A tutorial on SIR(-like) models

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Structure of day

- Bit of logistics (ppt)
- Introductory remarks (ppt)
- Equations (whiteboard)
    - Intuit epidemic curve
    - R0
    - Pc
- Numerical integration of ODEs (R)
    - Invasion towards endemic equilibria
    - Prevalence vs incidence
- Model explorations (Shiny)
- Model elaborations (whiteboard)
    - SEIR
    - Rates vs probabilities
- Further insights

Some logistics (1)

https://www.niss.org/events/nissasa-tutorial-susceptible-infected-recovered-sir-modeling

Two recent 2-page tutorials:

Bjørnstad, O.N., Shea, K., Krzywinski, M. and Altman, N., "Modeling infectious epidemics." Nature methods 17 (2020): 455-456.

with associated online Shiny App https://shiny.bcgsc.ca/posepi1/

Bjørnstad, O.N., Shea, K., Krzywinski, M. and Altman, N., "The SEIRS model for infectious disease dynamics." Nature methods 17 (2020): 557-558.

with associated online Shiny App https://shiny.bcgsc.ca/posepi2/

All the data and functions to be discussed are in the R-package: https://CRAN.R-project.org/package=epimdr

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Some logistics (2)

All the data and functions to be discussed are in the R-package: https://CRAN.R-project.org/package=epimdr

To follow along in RStudio install and attach key packages:

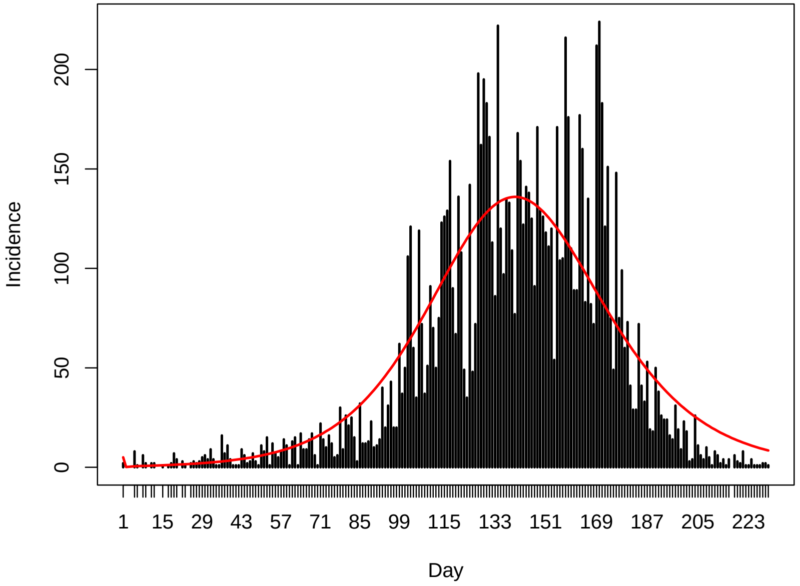
```
install.packages("epimdr")
install.packages("deSolve")
install.packages("shiny")
install.packages("polspline")

require("epimdr")
```

Bit of History

- There is no “*THE* SIR MODEL”.
- MathEpi shorthand for a class of more or less complicated compartmental models
- Original SIR model by Kermack and McKendrick (1927) was a set of elaborate integrodifferential renewal equations
    - Are there laws for the shape of epidemics?
    - Will everybody be infected?
- Bartlett 1957 Stoch Diff Eq versions
- Bailey 1956 introduced discrete time (“chain-binomial”) stochastic versions

- The short-hand today is most commonly used to refer to the simpler of the deterministic ordinary differential compartmental formulations

