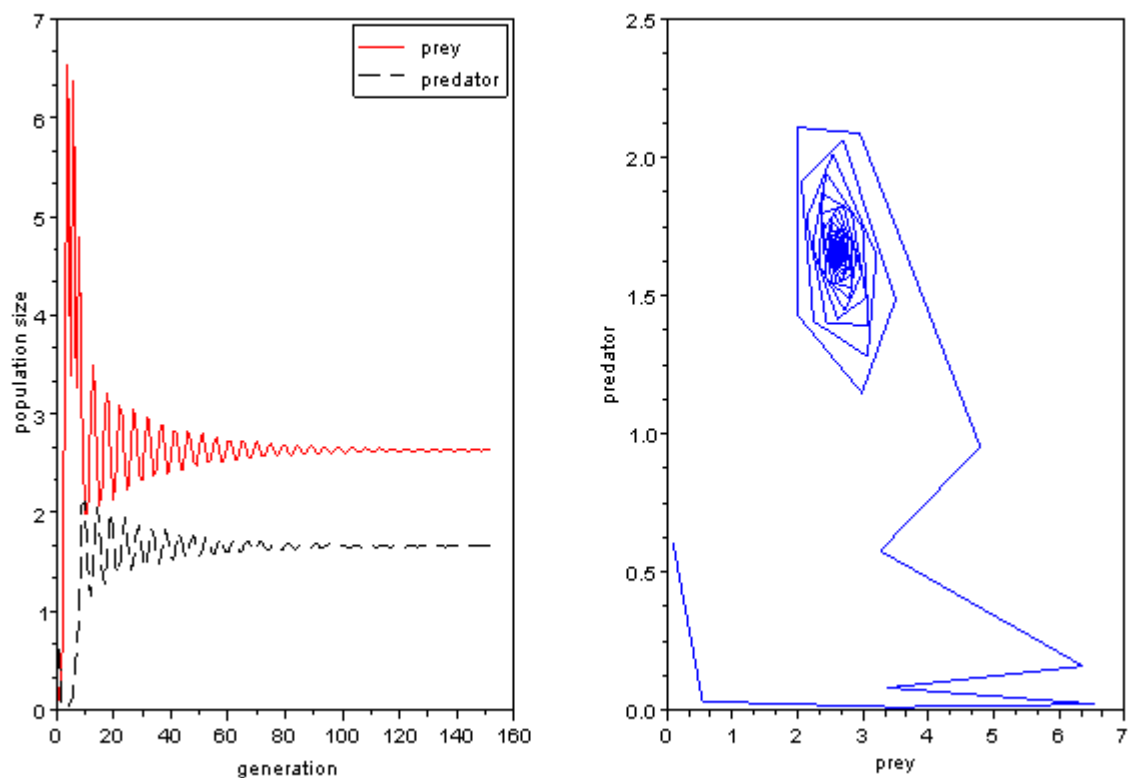
B.13   Predation

Note: After executing the file predator˙prey1.sce the following graph will appear:
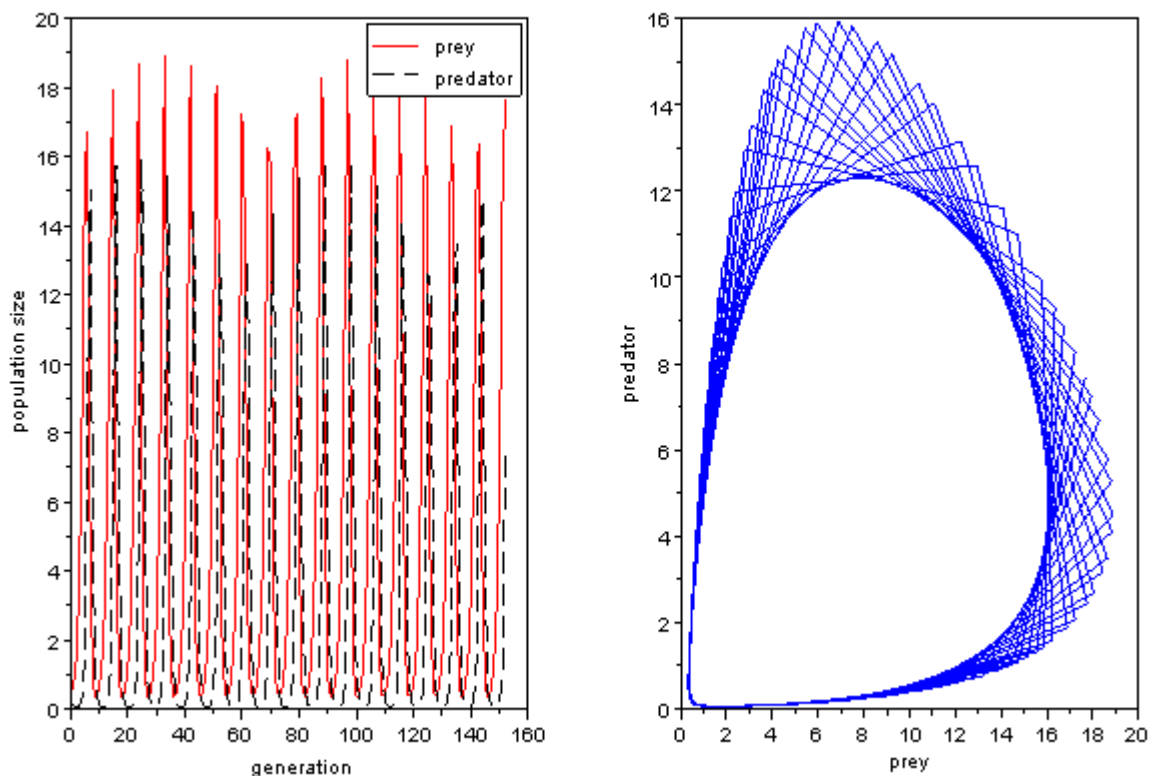
QUESTION: What are the similarities and differences between the behavior of this model and the behavior of the Lynx vs. Snowshoe Hare populations? What do you think the model is lacking to account for this difference? Explain why the qualitative behavior of the predator vs. prey graph on the right should be expected from the dynamics of the population vs. time graph on the left.

Solution: Both models exhibit cyclic or periodic behavior for both the predator and prey populations. But