Using C and C++ with R

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Plan

Calling foreign languages

Built-in `C` interface

The `Rcpp` package

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Foreign languages

- `C` , `C++`
- `Fortran`
- `Java`[1].

Other scripting languages

- R/Perl[2] and R/Python[3] bidirectional interfaces.
- There is also the `system()` function for direct access to OS functions.

[1] http://www.rforge.net/rJava/
[2] http://www.omegahat.org/RSPerl/
[3] http://www.omegahat.org/RSPython/

Robert Gentleman, in *R Programming for Bioinformatics*, 2008, about R's built-in C interfaces

> *Since R is not compiled, in some situations its performance can be substantially improved by writing code in a compiled language. There are also reasons not to write code in other languages, and in particular we caution against premature optimization, prototyping in R is often cost effective. And in our experience very few routines need to be implemented in other languages for efficiency reasons. Another substantial reason not to use an implementation in some other language is increased complexity. The use of another language almost always results in higher maintenance costs and less stability. In addition, any extensions or enhancements of the code will require someone that is proficient in both R and the other language.*

Rcpp does make some of the above caution statements slightly less critical.

- **Why?** `R` is getting slow or is not doing well in terms of memory management: for example `for` loops that can't be vectorised, recursion, ...
- **When?** `R` can't do better **and** the slow code has been identified $\rightarrow$ `Rprof`

- **Why?** `R` is getting slow or is not doing well in terms of memory management: for example `for` loops that can't be vectorised, recursion, ...
- **When?** `R` can't do better **and** the slow code has been identified $\rightarrow$ `Rprof`

- **Why?** Re-using existing infrastructure

Requirement for C/C++

Working compilers. On Windows, Rtools[1,2]. On Mac, Xcode[3,4].

1. http://cran.r-project.org/bin/windows/Rtools/
2. http://cran.r-project.org/doc/manuals/R-admin.html#The-Windows-toolset
3. http://cran.r-project.org/doc/manuals/R-admin.html#Installing-R-under-_0028Mac_0029-OS-X
4. http://cran.r-project.org/doc/manuals/R-admin.html#Mac-OS-X

We will be using the following packages:

- `inline` and the `cfunction` to write inline `C` code that is compiled on the fly. (There is also a `cxxfunction` for `C++` code).
- `Rcpp`, illustrating some of its functionality as well as the `cppFunction` for inline/on the fly compilation of `C++` code.

Example

We have a DNA sequence, represented by a string of A, C, G and T and we want to compute the GC content.

```
x <- "ACCGGGTTTT"
gccountr <- function(x) table(strsplit(x, "")[[1]])
gccountr(x)

##
## A C G T
## 1 2 3 4
```

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The `Rcpp` package

The R C API

- Very frequent in R but has its quirks.
- Better know how to program in C.
- Documentation is not always easy to follow: R-Ext, R Internals as well as R and other package's code.

`.C`

- Not recommended.
- Arguments and return values must be *primitives* (vectors of doubles or integers).

`.Call`

- Accepts any `R` data structures as arguments and return values as `SEXP`.
- Manual memory management: allocate memory, protect objects to avoid them being garbage collected and subsequently unprotect them.

S (or symbolic) expression

`SEXP` is a super-type that matches all `R` data structures. Each data type has its own `SEXP` sub-type.

- `REALSXP` and `INTSXP` for double and integer vectors
- `LGLSXP` and `STRSXP` for logical and character vectors
- `VECSXP` for a list (NB: `R` list are called vectors at the `C` level)
- ...

Function input and outputs are always `SEXP` and will have to be coerced to the appropriate `SXP` sub-type.
`Rinternals.h` defines all `C` functions, data types and macros.

```
file.path(R.home(), "include", "Rinternals.h")

## [1] "/usr/local/lib/R/include/Rinternals.h"
```

```
library("inline")

## From Hadley Wickham, devtools wiki, adapted from inspect.c
## https://github.com/hadley/devtools/wiki/C-interface
sexp_type <- cfunction(c(x = "ANY"), '
  switch (TYPEOF(x)) {
    case NILSXP:      return mkString("NILSXP");
    case SYMSXP:      return mkString("SYMSXP");
    case LISTSXP:     return mkString("LISTSXP");
    case CLOSXP:      return mkString("CLOSXP");
    case ENVSXP:      return mkString("ENVSXP");
    case PROMSXP:     return mkString("PROMSXP");
    case LANGSXP:     return mkString("LANGSXP");
    case SPECIALSXP:  return mkString("SPECIALSXP");
    case BUILTINSXP:  return mkString("BUILTINSXP");
    case CHARSXP:     return mkString("CHARSXP");
    case LGLSXP:      return mkString("LGLSXP");
    case INTSXP:      return mkString("INTSXP");
    case REALSXP:     return mkString("REALSXP");
    case CPLXSXP:     return mkString("CPLXSXP");
    case STRSXP:      return mkString("STRSXP");
    case DOTSXP:      return mkString("DOTSXP");
    case ANYSXP:      return mkString("ANYSXP");
    case VECSXP:      return mkString("VECSXP");
    case EXPRSXP:     return mkString("EXPRSXP");
    case BCODESXP:    return mkString("BCODESXP");
    case EXTPTRSXP:   return mkString("EXTPTRSXP");
    case WEAKREFSXP:  return mkString("WEAKREFSXP");
    case S4SXP:       return mkString("S4SXP");
    case RAWSXP:      return mkString("RAWSXP");
    default:          return mkString("<unknown>");
}')
```

```
source("src/sexp.R")
sexp_type(1:3)

## [1] "INTSXP"

sexp_type(10L)

## [1] "INTSXP"

sexp_type(TRUE)

## [1] "LGLSXP"

sexp_type(letters)

## [1] "STRSXP"

sexp_type(list(a = 1, b = letters))

## [1] "VECSXP"

sexp_type(ls)

## [1] "CLOSXP"
```

Garbage collection

Every `R` object that is created at the `C` level (not function arguments, that `R` is already aware of) must be `PROTECT`ed to avoid being garbage collected. Before the return statement, these must be explicitely `UNPROTECT`ed.

```
SEXP x;
PROTECT(x = ... )
## do stuff
UNPROTECT(1)
return(x)
```

Object creation

1. Allocate memory: `allocVector`, `allocMatrix`, `alloc3DArray`
2. Initialise objects: `memset`

```
SEXP x;
PROTECT(x = allocVector(INTSXP, 10) )
memset(INTEGER(x), 0, 10 * sizeof(int))
## do stuff
UNPROTECT(1)
return(x)
```

Accessing/setting SXP elements

- `REAL(x)[i]` if `x` is a `REALSXP`
- `INTEGER(x)[i]` if `x` is a `INTSXP`
- `LOGICAL(x)[i]` if `x` is a `LGLSXP`
- ...

- `STRING_ELT(x, i)` to access individual `CHARSXP` elements of a `STRSXP`
- `VECTOR_ELT(x, i)` to access individual elements of a `VECSXP`

- `SET_STRING_ELT(str, i, x))` to set an element in a string.
- `SET_VECTOR_ELT(vec, i, x))` to set an element in a list.

```c
SEXP gccount(SEXP inseq) {
  int i, l;
  char p;
  SEXP ans, dnaseq;

  PROTECT(dnaseq = STRING_ELT(inseq, 0)); // a CHARSXP
  l = length(dnaseq);

  PROTECT(ans = allocVector(INTSXP, 4));
  memset(INTEGER(ans), 0, 4 * sizeof(int));

  for (i = 0; i < l; i++) {
    p = CHAR(dnaseq)[i];
    if (p == 'A')
      INTEGER(ans)[0]++;
    else if (p == 'C')
      INTEGER(ans)[1]++;
    else if (p == 'G')
      INTEGER(ans)[2]++;
    else if (p == 'T')
      INTEGER(ans)[3]++;
    else
      error("Wrong alphabet");
  }
  UNPROTECT(2);
  return(ans);
}
```

1. `ingccount`: embedding the `C` directly in `R` using the `inline` package.
2. `gccount`: writing the `C` into its own code file and using `.Call`.

./src/ingccount.R

```
library("inline")

ingccount <- cfunction(
  sig = c(inseq = "character"),
  body = "
  int i, l;
  char p;
  SEXP ans, dnaseq;
  PROTECT(dnaseq = STRING_ELT(inseq, 0)); // a CHARSXP
  l = length(dnaseq);
  PROTECT(ans = allocVector(INTSXP, 4));
  memset(INTEGER(ans), 0, 4 * sizeof(int));
  for (i = 0; i < l; i++) {
    p = CHAR(dnaseq)[i];
    if (p == \'A\')
      INTEGER(ans)[0]++;
    else if (p == \'C\')
      INTEGER(ans)[1]++;
    else if (p == \'G\')
      INTEGER(ans)[2]++;
    else if (p == \'T\')
      INTEGER(ans)[3]++;
    else
      Rf_error(\"Wrong alphabet\");
  }
  UNPROTECT(2);
  return(ans);
")
```

```
source("./src/ingccount.R")
ingccount(x)

## [1] 1 2 3 4
```

src/gccount.c

```
#include <R.h>
#include <Rdefines.h>

SEXP gccount(SEXP inseq) {
  int i, l;
  char p;
  SEXP ans, dnaseq;

  PROTECT(dnaseq = STRING_ELT(inseq, 0)); // a CHARSXP
  l = length(dnaseq);

  PROTECT(ans = allocVector(INTSXP, 4));
  memset(INTEGER(ans), 0, 4 * sizeof(int));

  for (i = 0; i < l; i++) {
    p = CHAR(dnaseq)[i];
    if (p == 'A')
      INTEGER(ans)[0]++;
    else if (p == 'C')
      INTEGER(ans)[1]++;
    else if (p == 'G')
      INTEGER(ans)[2]++;
    else if (p == 'T')
      INTEGER(ans)[3]++;
    else
      error("Wrong alphabet");
  }
  UNPROTECT(2);
  return(ans);
}
```

Use directly

1. Create a shared library: `R CMD SHLIB gccount.c`
2. Load the shared object: `dyn.load("gccount.so")`
3. Create an `R` function that uses it:

```
gccountC <-
  function(inseq) .Call("gccount", inseq)
```

4. Use you `C` code:

```
gccountC(x)

## [1] 1 2 3 4
```

In a package

- The `C` code comes in the `src` directory.
- The `R` wrapper will be

```
gccount <- function(inseq)
  .Call("gccount", inseq, PACKAGE = "mypackage")
```

- Document the `R` function
- Export the `R` function and `useDynLib(mypackge)` in the `NAMESPACE`

```
library(sequences)
gccount

## function (inseq)
## {
##     .Call("gccount", inseq, PACKAGE = "sequences")
## }
## <environment: namespace:sequences>

gccount(x)

## [1] 1 2 3 4
```

We could check that

```
if (TYPEOF(inseq) != STRSXP)
  error("Need a character vector!");
```

although

```
gccountC(123)

## Error in gccountC(123):  STRING_ELT() can only be
applied to a 'character vector', not a 'double'
```

and type checking could easily be done at the R level. There is also `isReal(x)`, `isInteger(x)`, ... for atomics vectors.

There is of course much more to this . . . see references at the end.

Benchmarking

```
library(microbenchmark)
microbenchmark(gccountr(x),
               ingccount(x),
               gccountC(x),
               times = 1e4)
```

```
## Unit: nanoseconds
##           expr    min     lq       mean   median       uq      max neval
##   gccountr(x) 124900 130961 143460.812 134478.0 137706.5 37985890 10000
##  ingccount(x)    409    733   1213.308   1026.0   1538.0   991410 10000
##   gccountC(x)   4158   4707   6709.283   7891.5   8631.0    26680 10000
##  cld
##    b
##   a
##   a
```

Could we do better in R ? (should be asked first, really)

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```
gccountr2 <-
  function(x) tabulate(factor(strsplit(x, "")[[1]]))
```

Could we do better in R ? (should be asked first, really)

```
gccountr2 <-
  function(x) tabulate(factor(strsplit(x, "")[[1]]))
```

```
microbenchmark(gccountr(x),
               gccountr2(x),
               ingccount(x),
               gccountC(x),
               times = 1e4)

## Unit: nanoseconds
##           expr    min       lq      mean   median     uq      max neval  cld
##   gccountr(x) 125862 132247.0 139088.32 134932.0 137670 1498484 10000    d
##  gccountr2(x)  64077  68695.5  72472.12  70422.0  72422 1303895 10000   c
##  ingccount(x)    407    866.0   1242.09   1302.0   1528   22770 10000 a
##   gccountC(x)   6647   7438.0  10424.67  11581.5  11952   56256 10000  b
```

But, obviously, `table` and `tabular` do much more than `gccount`.

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The `Rcpp` package

The Rcpp package

- Dirk Eddelbuettel and Romain Francois, with contributions by Douglas Bates, John Chambers and JJ Allaire.
- A flexible framework that facilitates the integration of R and C/C++ .
- http://www.rcpp.org/

- It comes with **loads** of documentation and examples: `vignette(package = "Rcpp")`.
- All basic R types are implemented as C++ classes.
- No need to worry about garbage collection.

Associated packages

- `RcppArmadillo` – Armadillo templated C++ library for linear algebra.
- `RcppEigen` – high-performance Eigen linear algebra library.
- `RInside` – use `R` from inside another C++ by wrapping the existing `R` embedding API in an easy-to-use C++ class.

C++ classes

Scalar	Vector	Matrix
double	NumericVector	NumericMatrix
int	IntegerVector	IntegerMatrix
string	CharacterVector	CharacterMatrix
bool	LogicalVector	LogicalMatrix

And Function, List, DataFrame ...
Automatic conversions from R (C) to C++ (R) using as (wrap).

1. `ingccount2`: embedding the `C++` directly in `R` using the `Rcpp::cppFunction` package.
2. `gccount2`: in a package, writing the `C++` into its own code file and using `.Call`.
3. `gccountX`: using `sourceCpp` to source the `C++` file and export the function to `R` .

./src/ingccount2.R

```
1  IntegerVector ingccount2(CharacterVector inseq) {
2    IntegerVector ans(4);
3    std::string s = Rcpp::as<std::string>(inseq[0]);
4    int n = inseq[0].size();
5    for (int i = 0; i < n; i++) {
6      if (s[i] == 'A')
7        ans[0]++;
8      else if (s[i] == 'C')
9        ans[1]++;
10     else if (s[i] == 'G')
11       ans[2]++;
12     else if (s[i] == 'T')
13       ans[3]++;
14     else
15       Rf_error(\"Wrong alphabet\");
16   }
17   return wrap(ans);
18 }
```

./src/ingccount2.R

```
library("Rcpp")

cppFunction("
IntegerVector ingccount2(CharacterVector inseq) {
  IntegerVector ans(4);
  std::string s = Rcpp::as<std::string>(inseq[0]);
  int n = inseq[0].size();
  for (int i = 0; i < n; i++) {
    if (s[i] == 'A')
      ans[0]++;
    else if (s[i] == 'C')
      ans[1]++;
    else if (s[i] == 'G')
      ans[2]++;
    else if (s[i] == 'T')
      ans[3]++;
    else
      Rf_error(\"Wrong alphabet\");
  }
  return wrap(ans);
}
")
```

```
x <- "ACCGGGTTTT"
source("src/ingccount2.R")
ingccount2(x)

## [1] 1 2 3 4
```

./src/gccount2.cpp

```
#include <Rcpp.h>

using namespace Rcpp;

RcppExport SEXP gccount2(SEXP inseq)
{
  Rcpp::IntegerVector ans(4);
  Rcpp::CharacterVector dnaseq(inseq);
  std::string s = Rcpp::as<std::string>(dnaseq[0]);

  for (int i = 0; i < s.size(); i++) {
    char p = s[i];
    if (p=='A')
      ans[0]++;
    else if (p=='C')
      ans[1]++;
    else if (p=='G')
      ans[2]++;
    else if (p=='T')
      ans[3]++;
    else
      Rf_error("Wrong alphabet");
  }

  return(ans);
}
```

In a package

1. You will need a `Makevars` file in the `src` directory.
2. Modify `DESCRIPTION` file:
   ```
   Depends:  Rcpp (>= 0.10.1)
   LinkingTo:  Rcpp
   ```
3. Create an `R` function that uses it

   ```
   gccount2 <- function(inseq)
     .Call("gccount2", inseq, PACKAGE = "mypackage")
   ```

4. Document the `R` function
5. Export the `R` function and `useDynLib(mypackge)` in the `NAMESPACE`

Check the `sequences` package. But see `Rcpp.package.skeleton` below.

Using sourceCpp

- Write the C++ code into a cpp file, including headers and dedicated export statement (see next slide).
- Source it and use the R function.

```
sourceCpp("src/gccountX.cpp")
gccountX(x)
```

```
## [1] 1 2 3 4
```

./src/gccountX.R

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

// [[Rcpp::export]]
IntegerVector gccountX(CharacterVector inseq) {
  IntegerVector ans(4);
  std::string s = Rcpp::as<std::string>(inseq[0]);

  for (int i = 0; i < s.size(); i++) {
    if (s[i] == 'A')
      ans[0]++;
    else if (s[i] == 'C')
      ans[1]++;
    else if (s[i] == 'G')
      ans[2]++;
    else if (s[i] == 'T')
      ans[3]++;
    else
      Rf_error("Wrong alphabet");
  }
  return(ans);
}
```

sugar

sugar (for *syntactic sugar*) is a set of `C++` functions that (mostly) work and look like their `R` couterparts. Allows for example compact vectorised expression. Looks like `R` with the `C++` efficiency. (Rcpp-sugar vignette/paper)

- Vectorised arithmetic and logical operators: `+`, `>`, `!`, ...
- Functions: `seq_len`, `seq`, `sapply`, `rnorm`, `abs`, `sum`, ...

./src/cumsum.cpp

```
1  NumericVector cumsum1(NumericVector x){
2    // initialize an accumulator variable
3    double acc = 0;
4    // initialize the result vector
5    NumericVector res(x.size());
6    for(int i = 0; i < x.size(); i++){
7      acc += x[i];
8      res[i] = acc;
9    }
10   return res;
11 }
```

```cpp
NumericVector cumsum1(NumericVector x){
  // initialize an accumulator variable
  double acc = 0;
  // initialize the result vector
  NumericVector res(x.size());
  for(int i = 0; i < x.size(); i++){
    acc += x[i];
    res[i] = acc;
  }
  return res;
}
```

```cpp
NumericVector cumsum2(NumericVector x){
  return cumsum(x); // compute + return result
}
```

Translate these R functions into C or C++

```
sum
rowSums
pdistR <- function(x, ys)
  sqrt( (x - ys) ^ 2 )
sety <- function(x, y) {
    x[x > 0] <- y
    x[x < 0] <- -y
    x
}
lgl_biggerY <- function(x, y) x > y
biggerY <- function(x, y) x[x > y]
foo <- function(x, y) ifelse(x < y, x*x, -(y*y))
```

When possible, write two versions; one with an explicit `for` loop and another using sugar vectorised functions.
Hints: The `nrow` and `ncol` functions can be used to extract matrix dimensions. The matrix subsetting operator is `()` (instead of `[]`). To specify all indices, use the underscore.
Benchmark the R and C++ implementations.

