**AML 610 Fall 2014 Homework #8**

**Submit all files to** [**smtowers@asu.edu**](mailto:smtowers@asu.edu)**.**

**Due Mon Nov 10th, 2014 at noon.**

**Please submit with name format hwk8\_<first name>\_<initial of last name> Please provide your R and C++ files, and a Word file that gives the output to your screen, plots, etc.**

**All code must conform to good coding practices, as described in** [**http://sherrytowers.com/2012/12/14/good-programming-practices-in-any-language/**](http://sherrytowers.com/2012/12/14/good-programming-practices-in-any-language/) **and all plots must conform to good plotting practices, as described in** [**http://sherrytowers.com/2013/01/04/good-practices-in-producing-plots/**](http://sherrytowers.com/2013/01/04/good-practices-in-producing-plots/)

**Question 1**

a) Together with your project group, decide upon a journal that might be appropriate for publication of your analysis. Note that you need to avoid “predatory publishers”, for instance, all journals published by the OMICS group… to determine if your chosen journal is a scam journal, go to Google and type “<name of journal> scam” (without the quotes), or “<name of journal> predatory”. You can also look on the list compiled here: <http://scholarlyoa.com/individual-journals/>

If you want to discuss a shortlist of potential journals with me, please send me an email to set up an appointment to do that.

Go the “Instructions for Authors” page of your selected journal, and choose the appropriate article type (if you are given a choice, that is, because some journals just have one article type… If you are given a choice, an appropriate article type would be a “research article”, for instance), and download the latex or word template that they provide. You will be using this template for your project write-up, and you will be required to satisfy all of the Abstract, Title, and main body maximum word count requirements of that journal.

In your Word document submission for your homework, tell me the journal name, the article type (if applicable), and the word count requirements.

b) The typical sections in an article are:

Abstract

Introduction

Methods and Materials

Data

Model

Results

Discussion and Summary

Go to the module “How to write a good scientific paper (and get your work published as painlessly as possible)” and refresh yourselves on what each of these sections should contain

<http://sherrytowers.com/2014/09/02/how-to-write-a-good-scientific-paper/>

As a group, write the Introduction for your write-up (since you are already well aware of the motivation and objective, this should be straightforward), including all relevant references.

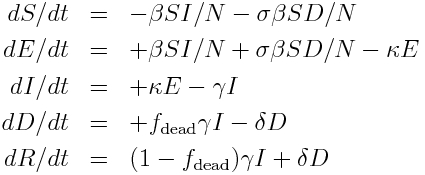
c) As a group, write the Methods:Data section. I want **all** the details of the sources of your data (references, if they were obtained from the published literature, and/or URL’s if they were obtained online). I also want the details of the population size being studied, the time frame over which the data was collected, the time steps of the time series of the data, etc. Just saying something like “we used flu data from the 2007-08 influenza season from the CDC” is not sufficient!

d) As a group, write the Methods:Model section, including the equations for your model, compartmental flow diagram, background references related to the model, description of the compartments and parameters, etc.

**Question 2**

a)

Download the files [www.sherrytowers.com/cpp\_deSolve.cpp](http://www.sherrytowers.com/deSolve.cpp) and [www.sherrytowers.com/cpp\_deSolve.h](http://www.sherrytowers.com/deSolve.h) and copy the code to your own personal files mycpp\_deSolve.cpp and mycpp\_deSolve.h. In the ModelEquations method, add code to the files to solve the following set of differential equations to simulate an Ebola outbreak



where S,E,I,D, and R represent the susceptible, exposed, infectious living, infectious dead, and “recovered” (ie; recovered and immune living, and safely buried no-longer-infectious dead). N = S+E+I+D+R. The parameter beta is the transmission rate from the living infectious, and sigma is the relative transmission scale from the infectious dead (some studies have indicated that sigma may be as high as 10). f\_dead is the fraction of infected that die, and delta is the burial rate.

When you write your code, assume the parameters are passed to the cpp\_deSolve methods in the following order:

http://rogercortesi.com/eqn/tempimagedir/eqn6978.jpg

b)

Write a C++ program, Ebola.cpp to use the methods you’ve coded up in the cpp\_deSolve class to solve the system of equations for a given set of model parameters. From observational studies of this outbreak, we know:

* 1/kappa~10 days,
* 1/gamma~10 days,
* 1/delta~2 days, and
* f\_dead~0.7

Using beta=0.2 and sigma=5 solve the equations of the model for time 0 to 300 days in steps of 0.01 days for a population of N=1,000,000 assuming one infected person is introduced to a completely susceptible population at time t=0.

Output the estimates for S, E, I, D, and R at each time step to a file called myebola.out.

c)

Write an R script Ebola.R to read in the results of C++ simulation.

Using methods in the deSolve library in R, solve the differential equations for the same model, with the same parameters for the same time steps.

Plot S,E,I,D, and R vs time from your C++ program, and overlay what you obtained using the R deSolve methods.

Plot vs time the values of I from your C++ program, minus the estimates of I from deSolve in R. Also plot the residuals divided by the estimates of I from deSolve in R (the “relative residuals”)

Your plot should look like this:

