(A bit of) Advanced R

Part 1 - towards better R-base programming

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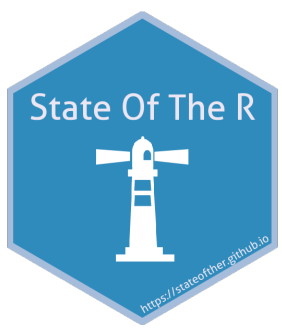


Outline

References

- R Core Team (2017): A Language and Environment for Statistical Computing https://www.R-project.org/
- Wickham (2014): Advanced R, retrieved from http://adv-r.had.co.nz/
- Gillespie & Lovelace (2016): efficient R programming https://bookdown.org/csgillespie/efficientR/

Prerequisites

Data Structure in base R

1. Atomic vector (integer, double, logical, character)
2. Recursive vector (list)
3. Factors
4. Matrices and array
5. Data Frame

$\rightsquigarrow$ Creation, Basic Operation, Manipulation, Representation

Resources

- Advanced R, chapters I.2, I.3 (Wickham, 2014, http://adv-r.had.co.nz/)
- An introduction to R programming
  http://julien.cremeriefamily.info/teachings_L3BI_ISV51.html

Outline

The [a-z]*pply family I

Example with factors (tapply)

```
data <- rnorm(100)
sexe <- factor( sample(c("H","F"), 100, replace = TRUE))
mean.1 <- tapply(data, sexe, mean) ## good
mean.2 <- c()  ## complicated
for (l in levels(sexe))
  mean.2 <- c(mean.2, mean(data[sexe == l]))
```

Example with list or data.frame (sapply/lapply)

The [a-z]*pply family II

```
data(oats, package = "MASS")
oats[1:2, ]
```

```
##   B       V      N   Y
## 1 I Victory 0.0cwt 111
## 2 I Victory 0.2cwt 130
```

```
sapply(oats, is.factor) ## readable
```

```
##     B     V     N     Y
##  TRUE  TRUE  TRUE FALSE
```

```
for (c in 1:ncol(oats)) ## less readable (I think)
    print(is.factor(oats[,c]))
```

```
## [1] TRUE
## [1] TRUE
## [1] TRUE
## [1] FALSE
```

The do.call function I

> *constructs and executes a function call from a name or a function and a list of arguments to be passed to it*

Suppose you have the outputs of 100 simulations at your disposable, stored in a list like that

```
res <- replicate(100, rbind(data.frame(method="lasso", mse=runif(1,.75,1) , timing=runif(1)),
                            data.frame(method="ridge", mse=runif(1,.5,.75), timing=runif(1)),
                            data.frame(method="bayes", mse=runif(1,.85,1) , timing=runif(1,100,
                              ), simplify=FALSE)
```

```
class(res)
```

```
## [1] "list"
```

```
res[[1]]
```

```
##   method       mse       timing
## 1  lasso 0.9397672   0.5130959
## 2  ridge 0.6686981   0.9713040
## 3  bayes 0.8816718 124.5252348
```

The do.call function II

```
length(res)
```

```
## [1] 100
```

How would you store them in a single data frame?

```
all.res <- do.call(rbind, res)
dim(all.res)
```

```
## [1] 300   3
```

The Reduce function

> *'Reduce' uses a binary function to successively combine the elements of a given vector*

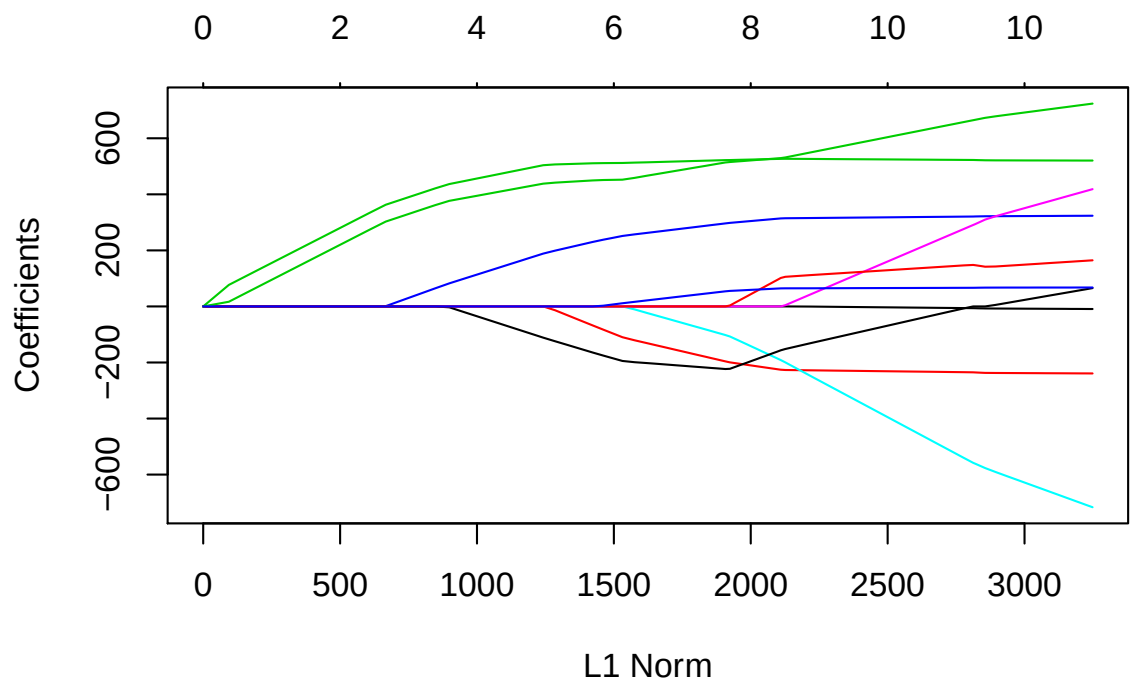
$\rightsquigarrow$ can be use to post-process your list of simulations obtained via `mclapply` just like `do.call`

Say more... (map, Reduce)

A Reduce example: "jacknifing" a lasso solution path

A single Lasso fit of the diabete data set

```
library(glmnet)
library(lars) # the diabetes data set (part of the lars package)
data(diabetes)
y <- diabetes$y
x <- diabetes$x
n <- length(y)
lasso <- glmnet(x,y)
plot(lasso)
```



A Reduce example: "jacknifing" a lasso solution path II I

Compute the regularization paths for all subsets, removing one individual at once