in the model, the periodic behavior is more regular in frequency and in intensity. The model doesn't take into account random events in nature which cause slight irregularities in the populations from year to year. The graph on the right shows the predator population vs. the prey population, and it cycles around with one population following the other, just as the graph on the left does. Just as the graph on the left shows that the cycles vary slightly in intensity, the graph on the right shows the size of the cycles also varies.
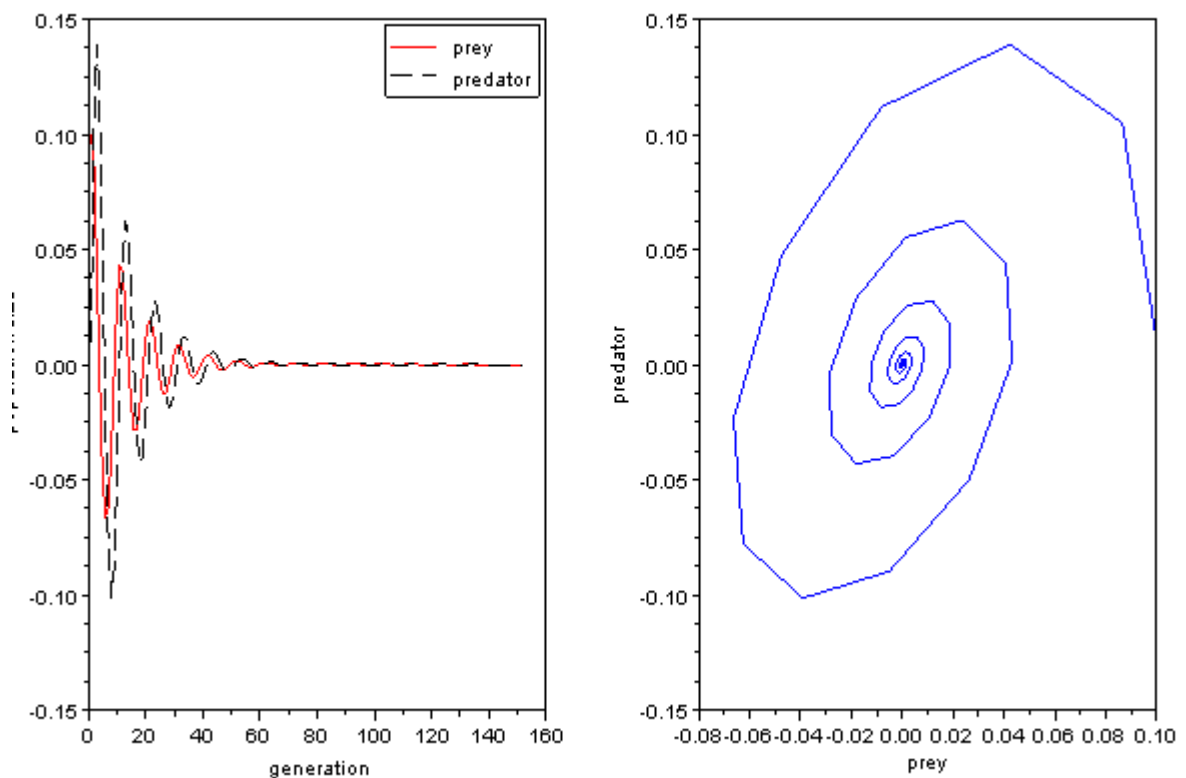
Note: After executing the file predator˙prey2.sce the following graph will appear:

QUESTION: What are the similarities and differences between the behavior of this model and the behavior of the previous model? Explain the qualitative behavior of the predator vs. prey graph on the right from the dynamics of the population vs. time graph on the left.

Solution: This model exhibits cyclic or periodic behavior just as the previous model did. But in this model, the populations are not as close in size as they were in the previous model and in this model, the intensity of the cycles decreases as time passes until the populations almost don't cycle at all.

Note: After executing the file predator‛prey3.sce the following graph will appear:

QUESTION: What modeling assumptions were used in constructing this model? What are the similarities and differences between the behavior of this model and the behavior of the previous models? Explain why the qualitative behavior of the predator vs. prey graph on the right should be expected from the dynamics of the population vs. time graph on the left.

Solution: The modeling assumptions here include the following:

1. The fraction of the prey population that survives declines proportional to the number of predators.

2. The prey have a net reproductive rate of r.

3. The rate of growth of the prey population is limited by the environmental carrying capacity, K.

4. Even in the absence of the prey, the predator population can still grow.

Like the previous model, this model exhibits cyclic or periodic behavior where the intensity of the cycles decreases over time. The size of the two populations is much closer to each other than in the previous model and they cycle much more smoothly about each other.

B.14 Population Ecology

QUESTION: Give a specific interpretation for c_{11}, c_{12}, c_{21}, c_{22}. Which ones represent interspecific competition and which ones represent intraspecific competition?

Solution: Since c_{ij} for $i, j = 1, 2$ represents the strength of the competition on species i by species j, then c_{11} is the strength of the competition on species 1 by species 1.

This represents intraspecific competition. c_{12} is the strength of the competition on species 1 by species 2 and it represents interspecific competition. c_{21} is the strength of the competition on species 2 by species 1 and it represents interspecific competition. c_{22} is the strength of the competition on species 2 by species 2 and it represents intraspecific competition.

