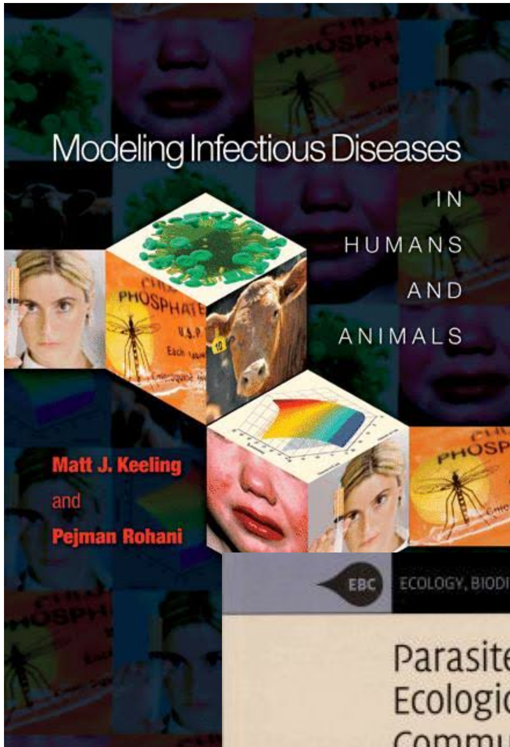
A practical guide to modelling epidemics:

Numerical simulations in R



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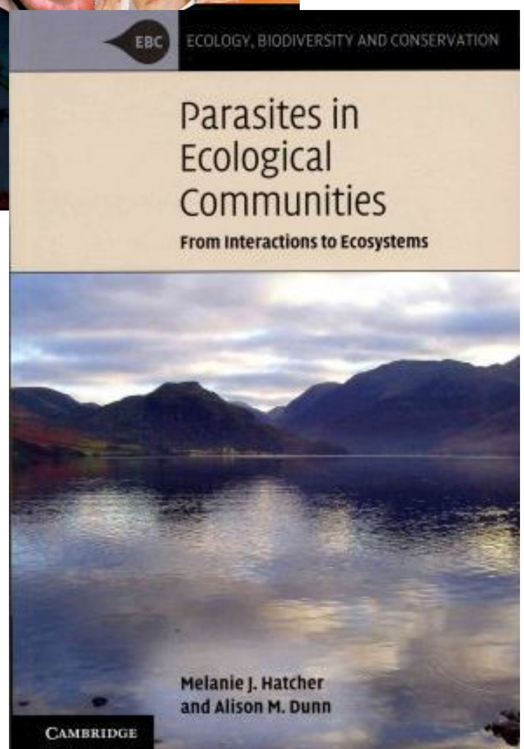

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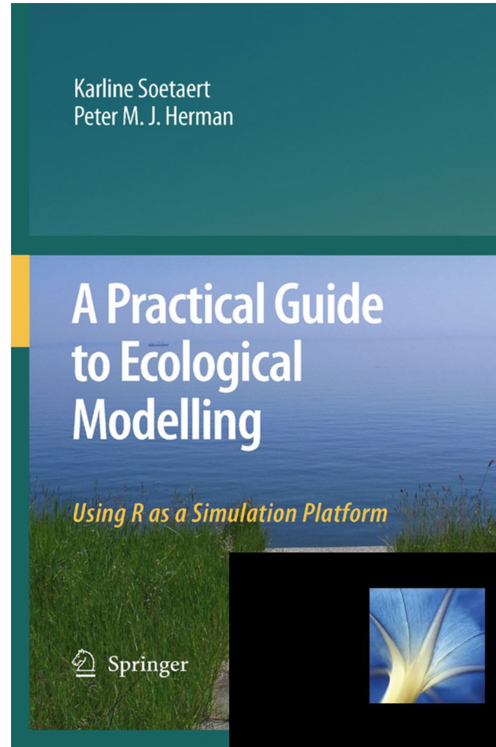

