

# Computational Statistics II

Unit A.2: Rcpp & RcppArmadillo

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## Main concepts

- Introduction to Rcpp & RcppArmadillo
- Some examples and comparisons with **R**
- The Gaussian model: Gibbs sampling using **R** and C++
- Associated **R** code: [https://tommasorigon.github.io/CompStat/exe/un\\_A2.html](https://tommasorigon.github.io/CompStat/exe/un_A2.html)

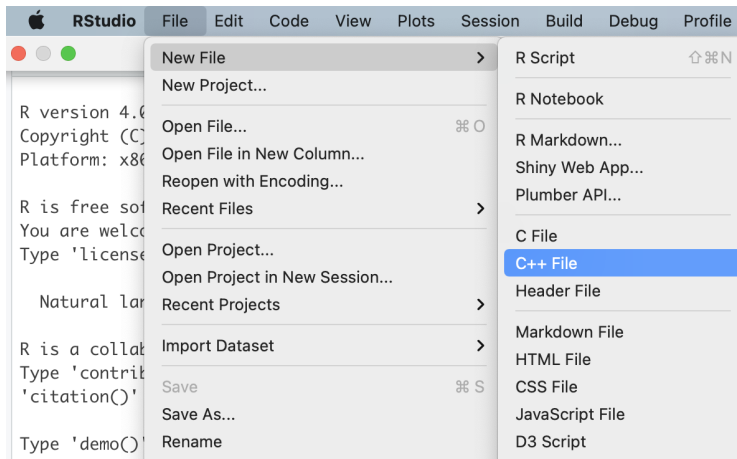
# Introduction

- The Rcpp package **simplifies the interface** between **R** and C++.
- The package RcppArmadillo extends Rcpp and simplifies the interface between **R** and armadillo, which is a “high quality **linear algebra** library for the C++ language, aiming towards a good balance between speed and ease of use”.
- The main advantage is that C++ code is usually **much faster than R** (and python), especially in non-vectorized settings.
- It is very hard to be faster than Rcpp, unless you code is indeed written in C++.

## Main references

- Eddebuettel, D. and Balamuta, J. J. (2018). Extending R with C++: A Brief Introduction to Rcpp. *The American Statistician*, 72(1), 28–36.
- Eddebuettel, D., and Sanderson, C. (2014). RcppArmadillo: Accelerating R with high-performance C++ linear algebra. *Computational Statistics and Data Analysis*, 71, 1054–1063.

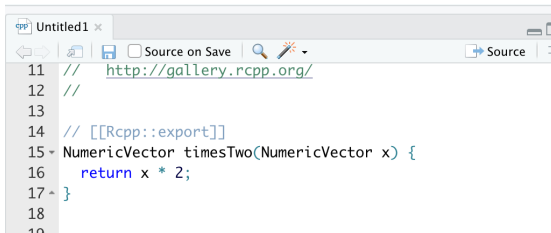
# Basic usage



- Nowadays, both packages (Rcpp and RcppArmadillo) are very well integrated within RStudio.

# Basic usage

- Provided you installed everything correctly (refer to the the Markdown A.2 available in the course website), the typical **coding pipeline** is straightforward.
- First, create an empty file, say `foo.cpp`, containing the C++ code.
- Save the C++ file and **compile it** using the `sourceCpp` function. Alternatively, you can press the “source” button if you are using RStudio.
- Use the functions contained in the C++ file within **R** as usual. The functions will appear in the environment.



```
11 // http://gallery.rcpp.org/
12 //
13
14 // [[Rcpp::export]]
15 NumericVector timesTwo(NumericVector x) {
16     return x * 2;
17 }
18
19
```

# The sum function in RcppArmadillo

---

```
#include <RcppArmadillo.h>
// [[Rcpp::depends(RcppArmadillo)]]
using namespace Rcpp;
using namespace arma;

// [[Rcpp::export]]
double arma_sum(vec x){
  double sum = 0;
  int n = x.n_elem; // Length of the vector x
  for(int i=0; i < n; i++){
    sum += x[i]; // Shorthand for: sum = sum + x[i];
  }
  return(sum);
}
```