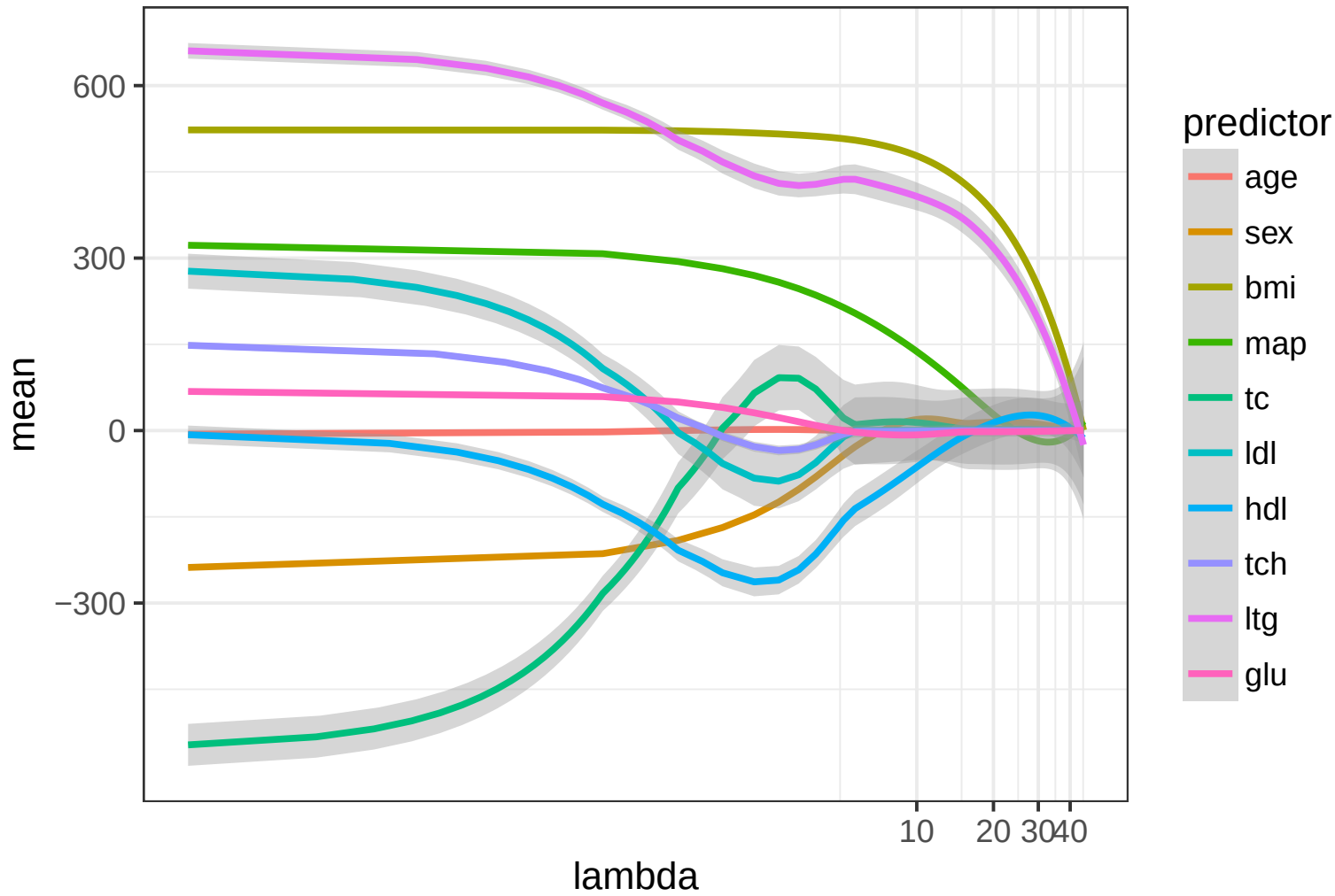
```
paths <- parallel::mclapply(1:n, function(i) {
    glmnet(x[-i, ], y[-i], lambda = lasso$lambda)$beta
}, mc.cores = 4)
```

Computing the envelop around the average regularization path with Reduce

```
mean.path <- Reduce("+", paths)/n
sdev.path <- sqrt(Reduce("+", lapply(paths, function(path) path**2))/n -
                  mean.path**2)
```

```
library(ggplot2)
library(reshape2)
mean.path <- t(as.matrix(mean.path)); rownames(mean.path) <- lasso$lambda
sdev.path <- t(as.matrix(sdev.path)); rownames(sdev.path) <- lasso$lambda
dplot <- cbind(reshape2::melt(mean.path), reshape2::melt(sdev.path)[, 3])
colnames(dplot) <- c("lambda","predictor","mean","sdev")
ggobj <- ggplot(dplot, aes(x=lambda, y=mean, group=predictor, color=predictor)) + geom_smooth(a
print(ggobj + coord_trans(x="log10"))
```

A Reduce example: "jacknifing" a lasso solution path II II



Outline

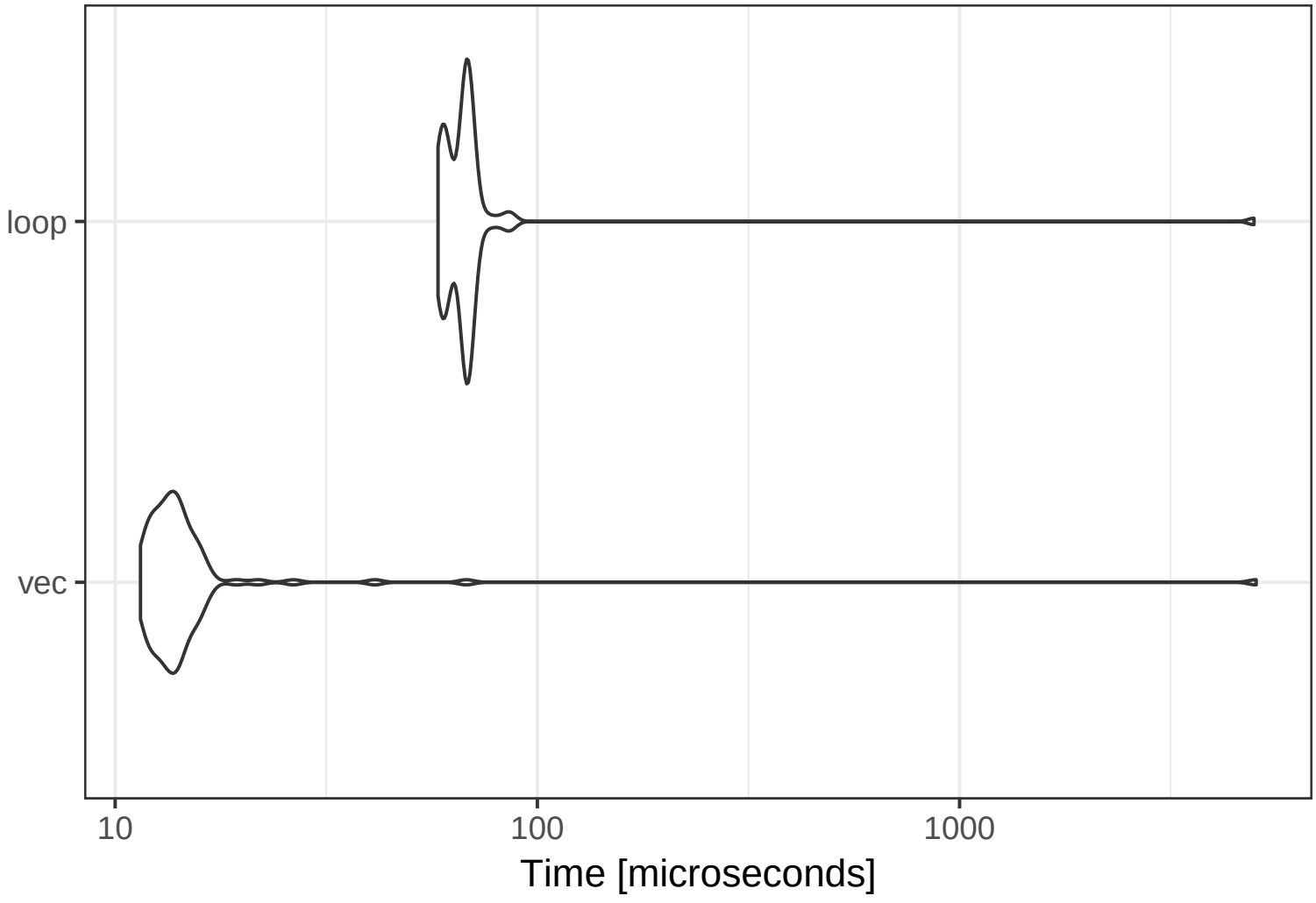
Vectorize any algebraic operation I

Example: compute $\exp(x) = \sum_{k=0}^{n} \frac{x^k}{k!}$

```
## the good way
exp_vec <- function(x, n){
  res <- sum(x^(0:n)/c(1,cumprod(1:n)))
  res
}
## the sad/bad/less readable way
exp_loop <- function(x, n){
  res <- 1
  for (k in 1:n) res <- res + 2^k/factorial(k)
  res
}
```

```
autoplot(microbenchmark(vec = exp_vec(2, 100), loop = exp_loop(2, 100)))
```

Vectorize any algebraic operation II



Vectorize, even for non-algebraic operation I

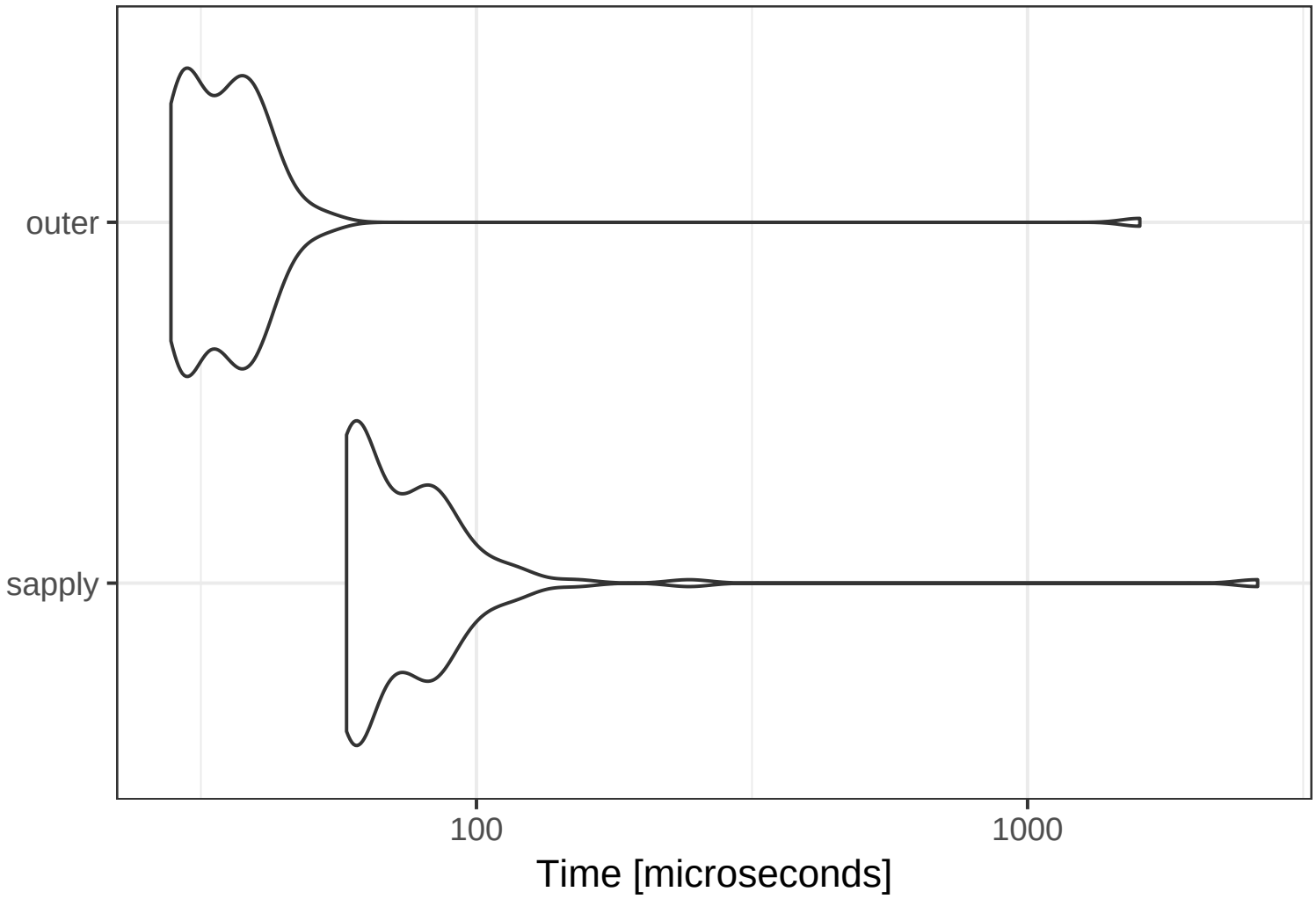
```
month_year_apply <- function(year) {
  sapply(month.name, function(month) paste(month, year, sep = "_"))
}

month_year_outer <- function(year) {
  outer(month.name, year, FUN = paste, sep = '_')
}
head(month_year_outer(c(2010, 2013)), 3)
```

```
##      [,1]            [,2]
## [1,] "January_2010"  "January_2013"
## [2,] "February_2010" "February_2013"
## [3,] "March_2010"    "March_2013"
```

```
autoplot(microbenchmark(
  sapply = month_year_apply(c(2011, 2013)),
  outer  = month_year_outer(c(2011, 2013)),
  times = 100))
```

Vectorize, even for non-algebraic operation II



Compile your functions with `base::compiler` I

If you cannot avoid a loop, you will save some time

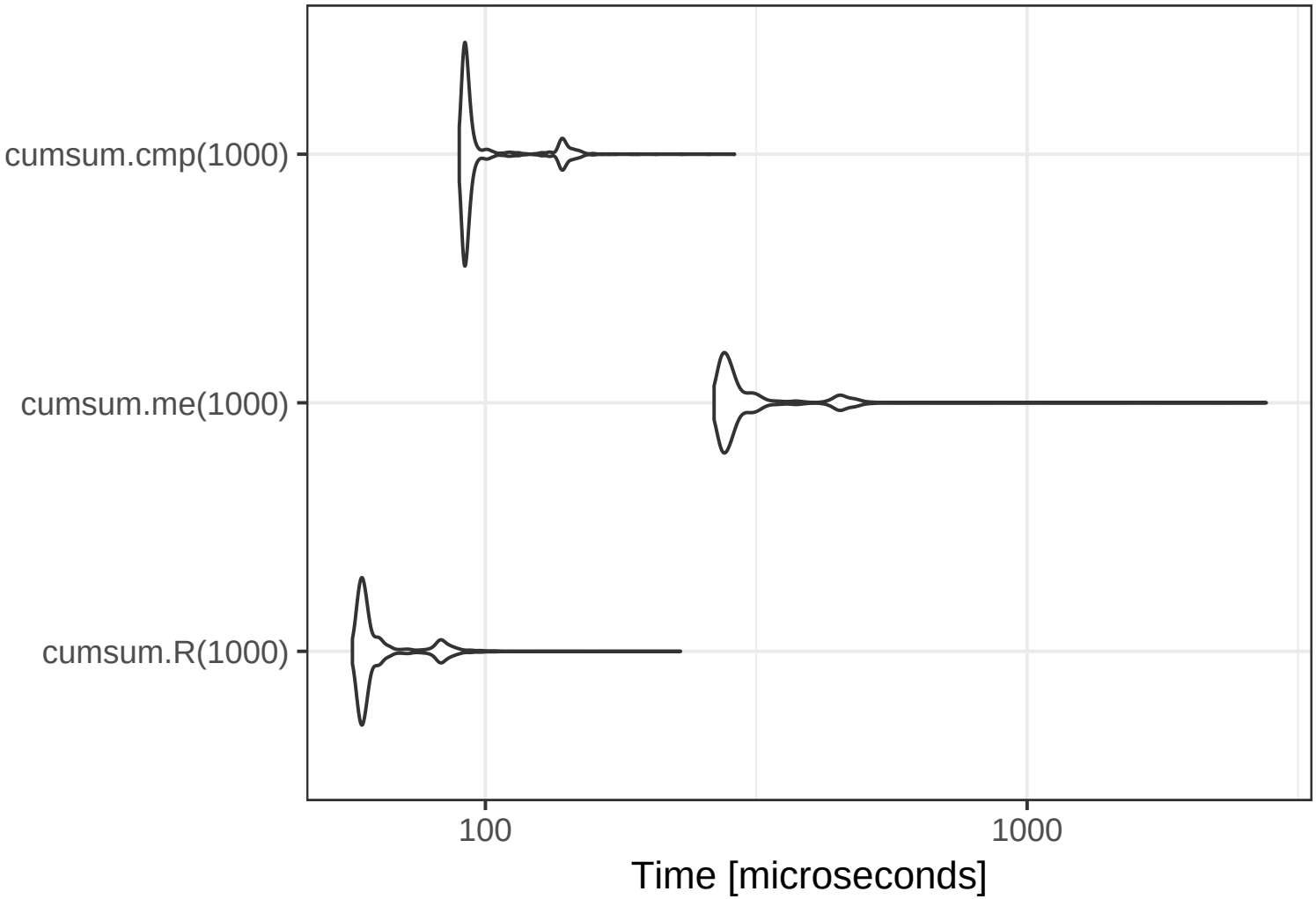
```
cumsum.R <- function(n) {
  x <- rnorm(n)
  cumsum(x)
}

cumsum.me <- function(n) {
  x <- rnorm(n)
  res <- 0
  for (i in 1:length(x))
    res <- res + x[i]
  res
}

cumsum.cmp <- compiler::cmpfun(cumsum.me)

autoplot(
  microbenchmark(
    cumsum.R(1000),
    cumsum.me(1000),
    cumsum.cmp(1000),
    times=1000)
)
```

