School of Mathematics & Applied Statistics

MATH111: Applied Mathematical Modelling
Assignment Week 11 Spring 2007

Student Name: _____ *Student Number:*_____

FULL WORKING is to be shown for all solutions.
Untidy or badly set out work will not be marked.
This assignment is to be handed in at the end of your during the Wednesday lecture of week 13.

Assignment Guidelines

You are expected to structure your assignments as if writing a report for presentation to people unfamiliar with the work covered by the assignment.

Your report should be structured as follows:

1. introductory remarks
   - state purpose of assignment; and
   - state proposed tasks.
2. discussion of theory (if appropriate)
3. discussion of results
   - present outputs of each task;
   - analyse outputs of each task, including
     - comment on what your mathematical results mean in terms of the underlying physical problem.
     - comment on unexpected results;
4. concluding remarks: state whether purpose of assignment was achieved. You should answer the following questions regarding this assignment.
   - What was the most important thing that you learnt? Why was it 'important'?
   - What was the most puzzling thing that you did? (If nothing was puzzling, say so!)
5. Bibliography (if required)
6. Appendices
   - MAPLE program(s), containing comment lines explaining the purpose of your code.
   - MAPLE outputs where you think they are required to further amplify comments you have made in your report. Do *not* include every output you generated.
7. If you are not certain what is required in your report you should speak to the lecturer before you hand it in. If you don't ask, don't whinge if you lose marks because you didn't do what you should have done.

Continued on next page

School of Mathematics & Applied Statistics **MATH111**: *Applied Mathematical Modelling*
Assignment Week **11** Spring 2007 Submission Receipt

Student Name: _____ *Student Number*: _____

Tutorial Class: _____ *Date Submitted:* _____ *Tutor Initials:* _____

Graphs and tables should be included at appropriate locations in the body of the report or as appendices at the end of the report. Please ensure all handwritten work is tidy and legible and that every page is present and in the intended order.

The grade a student receives will be the lab demonstrator's subjective assessment of how much effort that student seems to have put into creating their report. Please note that missing or incomplete outputs, inadequate discussions, and/or poor presentation will result in a low grade even if you have successfully completed all the assigned tasks. Note that marks to questions/tasks (if provided) is only indicative.

Here are some good ways to *lose* marks (5% for each one):

- No title ('MATH111 Assignment Week x' is not a satisfactory title).
- No introduction.
- No theory.
- No sections/section headings.
- Not including the model equations.
- Not discussing the model equations.
- No conclusions or summary.
- Non bibliography (when required).
- No figures.
- Inadequate referencing of sources.
- No appendices (if required).
- No page numbers.
- Repeating the questions in your report and answering them. You're supposed to write a report!
- Using the question/task numbers in your report. These don't make sense to a reader who hasn't read the assignment sheet.
- Including every graph you generated during your investigation. Summarise your findings where appropriate!
- Poor graphs: no title, no labels, too small, too large, not numbering figures etc.
- Stating that your graph uses colour, such as 'blue' and 'black' lines, but only providing a black and white graphic.
- Poor quality output: difficult to read; pages out of order.
- Not showing signs of having carried out further reading when you have been asked to read specific article(s). (**-10%**)

This list is *not* exhaustive.

Instructions

You should work you way through this assignment, answering questions and making notes where appropriate. Where appropriate you should adapt Maple programs that you have used in previous lab sessions.

You will find it very *useful* to save any programs that you write onto a disk which you bring to subsequent labs.

1. Use a text editor such as NotePad (Programs/Accessories/NotePad) to write your program.
2. Save your program onto a disk (or alternatively onto the C drive) as a *text* file.
3. To load your program into Maple enter `read "A:/file";` where `file` is the name of your program.
4. If your program generates an error message:
   (a) Enter the command `restart;` into Maple.
   (b) Look at your code for syntax errors. Correct the code and reload it.
   (c) If you can't find your error, ask for assistance.

SIR Endemics with and without vaccination

1 Instructions for group project

You may work on this assignment either on your own or in a group of two or three individuals. If you work as a group then you should submit one report. This report *must* include an appendix called "Group Work". This appendix should contain two sections, as outlined below.

1. The first section will explain how you organised the group project. You should answer the following points.
   - Did you do the maple component of the assignment as a group or as individuals? Did you split the work – if so, how did you decide to split it?
   - How did you write up the assignment?
2. In the second section each person in the group must write their own statement addressing the following points.
   - Why did you decide to do a group project rather than do the project on your own?
   - What did you learn from doing the maple assignment in a group that you would not have learnt from doing it on your own?

You will be penalised if you do not adequately address these questions.

2 Background

In this assignment you will investigate the dynamics of an endemic disease, that is a disease which is habitually prevalent in a population. For simplicity we consider a *non-fatal* disease.

