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Using Rcpp* packages for easy and fast Gibbs sampling MCMC from within R

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Outline

1. Short presentation of Rcpp* packages
   - Rcpp : extending R with C++
   - RcppGSL for fast random draws
   - RcppArmadillo for high-performance linear algebra
2. Rcpp for Gibbs sampling
   - Gibbs sampling and Bayesian statistics
   - Simple Gibb sampler
   - Linear regression example
3. The `jSDM` R package
   - Joint Species Distribution Models
   - Model specification
   - Comparison with `boral`/`JAGS`

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Rcpp R package

- **Rcpp** is an R package to extend R with C++ code
- Main advantage : C++ is fast, it accelerates R (see next sections)
- Written by **Dirk EDDELBUETTEL** and **Romain FRANCOIS**
- http://www.rcpp.org/

Simple Rcpp example

C++ code (in file `Code/addition.cpp`)

```
#include <Rcpp.h>
using namespace Rcpp;

// [[Rcpp::export]]
int addition(int a, int b) {
  return a + b;
}
```

R code

```
Rcpp::sourceCpp("Code/addition.cpp")
addition(2, 2)
```

```
## [1] 4
```

Rcpp advantages

Thanks to `Rcpp::sourceCpp()`

- Compile the C++ code
- Export the function to the R session
- Direct interchange of R objects (including S3, S4) between R and C++
- ... (many more, see `vignette("Rcpp-package")`)

In an R package

- `Rcpp.package.skeleton()` to generate a new Rcpp package (modifying `DESCRIPTION` and `NAMESPACE`)
- `Rcpp::compileAttributes()` scans the C++ files for `Rcpp::export` attributes and generates the code required to make the functions available in R.

GSL and RcppGSL

GNU Scientific Library

- Numerical library for C and C++ programmers
- Reliable random number generator algorithms
- Thoroughly tested and fast random number distributions
- Linear algebra (matrices and vectors)
- https://www.gnu.org/software/gsl/

RcppGSL

- Interface between R and GSL
- Using Rcpp to interface R and C
- http://dirk.eddelbuettel.com/code/rcpp.gsl.html

GSL random number distributions

- GSL v2.6 includes **38 random number distributions** (see GNU GSL)
- It's easy to implement additional random number distributions from the GSL base distributions (e.g. truncated normal distribution)
- For comparison, R API includes "only" 24 random number distributions (see Writing R Extensions)
- Random draws are faster with GSL than with R (eg. `gsl_ran_gamma()` vs. `R::rgamma()`)

RcppGSL example

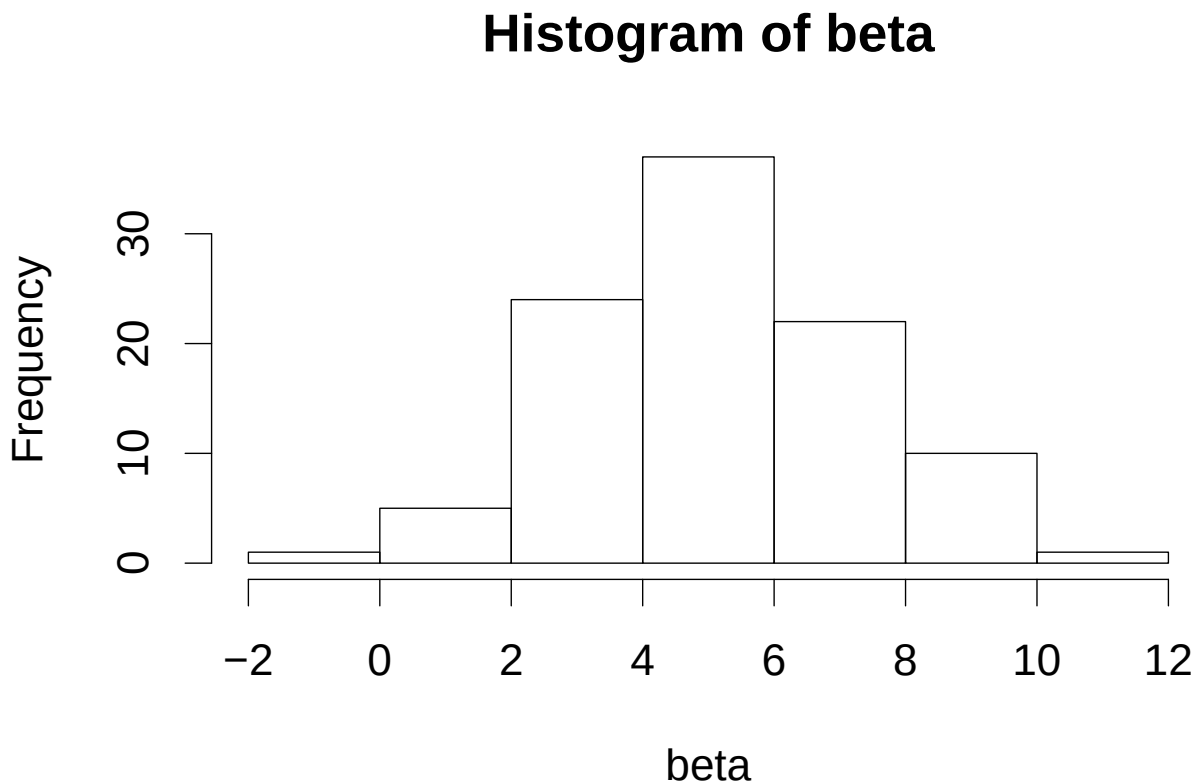
C++ code

```
#include <Rcpp.h>
#include <gsl/gsl_rng.h>
#include <gsl/gsl_randist.h>

using namespace Rcpp;

// [[Rcpp::depends(RcppGSL)]]

// [[Rcpp::export]]
Rcpp::NumericVector my_rnorm(int nsamp, double mu,
                             double sigma) {
    gsl_rng *s = gsl_rng_alloc(gsl_rng_mt19937); // Random seed
    Rcpp::NumericVector beta(nsamp);
    for (int i = 0; i < nsamp; i++) {
        beta[i] = mu + gsl_ran_gaussian(s, sigma); // Random draw
    }
    return beta;
}
```

