

Using R for mathematical modelling (the environment).

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Introduction

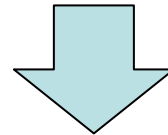
Dynamic differential equations
Steady-state solutions
Linear models
History/Outlook

Why models

Mass balance
In this talk..

Natural systems are very complex

Scientists want to understand this complexity and make quantitative predictions



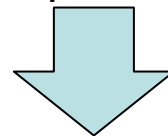
Model = simplifications of the complex natural environment

Test model to data

Quantification of unmeasured processes

Budgetting, interpolation in time/space

.....



Prediction of future behavior

Introduction

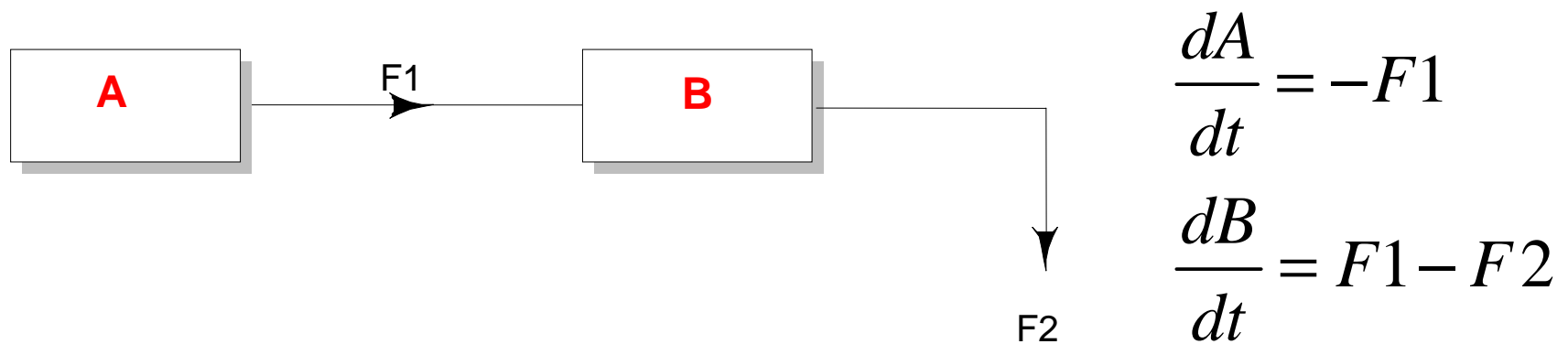
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In this talk..

- Mathematical model based on mass balance conservation



⇒ Differential equations

Introduction

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Mass balance

In this talk..

- ❑ Use R to solve mathematical mass balance models
- ❑ Three different types of models/solutions – three main packages
 - ❑ Integration (deSolve)
 - ❑ Steady-state solution (rootSolve)
 - ❑ Least-squares solutions (limSolve)

What was available + what is new

- ❑ Two examples
 - ❑ HIV model (dynamic / steady-state)
 - ❑ Deep-water coral food web

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HIV dynamics

Solving dynamic differential equations

Differential equations in R

The HIV/AIDS model in R

Example 1: hiv dynamics

Large interest in viral infection

Human disease

Marine animals, algae, bacteria are affected

⇒ Important role in biogeochemical cycles

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$$\frac{dH}{dt} = \lambda - \rho \cdot H - \beta \cdot H \cdot V$$

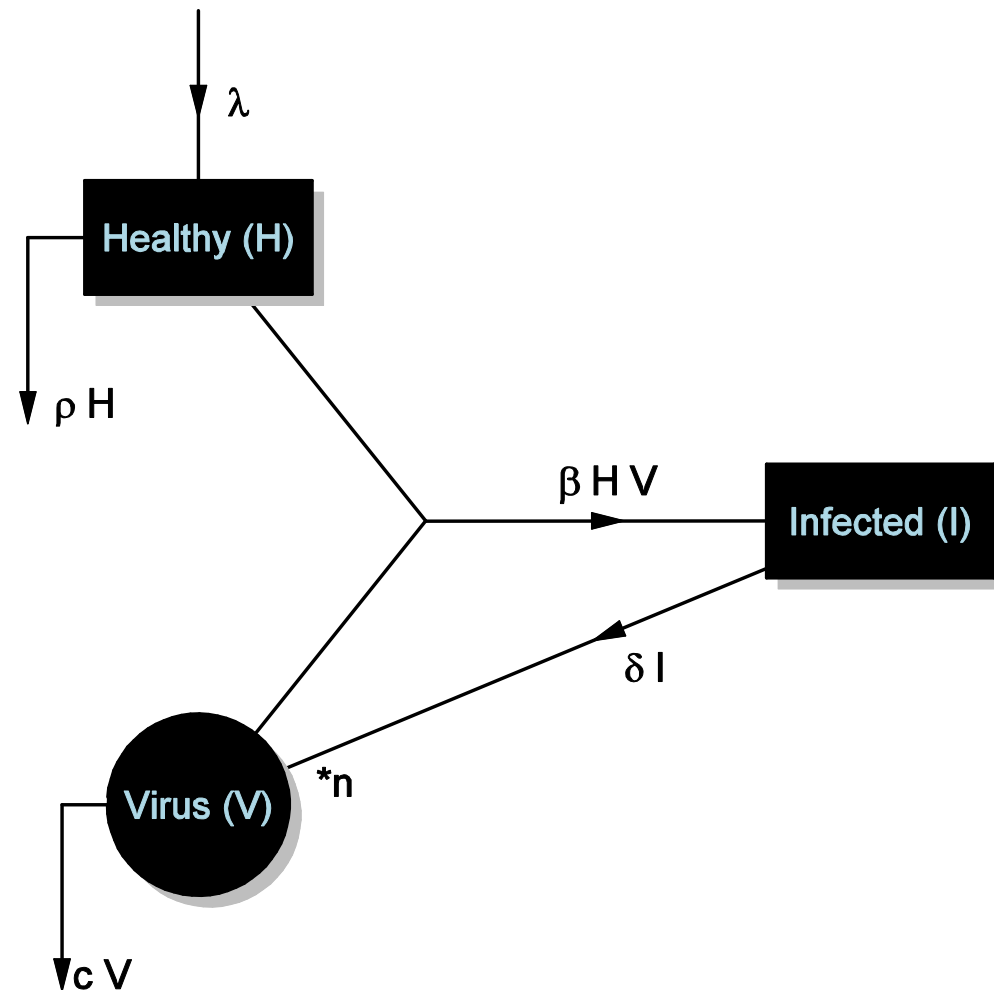
$$\frac{dI}{dt} = \beta \cdot H \cdot V - \delta \cdot I$$

$$\frac{dV}{dt} = n \cdot \delta \cdot I - c \cdot V - \beta \cdot H \cdot V$$

t = time

n, c, ... = parameter

H, I, V = state variable



Model formulation:*Derivative*

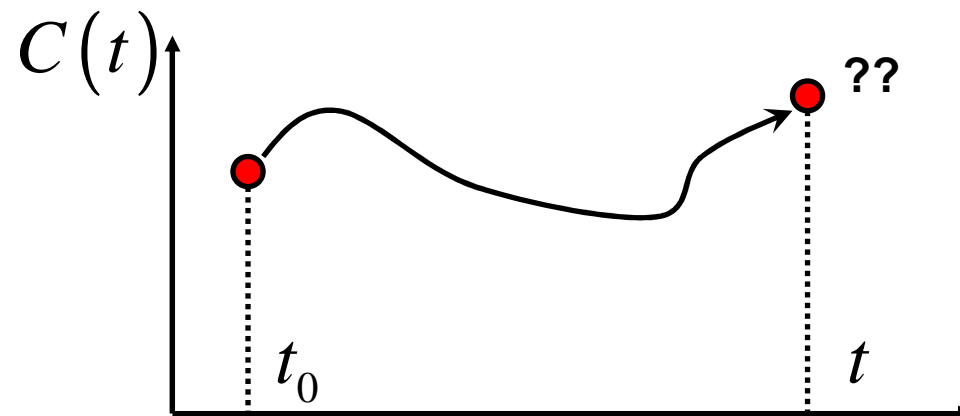
$$\frac{dC}{dt} = f(\Theta, C, t, u)$$

Initial condition

$$C_{t=0} = C_0$$

Model solution:*integration*

$$C(t) \quad \text{For } t > t_0$$



Previously on CRAN: **odesolve** (Setzer 2001)

- Nice interface
- Two integration routines:
 - RungeKutta*, not meant to be used
 - Isoda*, good for small, simple models
- Models implemented in R or compiled code DLL (fast)

BUT:

- Only simplest Ordinary Differential Equations (ODE)
- not flexible,
- not suited for large problems

Now on CRAN:

deSolve (Soetaert, Petzoldt, Setzer)

- Initial value problems

- > 10 integration routines

- Simple and complex ODE

- Differential algebraic equations (DAE)

- Partial differential equations: (PDE)

 - 1-D, 2-D, 3-D problems

- Flexible; Sparse, banded, full Jacobian

- Medium-sized to large problems (up to 80000 state variables)

bvpSolve (Soetaert)

- Boundary value problems

- 2 solution methods

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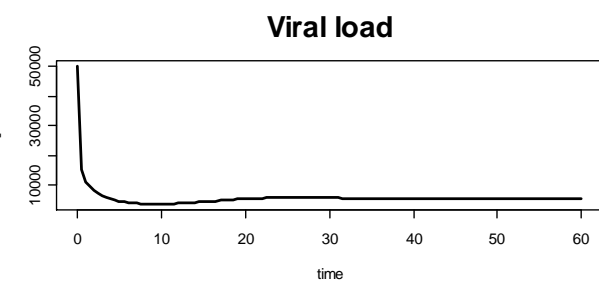
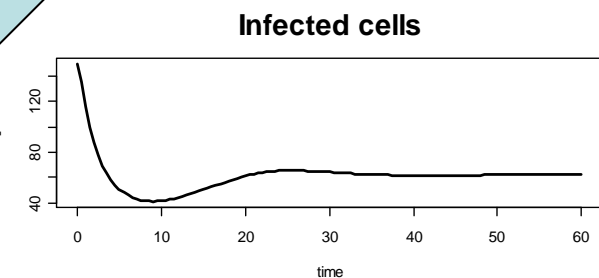
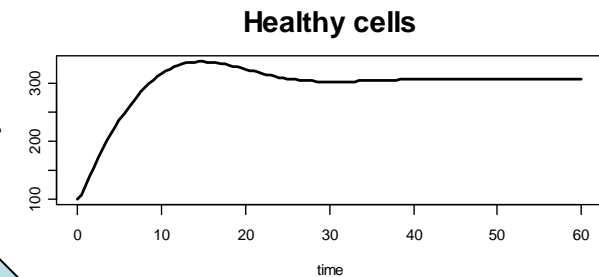
HIV dynamics

Solving dynamic differential equations

Initial value differential equations in R

The HIV/AIDS model in R

```
hiv<- function( time, y, pars) {  
  with (as.list(c(pars,y)), {  
  
    dH <- lam -rho*H - bet*H*V  
    dI  <- bet*H*V -delt*I  
    dV <- n*delt*I - c*V - bet*H*V  
  
    return( list(c(dH, dI, dV)) )  
  })  
}  
  
y <- c(H= 100,  I = 150,  v = 50000)  
  
times <- 0:60  
  
pars<- c(bet=0.00002,rho=0.15,delt=0.55,c=5.5,lam=80,n=900)  
  
out <- ode(y=y, parms=pars, times=times, func=hiv)  
  
plot(out[,,"time"], out[,,"H"])
```



Problem: dynamic models require many data:

$$\frac{dC}{dt} = \sum f_i(C, \Theta, t, u, \dots) - \sum f_j(C, \Theta, t, u, \dots)$$

- Knowledge of initial values
- Time-variable forcing functions (external data, u)

=> Not always available

Solution:

$$0 = \sum f_i(C, \Theta, \dots) - \sum f_j(C, \Theta, \dots)$$

- Assume **steady-state**
=> Systems of **nonlinear equations**
- Calculate **stability** properties

Previously on CRAN:

- uniroot* solves for one root of one nonlinear equation within interval

We need:

- Find all roots within one interval
- Functions to estimate gradient matrices, Jacobians (stability)
- Solve roots of n nonlinear equations (steady-state analysis)

Now on CRAN:

❑ **rootSolve** (Soetaert)