The population is divided into three classes:

susceptible: (S) individuals who *may* catch the disease.

invective: (I) individuals who are infected.

recovered: (R) individuals who have recovered from the disease.

The disease, in the absence of vaccination, is represented schematically below

$$\begin{array}{ccccccc} \stackrel{bN}{\rightarrow} & S & \stackrel{\beta IS}{\rightarrow} & I & \stackrel{cI}{\rightarrow} & R. \\ & \downarrow \gamma S & & \downarrow \gamma I & & \downarrow \gamma R \end{array}$$

In this figure

- b is the *per-capita* birth rate and N the total population size (assumed constant). The term bN is the total birth rate.

- γ is the *per-capita* death rate. S is the number of susceptibles. The term γS is the number of susceptibles who die from natural causes. (Remember that the disease is assumed to be non-fatal).
- β is the (*pairwise*) *infectious contact rate*. S and I are the number of susceptibles and infectives respectively. The term βIS is the rate at which infections occurs.
- γ is the *per-capita* death rate. I is the number of infectives. The term γI is the number of infectives who die from natural causes. (Remember that the disease is assumed to be non-fatal).
- c is the rate at which infected individuals recover from the disease. The term cI is the total number of individuals who recover from the disease.
- γ is the *per-capita* death rate. R is the number of people who have recovered from the disease (the 'recovereds'). The term γR is the number of recovereds who die from natural causes. (Remember that the disease is assumed to be non-fatal).

We further assume that the per-capita birth-rate (b) and the per-capita death rate (γ) are equal so that the total population (N) remains constant.

In this assignment we consider two important questions:

1. In the *absence* of vaccination what is the condition for a disease to be endemic/eradicated ?
2. For a disease that is endemic what fraction of the population needs to be vaccinated to eradicate the disease?

3 The model

The model equations can be written as

$$\frac{\mathrm{d}u}{\mathrm{d}t} = \frac{b}{b+c}(1-p-u) - R_0 uv, \tag{1}$$

$$\frac{\mathrm{d}v}{\mathrm{d}t} = (R_0 u - 1)\, v, \tag{2}$$

$$\frac{\mathrm{d}w}{\mathrm{d}t} = \frac{b}{b+c}p + \frac{c}{b+c}v - \frac{b}{b+c}w, \tag{3}$$

where p is the fraction of the population that is vaccinated. (We initially consider the case $p = 0$, i.e. there is no vaccination happening.) In these equations t represents time, measured in years.

In equations (1)–(3) u, v and w are the *fraction* of the population that are susceptible, infected and recovered respectively. They are defined by

$$u = \frac{S}{N},$$
$$v = \frac{I}{N},$$
$$w = \frac{R}{N}.$$

The parameter R_0 is known as the basic reproductive ratio of the disease. This is the expected number of infectious contacts made by a single infective in an otherwise totally susceptible population. The basic reproductive ratio is defined as

$$R_0 = \frac{\beta N}{b+c}. \tag{4}$$

4 Maple code

The same code is used to investigate the models with and without vaccination. This code is provided in appendix B. You do *not* need to retype this code. You can download it from

`http://www.uow.edu.au/~mnelson/teaching.dir/math111.dir/endemic.html`

We are primarily interested in the long-term behaviour of the model. In particular we want to know if in the limit of large time the fraction of infectives in the population ($v(t)$) tends to zero, in which case the disease is eradicated, or a positive number, in which case the disease is endemic.

Once you have saved this code you will need to remove any non-maple text that you have downloaded. You should carefully read through the Maple code — you may need to change parts of it to finish the assignment.

Points to remember:

1. You should read through the code before running it.
2. You will have to vary the value for `tend`. The 'right' value will depend upon which model you are investigating and the parameters values in the model. In your report you should indicate the value used for `tend` to generate each figure.
3. You may need to change various parameters in the plot commands. In particular, near the critical values you will find it extremely useful to change the command `view[0..0.1]`. (See the maple code for figure 3).
4. In order to determine the behaviour in the limit as $t \to \infty$ you may find it useful to construct a table showing the value of $v(t)$ for various values of t.
5. Do *not* include every figure in your report. Choose the figure(s) that best illustrate the point that you wish to make.

5 Tasks

5.1 No vaccination model

1. Run the default version of the code. Is the disease endemic or eradicated in the limit as $t \to \infty$?
2. Change the value of `R` in the code to `R=0.2;`. Is the disease endemic or eradicated in the limit as $t \to \infty$?
3. By carefully changing the value of R find the critical value of the basic reproductive number, R_{cr}, such that if $R = R_{cr}$ the disease is eradicated but if $R = R_{cr} + 0.01$ the disease is endemic.
4. Calculate the steady-state solution(s) of the no vaccination model. (See section A for how to do this). Which steady-state represents an endemic disease and which one represents an eradicated disease?

