# Rcpp Masterclass / Workshop Part IV: Applications

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RInside RcppArmadillo RcppGSL Simulations End Basics MPI Qt Building

- RInside
  - Basics
  - MPI
  - Qt
  - Building with RInside
- RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

### The first example

examples/standard/rinside\_sample0.cpp

#### We have seen this first example in part I:

Assign a variable, evaluate an expression—easy!

### A second example: part one

examples/standard/rinside\_sample1.cpp

### A second example: part two

examples/standard/rinside\_sample1.cpp

```
int main(int argc, char *argv[]) {
  RInside R(argc, argv); // create an embedded R instance
  const int mdim = 4; // let the matrices be 4 by 4; create, fill
  R["M"] = createMatrix (mdim); // assign data Matrix to R's 'M' var
  std::string str =
    "cat('Running ls()\n'); print(ls()); "
    "cat('Showing M\n'); print(M); "
    "cat('Showing colSums()\n'); Z <- colSums(M); "
                                    // returns Z
    "print(Z); Z";
  Rcpp::NumericVector v = R.parseEval(str); // eval. assign
  // now show vector on stdout
  exit(0);
```

Other example files provide similar R snippets and interchange.

## A third example: Calling R plot functions

examples/standard/rinside\_sample11.cpp

```
#include <RInside.h>
                                       // embedded R via RInside
int main(int argc, char *argv[]) {
                                     // create an embedded R instance
  RInside R(argc, argv);
  // evaluate an R expression with curve()
  std::string cmd = "tmpf <- tempfile('curve'); "</pre>
    "png(tmpf); curve(x^2, -10, 10, 200); "
    "dev.off(); tmpf";
  // by running parseEval, we get filename back
  std::string tmpfile = R.parseEval(cmd);
  std::cout << "Could use plot in " << tmpfile << std::endl;</pre>
  unlink(tmpfile.c_str()); // cleaning up
  // alternatively, by forcing a display we can plot to screen
  cmd = "x11(); curve(x^2, -10, 10, 200); Sys.sleep(30);";
  R.parseEvalQ(cmd);
  exit(0):
```

## A fourth example: Using Rcpp modules examples/standard/rinside\_module\_sample0.cpp

```
#include <RInside.h>
                                         // for the embedded R via RInside
// a c++ function we wish to expose to R
const char* hello( std::string who ) {
    std::string result( "hello " );
    result += who :
    return result.c str() ;
RCPP MODULE (bling) {
    using namespace Rcpp ;
    function ( "hello", &hello );
int main(int argc, char *argv[]) {
    // create an embedded R instance -- and load Rcpp so that modules work
    RInside R(argc, argv, true);
    // load the bling module
    R["bling"] = LOAD RCPP MODULE(bling) ;
    // call it and display the result
    std::string result = R.parseEval("bling$hello('world')");
    std::cout << "bling$hello('world') = '" << result << "'"
               << std::endl :
    exit(0);
```

RInside RcppArmadillo RcppGSL Simulations End Basics MPI Qt Building

## Other RInside standard examples

#### A quick overview:

- ex2 loads an Rmetrics library and access data
- ex3 run regressions in R, uses coefs and names in C++
- ex4 runs a small portfolio optimisation under risk budgets
- ex5 creates an environment and tests for it
- ex6 illustrations direct data access in R
- ex7 shows as<>() conversions from parseEval()
- ex8 is another simple bi-directional data access example
- ex9 makes a C++ function accessible to the embedded R
- ex10 creates and alters lists between R and C++

RInside RcppArmadillo RcppGSL Simulations End Basics MPI Qt Buildin

- RInside
  - Basics
  - MPI
  - Qt
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

### Parallel Computing with RInside

R is famously single-threaded.

High-performance Computing with R frequently resorts to fine-grained (multicore, doSMP) or coarse-grained (Rmpi, **pvm**, ...) parallelism. R spawns and controls other jobs.

But somebody's bug may be somebody's else's feature: Jianping Hua suggested to embed R via RInside in MPI applications.

Now we can use the standard and well understood MPI paradigm to launch multiple R instances, each of which is indepedent of the others.

## examples/standard/rinside\_sample2.cpp

```
#include <mpi.h> // mpi header
#include <RInside.h> // for the embedded R via RInside
int main(int argc, char *argv[]) {
                                                  // mpi initialization
  MPI::Init(argc, argv);
                                                  // current node rank
  int myrank = MPI::COMM WORLD.Get rank();
  int nodesize = MPI::COMM WORLD.Get size(); //total nodes running.
                                                  // embedded R instance
  RInside R(argc, argv);
  std::stringstream txt;
  txt << "Hello from node " << myrank  // node information
      << " of " << nodesize << " nodes!" << std::endl;
                                                  // assign to R var 'txt'
  R["txt"] = txt.str();
                                                  // eval, ignore returns
  R.parseEvalQ("cat(txt)");
  MPI::Finalize():
                                                  // mpi finalization
  exit(0);
```

### A first example: Output

examples/standard/rinside\_sample2.cpp

```
edd@max:/tmp$ orterun -n 8 ./rinside_mpi_sample2
Hello from node 5 of 8 nodes!
Hello from node 7 of 8 nodes!
Hello from node 1 of 8 nodes!
Hello from node 0 of 8 nodes!
Hello from node 2 of 8 nodes!
Hello from node 3 of 8 nodes!
Hello from node 4 of 8 nodes!
Hello from node 6 of 8 nodes!
Hello from node 6 of 8 nodes!
```

This uses Open MPI just locally, other hosts can be added via -H node1, node2, node3.

The other example(s) shows how to gather simulation results from MPI nodes.

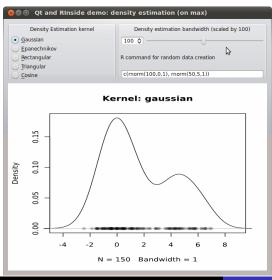
- RInside
  - Basics
  - MPI
  - Qt
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

## Application example: Qt RInside examples/gt/

The question is sometimes asked how to embed **RInside** in a larger program.

We just added a new example using Qt:

## Application example: Qt density slider



This uses standard **Qt** / GUI paradigms of

- radio buttons
- sliders
- textentry

all of which send values to the R process which provides an SVG image that is plotted.

## Application example: Qt density slider RInside examples/qt/

The actual code is pretty standard **Qt** / GUI programming (and too verbose to be shown here).

The qtdensity.pro file is interesting as it maps the entries in the Makefile (discussed in the next section) to the **Qt** standards

It may need an update for OS X—we have not tried that yet.

- RInside
  - Basics
  - MPI
  - Qt
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

### **Building with RInside**

RInside needs headers and libraries from several projects as it

embeds R itself so we need R headers and libraries
uses Rcpp so we need Rcpp headers and libraries
RInside itself so we also need RInside headers and libraries

#### Use the Makefile in examples/standard

The Makefile is set-up to create an binary for example example file supplied. It uses

```
R CMD config to query all of -cppflags, -ldflags,
          BLAS LIBS and LAPACK LIBS
   Rscript to query Rcpp:::CxxFlags and
          Rcpp:::LdFlags
   Rscript to query RInside:::CxxFlags and
          RInside:::LdFlags
```

The gtdensity.pro file does the equivalent for Qt.

- RInside
  - Basics
  - MPI
  - Ot
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

#### Armadillo

#### From arma.sf.net and slightly edited

Armadillo is a C++ linear algebra library aiming towards a good balance between speed and ease of use. Integer, floating point and complex numbers are supported, as well as a subset of trigonometric and statistics functions. Various matrix decompositions are provided.

A delayed evaluation approach is employed (during compile time) to combine several operations into one and reduce (or eliminate) the need for temporaries. This is accomplished through recursive templates and template meta-programming.

This library is useful if C++ has been decided as the language of choice (due to speed and/or integration capabilities).

## Armadillo highlights

- Provide integer, floating point and complex vectors, matrices and fields (3d) with all the common operations.
- Very good documentation and examples at website http://arma.sf.net, and a recent technical report (Sanderson, 2010).
- Modern code, building upon and extending from earlier matrix libraries.
- Responsive and active maintainer, frequent updates.

## RcppArmadillo highlights

- Template-only builds—no linking, and available everywhere R and a compiler work (but Rcpp is needed to)!
- Easy to use, just add LinkingTo: RcppArmadillo,
   Rcpp to DESCRIPTION (i.e., no added cost beyond Rcpp)
- Really easy from R via Rcpp
- Frequently updated, easy to use

RInside RcppArmadillo RcppGSL Simulations End Armadillo Example Example: VAR(1) Simulatio

- RInside
  - Basics
  - MPI
  - Ot
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

## Complete file for fastLM RcppArmadillo src/fastLm.cpp

```
#include <RcppArmadillo.h>
extern "C" SEXP fastLm(SEXP ys, SEXP Xs) {
 try {
    arma::colvec y = Rcpp::as<arma::colvec>(ys); // direct to arma
    arma::mat X = Rcpp::as<arma::mat>(Xs);
    int df = X.n rows - X.n cols;
    arma::colvec coef = arma::solve(X, v);
                                           // fit model y \sim X
                                                 // residuals
    arma::colvec res = y - X*coef;
    double s2 = std::inner_product(res.begin(), res.end(),
                      res.begin(), 0.0)/df; //std.errors of coefs
    arma::colvec std_err = arma::sqrt(s2 *
               arma::diagvec(arma::pinv(arma::trans(X)*X)));
    return Rcpp::List::create(Rcpp::Named("coefsficients")=coef,
                             Rcpp::Named("stderr") = std err,
                             Rcpp::Named("df") = df);
  } catch( std::exception &ex ) {
      forward_exception_to_r( ex );
  } catch(...) {
      ::Rf_error( "c++ exception (unknown reason)" );
  return R NilValue; //-Wall
```

## Core part of fastLM

RcppArmadillo src/fastLm.cpp

```
arma::colvec y = Rcpp::as<arma::colvec>(ys); // to arma
arma::mat X = Rcpp::as<arma::mat>(Xs);
int df = X.n rows - X.n cols;
arma::colvec coef = arma::solve(X, y);
                                             // fit v \sim X
arma::colvec res = y - X*coef;
                                              // residuals
double s2 = std::inner_product(res.begin(), res.end(),
                  res.begin(), 0.0)/df; //std.err coefs
arma::colvec std_err = arma::sqrt(s2 *
         arma::diagvec(arma::pinv(arma::trans(X)*X)));
return Rcpp::List::create(Rcpp::Named("df") = df,
              Rcpp::Named("stderr") = std_err,
              Rcpp::Named("coefficients") = coef);
```

## Easy transfer from (and to) R

RcppArmadillo src/fastLm.cpp

```
arma::colvec y = Rcpp::as<arma::colvec>(ys); // to arma
arma::mat X = Rcpp::as<arma::mat>(Xs);
int df = X.n rows - X.n cols;
arma::colvec coef = arma::solve(X, v);
                                             // fit v \sim X
arma::colvec res = y - X*coef;
                                              // residuals
double s2 = std::inner_product(res.begin(), res.end(),
                  res.begin(), 0.0)/df; //std.err coefs
arma::colvec std_err = arma::sqrt(s2 *
         arma::diagvec(arma::pinv(arma::trans(X)*X)));
return Rcpp::List::create(Rcpp::Named("df") = df,
              Rcpp::Named("stderr") = std_err,
              Rcpp::Named("coefficients") = coef);
```

### Easy linear algebra via Armadillo

```
arma::colvec y = Rcpp::as<arma::colvec>(ys); // to arma
arma::mat X = Rcpp::as<arma::mat>(Xs);
int df = X.n rows - X.n cols;
                                              // fit v \sim X
arma::colvec coef = arma::solve(X, y);
                                              // residuals
arma::colvec res = y - X*coef;
double s2 = std::inner_product(res.begin(), res.end(),
                  res.begin(), 0.0)/df; //std.err coefs
arma::colvec std_err = arma::sqrt(s2 *
         arma::diagvec(arma::pinv(arma::trans(X)*X)));
return Rcpp::List::create(Rcpp::Named("df") = df,
              Rcpp::Named("stderr") = std err,
              Rcpp::Named("coefficients") = coef);
```

RInside RcppArmadillo RcppGSL Simulations End Armadillo Example Example: VAR(1) Simulatio

- RInside
  - Basics
  - MPI
  - Ot
  - Building with RInside
- 2 RcppArmadillo
  - Armadillo
  - Example: FastLM
  - Example: VAR(1) Simulation

## Example: VAR(1) Simulation examples/part4/varSimulation.r

Lance Bachmeier started this example for his graduate students: Simulate a VAR(1) model row by row:

## Example: VAR(1) Simulation – Compiled R examples/part4/varSimulation.r

#### With R 2.13.0, we can also compile the R function:

```
R> ## Now let's load the R compiler (requires R 2.13 or later)
R> suppressMessages (require (compiler))
R> compRsim <- cmpfun(rSim)
R> compRData <- compRsim(a,e) # gen. by R 'compiled'
R> stopifnot (all.equal (rData, compRData)) # checking results
```

## Example: VAR(1) Simulation – RcppArmadillo examples/part4/varSimulation.r

```
R> ## Now load 'inline' to compile C++ code on the fly
R> suppressMessages(require(inline))
R> code <- '
    arma::mat coeff = Rcpp::as<arma::mat>(a);
    arma::mat errors = Rcpp::as<arma::mat>(e);
    int m = errors.n_rows; int n = errors.n_cols;
    arma::mat simdata(m,n);
    simdata.row(0) = arma::zeros<arma::mat>(1,n);
+
    for (int row=1; row<m; row++) {
      simdata.row(row) = simdata.row(row-1) *
                          trans(coeff)+errors.row(row);
+
    return Rcpp::wrap(simdata);
R> ## create the compiled function
R> rcppSim <- cxxfunction(signature(a="numeric",e="numeric"),</pre>
                          code,plugin="RcppArmadillo")
                                              # generated by C++ code
R> rcppData <- rcppSim(a,e)
R> stopifnot(all.equal(rData, rcppData)) # checking results
```

## Example: VAR(1) Simulation – RcppArmadillo

examples/part4/varSimulation.r

```
R> ## now load the rbenchmark package and compare all three
R> suppressMessages(library(rbenchmark))
R> res <- benchmark(rcppSim(a,e),
                   rSim(a,e).
                   compRsim(a,e),
                   columns=c("test", "replications",
                              "elapsed", "relative"),
                   order="relative")
R> print(res)
            test replications elapsed relative
   rcppSim(a, e)
                          100 0.038 1.0000
                          100 2.011 52.9211
 compRsim(a, e)
      rSim(a, e)
                          100 4.148 109.1579
R>
```

## Example: VAR(1) Simulation – RcppArmadillo examples/part4/varSimulation.r

```
R> ## now load the rbenchmark package and compare all three
R> suppressMessages(library(rbenchmark))
R> res <- benchmark(rcppSim(a,e),
                   rSim(a,e),
                   compRsim(a,e),
                   columns=c("test", "replications",
                              "elapsed", "relative"),
                   order="relative")
R> print (res)
            test replications elapsed relative
                          100 0.038 1.0000
   rcppSim(a, e)
                          100 2.011 52.9211
 compRsim(a, e)
                         100 4.148 109.1579
      rSim(a, e)
R>
```

This is now in SVN for **RcppArmadillo** and will be in the next version.

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
  - R
  - RcppArmadillo
  - Rcpp
  - Performance

RInside RcppArmadillo RcppGSL Simulations End Overview

### RcppGSL

#### RcppGSL is almost as user-friendly as RcppArmadillo

But given that the **GSL** is a C library, we need to

- do memory management and free objects
- arrange for the GSL linker to be found

**RcppGSL** may still be a convenient tool for programmers more familiar with C than C++ wanting to deploy GSL algorithms.

- RcppGSL
  - Overview
  - Example
- - Intro

## Vector norm example—c.f. GSL manual

examples/part4/gslNorm.cpp

```
#include <RcppGSL.h>
#include <gsl/gsl_matrix.h>
#include <gsl/gsl_blas.h>
extern "C" SEXP colNorm(SEXP sM) {
 try {
   int k = M.ncol():
   Rcpp::NumericVector n(k);
                                     // to store results
   for (int j = 0; j < k; j++) {
     RcppGSL::vector_view<double> colview =
                       gsl matrix column (M, j);
     n[j] = gsl_blas_dnrm2(colview);
   M.free():
   return n:
                                    // return vector
  } catch( std::exception &ex ) {
   forward_exception_to_r( ex );
  } catch(...) {
    ::Rf_error( "c++ exception (unknown reason)" );
 return R NilValue; //-Wall
```

# Core part of example examples/part4/gslNorm.cpp

## Core part of example

Using standard GSL functions: examples/part4/gslNorm.cpp

RInside RcppArmadillo RcppGSL <mark>Simulations</mark> End Intro R RcppArmadillo Rcpp Performance

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
  - R
  - RcppArmadillo
  - Rcpp
  - Performance

RInside RcppArmadillo RcppGSL Simulations End Intro R RcppArmadillo Rcpp Performance

## **Accelerating Monte Carlo**



Albert. Bayesian Computation with R, 2nd ed. Springer, 2009

Albert introduces simulations with a simple example in the first chapter.