---

```
sourceCpp("../cpp/sum.cpp")
x <- c(10, 20, 5, 30, 21, 78, pi, exp(7))
arma_sum(x) # sum of the vector x
# [1] 1263.775
sum(x) # sum of the vector x - usual command
# [1] 1263.775
```

---

# Example 1: Euclidean distance

- The **R** code is typically **slow** in presence of (nested) for loops.
- We are given a matrix **X** of dimension  $n \times p$ , whose rows are  $x_i = (x_{i1}, \dots, x_{ip})^T$ .
- We are interested in computing the matrix of euclidean distances **D** of dimension  $n \times n$  whose entries are equal to

$$d_{ii'} = \sqrt{\sum_{j=1}^p (x_{ij} - x_{i'j})^2}, \quad i, i' \in \{1, \dots, n\}.$$

---

```
R_dist <- function(X) {  
  n <- nrow(X)  
  D <- matrix(0, n, n) # Pre-allocate the output  
  for (i in 1:n) {  
    for (k in 1:i) {  
      D[i, k] <- D[k, i] <- sqrt(sum((X[i, ] - X[k, ])^2))  
    }  
  }  
  D  
}
```

---

# Example 1: Euclidean distance

- The corresponding RcppArmadillo implementation is quite simple as well.

---

```
#include <RcppArmadillo.h>
// [[Rcpp::depends(RcppArmadillo)]]
using namespace Rcpp;
using namespace arma;

// [[Rcpp::export]]
mat arma_dist(const mat& X){
  int n = X.n_rows;
  mat D(n, n, fill::zeros); // Allocate a matrix of dimension n x n
  for (int i = 0; i < n; i++) {
    for(int k = 0; k < i; k++){
      D(i, k) = sqrt(sum(pow(X.row(i) - X.row(k), 2)));
      D(k, i) = D(i, k);
    }
  }
  return D;
}
```

---



# Example 1: benchmark

```
X <- as.matrix(USArrests) # Example dataset
```

```
benchmark(  
  arma_dist = arma_dist(X), # Armadillo implementation  
  R_dist = R_dist(X), # Naive R implementation  
  dist = as.matrix(dist(X)), # Built-in R function (C++)  
  columns = c("test", "replications", "elapsed", "relative"),  
  replications = 1000  
)
```

```
#      test replications elapsed relative  
# 1 arma_dist      1000   0.015    1.000  
# 3 dist          1000   0.080    5.333  
# 2 R_dist         1000  2.445  163.000
```

- Let us use the USArrests dataset for a quick **benchmark**.
- The RcppArmadillo implementation is about **150 times faster** than the naive **R** version, due to the presence of nested for loops.
- Actually, the RcppArmadillo version is slightly faster the **dist** built-in **R** function!

## Example 2: linear models

- **R** code is not necessarily slower than Armadillo when linear algebra is involved.
- Suppose we are interested in obtaining the least squares estimate  $\hat{\beta}$  from the design matrix  $\mathbf{X}$  and the response  $\mathbf{y}$ , namely  $\hat{\beta} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y}$ .
- In first place, let us compare two slightly different **R** implementations.
- As a rule of thumb, do not invert matrices if the actual goal is solving linear systems.

---

*# Using matrix multiplication commands*

```
lm_coef1 <- function(X, y) {  
  solve(t(X) %*% X) %*% t(X) %*% y  
}
```

*# Better (no matrix inversion!) and faster implementation*

```
lm_coef2 <- function(X, y) {  
  solve(crossprod(X), crossprod(X, y))  
}
```

---

## Example 2: linear models

- The `solve` function here can be used directly on the objects  $\mathbf{X}$  and  $\mathbf{y}$ .