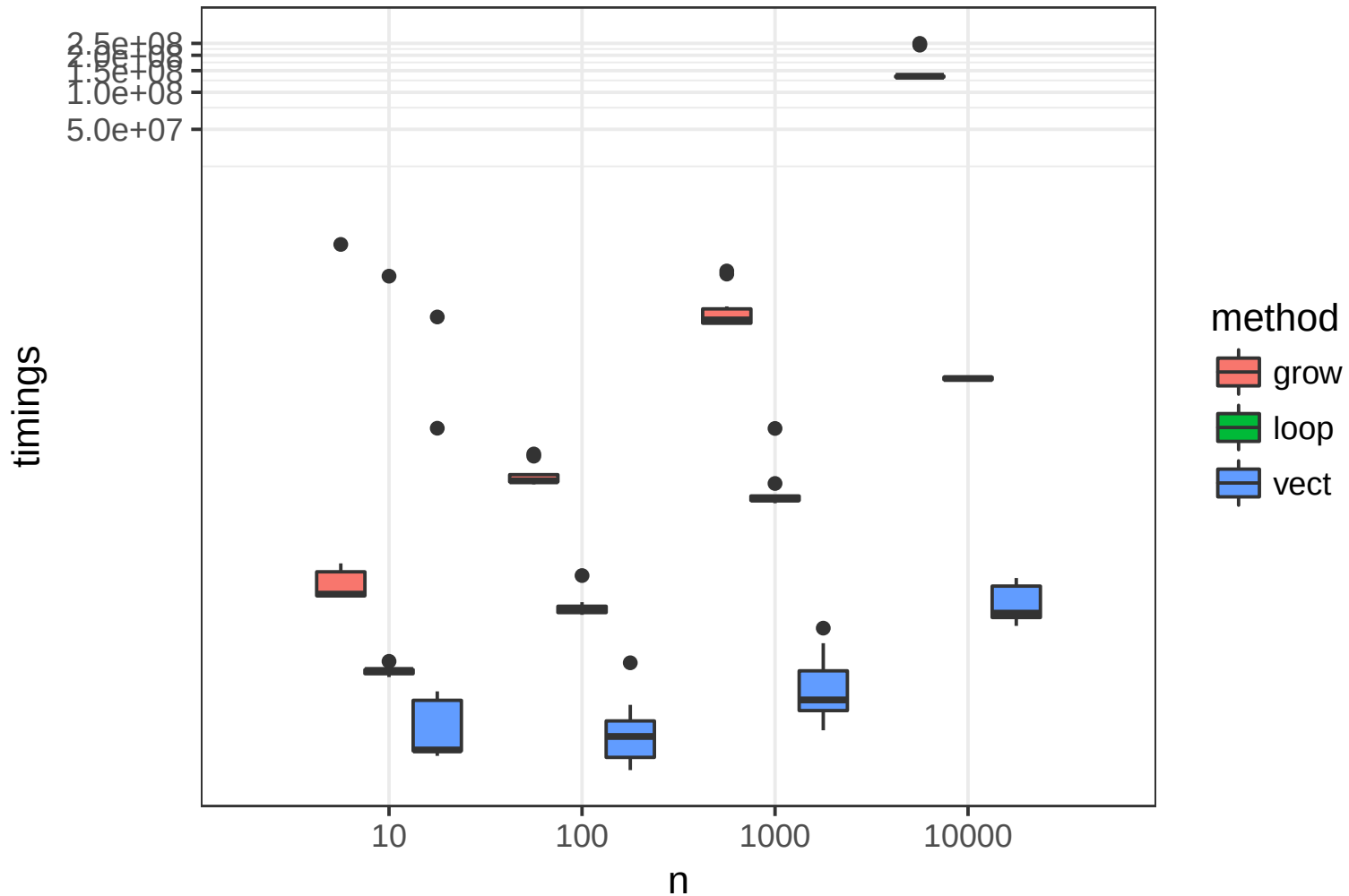
Compile your functions with `base::compiler` II



⇝ Can be set automatically with `compiler::enableJIT(3)`

Preallocate whenever it is possible

```
grow <- function(n) {vec <- numeric(0); for (i in 1:n) vec <- c(vec,i)}
loop <- function(n) {vec <- numeric(n); for (i in 1:n) vec[i] <- i}
vect <- function(n) {1:n}
```



Do not stack objects I

Even if it is tempting when the final size is unknown.

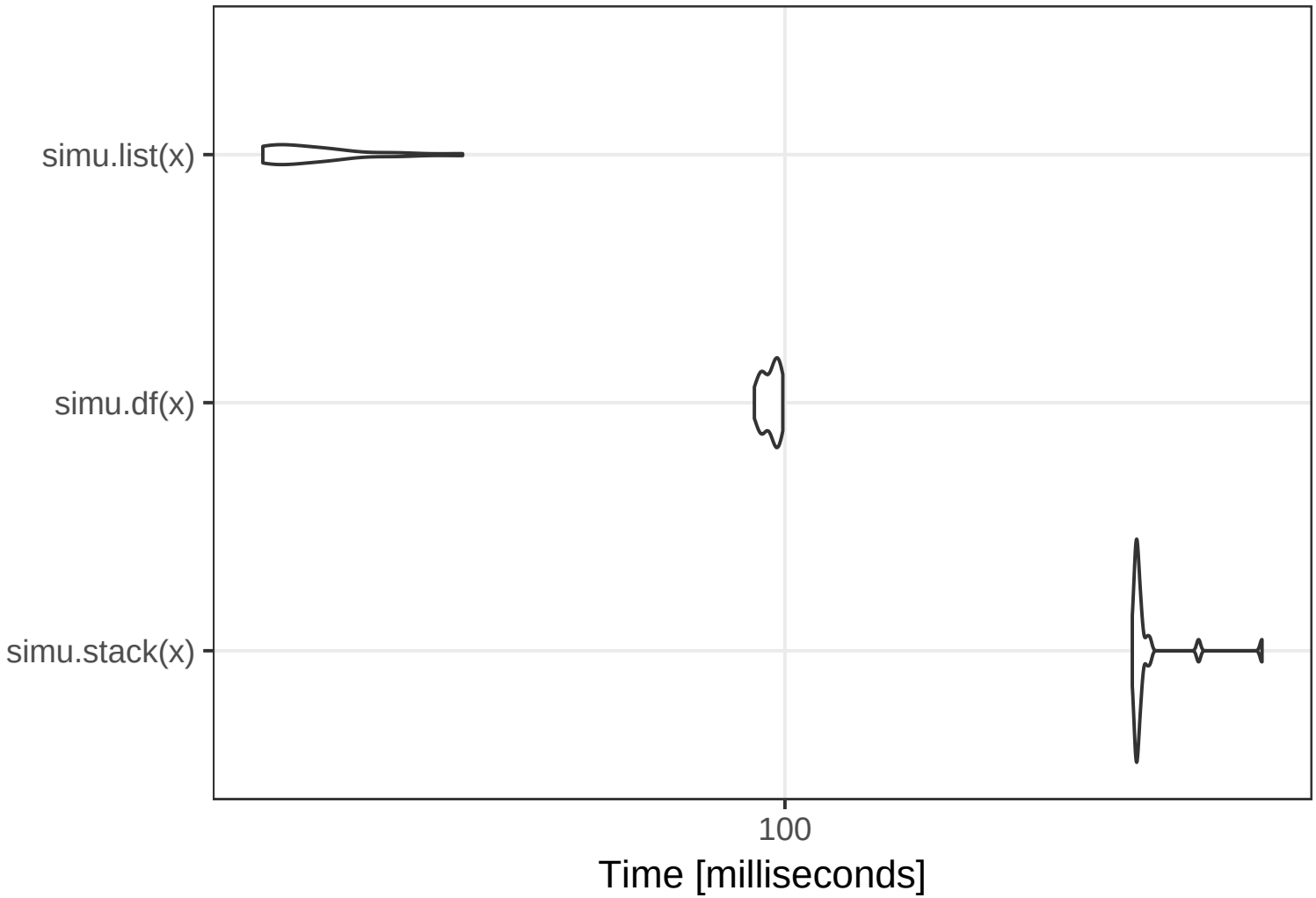
```
simu.stack <- function(x) { ## x is a n x p matrix
  out <- data.frame(mean = numeric(0), sd = numeric(0))
  for (i in 1:n)
    out <- rbind(out, data.frame(mean = mean(x[i,]), sd = sd(x[i, ])) )
  return(out)
}

simu.df <- function(x) {
  out <- data.frame(mean = numeric(n), sd = numeric(n))
  for (i in 1:n)
    out[i, ] <- c(mean = mean(x[i,]), sd = sd(x[i, ]))
  return(out)
}

simu.list <- function(x) {
  my.list <- lapply(1:n, function(i) c(mean(x[i,]), sd(x[i, ])))
  out <- data.frame(do.call(rbind, my.list))
  colnames(out) <- c("mean","sd")
  return(out)
}
```

```
n <- 1000; p <- 10; x <- matrix(rnorm(n*p), n, p)
autoplot(microbenchmark(simu.stack(x), simu.df(x), simu.list(x), times=20))
```