- ❑ *uniroot.all* , *jacobian*: stability analysis
- ❑ *multiroot* : roots of general nonlinear functions (Newton-Raphson)
- ❑ *steady*, *steady.1D*, *steady.2D*, *steady.3D*, *runsteady* :
steady-state solvers
 - ❑ Fully compatible with integration routines from **deSolve**
 - ❑ Suited for large problems (~100 000 equations)
 - ❑ Sparse, banded, full Jacobian

```
STD <- runsteady(y=y, func=hiv, parms=parms)
```

```
eigen( jacobian.full (y=STD$y, func=hiv, parms=parms) )$values
```

Problem:

- mechanistic nonlinear models have many parameters (θ):

- ⇒ Many are unknown
- ⇒ need to be fitted to data
- ⇒ Data not always available

$$\frac{dC}{dt} = \sum f_i(C, \Theta, t, \dots) - \sum f_j(C, \Theta, t, \dots)$$

- nonlinear equations may not be known

Solution:

- Avoid nonlinear equations
- No parameters
- The sources and sinks ($f_{i \rightarrow j}$) are the unknowns
⇒ Linear model

$$\frac{dC_j}{dt} = \underbrace{\sum f_{i \rightarrow j}}_{\text{Sources}} - \underbrace{\sum f_{j \rightarrow k}}_{\text{Sinks}}$$

$$\frac{d\mathbf{C}}{dt} = \mathbf{A} \cdot \mathbf{x}$$



Example 2: Deep-water coral food webs

Corals are commonly found at ~ 800-1000 m water depth.

A large number of animals are living in the coral reefs

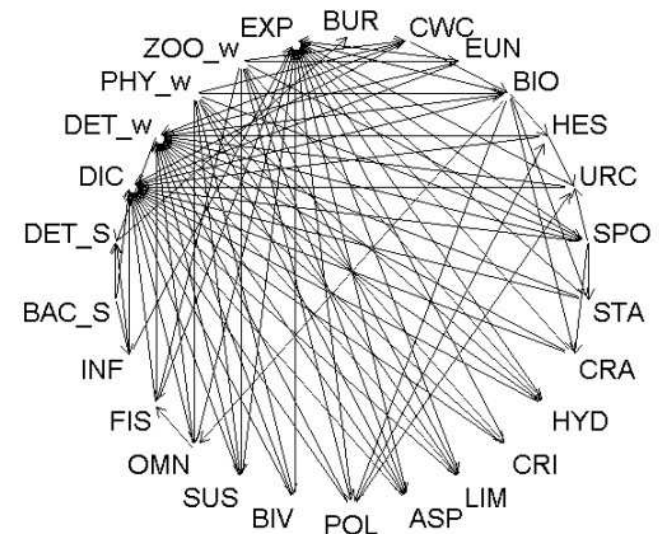


It is very expensive to do research there

⇒ Data are very fragmentary

⇒ Who is eating who? How much do they eat?

⇒ A model is needed to see the global picture



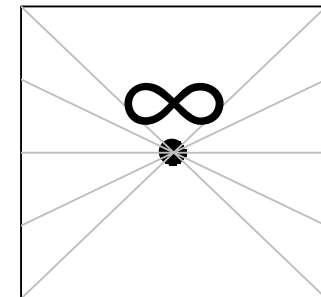
Problem:

number of equations \lll number of unknowns (under determined)

Coral food web: 51 equations \sim 140 unknowns

\Rightarrow There is no unique solution
(\sim fitting a straight line through one point)

underdetermined



Solution 1. Add data from other sources to equalities
 \Rightarrow achieve overdeterminacy (1 solution)

Solution 2. Data from other sources as "inequalities"

equality equation:
(in situ data, mass balance)

$$\mathbf{E}\mathbf{x} = \mathbf{f}$$

inequality equation:
(literature data, physiological constraints,..)

$$\mathbf{G}\mathbf{x} \geq \mathbf{h}$$



$$\underbrace{\begin{pmatrix} a & -b & 0 \\ \vdots & & \end{pmatrix}}_{\text{linear functions}} \cdot \underbrace{\begin{pmatrix} f_1 \\ \vdots \\ f_n \end{pmatrix}}_{\text{food web flows}} \geq \underbrace{\begin{pmatrix} C1 \\ \vdots \end{pmatrix}}_{\text{numerical data}}$$

