

## Benchmarking

```
m <- matrix(rnorm(1e6), ncol=100)
f1 <- function(x, t = 0.3) {
  xx <- 0
  for (i in 1:nrow(x)) {
    xx <- c(xx, sum(m[i, ]))
  }
  mean(xx, trim = t)
}
f2 <- function(x, t = 0.3) mean(rowSums(x), trim = t)

library(rbenchmark)
benchmark(f1(m), f2(m),
          columns=c("test", "replications",
                    "elapsed", "relative"),
          order = "relative", replications = 10)
```

## Lotka–Volterra equations

Describe simple models of populations dynamics of species competing for some common resource. When two species are not interacting, their population evolve according to the logistic equations and the rate of reproduction is proportional to both the existing population and the amount of available resources

$$\begin{aligned}\frac{\partial x}{\partial t} &= r_1 x \left(1 - \frac{x}{k_1}\right) \\ \frac{\partial y}{\partial t} &= r_2 y \left(1 - \frac{y}{k_2}\right)\end{aligned}$$

where the constant  $r_i$  defines the growth rate and  $k_i$  is the carrying capacity of the environment.

## Outline

Key unix tools and languages

C and C++ from R

Not only local

Handling large files / databases

Parallel processing

A few more words about about R

Differential equations and phase plane analysis

Conclusions

## Competitive Lotka–Volterra equations

When competing for the same resource, the animals have a negative influence on their competitors growth.

$$\begin{aligned}\frac{\partial x}{\partial t} &= r_1 x \left(1 - \frac{x}{k_1}\right) - axy \\ \frac{\partial y}{\partial t} &= r_2 y \left(1 - \frac{y}{k_2}\right) - bxy\end{aligned}$$

## Rabbits vs sheep (Strogatz, p155)

Here is an example with  $r_1 = 3$ ,  $k_1 = 3$ ,  $a = 2$ ,  $r_2 = 2$ ,  $k_2 = 2$ ,  $b = 1$ , which simplifies to

$$\begin{aligned}\frac{\partial r}{\partial t} &= r(3 - r - 2s) \\ \frac{\partial s}{\partial t} &= s(2 - r - s)\end{aligned}$$

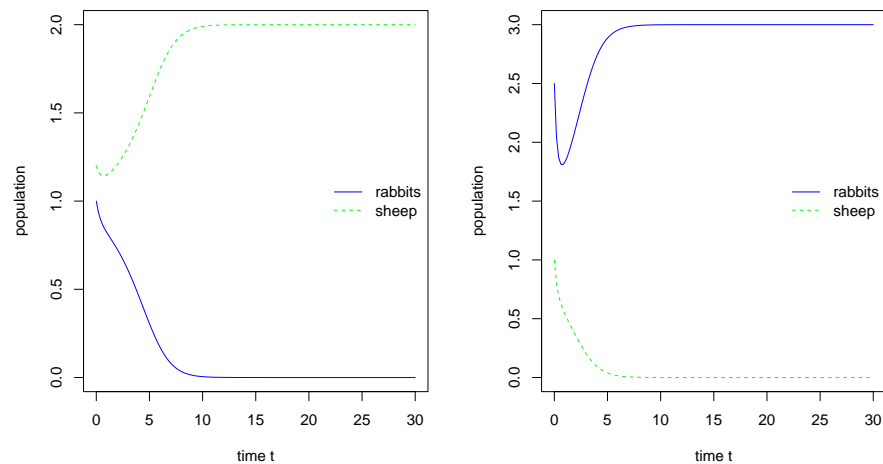
## Computing a trajectory over time

i.e. use numerical integration, with  $r_0 = 1$  and  $s_0 = 1.2$

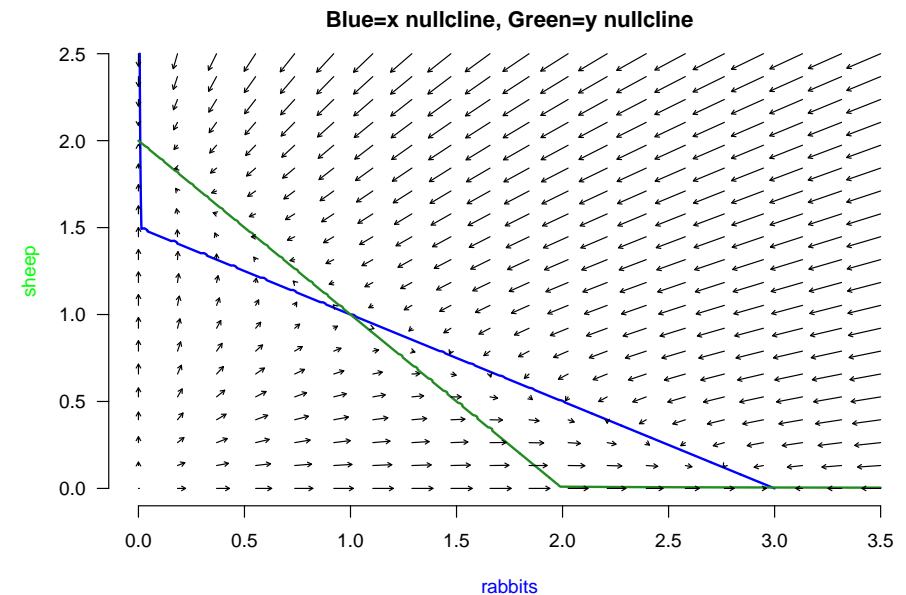
```
library(deSolve)
Sheep <- function(t, y, parms) {
  r=y[1]; s=y[2]
  drdt = r * (3 - r - (2*s))
  dsdt = s * (2 - r - s)
  list(c(drdt, dsdt))
}

x0 <- c(1, 1.2)
times <- seq(0, 30, by=0.2)
parms <- 0
out <- rk4(x0, times, Sheep, parms)
head(out)
```

## Plotting population growth



## Phase plane analysis



## Starting points

- ▶ deSolve package
- ▶ phase planes and nullclines (DMBppplane.r from DMB site, modified from Daniel Kaplan)
- ▶ integrate() – quadrature
- ▶ D() – symbolic differentiation
- ▶ optimize() (1d) and optim() (n-d)
- ▶ Steven Strogatz. Nonlinear dynamics and chaos.
- ▶ NR: William Press et al. Numerical Recipes in C/C++
- ▶ More slides about DE and phase plane – [de.pdf](#)

## Conclusions

- ▶ Looking for packages
  - ▶ CRAN Task Views <http://cran.r-project.org/web/views/>
  - ▶ Bioconductor biocViews  
<http://bioconductor.org/packages/release/BiocViews.html>
- ▶ Reproducibility is crucial
- ▶ Have several tools at hand
  - ▶ editor, programming languages, shell, ...
- ▶ Practice to keep learning
- ▶ Have fun! ☺

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