

# 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
  - $R_0$
  - $P_c$
- 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")
```

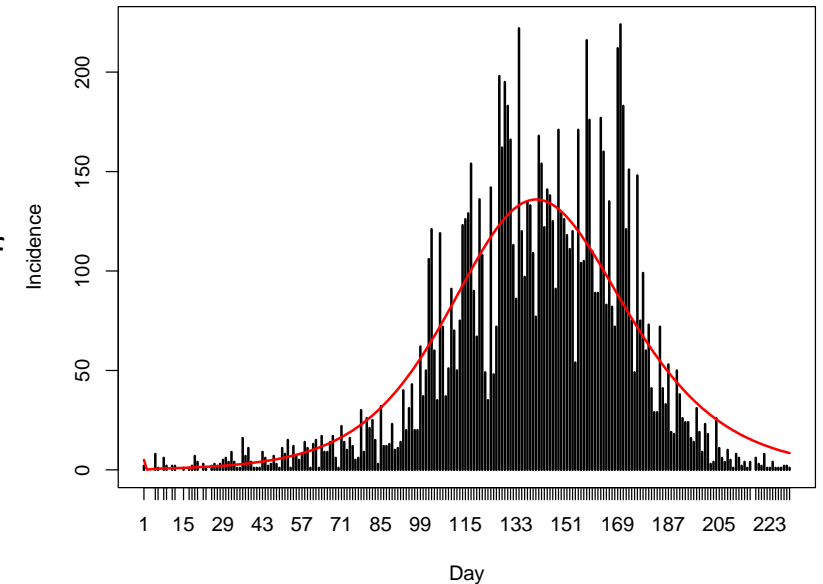
```
install.packages("polspline")
```

```
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

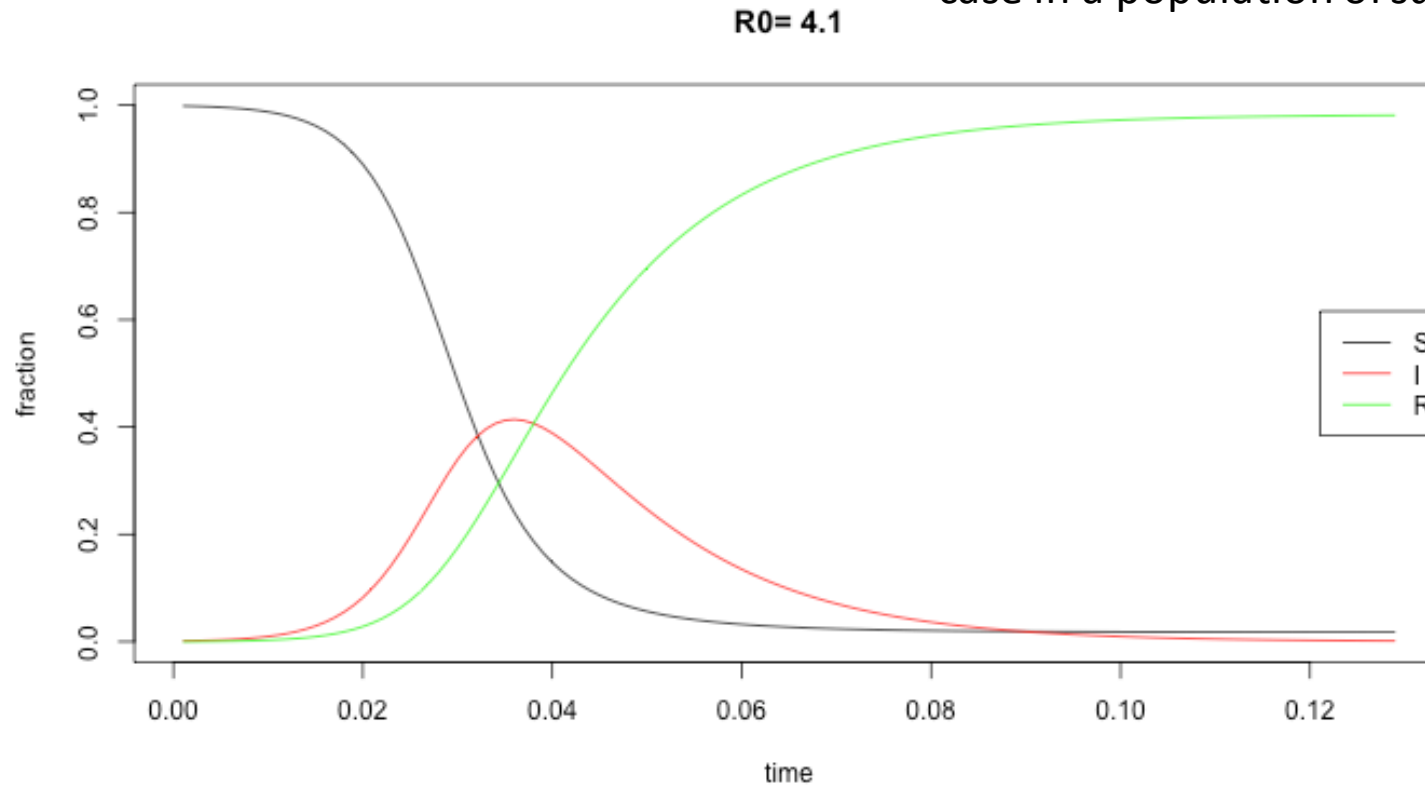
(E – “Exposed” – Infected but not yet infectious)