Question 1 *One of the reasons for making models of infectious disease is to enable the design of policies aimed at eradicating or at least controlling them. Control methods for disease involving animals include: slaughtering infected animals (increasing γ), disinfection and movement controls (reducing β) and slaughtering potential contacts of infected animals (reducing N). Explain how these control policies work by considering their effect on the basic reproductive ratio defined in equation* (4).

5.2 Vaccination model

1. A typical value of R_0 for smallpox is $R_0 = 3$. Change the value of the basic reproductive number in the code to `R=3;`.
   (a) With no vaccination is the disease eradicated or endemic?

(b) Set the vaccination fraction to 0.5 (`vac=0.5;`). Is the disease eradicated or endemic?

(c) Set the vaccination level to 0.8 (`vac=0.8;`). Is the disease eradicated or endemic?

(d) By carefully changing the vaccination level find a critical vaccination number, vac_{cr}, such that if `vac` $= \text{vac}_{\text{cr}}$ the disease is eradicated but if `vac` $= \text{vac}_{\text{cr}} - 0.01$ the disease is endemic. Comment on the practical implications of your finding.

2. The following table gives typical values for the basic reproductive number for some common diseases

Infection	R_0
Measles	12
Pertussis (whooping cough)	15
Rubella (German measles)	7
Chickenpox	9
Diphtheria	4
Scarlet fever	5
Mumps	6.5
Poliomyewlitis	6

Choose four diseases. For each one

(a) Determine the critical vaccination number.

(b) Write one paragraph describing the disease. Clearly cite any web page that you use as source of information.

6 Marking

Every student starts with a mark of 100. The questions and tasks for this assignment are worth a certain number of marks. Every time your answer to a question or task is incomplete or wrong you lose marks. In addition to losing marks in this way can also lose marks for a badly written report. There is no upper bound on the number of marks you can lose. If you make 17 bad mistakes (see the list on page two) then you will lose 85 marks. However, your mark will not be reduced below zero.

A maximum of five bonus marks can be obtained for this assignment. However, the maximum mark on an assignment is 100%. Reasons for gaining a bonus mark include: showing exceptional insight into a mathematical problem, making a particularly interesting comment, finding something interesting from a literature search and having a particularly well-written report. This is not an exhaustive list.

A Optional question on the vaccination model

This question is optional. You will not be penalised for not attempting this question nor for answering it incorrectly. If you answer it correctly, you will receive a bonus. However, your final mark can not be increased over 100%.

The vaccination model is given by

$$\begin{aligned}
\frac{\mathrm{d}u}{\mathrm{d}t} &= \frac{b}{b+c}\left(1-p-u\right) - R_0 uv, \\
\frac{\mathrm{d}v}{\mathrm{d}t} &= \left(R_0 u - 1\right) v, \\
\frac{\mathrm{d}w}{\mathrm{d}t} &= \frac{b}{b+c}p + \frac{c}{b+c}v - \frac{b}{b+c}w.
\end{aligned}$$

An important observation is that the variable $w(t)$ does not appear in the first two-equations. Therefore to understand the properties of this model we only need study the system

$$\frac{\mathrm{d}u}{\mathrm{d}t} = \frac{b}{b+c}(1-p-u) - R_0 uv, \tag{5}$$

$$\frac{\mathrm{d}v}{\mathrm{d}t} = (R_0 u - 1)\, v. \tag{6}$$

The steady-state(s) of a system of two differential equations

$$\begin{aligned} \frac{\mathrm{d}x}{\mathrm{d}t} &= f(x,y), \\ \frac{\mathrm{d}y}{\mathrm{d}t} &= g(x,y), \end{aligned} \tag{7}$$

are found by solving the system of simultaneous equations

$$\begin{aligned} f(x^*,y^*) &= 0, \\ g(x^*,y^*) &= 0. \end{aligned} \tag{8}$$

To calculate the stability of a steady-state solution (x^*, y^*) we need to find the eigenvalues of the *Jacobian matrix* J which is defined by

$$J = \begin{pmatrix} \frac{\partial f}{\partial x} & \frac{\partial f}{\partial y} \\ \frac{\partial g}{\partial x} & \frac{\partial g}{\partial y} \end{pmatrix}_{(x^*,y^*)}. \tag{9}$$

The eigenvalues, λ, of the Jacobian defined by equation (9) are given by

$$|J - \lambda I| = 0 \tag{10}$$

$$\Rightarrow \lambda^2 - (\mathrm{tr}\, J)\,\lambda + \det J = 0 \tag{11}$$

The steady-state solution (x^*, y^*) is *stable* if the real part of each eigenvalues is less than zero, i.e.

$$\mathrm{Re}\lambda < 0.$$

This is true provided that

$$\mathrm{tr}\, J < 0 \quad \text{and} \quad \det J > 0, \tag{12}$$

where $\mathrm{tr}\, J$ and $\det J$ are respectively the trace and determinant of the Jacobian matrix evaluated at the steady-state solution.