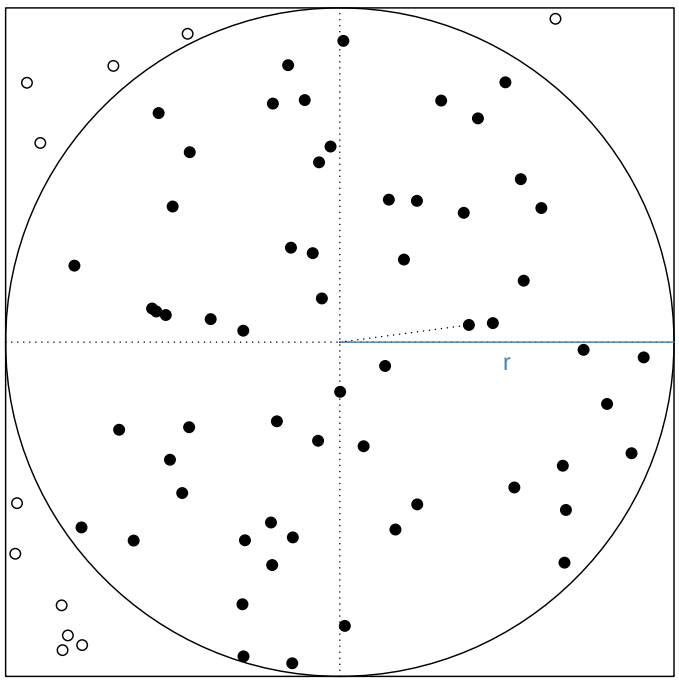
Modification of the function arguments!

```
1  // [[Rcpp::export]]
2  IntegerVector modifyX(IntegerVector x) {
3    int n = x.size();
4    for (int i = 0; i < n; i++) {
5      x[i] = i;
6    }
7    return x;
8  }
```

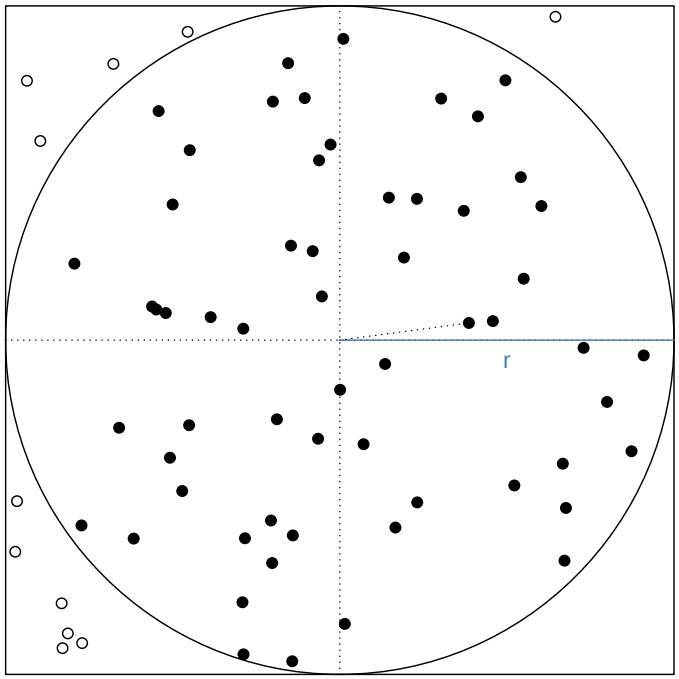
```
sourceCpp("src/modify.cpp")
(x <- 3:1)

## [1] 3 2 1

modifyX(x)

## [1] 0 1 2

x

## [1] 0 1 2
```

Cloning

```
1  IntegerVector nomodifyX(IntegerVector x) {
2    IntegerVector y = clone(x);
3    int n = x.size();
4    for (int i = 0; i < n; i++) {
5      y[i] = i;
6    }
7    return y;
8  }
```