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

-> White board

The “closed SIR epidemic” (no susceptible recruitment)

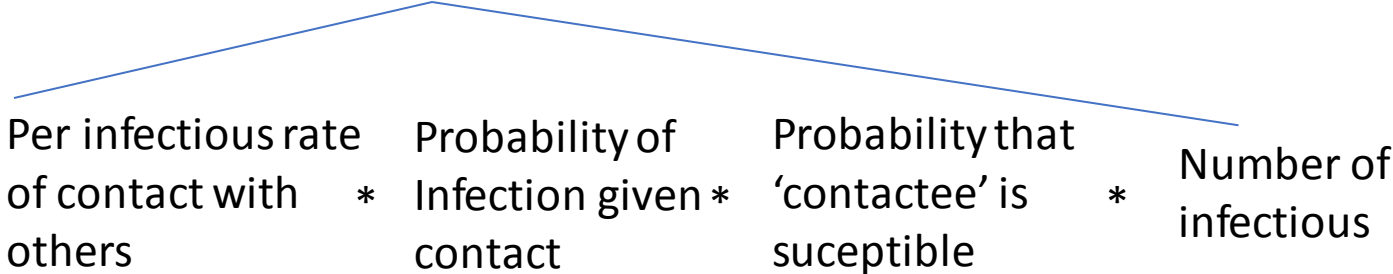
$R_0 = \#$  of infecteds expected from index case in a population of susceptibles



- 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

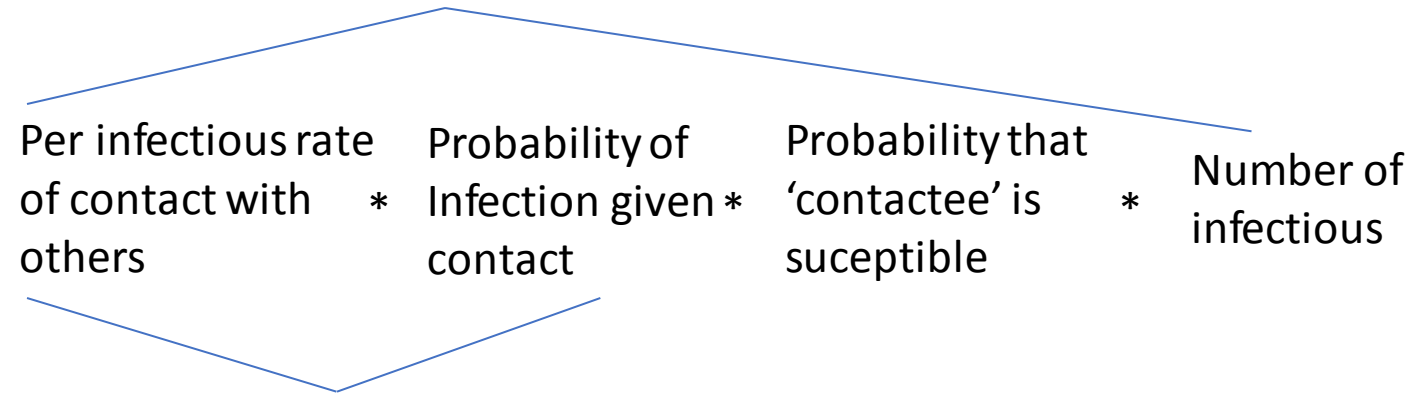
Change in S = + new births – new infections - deaths





# The simple S-I-R model

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



Transmission rate,  $\beta$

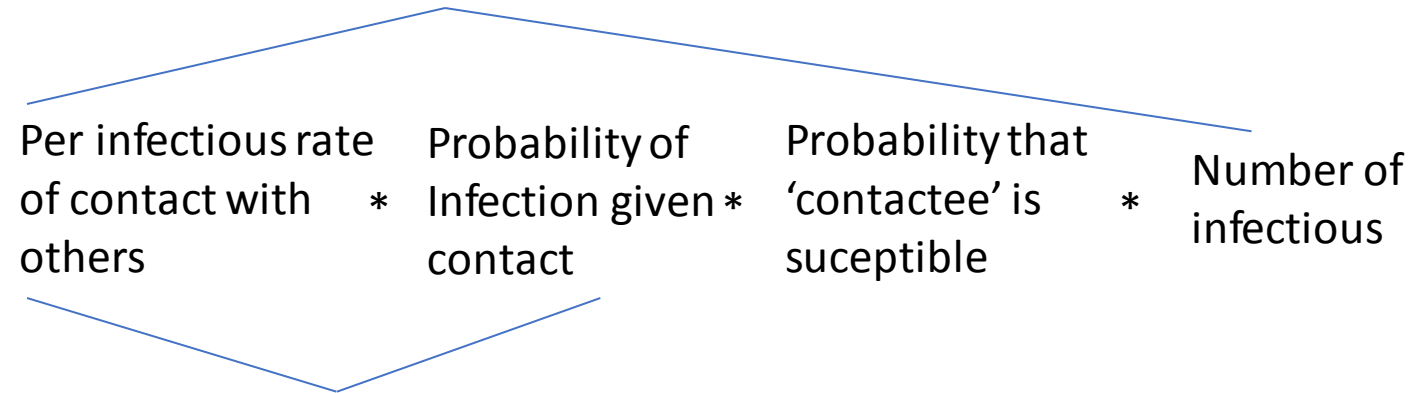
$$\frac{dS}{dt} = \nu N - \beta \frac{S}{N} I - \mu S$$

$\nu$  = natality rate

$\mu$  = mortality rate

# The simple S-I-R model

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



Transmission rate,  $\beta$

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

$\nu$  = natality rate

$\mu$  = 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

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

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

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

$R_0$  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:

- Inter epidemic interval

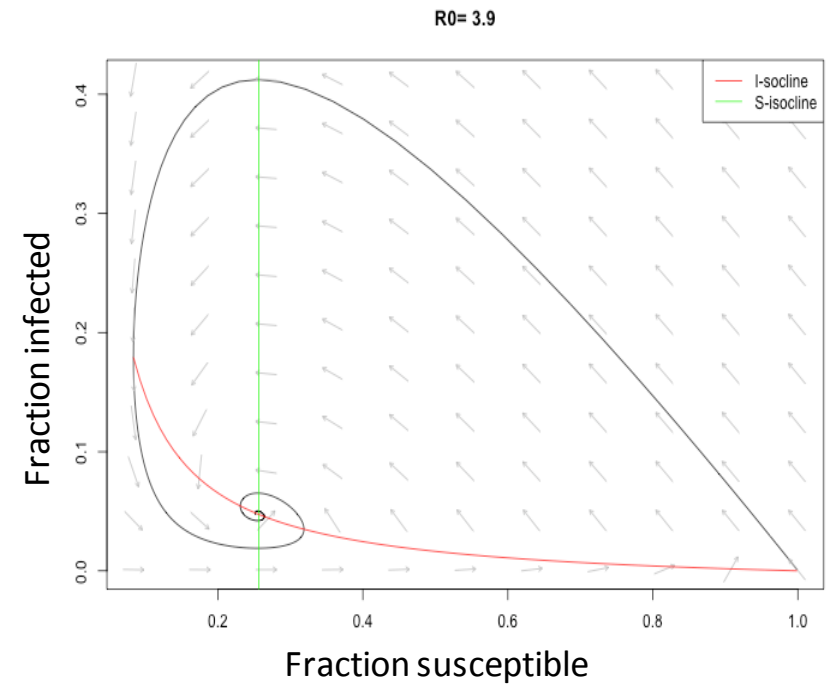
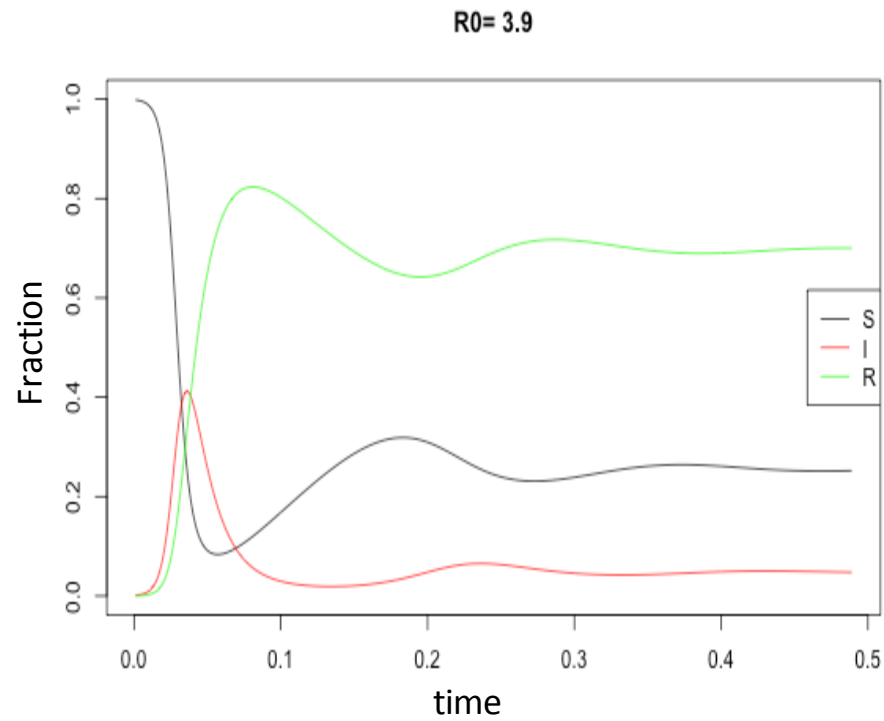
SI & SIS -> logistic invasion

SIR, SEIR, SEIRS -> epidemic invasion

- $S^* = 1/R_0$

- 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  $R_0$  below 1.