» the matrix equations are solved for the vector with food web flows

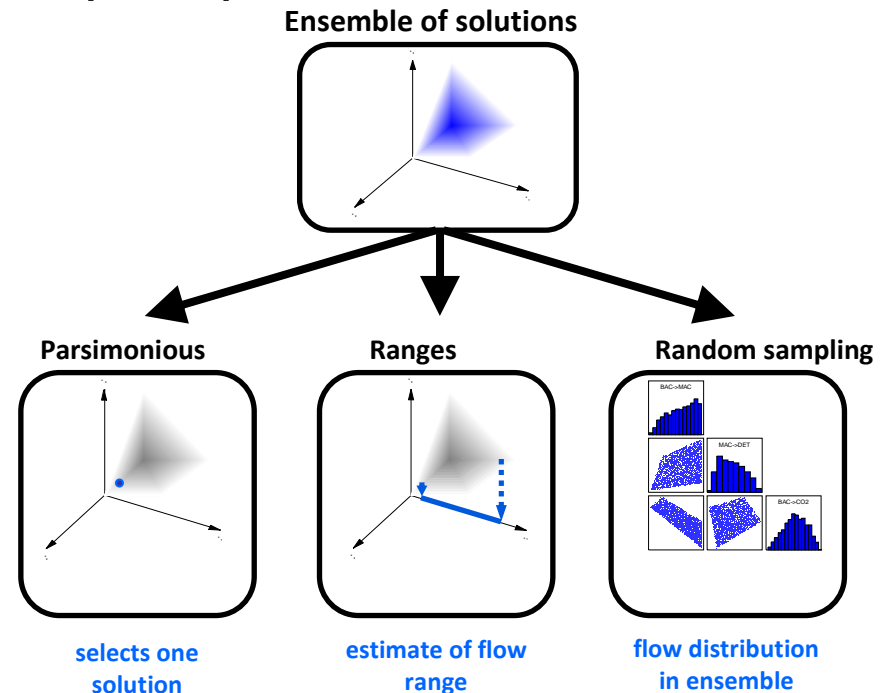
Dealing with the underdeterminacy:

$$\mathbf{E}\mathbf{x} = \mathbf{f}$$

Coral : Solution is a 140-dimensional SPACE!
 ⇒ Within this space, every point equally likely

$$\mathbf{G}\mathbf{x} \geq \mathbf{h}$$

⇒ 3 different ways of solving:



$$\min \|\mathbf{A}\mathbf{x} \approx \mathbf{b}\|$$

$$\min(x)$$

$$\min(\sum x^2)$$

$$\max(x)$$

Previously on CRAN

- ❑ *solve.qp*, (**quadprog**): quadratic programming

$$\min \|\mathbf{Ax} \approx \mathbf{b}\|, \mathbf{Ex} = \mathbf{f}, \mathbf{Gx} \geq \mathbf{h}$$

- ❑ *lp*, (**lpSolve**): linear programming

$$\min(\sum a_i x_i), \mathbf{Ex} = \mathbf{f}, \mathbf{Gx} \geq \mathbf{h}$$

But:

- ❑ *solve.qp* tends to fail for some problems
- ❑ *lp* requires x to be positive (linear programming)
- ❑ *lp* and *solve.qp* are not compatible
- ❑ No monte carlo sampling of underdetermined systems
- ❑ Implementing large matrices: error-prone

Now on CRAN:

limSolve (Soetaert, van Oevelen, van den Meersche)

- least squares,
- linear programming,
- least distance programming
- xranges*, *xsample*: range estimation and random sampling

LIM (Soetaert, van Oevelen)

- Models are specified in text files

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Simplification may be necessary
 Deep-water coral food web
 Linear inverse models
 Linear inverse model solutions
 Solving Linear Inverse Models in R
Implementing LIM in R

Flowto(CO2) = 100

coral -> CO2 = [0.2,0.4] * Flowto(coral)

...