Measles Niamey, Niger 2003-2004



Flows of transmisson

S – Susceptible

I – Infected and infectious

R – Recovered and immune

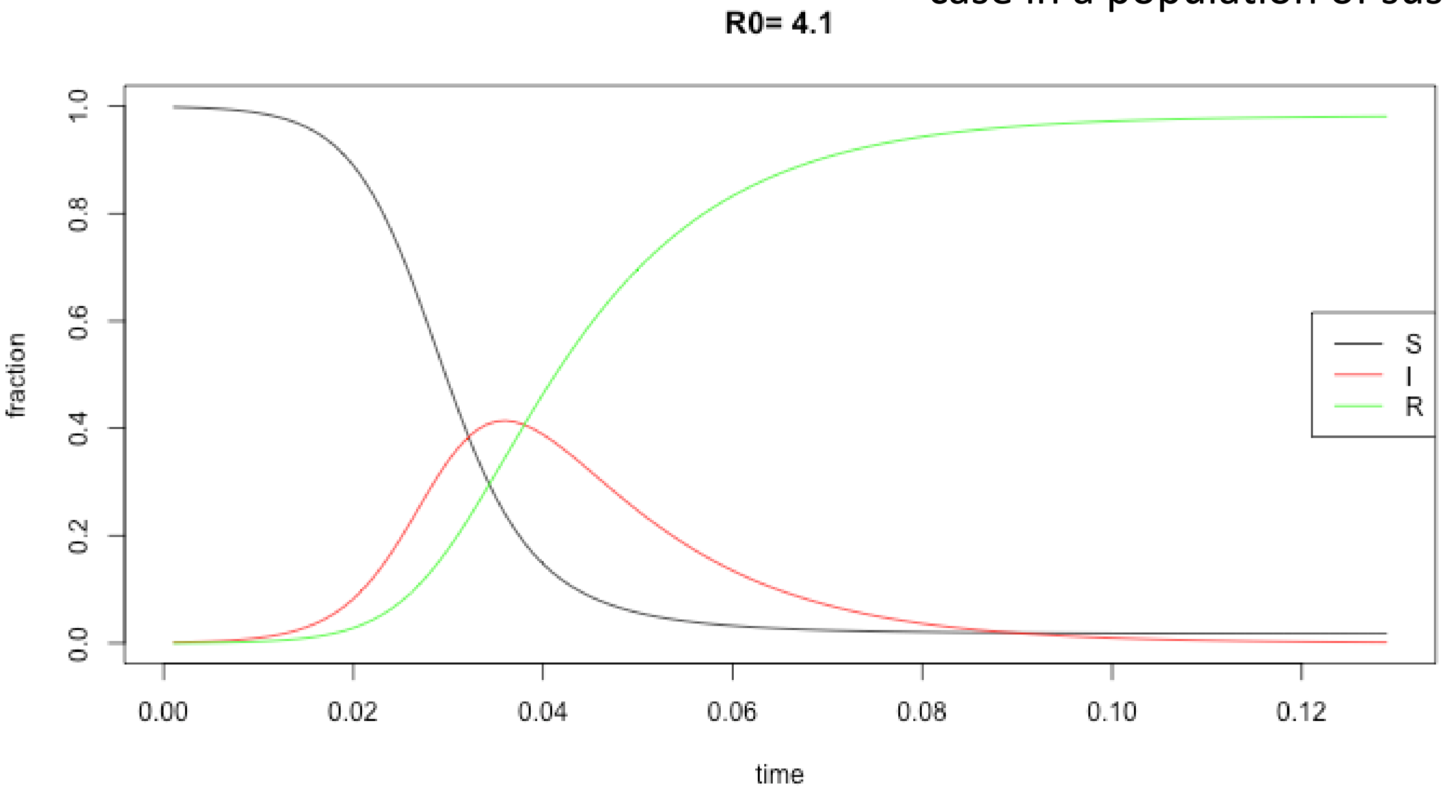
(E – “Exposed” – Infected but not yet infectious)

- Infection is for life: S -> I
- Immunity following infection is for life: S -> I -> R
- Significant lag between exposure and infectious: S -> E -> I -> R
- Impermanent immunity: S -> (E ->) -> I -> R -> S

-> White board

The “closed SIR epidemic” (no susceptible recruitment)

R_0 = # of infecteds expected from index case in a population of susceptibles



- Initial exponential growth (and exponential depletion of S)

- Turning-point is when contacts among infecteds and susceptibles becomes too rare for replacement ($S = 1/R_0$).
- Vaccine target for herd immunity = $1 - 1/R_0$

- In absence of births epidemics will self-extinguish with a fraction of S left behind ($\approx \exp[-R_0]$)

The S-I-R model

Change in S = + new births – new infections - deaths

Per infectious rate of contact with others * Probability of Infection given contact * Probability that ‘contactee’ is suceptible * Number of infectious

The simple S-I-R model

Change in S = + new births – new infections - deaths

Per infectious rate of contact with others ∗ Probability of Infection given contact ∗ Probability that ‘contactee’ is suceptible ∗ Number of infectious