Note: After executing the file competition.sce, the following graphs will appear:
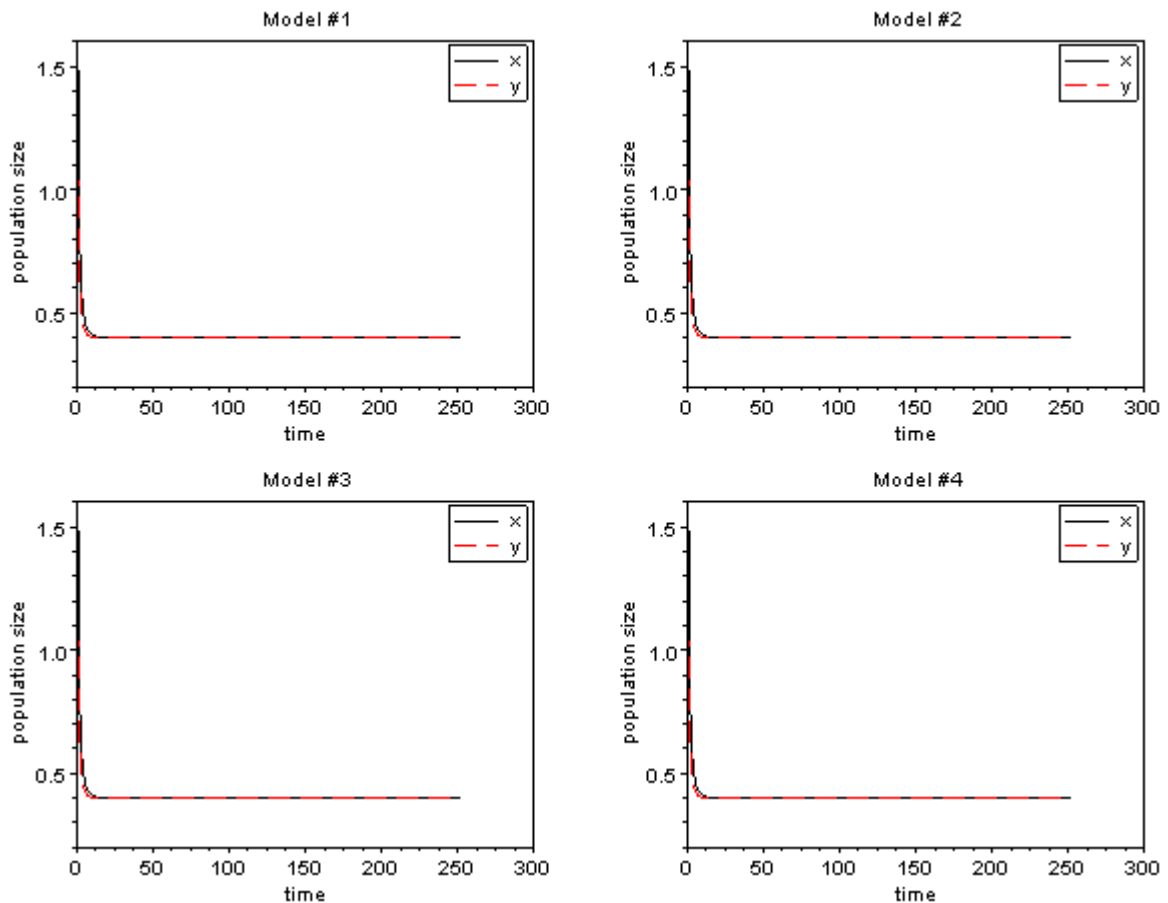
QUESTION: Find a set of parameter values which allows both species to coexist, but come to equilibrium at different population levels. *Hint*: Use the four graphs to make various changes and simultaneously compare the changes.

Solution: Answers will vary by student, but as long as the levels of competition aren't equal, the species should have different equilibrium values, and as long as the difference in competition isn't too much then both species should be able to coexist. For example, decreasing c_{12} to .15 and increasing c_{21} to .5, while increasing c_{11} to 11.25 and decreasing c_{22} to .75 would allow both species to coexist at different levels.

QUESTION: Find two sets of parameter values which allows Species 1 to exclude Species 2 (Species 1 exists but Species 2 becomes extinct). First do it by changing only the growth rates then do it by changing only the interspecific competition.

Solution: Answers will vary by student. For changing the growth rates, the growth rate of Species 1 needs to be sufficiently bigger than the growth rate of Species 2. For example, set $b_1 = 2.5$ and $b_2 = .5$. For changing the interspecific competition, the competition on Species 2 needs to be sufficiently more than the competition on Species 1. For example, set $c_{12} = .1$ and $c_{21} = 1.1$.

QUESTION: Can changing the strength of the intraspecific competition save Species 2 in either set of parameter values in the previous problem?

Solution: If the differences in growth rate or interspecific competition aren't too high and the level of intraspecific competition is reduced sufficiently, then Species 2 can be saved.

QUESTION: What, if any, interesting, unexpected, or different phenomena did you discover while searching for the sets of parameter values you were asked to find?

Solution: Answers will depend on what parameter choices they made while trying to answer the previous problems. One possibility would be if students left $b_1 =$

1.5, $b_2 = 1.5$, $c_{11} = 1$, $c_{12} = .25$, and $c_{22} = 1$ but changed $c_{21} = 1$, then Species 1 would exclude Species 2, but if they then decrease the intraspecific competition for Species 2 to $c_{22} = .1$ then not only would that save Species 2, but Species 2 would then exclude Species 1, driving them to extinction.