$$\frac{d}{n} = \frac{\pi r^2}{4r^2} = \pi/4$$
$$\pi \approx \frac{4d}{n}$$



$$\frac{d}{n} = \frac{\pi r^2}{4r^2} = \pi/4$$
$$\pi \approx \frac{4d}{n}$$

```
piR <- function(N) {
    x <- runif(N)
    y <- runif(N)
    d <- sqrt(x^2 + y^2)
    4 * sum(d < 1.0) / N
}
```

```r
piR <- function(N) {
    x <- runif(N)
    y <- runif(N)
    d <- sqrt(x^2 + y^2)
    return(4 * sum(d < 1.0) / N)
}
```

```r
piR <- function(N) {
    x <- runif(N)
    y <- runif(N)
    d <- sqrt(x^2 + y^2)
    return(4 * sum(d < 1.0) / N)
}
```

```cpp
#include <Rcpp.h>
using namespace Rcpp;
// [[Rcpp::export]]
double piSugar(const int N) {
    RNGScope scope; // ensure RNG gets set/reset
    NumericVector x = runif(N);
    NumericVector y = runif(N);
    NumericVector d = sqrt(x*x + y*y);
    return 4.0 * sum(d < 1.0) / N;
}
```

src/sugar.R

```
source("src/pi.R")

library("Rcpp")
sourceCpp("src/pi.cpp")

N <- 1e6
set.seed(42)
resR <- piR(N)

set.seed(42)
resCpp <- piSugar(N)
stopifnot(identical(resR, resCpp))
```

```
library(rbenchmark)
res <- benchmark(piR(N), piSugar(N),
                 order="relative")
print(res[,1:4])

##          test replications elapsed relative
## 2 piSugar(N)          100   3.724    1.000
## 1     piR(N)          100  13.000    3.491
```

Missing values

There are type specific `NA_REAL`, `NA_INTEGER`, `NA_STRING`, `NA_LOGICAL`. A vector can be tested with `is_na`. To test a scalar, use `R_IsNA`.
Sugar also provides `all` and `any`.

```
is.na
foo <- function(x, y) ifelse(x < y, x*x, -(y*y))
```

Recursion

```
fr <- function(n) {
    if (n < 2) return(n)
    return(fr(n-1) + fr(n-2))
}
```

Calling a function

```
// [[Rcpp::export]]
NumericVector callFunction(NumericVector x,
    Function f) {
  NumericVector res = f(x);
  return res;
}

## in R
callFunction(x, summary)
```

sapply in C++

```
double square( double x ){
  return x*x ;
}

// [[Rcpp::export]]
NumericVector applyC(NumericVector xx){
  return sapply(xx, square);
}
```

Rcpp modules

Using S4 Reference Classes to reflect C++ classes and methods (see the Rcpp-modules vignette).

Interface to the Standard template library

C++ library with data structure and algorithms: vectors, arrays, stacks, iterators, accumulators, ... (see the Rcpp-sugar vignette).

```
1  NumericVector cumsum3(NumericVector x) {
2    NumericVector res(x.size());
3    std::partial_sum(x.begin(), x.end(), res.begin());
4    return res;
5  }
```

Using Rcpp in packages

```
Rcpp.package.skeleton("mypackage")
```

```
mypackage
|-- DESCRIPTION
|-- man
|   |-- mypackage-package.Rd
|    -- rcpp_hello_world.Rd
|-- NAMESPACE
|-- R
|    -- rcpp_hello_world.R
|-- Read-and-delete-me
 -- src
    |-- Makevars
    |-- Makevars.win
    |-- rcpp_hello_world.cpp
     -- rcpp_hello_world.h
```

```
Rcpp.package.skeleton("mypackage", attribute = TRUE)
Rcpp.package.skeleton("mypackage", module = TRUE)
Rcpp.package.skeleton("mypackage",
                      cpp_files = c("convolve.cpp"))
```

Further reading

- Writing R Extensions, R Core team.
- Robert Gentleman, R Programming for Bioinformatics, 2008.
- Rcpp documentation and Rcpp.org.
- Dirk Eddelbuettel, Seamless R and C++ Integration with Rcpp, Springer, 2013.
- Dirk Eddelbuettel and Romain Francois, *Rcpp: Seamless R and C++ Integration*, Journal of Statistical Software, Vol. 40, Issue 8, Apr 2011, http://www.jstatsoft.org/v40/i08/.
- Relevant devtools sections: *C interface* and *Rcpp*.

- Course web page and more material:
  https://github.com/lgatto/TeachingMaterial

Thank you for you attention