Do not stack objects II



Outline

Quick (and dirty) benchmarking with `system.time()`

One usually relies on the command `system.time(expr)` to evaluate the timings:

```
func.one <- function(n) {return(rnorm(n,0,1))}
func.two <- function(n) {return(rpois(n,1))}

n <- 1000
system.time(replicate(100, func.one(n)))
```

```
##    user  system elapsed
##   0.012   0.000   0.011
```

```
system.time(replicate(100, func.two(n)))
```

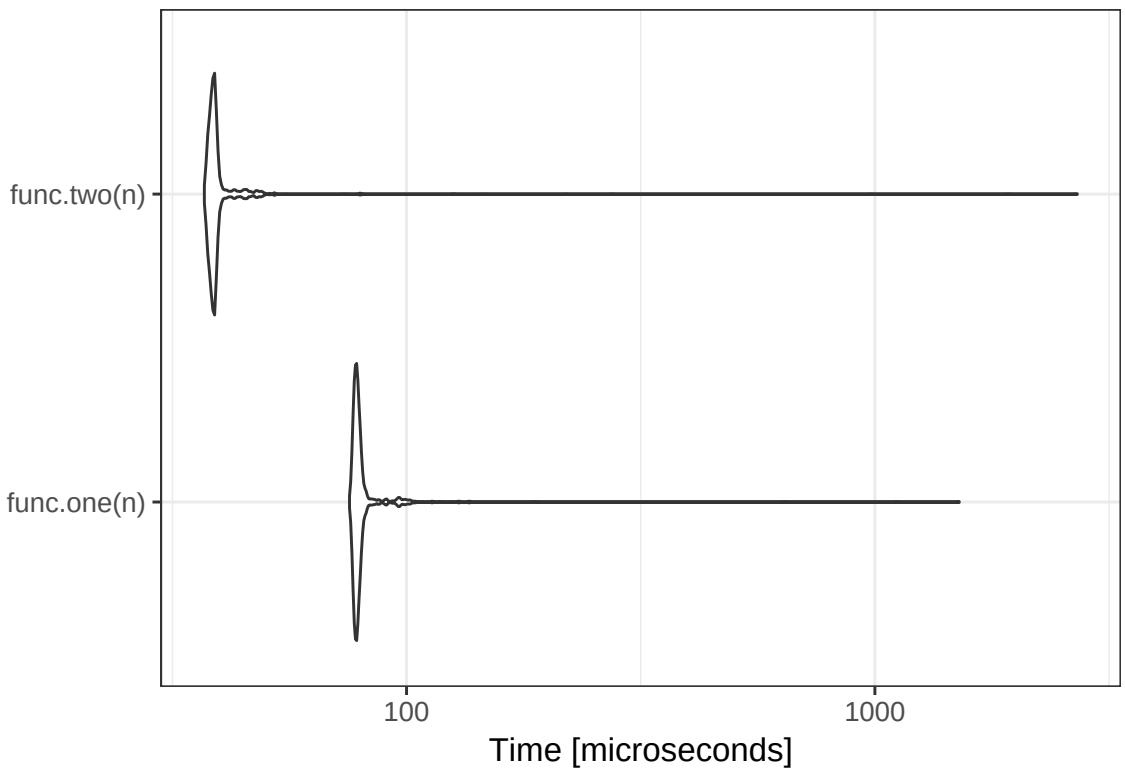
```
##    user  system elapsed
##   0.008   0.000   0.010
```

Quick benchmarking with `microbenchmark`

```
func.one <- function(n) {return(rnorm(n,0,1))}
func.two <- function(n) {return(rpois(n,1))}

library(microbenchmark)

n <- 1000
res <- microbenchmark(func.one(n), func.two(n), times=1000)
ggplot2::autoplot(res)
```



Profile your code

Suppose you want to evaluate which part of the following function is hot:

```
## generate data, center/scale and perform ridge regression
my_func <- function(n,p) {

  require(MASS)

  ## draw data
  x <- matrix(rnorm(n*p),n,p)
  y <- rnorm(n)

  ## center/scale
  xs <- scale(x)
  ys <- y - mean(y)

  ## return ridge's coefficients
  ridge <- lm.ridge(ys~xs+0,lambda=1)

  return(ridge$coef)
}
```