Transmisssion rate, β

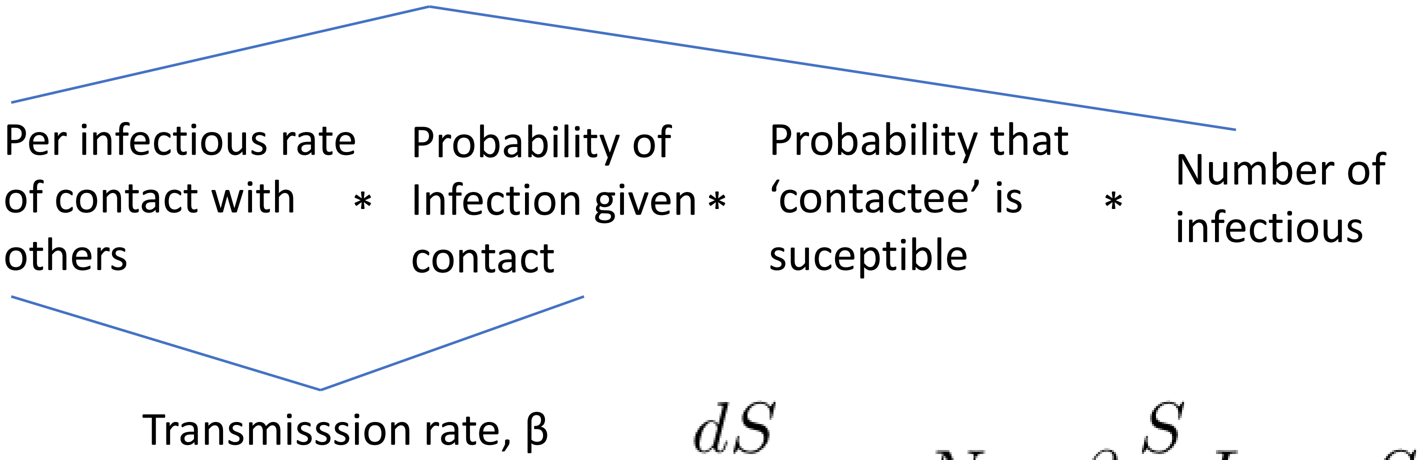
$$\frac{dS}{dt} = \nu N - \beta \frac{S}{N} I - \mu S$$

$\nu = \text{natality rate}$

$\mu = \text{mortality rate}$

The simple S-I-R model

Change in S = + new births – new infections - deaths



Per infectious rate of contact with others * Probability of Infection given contact * Probability that ‘contactee’ is suceptible * Number of infectious

Transmisssion rate, β

$$\frac{dS}{dt} = \nu N - \beta \frac{S}{N} I - \mu S$$

$\nu = \text{natality rate}$

$\mu = \text{mortality rate}$

In stable pop: mu=nu

Change in I = + new infections – new recovered - deaths

When calculating we usually set N = 1 so each variable is the fraction of population

$$\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I - \mu I$$

$$\gamma = \frac{1}{\text{latent+infectious period}}$$

The recipe for integrating the SIR ode's (and other ode's in R)

Step1: require(deSolve)

Step2: *gradient-function*

Step3: parameter values

Step4: initial values

Step5: time points

Step6: call ode()-function

https://shiny.bcgsc.ca/posepi1/

```
#1      require(deSolve)

#2      sirmod=function(t, y, parms){
        S=y[1];  I=y[2]; R=y[3]
        beta= parms["beta"]; mu= parms["mu"]
        gamma= parms["gamma"]; N= parms["N"]
        dS = mu * (N  - S)  - beta * S * I / N
         dI = beta * S * I / N - (mu + gamma) * I
        dR = gamma * I - mu * R
        res=c(dS, dI, dR)
        list(res) }

#3      paras  = c(mu = 0, N = 1, beta =  2, gamma = 1/2)
#4      start = c(S=0.999, I=0.001, R = 0)
#5      times  = seq(0, 26, by=1/10)

#6      out = ode(y = start, times = times, func = sirmod,
            parms = paras)
```

Further insights 1

R0 determines

- Final epidemic size
- Time and height of peak
- The critical vaccine cover

(Endemic mean age of infection)