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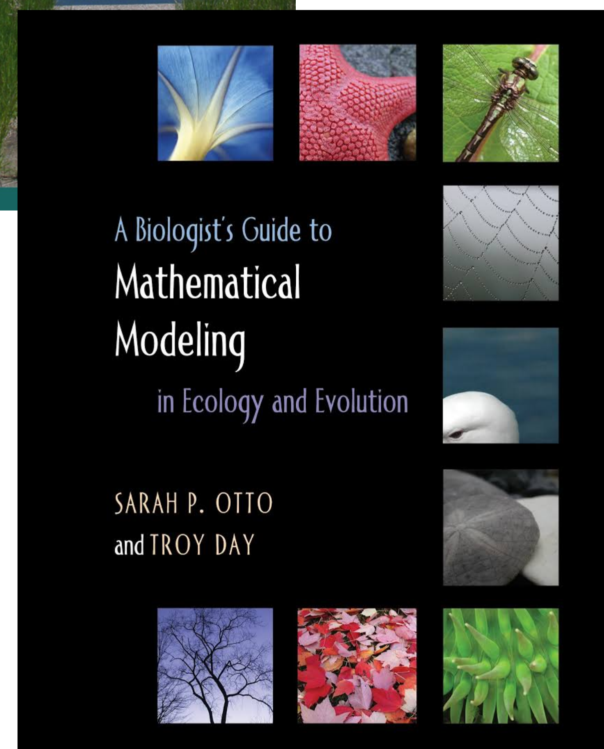

A Biologist's Guide to
Mathematical Modeling
in Ecology and Evolution
SARAH P. OTTO
and TROY DAY

Overview

1. An introduction to epidemic models (SIS model)
2. Implementation in R

1. An introduction to epidemic models (SIS model)

An epidemic model

- SIS model (ODEs)

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + \gamma I \\ \frac{dI}{dt} &= \beta SI - \gamma I\end{aligned}$$

An epidemic model

- SIS model (ODEs)

Change in number of susceptibles & Infecteds over time

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An epidemic model

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Number of new infections per unit time

Number of recovered hosts per unit time

Assumptions:

- No births, deaths, and migration
- Mass action
- Recovery without immunity memory

An epidemic model

- On β:
  - β is a rate, NOT a probability
  - Each infected individual makes β infectious contacts per unit time
  - $\beta \times I$ is the incoming transmission rate per susceptible individual, the force of infection

More on β: Keeling and Rohani: Box 2.1

An epidemic model

- On ɣ:
  - ɣ is also a constant rate
  - Exponential distribution:
    - E[waiting time] = 1/rate
    - 1/ ɣ = expected time until recovery
    - 1/ ɣ = duration of infection (if there is no mortality)