Profile your code with base Rprof I

One can rely on the default Rprof function, with somewhat technical outputs

```
Rprof(file="profiling.out", interval=0.05)
res <- my_func(1000,500)
Rprof(NULL)
```

```
summaryRprof("profiling.out")$by.self
```

```
##                      self.time self.pct total.time total.pct
## "La.svd"                  1.20    68.57       1.20     68.57
## "aperm.default"           0.15     8.57       0.15      8.57
## "is.finite"               0.15     8.57       0.15      8.57
## "na.omit.data.frame"      0.10     5.71       0.10      5.71
## "lapply"                  0.05     2.86       1.75    100.00
## "array"                   0.05     2.86       0.05      2.86
## "rnorm"                   0.05     2.86       0.05      2.86
```

```
summaryRprof("profiling.out")$by.total
```

Profile your code with base Rprof II

```
##                       total.time total.pct self.time self.pct
## "lapply"                    1.75    100.00      0.05     2.86
## "block_exec"                1.75    100.00      0.00     0.00
## "call_block"                1.75    100.00      0.00     0.00
## "evaluate"                  1.75    100.00      0.00     0.00
## "evaluate_call"             1.75    100.00      0.00     0.00
## "evaluate::evaluate"        1.75    100.00      0.00     0.00
## "FUN"                       1.75    100.00      0.00     0.00
## "in_dir"                    1.75    100.00      0.00     0.00
## "knit"                      1.75    100.00      0.00     0.00
## "knitr::knit"               1.75    100.00      0.00     0.00
## "process_file"              1.75    100.00      0.00     0.00
## "process_group"             1.75    100.00      0.00     0.00
## "process_group.block"       1.75    100.00      0.00     0.00
## "rmarkdown::render"         1.75    100.00      0.00     0.00
## "withCallingHandlers"       1.75    100.00      0.00     0.00
## "eval"                      1.70     97.14      0.00     0.00
## "handle"                    1.70     97.14      0.00     0.00
## "my_func"                   1.70     97.14      0.00     0.00
## "timing_fn"                 1.70     97.14      0.00     0.00
## "withVisible"               1.70     97.14      0.00     0.00
## "lm.ridge"                  1.45     82.86      0.00     0.00
## "svd"                       1.35     77.14      0.00     0.00
## "La.svd"                    1.20     68.57      1.20    68.57
## "aperm"                     0.20     11.43      0.00     0.00
## "scale"                     0.20     11.43      0.00     0.00
## "scale.default"             0.20     11.43      0.00     0.00
```

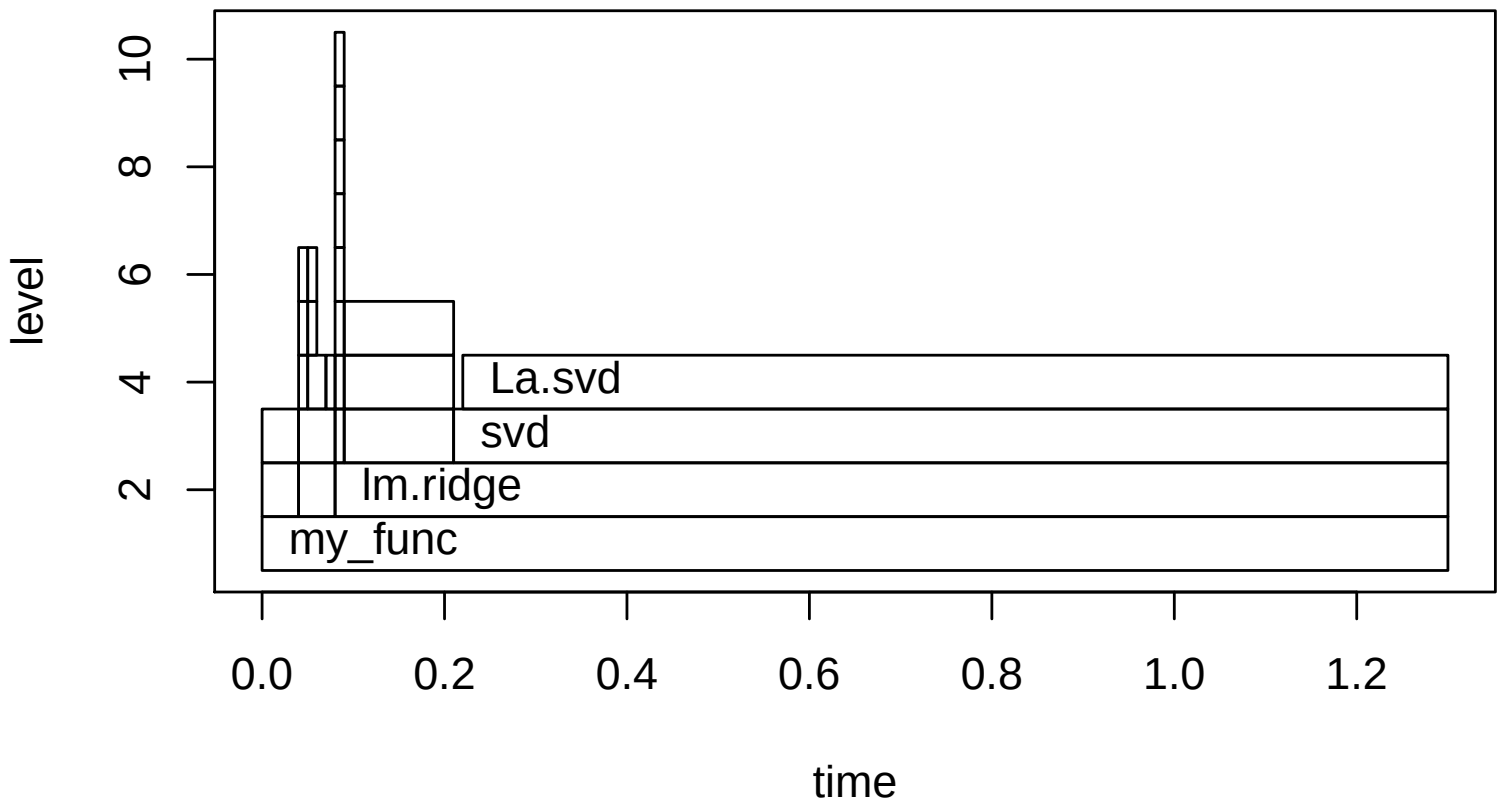
Profile your code with base Rprof III

```
## "aperm.default"           0.15      8.57      0.15      8.57
## "is.finite"               0.15      8.57      0.15      8.57
## "apply"                   0.15      8.57      0.00      0.00
## "na.omit.data.frame"      0.10      5.71      0.10      5.71
## "eval.parent"             0.10      5.71      0.00      0.00
## ".External2"              0.10      5.71      0.00      0.00
## "model.frame.default"     0.10      5.71      0.00      0.00
## "na.omit"                 0.10      5.71      0.00      0.00
## "stats::model.frame"      0.10      5.71      0.00      0.00
## "array"                   0.05      2.86      0.05      2.86
## "rnorm"                   0.05      2.86      0.05      2.86
## "handle_output"           0.05      2.86      0.00      0.00
## "matrix"                  0.05      2.86      0.00      0.00
## "par"                     0.05      2.86      0.00      0.00
## "plot_snapshot"           0.05      2.86      0.00      0.00
## "sweep"                   0.05      2.86      0.00      0.00
## "unlist"                  0.05      2.86      0.00      0.00
## "w$get_new"               0.05      2.86      0.00      0.00
```