RcppGSL example

R code

```
library(Rcpp)
library(RcppGSL)
beta <- my_rnorm(100, 5, 2)
par(cex=2)
hist(beta)
```



Armadillo and RcppArmadillo

Armadillo

- C++ library for linear algebra and scientific computing
- Provides high-level syntax and functionality : speed and ease of use
- Classes for vectors, matrices and cubes
- Matrix operations, matrix decomposition, linear model solver, etc.
- http://arma.sourceforge.net/

RcppArmadillo

- Interface between R and Armadillo
- Using Rcpp to interface R and C++
- http://dirk.eddelbuettel.com/code/rcpp.armadillo.html

RcppArmadillo example

C++ code

```
#include <RcppArmadillo.h>

// [[Rcpp::depends(RcppArmadillo)]]

// [[Rcpp::export]]
Rcpp::List fastLm(const arma::mat& X, const arma::colvec& y) {
    int n = X.n_rows, k = X.n_cols;

    arma::colvec coef = arma::solve(X, y);    // fit model y ~ X
    arma::colvec res  = y - X*coef;           // residuals

    // std.errors of coefficients
    double s2 = std::inner_product(res.begin(),
                                   res.end(),
                                   res.begin(), 0.0)/(n - k);

    arma::colvec std_err = arma::sqrt(s2 *
      arma::diagvec(arma::pinv(arma::trans(X)*X)));

    return Rcpp::List::create(Rcpp::Named("coefficients") = coef,
                              Rcpp::Named("stderr")       = std_err,
                              Rcpp::Named("df.residual")  = n - k);
}
```

RcppArmadillo example

R code

```
library(Rcpp)
library(RcppArmadillo)
# Trees data-set
y <- log(trees$Volume)
X <- cbind(1, log(trees$Girth))
# fastLm
mod <- fastLm(X, y)
mod$coef
```

```
##           [,1]
## [1,] -2.353325
## [2,]  2.199970
```

Licenses

- Licenses : GNU General Public License, Apache License 2.0 for Armadillo
- Free software licenses : we can use, modify and redistribute these softwares

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Gibbs sampling

Gibbs sampling is commonly used for **statistical inference**.

$\Theta = (\theta_1, \ldots, \theta_n)$ from a joint distribution $p(\theta_1, \ldots, \theta_n)$.

1. Begin with some initials values $\Theta^{(i)}$.
2. Next sample $\Theta^{(i+1)} = (\theta_1^{(i+1)}, \ldots, \theta_n^{(i+1)})$?
   We sample iteratively the parameters.
   Update $\theta_j^{(i+1)}$ according to $p(\theta_j^{(i+1)} | \theta_0^{(i+1)}, \ldots, \theta_{j-1}^{(i+1)}, \theta_{j+1}^{(i)}, \ldots, \theta_n^{(i)})$
3. We repeat the above steps k times (Markov chain Monte Carlo).