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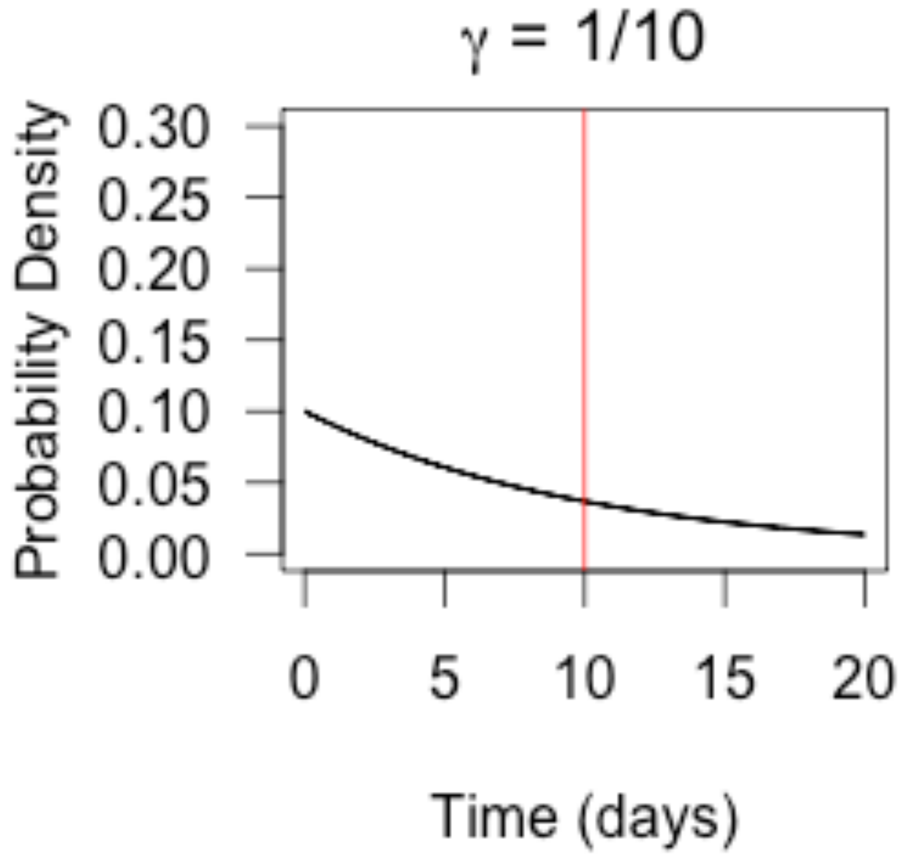

An epidemic model

- On R_0:
  - The number of secondary infections per infected host in a fully susceptible population
  - Maximum reproductive potential for the parasite population
  - Tons of different methods and they rarely agree with each other (for complex models).

  - Deriving intuitively from an ODE model:
    - $R_0 = Transmission\ rate \times duration\ of\ infection$
    - For a SIS model: $R_0 = \beta/\gamma$

Modelling considerations

- Time
  - Continuous
  - Discrete
- Deterministic (large pop.) vs. stochastic (small pop.)
- Host demography
  - Constant population size
  - Constant input (strong externally regulation)
  - Logistic growth (similar to constant population size near K)
  - Per capita growth rate
- Host immunity
  - (waning) immune memory (SIR model)
  - No immune memory (SIS model)
- Mode of transmission
  - Density or frequency (STI and vector-borne) dependent
  - Vertical or horizontal
  - Direct, indirect or environmental
- Parasite development
  - Infected, but not infectious (exposed class)
- Parasite-induced harm
  - Mortality through infection?

Assessing epidemiological consequences

- Examples of useful metrics
  - R_0 and its relatives (emergence)
  - Emergence probability (stochastic models)
  - Peak infection prevalence (SIR models, in particular)
  - Endemic equilibrium prevalence
  - Stability (disease free & endemic equilibrium)

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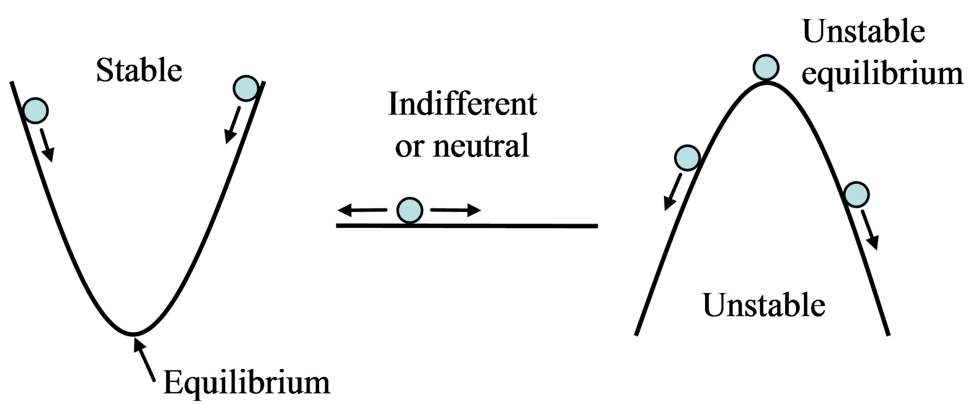