Together with infectious period, initial rate of exponential increase

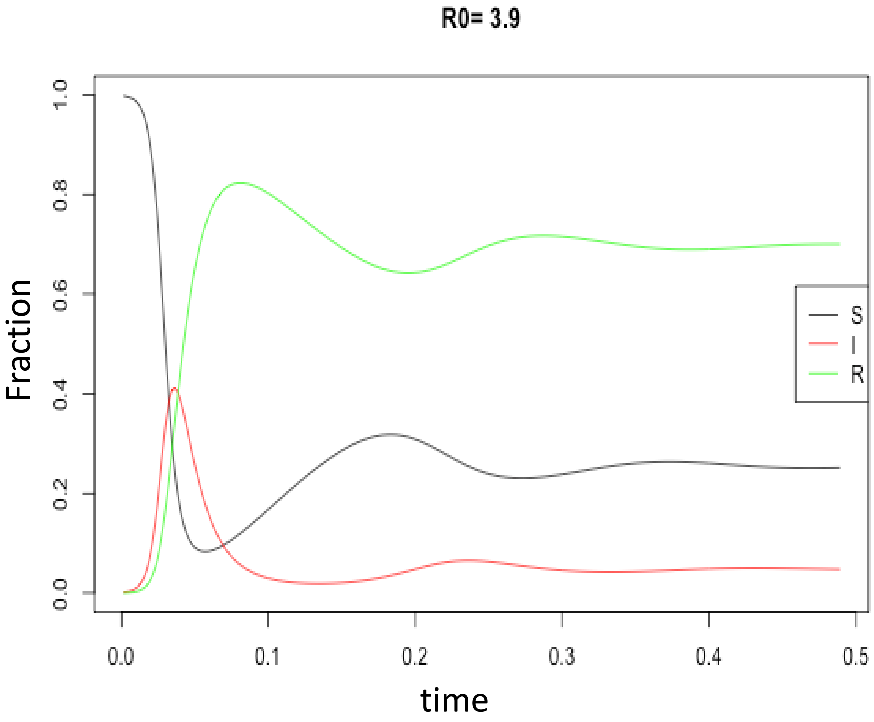
The “open epidemic” – susceptible recruitment

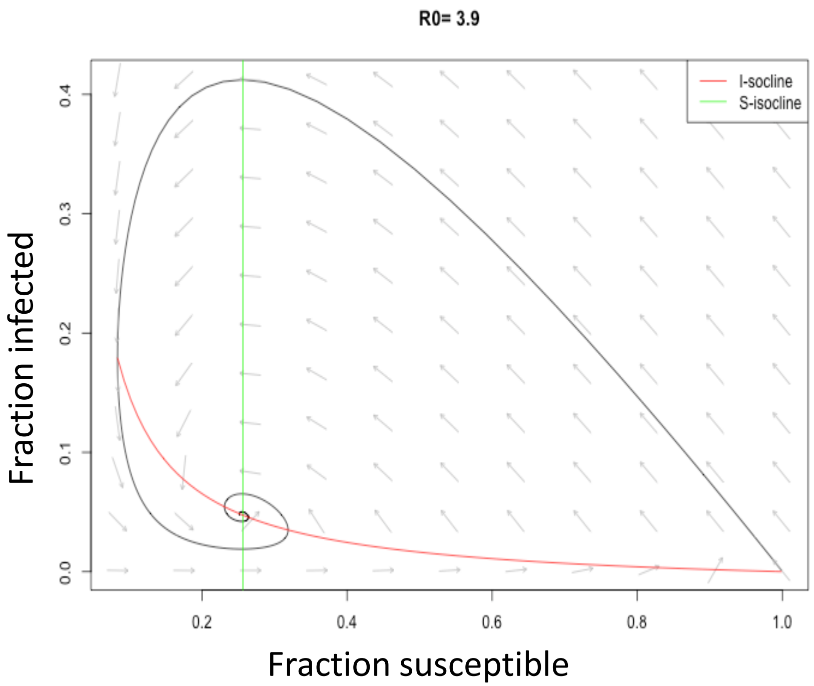
> SIR.app

Further insights 2:

SI & SIS -> logistic invasion
SIR, SEIR, SEIRS -> epidemic invasion

- Inter epidemic interval
- S* = 1/R0
- Endemic mean age of infection
- “Natural herd immunity” does not exist – epidemic spread will *slow* as immunity builds up, but in large cities will never go extinct unless vaccination or other interventions reduce R0 below 1.