“coral.input”

require(LIM)

coral.lim <- Setup(“coral.input”)

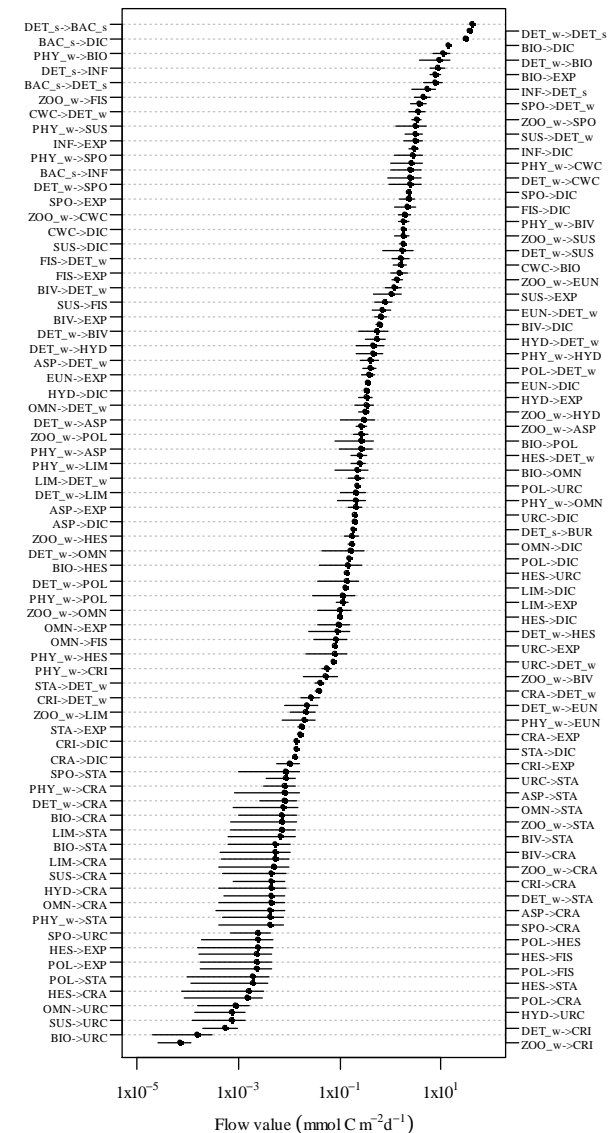
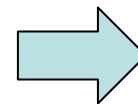
Parsimonious <- Ldei(coral.lim)

Ranges <- Xranges(coral.lim)

Xs <- Xsample(coral.lim, iter=10000)

Plotranges(order(colMeans(Xs)),...)

...



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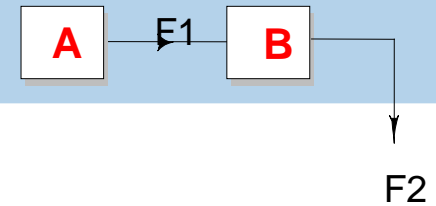
Linear models

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In this talk..



Linear

limSolve

LIM

Steady-state

nonlinear

rootSolve

Dynamic

deSolve

$$\frac{dC_j}{dt} = \overbrace{\sum flow_{i \rightarrow j}}^{input} - \overbrace{\sum flow_{j \rightarrow k}}^{output}$$

$$0 = \sum f_i(C, \Theta, \dots) - \sum f_j(C, \Theta, \dots)$$

$$\frac{dC}{dt} = \sum f_i(C, \Theta, t, u, \dots) - \sum f_j(C, \Theta, t, u, \dots)$$

reality

complexity

data availability

- ❑ Before 2006: Fortran, Excel, Powerpoint, Sigmaplot, own software
- ❑ End 2005. First acquaintance with R
- ❑ End 2006. Decision to use R for our scientific programming / graphics
 - ⇒ Implement functions not yet available

Three years later...

⇒ Basic solution methods available

⇒ 5 Solver packages (deSolve, rootSolve, bvpSolve, limSolve, LIM)

⇒ Specific model applications

Reactive transport models, (ReacTran)

⇒ rivers, estuaries, lakes, sediments

Toxicology, (ToxWebs)

⇒ toxic substances in marine organisms

Ecological network analysis (NetIndices)

.....

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History
Now and Future

THANK YOU

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Soetaert K. and P.M.J. Herman, 2009. A practical guide to ecological modelling – using R as a simulation platform. Springer, 372 pp

Soetaert, K., van Oevelen, D., 2009. Modeling food web interactions in benthic deep-sea ecosystems: a practical guide. Oceanography (22) 1: 130-145.