Assessing epidemiological consequences

- Examples of useful metrics
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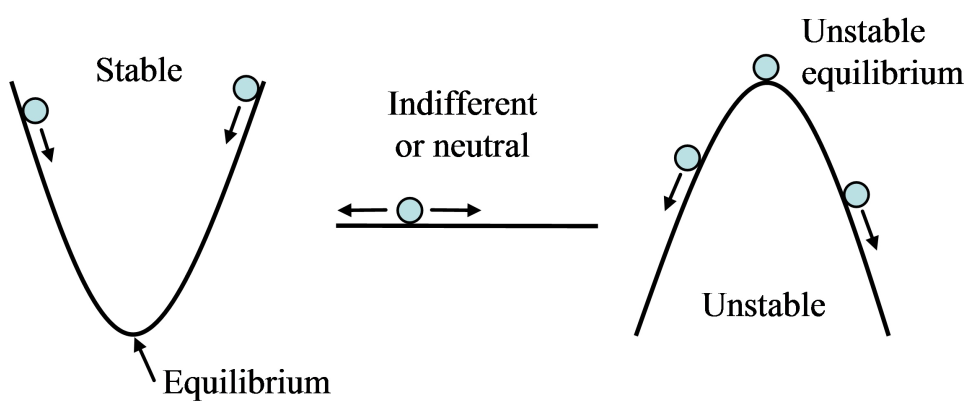


Calculating infection prevalence

Rate of change

$$\frac{dS}{dt} \Longrightarrow S(t)$$

$$\frac{dI}{dt} \Longrightarrow I(t)$$

Density at time t

Calculating infection prevalence

$$\frac{dS}{dt} \Longrightarrow S(t)$$

Rate of change Integration **Density at time t**

$$\frac{dI}{dt} \Longrightarrow I(t)$$

Calculating infection prevalence

Rate of change

$$\frac{dS}{dt} \Longrightarrow S(t)$$

Integration

$$\frac{dI}{dt} \Longrightarrow I(t)$$

Density at time t

- But, often impossible to integrate complex systems models analytically
  - So we resort to calculating numerical values that approximate the system
  - R offers ready-to-use numerical integrators

2. Implementation in R

Useful R packages for ODE models

- deSolve
  - Numerical integration algorithms: lsoda()
- rootSolve
  - Finding steady states (equilibrium): runsteady()
  - Stability: jacobian.full()
- GillespieSSA
  - Stochastic model
- FME
  - Sensitivity analysis

R implementation (SIS model):

1. Describing the model
2. Setting up initial conditions
3. Running the model through time
4. Finding a steady state (equilibrium)
5. Assessing stability
6. (Sensitivity analysis)

R implementation (SIS model):

1. Describing the model

```
#####  Model description  #####
SISmodel=function(t,y,parameters)
{
  ## Variables
  S=y[1]; I=y[2];

  ## Parameters
  beta = parameters[1]; gamma = parameters[2]

  ## Ordinary differential equations
  dSdt = - beta * S * I + gamma * I
  dIdt = beta * S * I - gamma * I

  return(list(c(dSdt,dIdt)));
}
###############################
```

R implementation (SIS model):

2. Setting up initial conditions

```
#####  Intial condition  #####
## Parameters
parameters=c(beta=0.001, gamma=1/10)

## Initial state
variables0=c(S0=999,I0=1)

## Times at which estimates of the variables are returned
timevec=seq(0,30,1)
################################
```