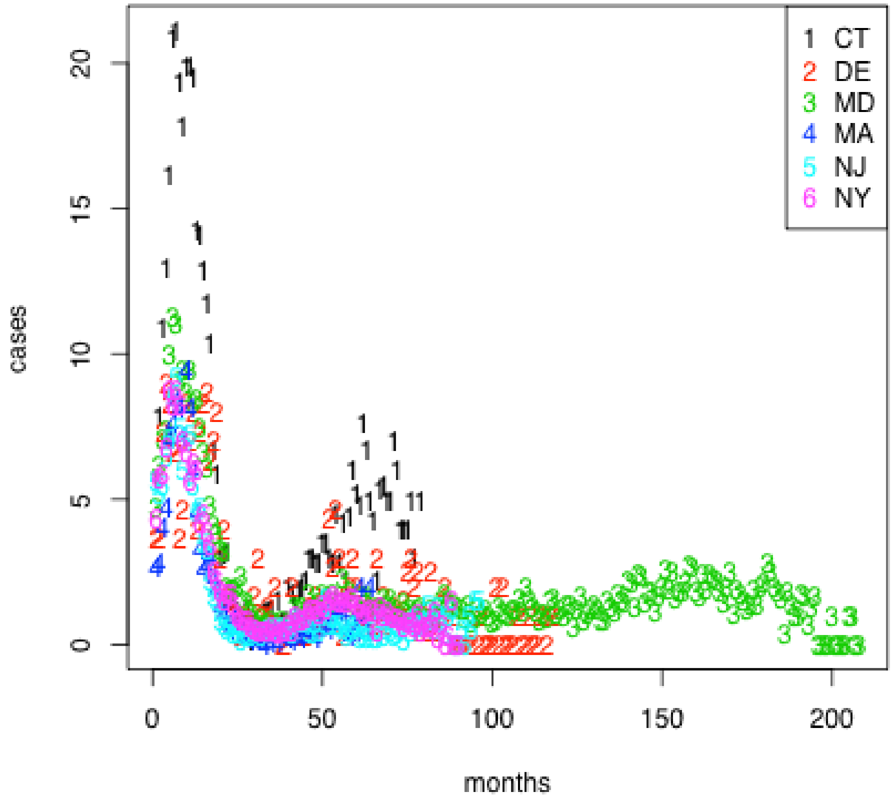
- With susceptible recruitment, (dampened) epidemic cycles appear

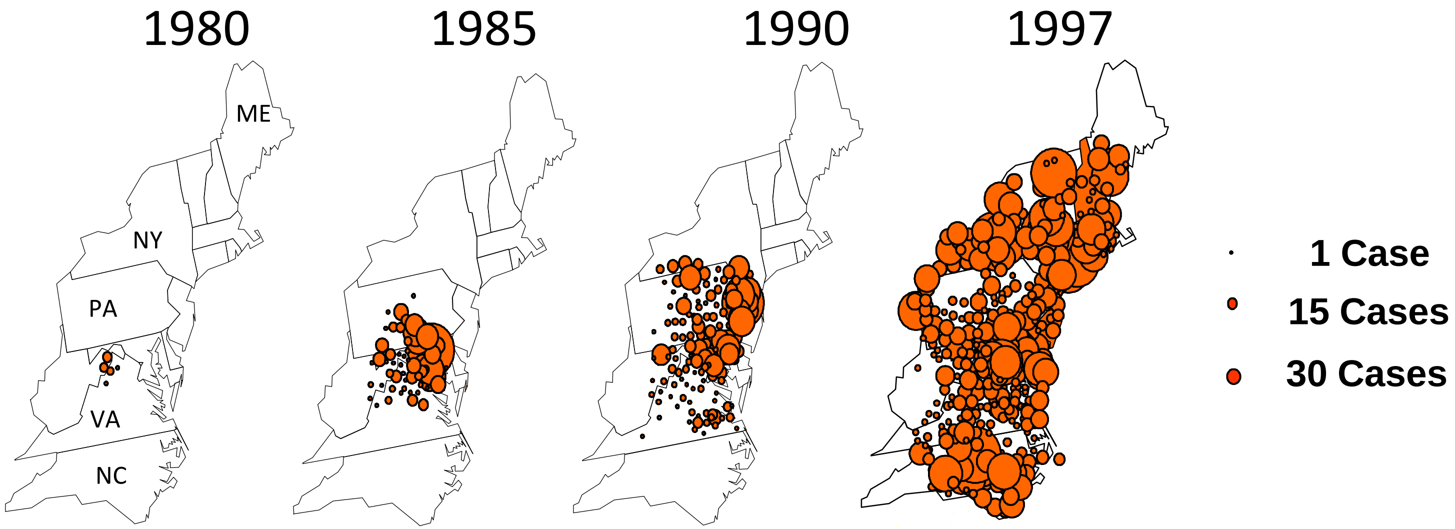
- Inter-epidemic interval depends on
  - Transmission rate
  - Infectious period
  - Birth rate
  - (duration of immunity)

  >>Shiny App

Invasion of rabies in NE US raccoons

A simple SIR-like model predicts 39 months interepidemic period (9 mos) too short





Model elaborations (& R0)

- SEIR with disease induced mortality
- Scaling of transmission with density
- (Jaccibians and inter epidemic periods)
- (Next generation method)

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Standalone Shiny-embedded Rmarkdowns
https://github.com/objornstad/ecomodelmarkdowns

Epidemics: models and data using R:
https://github.com/objornstad/epimdr