---

```
#include <RcppArmadillo.h>
// [[Rcpp::depends(RcppArmadillo)]]
using namespace Rcpp;
using namespace arma;

// [[Rcpp::export]]
vec lm_coef3(const mat& X, const vec& y) {
  vec coef = solve(X, y);
  return(coef);
}
```

---

```
set.seed(123)
X <- cbind(1, rnorm(10^4))
y <- rowSums(X) + rnorm(10^4)

cbind(lm_coef1(X, y), lm_coef2(X, y), lm_coef3(X, y)) # Same results
```

---

```
#           [,1]      [,2]      [,3]
# [1,] 0.9909079 0.9909079 0.9909079
# [2,] 1.0060394 1.0060394 1.0060394
```

---

## Example 2: benchmark

```
benchmark(R_matrix_inv = lm_coef1(X, y),
  R_no_matrix_inv = lm_coef2(X, y),
  Rcpp = lm_coef3(X, y),
  lm = coef(lm(y ~ X, data = cars)),
  columns = c("test", "replications", "elapsed", "relative"),
  replications = 1000
)
```

#		<i>test</i>	<i>replications</i>	<i>elapsed</i>	<i>relative</i>
# 4	<i>lm</i>		1000	2.487	25.378
# 1	<i>R_matrix_inv</i>		1000	0.365	3.724
# 2	<i>R_no_matrix_inv</i>		1000	0.098	1.000
# 3	<i>Rcpp</i>		1000	0.141	1.439

- In this case, the Rcpp implementation is approximately as fast as the R version.
- Indeed, the “difficult” part (i.e. solution of the linear system) in all cases is handled by well-optimized C routines.
- The usual `lm` R functions is slower, but it is calculating many additional quantities.

# Gibbs sampling (recap)

- Recall that  $\pi(\boldsymbol{\theta} \mid \mathbf{X})$  denotes the posterior distribution of  $\boldsymbol{\theta} \in \Theta \subseteq \mathbb{R}^p$  given the data.
- Let us partition the parameter vector  $\boldsymbol{\theta} = (\theta_1, \dots, \theta_B)$  into  $B$  blocks of parameters. Sometimes we will have as many blocks as parameters, so that  $\boldsymbol{\theta} = (\theta_1, \dots, \theta_p)$ .

- Let  $\pi(\boldsymbol{\theta}_b \mid -)$  be the so-called **full-conditional** of  $\boldsymbol{\theta}_b$ , that is

$$\pi(\boldsymbol{\theta}_b \mid -) = \pi(\boldsymbol{\theta}_b \mid \mathbf{X}, \boldsymbol{\theta}_1, \dots, \boldsymbol{\theta}_{b-1}, \boldsymbol{\theta}_{b+1}, \dots, \boldsymbol{\theta}_B), \quad b = 1, \dots, B,$$

namely the conditional distribution of  $\boldsymbol{\theta}_b$  given the data and the other parameters.

- Repeatedly sampling  $\boldsymbol{\theta}_b$ , for  $b = 1, \dots, B$ , from the corresponding full conditionals leads to a MCMC algorithm targeting the posterior distribution  $\pi(\boldsymbol{\theta} \mid \mathbf{X})$ .
- In the next units (B.2, C.1, C.2, C.3), we will see extensions of this basic strategy, but at the moment we will focus on its **implementation**.

## Example 3: conditionally-conjugate Gaussian model

- Let us assume the observations  $\mathbf{X} = (X_1, \dots, X_n)$  are draws from

$$(X_i \mid \mu, \sigma^2) \stackrel{\text{iid}}{\sim} \mathcal{N}(\mu, \sigma^2), \quad i = 1, \dots, n.$$

with independent priors  $\mu \sim \mathcal{N}(\mu_\mu, \sigma_\mu^2)$  and  $\sigma^{-2} \sim \text{Ga}(a_\sigma, b_\sigma)$ .

- The full conditional distribution for the **mean**  $\mu$  is:

$$(\mu \mid -) \sim \mathcal{N}(\mu_n, \sigma_n^2), \quad \mu_n = \sigma_n^2 \left( \frac{\mu_\mu}{\sigma_\mu^2} + \frac{1}{\sigma^2} \sum_{i=1}^n x_i \right), \quad \sigma_n^2 = \left( \frac{n}{\sigma^2} + \frac{1}{\sigma_\mu^2} \right)^{-1}.$$