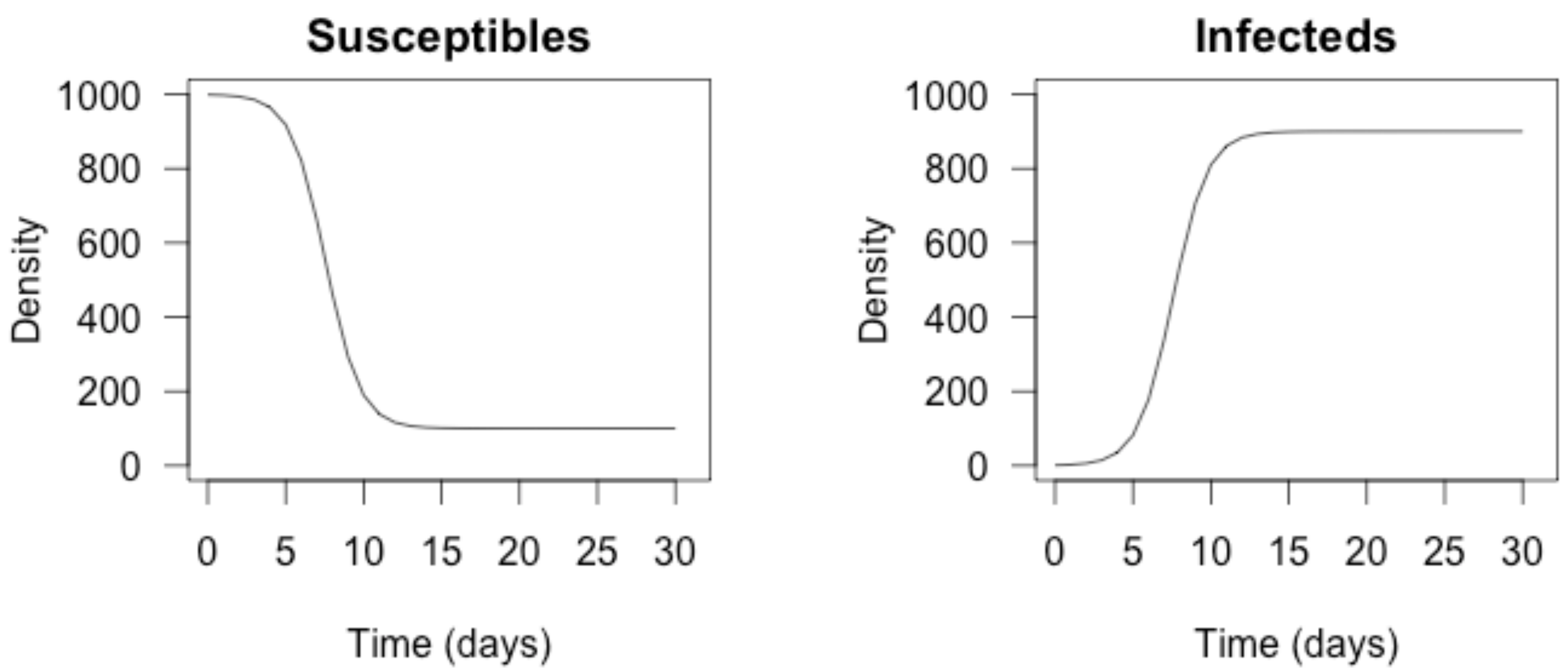
R implementation (SIS model):

3. Running the model through time

```
#####  Running the model   #####
## Numerical integration through time
output=lsoda(y = variables0,    # intial values
             times = timevec,   # time vector
             func = SISmodel,   # model
             parms = parameters # constant parameters
             )
################################
```

R implementation (SIS model):

3. Running the model through time



R implementation (SIS model):