1. Find the *two* steady-state solutions of equations (5) & (6).
2. Evaluate the Jacobian matrix for the trivial steady-state solution. Assuming $R_0 > 1$ what are the conditions on the value of p for the trivial steady-state solution to be stable and unstable?
3. Hence suggest a condition that ensures that the disease is eradicated. Why is this condition useful to know?

B Maple code

```
# endemic.maple   Maple code to integrate a simple SIR model for an
# 14.10.03        endemic disease with vaccination.
# 10.10.07        Revised to run on maple 10.
#
with(linalg):
with(plots):
```

```
R  :=10.0;   # the basic reproductive number.
vac:= 0.00;    # the fraction of the population that is vaccinated.

tstart := 0;    # the initial value for time.
tend   := 10;   # the final value for time.

# define the differential equations
de1 := diff(u(t),t) = b/(b+c)*(1-vac-u(t)) -R*u(t)*v(t);
de2 := diff(v(t),t) = (R*u(t)-1)*v(t);
de3 := diff(w(t),t) = b*vac/(b+c) +c/(c+b)*v(t) -b/(b+c)*w(t);

interval := 5.0:      # number of points calculated per unit of time.
susceptibles := 0.98; # initial fraction of population that are susceptibles.

ic1 := u(0) = susceptibles;   # initial pop'n fraction that are susceptibles.
ic2 := v(0) = 1-susceptibles; # initial pop'n fraction that are infected.
ic3 := w(0) = 0;              # initial pop'n fraction that are immune.

deqs := {de1,de2,de3}:        # define the system of DEs.
ics  := {ic1,ic2,ic3}:        # define the initial conditions.
vars := {u(t),v(t),w(t)}:     # define the dependent variables.

b := 10.0;                    # per-capita birth rate.
c := 10*b;                    # the rate at which invected people recover
                              # from the disease.

# define the values of time at which the output is calculated.
ans := array([seq(i/interval,i=tstart..(interval*tend))]):
# integrate the system of differential equations
#
solnum := dsolve(deqs union ics,vars, \
                     type=numeric, output=ans, maxfun=300000):

# Print the values of the independent and dependent variables at the final
# integration point (tend).  NOTE that the output is NOT necessarily in the
# format u(t), v(t), w(t).
#
# The next command pulls out an array that contains the time and the
# solution points.
solmatrix := eval(solnum[2,1]):
rowsize   := rowdim(solmatrix):
eval(solnum[1,1]);      # this gives us the output order
row(solmatrix,rowsize); # the output at the final integration point

# Plot some figures.  You WILL need to play around with these
# commands to get the best possible figures for your report.
#

# Figure One. Plot the solution in the susceptible-invected plane.
odeplot(solnum,[u(t),v(t)],labels=["u(t)","v(t)"]);

# Figure Two. Plot the susceptible-time and invected-time data on the
#             same figure.  Make sure you know which one is which.
p1 := odeplot(solnum,[t,u(t)],colour=BLUE):
p2 := odeplot(solnum,[t,v(t)],colour=RED):
display({p1,p2},title="Susceptibles and Infectives",\
                labels=["time","fractional population"]);
```

```
# Figure Three.  Plot the fraction of infected people in the population.
#                You may find it useful to change the 'y'-view to
#                clarrify the long-term behaviour: is it heading towards zero?
odeplot(solnum,[t,v(t)],colour=RED,labels=["time","v(t)"],\
        title="Fractional infected population",\
        view=[tstart..tend,0..0.1]);
# Figure Four.  Plot the immune-time data.
odeplot(solnum,[t,w(t)],labels=["t","w(t)"]);

R := 'R':
b      := 'b':
c      := 'c':
deqs   := 'deqs':
de1    := 'de1':
de2    := 'de2':
de3    := 'de3':
ics    := 'ics':
ic1    := 'ic1':
ic2    := 'ic2':
ic3    := 'ic3':
interval := 'interval':
output := 'output':
p1     := 'p1':
p2     := 'p2':

rowsize := 'rowsize':
solmatrix := 'solmatrix':
solnum := 'solnum':
susceptibles := 'susceptibles':
tend   := 'tend':
tstart := 'tstart':
vac    := 'vac':
vars   := 'vars':
```