

1 Epidemic Modelling Intro



Mathematics
and Statistics

$$\int_M d\omega = \int_{\partial M} \omega$$

Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 1
Epidemic Modelling Intro
Monday 7 January 2019

Where to find course information

- The course web page:
<http://www.math.mcmaster.ca/earn/4MB3>
- Click on “Course information sheet”.
- Download pdf or read online.
- Let's [have a look now...](#)

Who is NOT available at these times?

- Monday 9:30-10:30
- Wednesday 9:30-10:30
- Thursday 9:30-10:30
- Thursday 11:30-12:20
- Friday 12:30-1:20
- Friday 2:30-3:20

Group formation

Most work in this course will be done in groups.

- Attempt to form a group of 4 students (you and 3 others) **no later than Wednesday night this week.**
- After you have done your best to form a group of four, **exactly one** member of your group must **e-mail the instructor no later than Wednesday night this week:**
 - Include “Math 4MB3” and your proposed group name in the subject line.
 - **Copy your message to all members of your proposed group so I have everyone’s e-mail in the thread.**
- If you were unable to form a group, then e-mail the instructor explaining what you did to try to form a group, and describe your skills/preferences. (*This is a last resort – please try your best to form a group.*)
- *Instructor may change groups based on survey results.*

Online Surveys

You will be required to fill in online surveys during this course. Doing so in a timely manner contributes to your participation mark.

The first online survey has been posted:

- Go to the [Surveys page](#) on the [course web site](#).
- Follow the link for [Background and Group formation Survey](#).
- Complete the survey **no later than 11:59pm this Wednesday (9 Jan 2019)**.
- It should take only ~ 5 minutes.
- Note that *surveys sometimes fail to save*.
 - Type long answers into a file first and paste them into the survey. Then you won't get as frustrated if it fails to save.

Software

- **ASAP**, install the software discussed on the [Software page](#) on the [course web site](#):

- L^AT_EX



- R



- RStudio



- XPPAUT

- Emacs

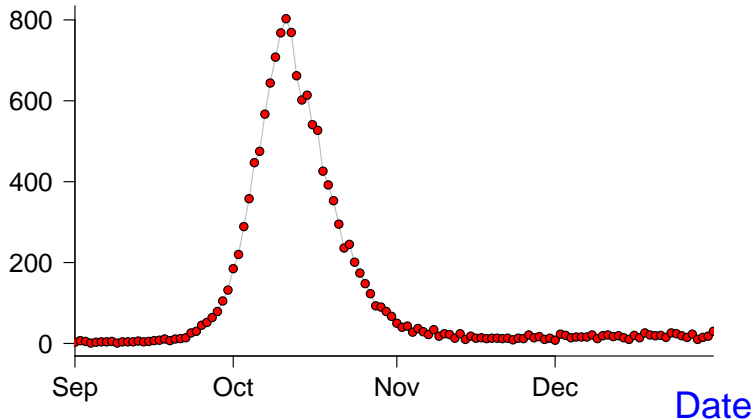


- If you have installation problems, please contact [Ken Moyle](#) <moylek@mcmaster.ca>, who created the [Software page](#).
- **Note:** the [Software page](#) also contains some info about spell-checking and counting words in L^AT_EX documents.

Epidemic Modelling

Pneumonia & Influenza Mortality, Philadelphia, 1918

P&I Deaths



Modelling challenge

Develop a model that helps us understand the [graph on the previous slide](#), based on mechanisms of disease spread.

- Only one variable is observed (P&I deaths per day) so construct a model containing only one variable.
- Think about how disease spreads and express your thoughts with mathematical notation.
- Derive a differential equation that models the process of disease transmission.
- Analyze the model and determine its strengths and weaknesses/limitations.

Make (Biological) Assumptions Clear

- 1 *Assume* the disease is transmitted by contact between an infected individual and a susceptible individual.
- 2 *Assume* the latent period (delay between being infected and becoming infectious) is so short that it can be ignored (technically assume it is zero).
- 3 *Assume* all members of the population are identical and respond identically to the disease. In particular, all susceptible individuals are equally susceptible and all infected individuals are equally infectious.
- 4 *Assume* the population size is fixed during the epidemic, *i.e.*, ignore births, migration, and deaths from causes other than the disease, and count individuals who have died from the disease as part of the population.

About Assumptions. . .

- Note that the first assumption on the [previous slide](#) is actually correct.
- The other assumptions are wrong, but are reasonable approximations.
- It is best to *start as simple as possible and add complexity later*, in order to:
 - obtain a model that actually succeeds in explaining [the data](#) with as few assumptions as possible;
 - check that inferences we draw from our model(s) are robust to the inclusion of more biological details/realism.

What variables should we include in our model?

- Independent variable: time (t)
- Dependent variable: Many options, e.g.,
 - Incidence (number of new infections per unit time)
 - Prevalence (total current number of infected individuals)
 - Death rate (number of deaths per unit time)
 - Death toll (number of deaths so far)
- So, what would be best?
- Not deaths, because whether or not you die may be unrelated to how much you transmit.
- But deaths are what **we observe!** What to do?!?
- Make another assumption. . .

Additional assumption(s)

- We actually want to know incidence or prevalence, but we **observe deaths**.
- Under what circumstances would daily deaths be a good estimate of incidence? (*i.e.*, What must we assume in addition to the **assumptions we have already made**.)
 - 5 **Assume** that the time from infection to death is exactly the same (a certain number of days) for every individual who dies.
 - 6 **Assume** that the probability of dying from the disease is the same for every individual who is infected.
- Then daily death counts are proportional to daily incidence a certain number of days in the past, *i.e.*, the “mortality curve” that **we observe** is a translated and scaled version of the “epidemic curve” (new cases per day).

So... what variables should we include in our model?

- Independent variable: time (t)
- Dependent variable: one of:
 - Incidence (number of new infections per unit time)
 - Prevalence (total current number of infected individuals)
- Which one?
- Choose prevalence (I) because anybody who is currently infectious can infect others, so it will probably be easier to formulate a transmission model based on prevalence. (Try not to lose sight of underlying biological mechanisms.)
- But our **mortality curve** is related to incidence, not prevalence!?! Argh. What to do?!?
- Let's work with prevalence and see how it works out. Maybe we'll be able to derive the incidence curve from a model based on prevalence.

Notational note

- We use I for prevalence because prevalence is the number of infected individuals.

- So, let's try to write down a model...