The samples approximate the joint distribution of all variables.

Can incorporate various algorithms (Metropolis-Hastings, slice sampling, adaptive rejection sampling, Hamiltonian Monte-Carlo) to implement one or more of the sampling steps.

Gibbs sampling

- Involves several loops : MCMC step, parameters.
- Random draws.
- Matrix computations in case of conjugated priors in Bayesian statistics.

Rcpp (C++), RcppGSL (random draws) and RcppArmadillo (matrix computations) are useful for efficient Gibbs sampling.

R code

```r
gibbs_r <- function(N, thin) {
    mat <- matrix(nrow = N, ncol = 2)
    x <- y <- 0

    for (i in 1:N) {
        for (j in 1:thin) {
            x <- rgamma(1, 3, y * y + 4) # Gamma(shape, rate) with R
            y <- rnorm(1, 1 / (x + 1), 1 / sqrt(2 * (x + 1)))
        }
        mat[i, ] <- c(x, y)
    }
    mat
}
```

Rcpp

C++ code with Rccp

```cpp
#include <Rcpp.h>
using namespace Rcpp;

// [[Rcpp::export]]
NumericMatrix gibbs_rcpp(int N, int thin) {
    NumericMatrix mat(N, 2);
    double x = 0, y = 0;

    for(int i = 0; i < N; i++) {
        for(int j = 0; j < thin; j++) {
            x = R::rgamma(3, 1 / (y * y + 4)); // R::rgamma(shape, scale)
            y = R::rnorm((1 / (x + 1)), 1 / sqrt(2 * (x + 1)));
        }
        mat(i, 0) = x;
        mat(i, 1) = y;
    }

    return(mat);
}
```

Rcpp + RcppArmadillo + RcppGSL

C++ code with RccpArmadillo and RcppGSL

```
#include <RcppArmadillo.h>
#include <gsl/gsl_rng.h>
#include <gsl/gsl_randist.h>
// [[Rcpp::depends(RcppArmadillo)]]
// [[Rcpp::depends(RcppGSL)]]

// [[Rcpp::export]]
arma::mat gibbs_rcpp_arma_gsl(int N, int thin) {
    gsl_rng *s = gsl_rng_alloc(gsl_rng_mt19937); // Create RNG seed
    arma::mat mat; mat.zeros(N, 2);
    double x = 0, y = 0;
    for(int i = 0; i < N; i++) {
        for(int j = 0; j < thin; j++) {
            x = gsl_ran_gamma(s, 3,
                      1 / (y * y + 4)); // Gamma(shape, scale)
            y = (1 / (x + 1)) +
                gsl_ran_gaussian_ziggurat(s, 1 / sqrt(2 * (x + 1)));
        }
        mat(i, 0) = x;
        mat(i, 1) = y;
    }
    gsl_rng_free(s); // Free memory
    return(mat);
}
```

Benchmark

```
# Libraries
library(rbenchmark)
# Benchmark
Benchmark <- benchmark(
    "R" = {gibbs_r(100, 10)},
    "rcpp" = {gibbs_rcpp(100, 10)},
    "rcpp_arma_gsl" = {gibbs_rcpp_arma_gsl(100, 10)},
    replications=30,
    columns = c("test", "elapsed", "relative")
)
Benchmark
```

```
##            test elapsed relative
## 1             R   0.186       62
## 2          rcpp   0.009        3
## 3 rcpp_arma_gsl   0.003        1
```

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JSDM utility

- Fit species distribution
- Account for species interaction

Data to fit JSDM

- Species presence/absence on sites
- Environmental variables (climate, lancover) at each sites

```
df <- read.csv("tabs/jSDM_tab.csv")
df
```

```
##         Sites Sp_1 Sp_2 Sp_nsp    X1 X2 X_nvar
## 1      Site_1    0    0      1 -0.21 -1  -1.24
## 2      Site_2    0    1      1  0.25  0  -0.53
## 3 Site_nsite    1    0      1  0.82  1   0.34
```

Statistical model

Complexity of the model

- Multi-dimensionality (parameters for sites and species)
- Non Gaussian
- Latent-variables
- Mixed model with site random effects

jSDM R package

. . . Thank you for attention . . .

https://ecology.ghislainv.fr/jSDM