1 Epidemic Modelling Intro

McMaster University

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 8 January 2018

Where to find course information

- The course web page:
  http://www.math.mcmaster.ca/earn/4MB3
- Click on "Course information".
- Download pdf or read online.
- Let's have a look now...

Who is NOT available at these times?

- Monday 10:30-11:30
- Monday 12:30-1:30
- Wednesday 10:30-11:30
- Wednesday 12:30-1:30
- Friday 12:30–1:30
- 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 Thursday 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 Thursday 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 Thursday (11 Jan 2018)**.
- 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

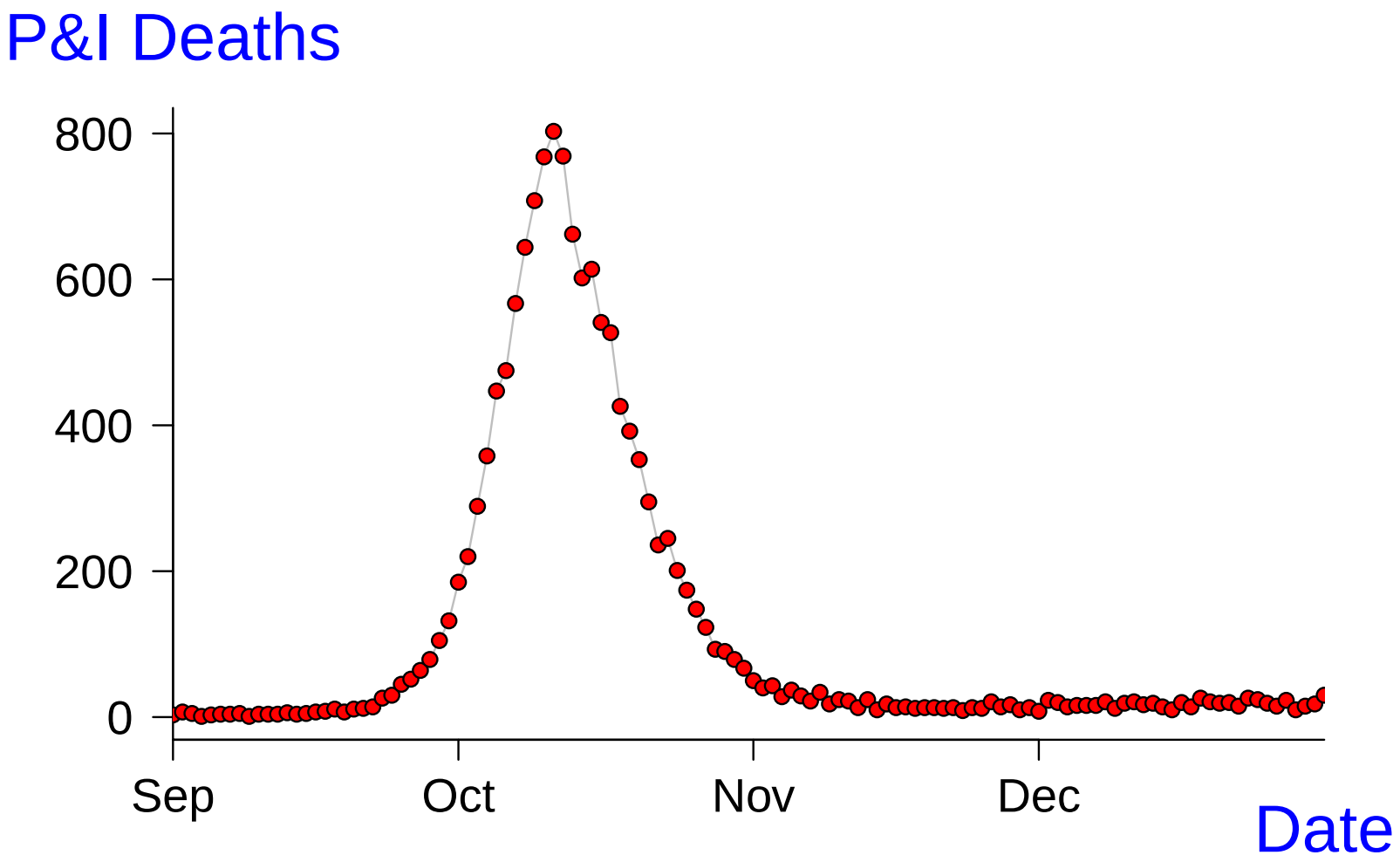
- **ASAP**, install the software discussed on the Software page on the course web site:
  - LaTeX

  - 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 LaTeX documents.

Epidemic Modelling

Pneumonia & Influenza Mortality, Philadelphia, 1918



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.