Mathematics 4MB3/6MB3 Mathematical Biology
2016 ASSIGNMENT 4

Group Name: Muse

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This assignment was due on Wednesday 14 March 2018 at 11:30am.

1 Time Series analysis of Recurrent Epidemics

(a) You should have received the following data files by e-mail:

<div align="center">

`meas_uk__lon_1944-94_wk.csv`
`meas_uk__lpl_1944-94_wk.csv`

</div>

These plain text comma-separated-value files list weekly cases of measles (in London and Liverpool, England, from 1944 to 1994). Depending on which research direction you select, you might receive other files in the same `ymdc` (year,month,day,count) format, where the count column might contain cases or deaths, for example. Write the following ® functions:

(i) `read.ymdc()`. Read a file in `ymdc` format and return a data frame containing these data and including a `date` column that has ®'s `Date` class. The first (and potentially only) argument to this function should be the `filename` of the data file to be read.

Proof. . . . beautifully clear and concise text to be inserted here. . . □

(ii) `time.plot()`. Given a data frame produced using `read.ymdc()`, display the associated time plot. The first argument of the function should be the data frame. Further optional argument(s) should allow the user to smooth the time series with a moving average. By default, this function should create a new plot but there should be an option to add to an existing plot. Implement this by having a logical `add` argument that is false by default (`add=FALSE`). This will allow you to add a smoothed version of the time series on top of the raw data, for example. The final argument should be the ellipsis (. . .) so that details such as colour and line style can be passed to the plotting commands used in this function.

Proof. . . . beautifully clear and concise text to be inserted here. . . □

(iii) `periodogram()`. Given a data frame produced using `read.ymdc()`, display the associated *period periodogram* (power spectrum as a function of period). The first argument of the function should be the data frame. By default, the entire time series should be used, but optional argument(s) should allow the user to specify a time range of interest. Use ℝ's `spectrum()` function to compute the power spectrum. Have `add` and `...` arguments as in `time.plot()`. Note that if `v` is a vector containing a time series of interest, you can obtain and plot its *frequency* periodogram as follows.

```
s <- spectrum(v, plot=FALSE)
plot( s$freq, s$spec, type="l")
```

Proof. ... beautifully clear and concise text to be inserted here... □

(b) Using your functions, make a multi-panel plot that clearly shows the temporal pattern of the time series and how its frequency structure changes over time. Think carefully about how to make this multi-panel figure as clear as possible for yourselves and your readers. Describe your figure, explaining what aspects of your figure you feel are puzzling or interesting and may be possible to understand using mechanistic mathematical modelling. (Repeat this for each of the epidemic time series you are given.)

Proof. ... beautifully clear and concise text to be inserted here... □

2 Stochastic Epidemic Simulations

Consider the SI model,

$$\frac{dI}{dt} = \beta(N - I)I\,, \qquad I(0) = I_0, \tag{1}$$

where β is the transmission rate, N is the population size and $I(t)$ is the number of infected individuals at time t.

(a) Write an ℝ function `SI.Gillespie()` that uses the Gillespie algorithm to produce a realization of a stochastic process whose mean field dynamics are given by equation (1) in the limit $N \to \infty$. Your function should have arguments `beta`, `N`, `I0` and `tmax` (the time at which to end the simulation). You may find it helpful (conceptually) to write equation (1) in two-variable form:

$$\frac{dS}{dt} = -\beta SI\,, \qquad S(0) = N - I_0, \tag{2a}$$

$$\frac{dI}{dt} = \beta SI\,, \qquad I(0) = I_0. \tag{2b}$$

Note that there is only one type of event that can occur, so the second part of the Gillespie algorithm (what type of event occurred) is trivial for this model.

Proof. ...beautifully clear and concise text to be inserted here... □

(b) Make a multi-panel plot comparing the deterministic and stochastic dynamics of the SI model for $\beta = 1$, $I_0 = 1$ and $N \in \{32, 10^2, 10^3, 10^4\}$ ($N = 32$ is close to $10^{1.5}$). Each panel should correspond to a different value of N and should show 30 stochastic realizations together with the deterministic solution.

   Note: To make stochastic simulations exactly reproducible use `set.seed()`.

   Proof. ...beautifully clear and concise text to be inserted here... □

3 $\mathcal{R}_0$ for smallpox

The natural history of smallpox is shown in Figure 1. The US Centers for Disease Control and Prevention (CDC) has recently discovered that a group of bioterrorists plans to reintroduce smallpox to the United States. The CDC has reason to believe that the terrorists are also bioengineers and have successfully altered the virus so that it causes the early rash stage to be twice as long as it was when the virus was last circulating naturally in the 1970s. Moreover, the existing smallpox vaccine apparently provides no protection against the altered virus. The CDC wants your opinion on how the alterations to the virus will affect $\mathcal{R}_0$ and the expected final size of an epidemic if the planned attack is successful.

(a) Construct a compartmental (ODE) smallpox transmission model based on the natural history specified in Figure 1, including vital dynamics but ignoring disease-induced death.

   Proof. ...beautifully clear and concise text to be inserted here... □

(b) Use a biological argument to find a formula for $\mathcal{R}_0$.

   Proof. ...beautifully clear and concise text to be inserted here... □

(c) Calculate $\mathcal{R}_0$ using the next generation matrix approach. *Note:* Your solution should include $\mathcal{F}$, $\mathcal{V}$, F, V, and FV^{-1}, in the most human-friendly form you can find. However, feel free to use symbolic manipulation software such as `Maple`, *Mathematica* or sage to help with the necessary algebra and matrix computations.

   Proof. ...beautifully clear and concise text to be inserted here... □

(d) Based on your model, and $\mathcal{R}_0 \sim 5$ for unaltered smallpox, what can you say about the difference in $\mathcal{R}_0$ that can be expected for the newly engineered virus vs. the original virus?

   Proof. ...beautifully clear and concise text to be inserted here... □

(e) Write a paragraph that you can imagine e-mailing to the CDC, in which you do your best to answer their questions.

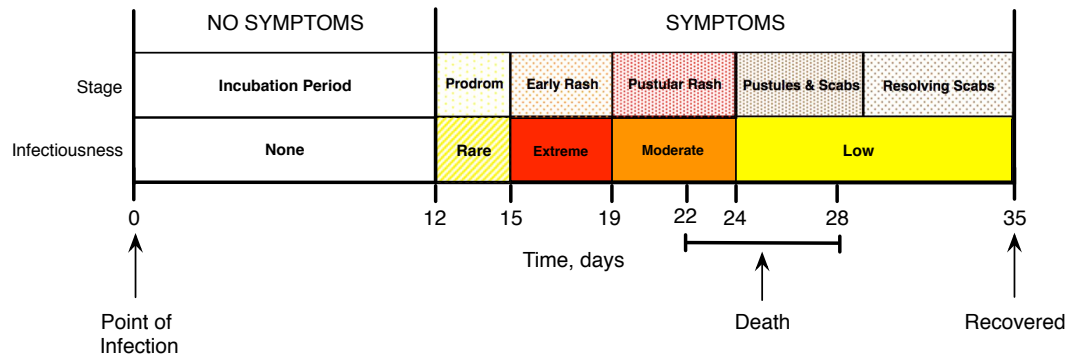*Proof.* . . . beautifully clear and concise text to be inserted here. . . ◻

Figure 1: The natural history of smallpox infection. The prodrom stage begins with fever but the patient is very rarely contagious. Early rash is the most contagious stage, when the rash develops and transforms into bumps. During the pustular rash stage bumps become pustules, which then turn into scabs during the pustules and scabs stage and fall off during the resolving scabs stage. The infected person is contagious until the last scab falls off. (*This is Figure 3.4 from page 82 of Olga Krylova's 2011 McMaster University PhD thesis.*)

— **END OF ASSIGNMENT** —

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