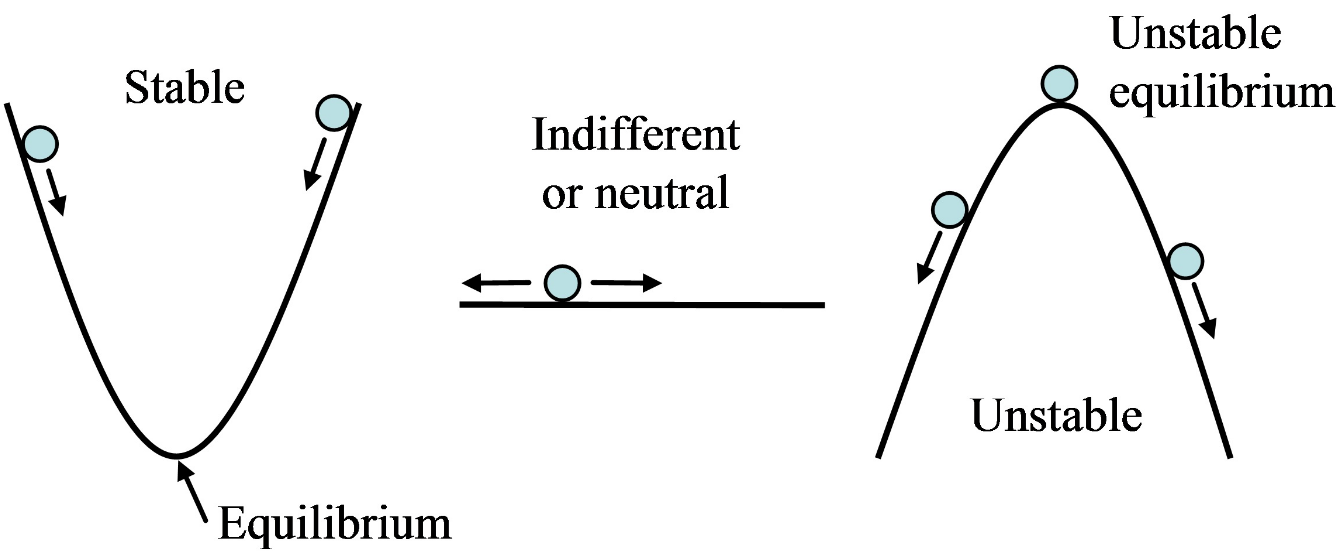
4. Finding a steady state (equilibrium)

```
##### Finding steady state #####
steadyState=runsteady(y = variables0,
                      fun = SISmodel,
                      parms = parameters)
steadyState$y
################################
```

```
> steadyState$y
 S0  I0
100 900
```

R implementation (SIS model):

5. Assessing stability of the equilibrium



More on stability analysis: Otto and Day, Chapter 5, Chapter 8

R implementation (SIS model):

5. Assessing stability of the equilibrium
   - When the dominant Eigenvalue of the Jacobian matrix is negative -> the equilibrium is stable

$$J = \begin{bmatrix} \frac{\partial S'}{\partial S} & \frac{\partial S'}{\partial I} \\ \frac{\partial I'}{\partial S} & \frac{\partial I'}{\partial I} \end{bmatrix}$$

R implementation (SIS model):

5. Assessing stability of the equilibrium
   - When the dominant Eigenvalue of the Jacobian matrix is negative -> the equilibrium is stable

```
##### Assessing the stability of the steady state #####
## Stability
Jmatrix=jacobian.full(y = steadyState$y,
                      func = SISmodel,
                      parms = parameters)
dEigenV=max(Re(eigen(Jmatrix)$values))
#######################################################
```

R implementation (SIS model):

6. (Sensitivity analysis: FME package)
   - Local sensitivity (elasticity) analysis