- The full conditional distribution for the **precision**  $\sigma^{-2}$  is:

$$(\sigma^{-2} \mid -) \sim \text{Ga}(a_n, b_n), \quad a_n = a_\sigma + n/2, \quad b_n = b_\sigma + \frac{1}{2} \sum_{i=1}^n (x_i - \mu)^2.$$

## Example 3: implementation in R

```
gibbs_R <- function(x, mu_mu, sigma2_mu, a_sigma, b_sigma, R, burn_in) {  
  # Initialization  
  n <- length(x); xbar <- mean(x)  
  out <- matrix(0, R, 2)  
  # Initial values for mu and sigma  
  sigma2 <- var(x); mu <- xbar  
  for (r in 1:(burn_in + R)) {  
    # Sample mu  
    sigma2_n <- 1 / (1 / sigma2_mu + n / sigma2)  
    mu_n <- sigma2_n * (mu_mu / sigma2_mu + n / sigma2 * xbar)  
    mu <- rnorm(1, mu_n, sqrt(sigma2_n))  
    # Sample sigma2  
    a_n <- a_sigma + 0.5 * n  
    b_n <- b_sigma + 0.5 * sum((x - mu)^2)  
    sigma2 <- 1 / rgamma(1, a_n, b_n)  
    # Store the values after the burn-in period  
    if (r > burn_in) {  
      out[r - burn_in, ] <- c(mu, sigma2)  
    }  
  }  
  out  
}
```

## Example 3: implementation in RcppArmadillo

```
mat gibbs_arma(vec x, double mu_mu, double sigma2_mu,
double a_sigma, double b_sigma, int R, int burn_in){
  // Initialization
  double n = x.n_elem; double xbar = mean(x);
  mat out(R,2);
  // Initial values for mu and sigma
  double sigma2 = var(x); double mu = mean(x);
  for (int r = 0; r < R + burn_in; r++) {
    // Sample mu
    double sigma2_n = 1.0 / (1.0 / sigma2_mu + n / sigma2);
    double mu_n = sigma2_n * (mu_mu / sigma2_mu + n / sigma2 * xbar);
    mu = rnorm(1, mu_n, sqrt(sigma2_n))[0];
    // Sample sigma2
    double a_n = a_sigma + 0.5 * n;
    double b_n = b_sigma + 0.5 * sum(pow(x - mu, 2));
    sigma2 = 1.0 / rgamma(1, a_n, 1.0 / b_n)[0]; // NOTE: rgamma in Rcpp use scale not rate
    if (r > burn_in) {
      out(r - burn_in, 0) = mu;
      out(r - burn_in, 1) = sigma2;
    }
  }
  return out;
}
```



## Example 3: benchmark

- In this dataset, the RcppArmadillo implementation is about **25 times faster** than R.

---

```
data(sleep)
x <- sleep$extra[sleep$group == 1]

library(tictoc) # Library for "timing" the functions
set.seed(123)

# Hyperparameter settings
mu_mu <- 0; sigma2_mu <- 50
a_sigma <- b_sigma <- 2
R <- 50000; burn_in <- 5000

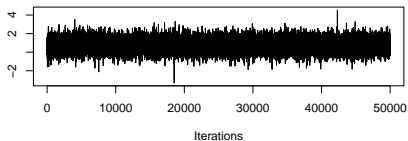
tic()
fitR <- gibbs_R(x, mu_mu, sigma2_mu, a_sigma, b_sigma, R, burn_in)
toc()
# 0.415 sec elapsed

tic()
fitRcpp <- gibbs_arma(x, mu_mu, sigma2_mu, a_sigma, b_sigma, R, burn_in)
toc()
# 0.015 sec elapsed
```

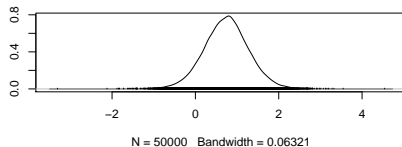
---

# Traceplots and posterior distribution

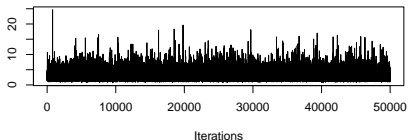
Trace of var1



Density of var1



Trace of var2



Density of var2