We will study this example and translate it to R using RcppArmadillo (and Rcpp).

The idea is to, for a given level  $\alpha$ , and sizes n and m, draw a number N of samples at these sizes, compoute a t-statistic and record if the test statistic exceeds the theoretical critical value given the parameters.

This allows us to study the impact of varying  $\alpha$ , N or M — as well as varying parameters or even families of the random vectors.

## Restating the problem

• With two samples  $x_1, \ldots, x_m$  and  $y_1, \ldots, y_n$  we can test

$$H_0: \mu_{\mathsf{X}} = \mu_{\mathsf{Y}}$$

• With sample means  $\bar{X}$  and  $\bar{Y}$ , and  $s_x$  and y as respective standard deviations, the standard test is

$$T = \frac{\bar{X} - \bar{Y}}{s_P \sqrt{1/m + 1/n}}$$

whew  $s_p$  is the pooled standard deviation

$$s_p = \sqrt{\frac{(m-1)s_x^2 + (n-1)s_y^2}{m+n-2}}$$

RInside RcppArmadillo RcppGSL Simulations End Intro R RcppArmadillo Rcpp Performance

## Restating the problem

- Under  $H_0$ , we have  $T \sim t(m+n-2)$  provided that
  - $x_i$  and x + i are NID
  - the standard deviations of populations x and y are equal.
- For a given level  $\alpha$ , we can reject H if

$$|T| \geq t_{n+m-2,\alpha/2}$$

- But happens when we have
  - unequal population variances, or
  - non-normal distributions?
- Simulations can tell us.

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
  - R
  - RcppArmadillo
  - Rcpp
  - Performance

#### Basic R version

Core function: examples/part4/montecarlo.r

```
## Section 1.3.3
## simulation algorithm for normal populations
sim1 3 3 R <- function() {
    alpha <- .1; m <- 10; n <- 10 # sets alpha, m, n
                                         # sets nb of sims
    N < -10000
                                         # number of rejections
    n.reject <- 0
    crit \leftarrow qt (1-alpha/2, n+m-2)
    for (i in 1:N) {
         x <- rnorm (m, mean=0, sd=1) # simulates xs from population 1
         y <- rnorm (n, mean=0, sd=1) # simulates ys from population 2
         t.stat <- tstatistic(x,y) # computes the t statistic
         if (abs(t.stat)>crit)
              n.reject=n.reject+1 # reject if |t| exceeds critical pt
    true.sig.level <- n.reject/N
                                         # est. is proportion of rejections
```

#### Basic R version

Helper function for t-statistic: examples/part4/montecarlo.r

#### ## helper function

```
tstatistic <- function(x,y) {
    m <- length(x)
    n <- length(y)
    sp <- sqrt(((m-1)*sd(x)^2 + (n-1)*sd(y)^2) / (m+n-2))
    t.stat <- (mean(x) - mean(y)) / (sp*sqrt(1/m + 1/n))
    return(t.stat)
}</pre>
```

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
  - R
  - RcppArmadillo
  - Rcpp
  - Performance

## RcppArmadillo version

Main function: examples/part4/montecarlo.r

```
sim1_3_3_arma <- cxxfunction(, plugin="RcppArmadillo",</pre>
                            inc=tstat arma, body='
  RNGScope scope; // properly deal with RNGs
  double alpha = 0.1:
  int m = 10, n = 10; // sets alpha, m, n
  int N = 10000; // sets the number of sims
  double n reject = 0; // counter of num. of rejects
  double crit = ::Rf_qt(1.0-alpha/2.0, n+m-2.0,true,false);
  for (int i=0; i<N; i++) {
    Numeric Vector x = rnorm(m, 0, 1); // sim xs from pop 1
   Numeric Vector y = rnorm(n, 0, 1); // sim ys from pop 2
    double t_stat = tstatistic(Rcpp::as<arma::vec>(x),
                              Rcpp::as<arma::vec>(v));
    if (fabs(t_stat) > crit)
     n reject++: // reject if |t| exceeds critical pt
  double true_siq_level = 1.0*n_reject / N; // est. prop rejects
  return(wrap(true_sig_level));
′)
```