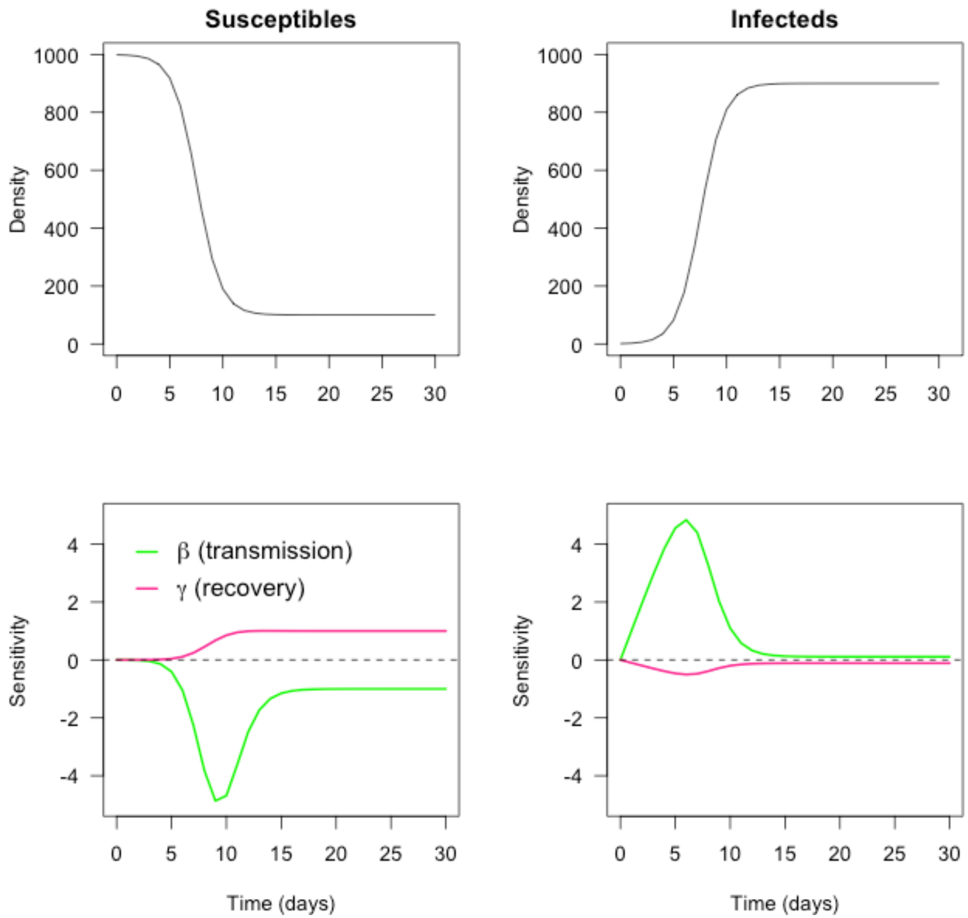
$$\frac{\partial y_i}{\partial \Theta_j} \cdot \frac{w_{\Theta_j}}{w_{y_i}}$$

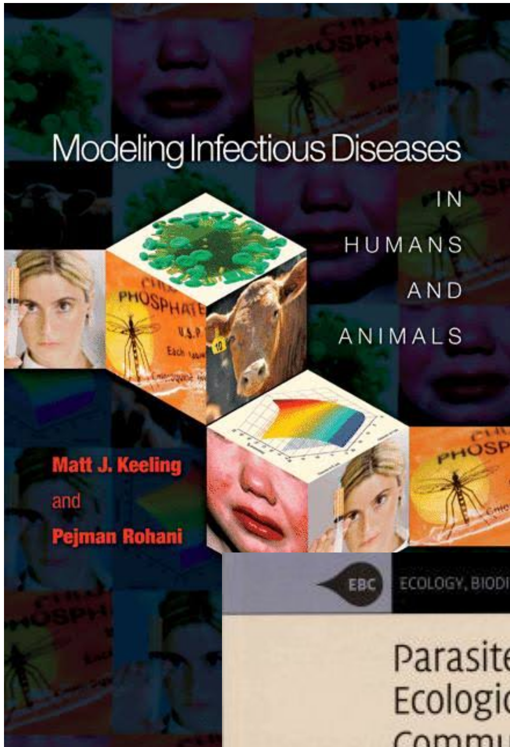
     - Where y_i is the i^{th} variable and Θ_j is the j^{th} parameter and w is a scaling factor.

   - Soetaert, K. and Petzoldt, T., 2010. Inverse modelling, sensitivity and Monte Carlo analysis in R using package FME. *Journal of Statistical Software*, *33*(3), pp.1-28.