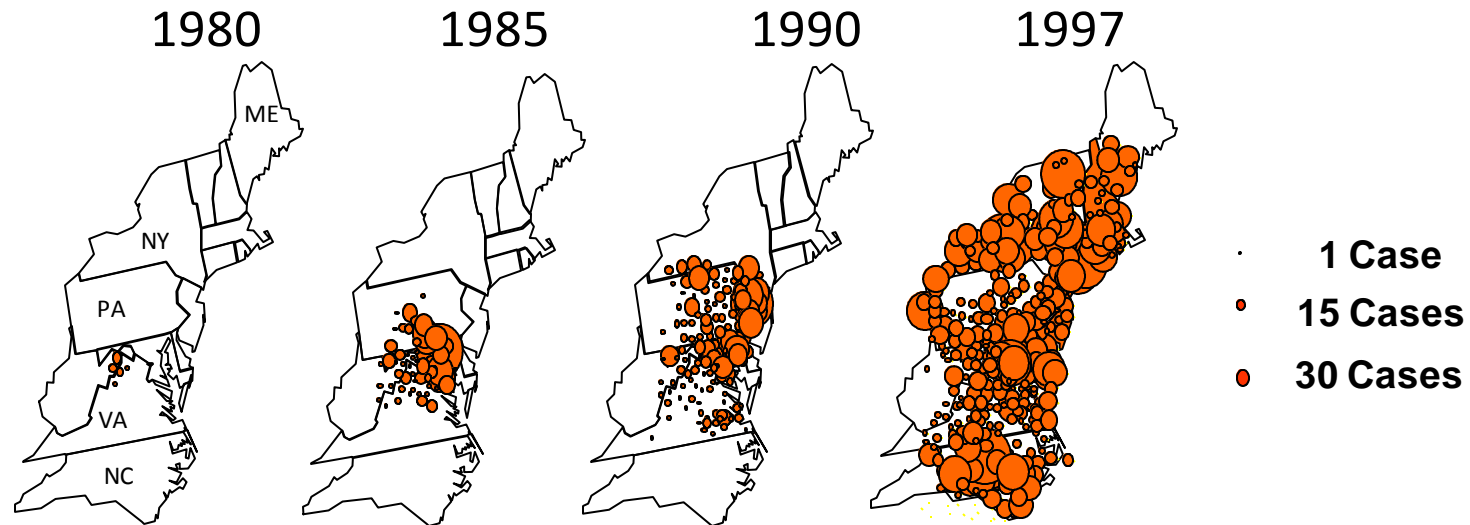
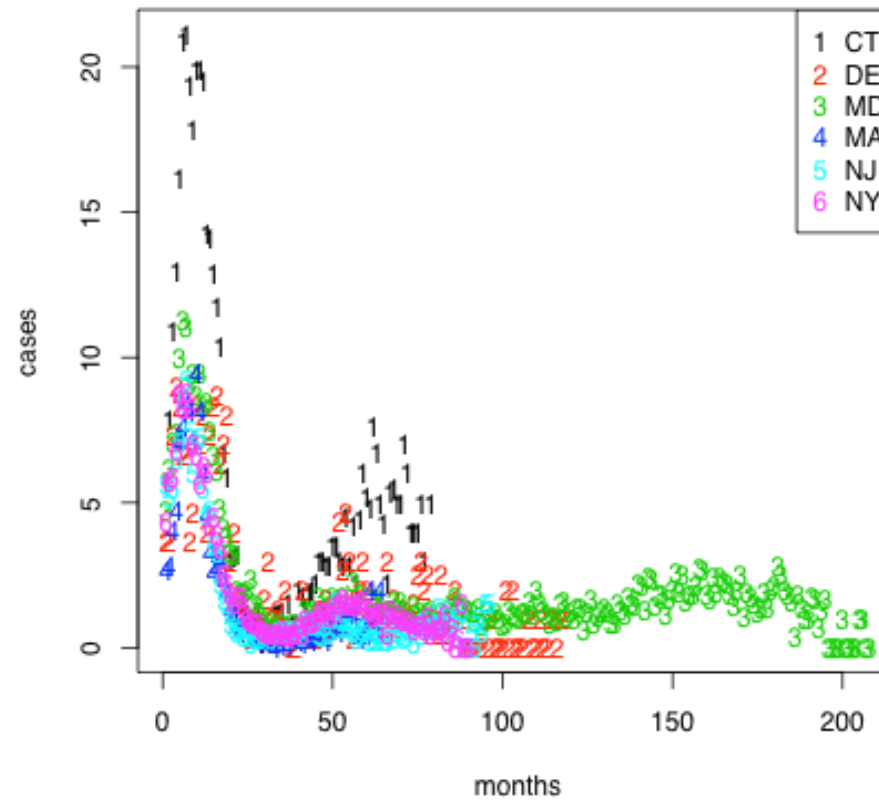


- With susceptible recruitment, (dampened) epidemic cycles appear
- Inter-epidemic interval depends on
  - Transmission rate
  - Infectious period
  - Birth rate
  - (duration of immunity)

>>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 (& $R_0$ )

- 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>