## RcppArmadillo version

Helper function for t-statistic: : examples/part4/montecarlo.r

## Rcpp version—using SVN version with mean, sd, ... Main function: examples/part4/montecarlo.r

```
sim1_3_3_rcpp <- cxxfunction(, plugin="Rcpp",</pre>
                            inc=tstat rcpp, body='
  RNGScope scope; // properly deal with RNG settings
  double alpha = 0.1:
  int m = 10, n = 10; // sets alpha, m, n
  int N = 10000; // sets the number of simulations
  double n_reject = 0; // counter of num. of rejections
  double crit = ::Rf_qt(1.0-alpha/2.0, n+m-2.0, true, false);
  for (int i=0; i<N; i++) {
   Numeric Vector x = rnorm(m, 0, 1); // sim xs from pop 1
   Numeric Vector y = rnorm(n, 0, 1); // sim ys from pop 2
    double t_stat = tstatistic(x, y);
    if (fabs(t stat) > crit)
     n reject++: // reject if |t| exceeds critical pt
  double true_sig_level = 1.0*n_reject / N; // est. prop rejects
  return(wrap(true_sig_level));
```

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
    - R
    - RcppArmadillo
    - Rcpp
    - Performance

## Rcpp version—using SVN version with mean, sd, ... Helper function: examples/part4/montecarlo.r

- RcppGSL
  - Overview
  - Example
- Simulations
  - Intro
  - R
  - RcppArmadillo
  - Rcpp
  - Performance

## Benchmark results

examples/part4/montecarlo.r

```
R> library(rbenchmark)
R> res <- benchmark(sim1_3_3_R(),
                  sim1 3 3 Rcomp(),
                  sim1 3 3 arma().
                  sim1_3_3_rcpp(),
                  columns=c("test", "replications",
                            "elapsed", "relative",
                            "user.self").
                  order="relative")
R> res
             test replications elapsed relative user.self
                           100 2.118 1.00000
                                                    2.12
3
  sim1 3 3 arma()
  sim1 3 3 rcpp()
                           100 2.192 1.03494 2.19
     sim1 3 3 R()
                          100 153.772 72.60246 153.70
2 sim1_3_3_Rcomp()
                          100 154.251 72.82861 154.19
R>
```

RInside RcppArmadillo RcppGSL Simulations End Intro R RcppArmadillo Rcpp Performance

### Benchmark results

```
R> res

test replications elapsed relative user.self
3 sim1_3_3_arma() 100 2.118 1.00000 2.12
4 sim1_3_3_rcpp() 100 2.192 1.03494 2.19
1 sim1_3_3_R() 100 153.772 72.60246 153.70
2 sim1_3_3_Rcomp() 100 154.251 72.82861 154.19
R>
```

In this example, the R compiler does not help at all. The difference between **RcppArmadillo** and **Rcpp** is neglible.

Suggestions (by Albert): replace n, m, standard deviations of Normal RNG, replace Nornal RNG, ... which, thanks to **Rcpp** and 'Rcpp sugar' is a snap.

RInside RcppArmadillo RcppGSL Simulations End Intro R RcppArmadillo Rcpp Performance

## Simulation results

examples/part4/montecarlo.r

#### Albert reports this table:

Populations	True Sign. Level
Normal pop. with equal spreads Normal pop. with unequal spreads $t(4)$ distr. with equal spreads Expon. pop. with equal spreads Normal + exp. pop. with unequal spreads	0.0986 0.1127 0.0968 0.1019 0.1563

Table: True significance level of *t*-test computed by simulation; standard error of each estimate is approximately 0.003.

Given that our simulations are  $\approx$  70-times faster, we can reduce the standard error to  $\sqrt{0.1\times0.9/1,000,000}=0.0003$ .

## That's it, folks!

#### Want to learn more ?

- Check the vignettes
- Ask questions on the Rcpp-devel mailing list
- Inquire about commercial support

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