R implementation (SIS model):

6. (Sensitivity analysis: FME package)

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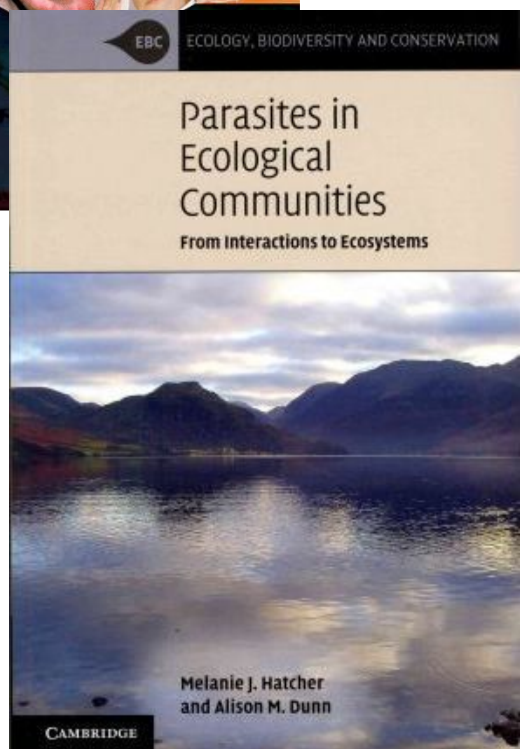
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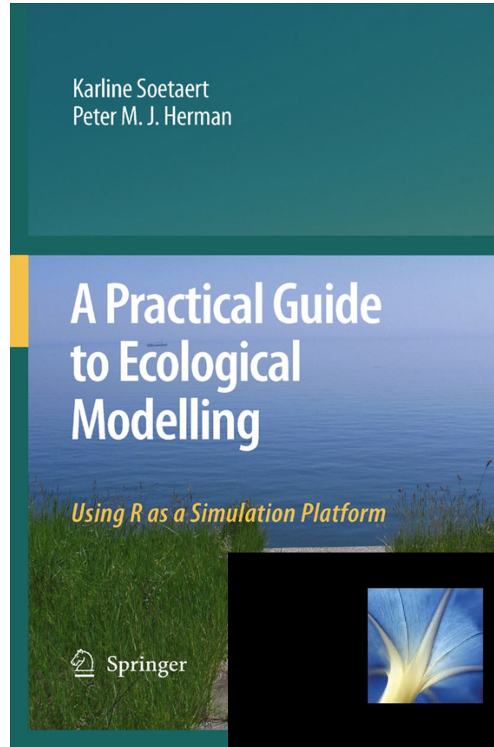
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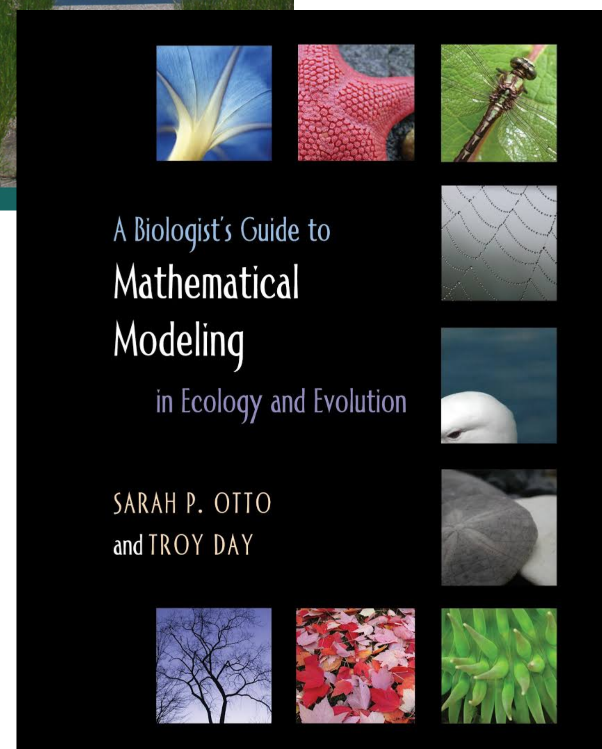
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