Profile your code with `profr`

The *profr* package is maybe a little easier to understand. . .

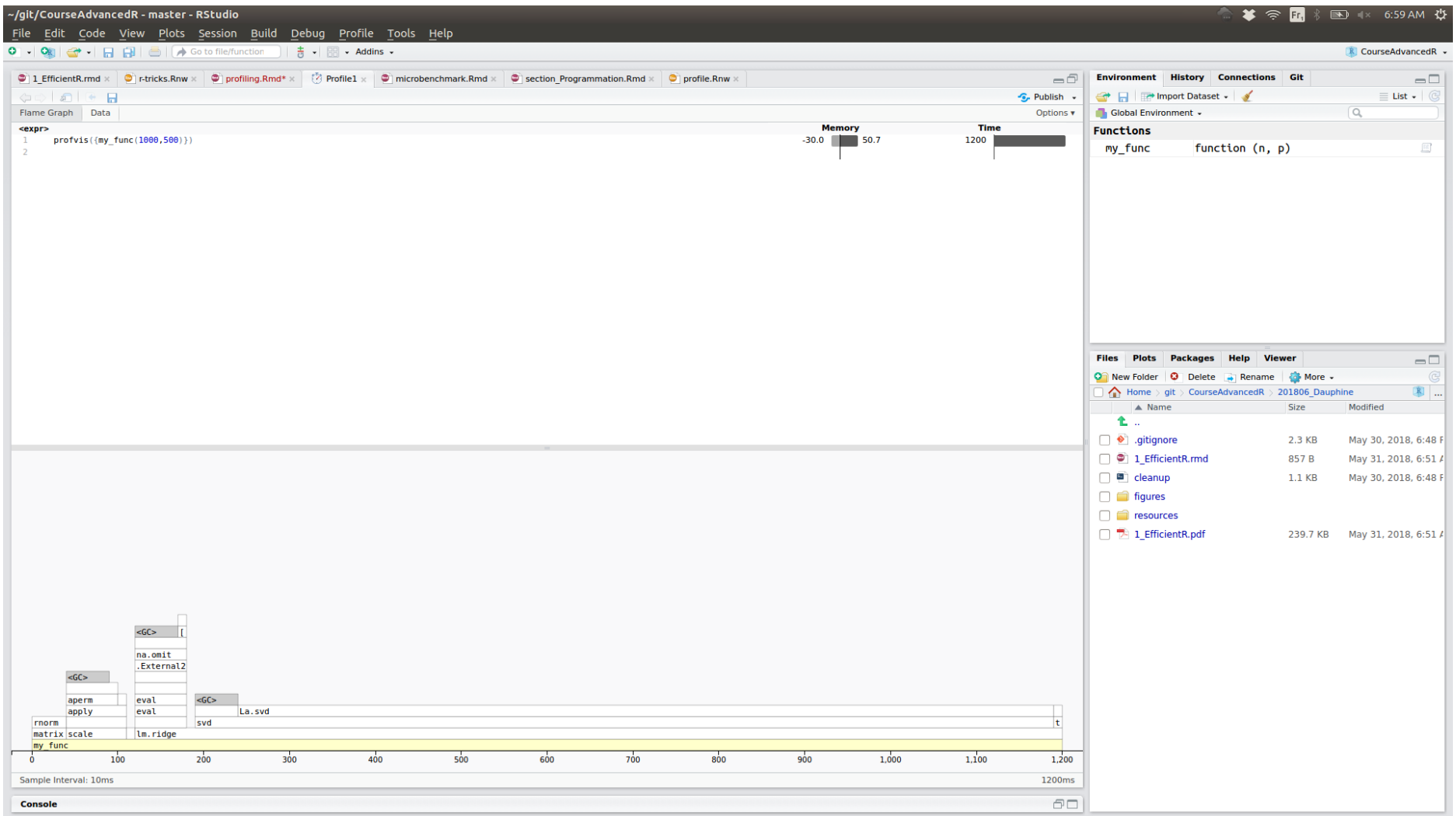
```
library(profr)
profiling <- profr({my_func(1000,500)}, interval = 0.01)
plot(profiling)
```



Profile your code within R Studiow with `profvis`

Profvis integrates the profiling to the Rstudio API

```
library(profvis)
profvis({my_func(1000,500)})
```



Outline

Parallel computing

Usual Roadmap

1. Start up and intialize M 'worker' processes
2. Send data required for each task to the workers
3. Split the task into M roughly equally-sized chunks and send them (including the R code needed) to the workers
4. Wait for all the workers to complete their tasks, and ask them for their results
5. Repeat steps (2–4) for any further tasks
6. Shut down the worker processes

Socketing vs Forking

Two approaches achieving the same goal

The socket approach

- launches a new version of R on each core
- connection is done via networking all happening on your own computer

The forking approach

- copies the entire current version of `R` and moves it to a new core
- several processes acheive the same task resulting in different outputs

$\rightsquigarrow$ Forking is only possible on Unix systems (Linux, Mac OS)

Parallel computing with parallel

Package parallel

- merge of packages multicore and snow
- included in base R and maintained by the R Core team

Check your computer

```
library(parallel) ## embedded with R since version 2.9 or something
cores <- detectCores() ## How many cores do I have?
print(cores)
```

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

⇝ parallel features both socketing (parLapply) and forking (mclapply)

Forking approach with `parallel::mclapply`

Very easy: use parallel features as soon as you do simulations !

Example: estimates the test error from ridge regression

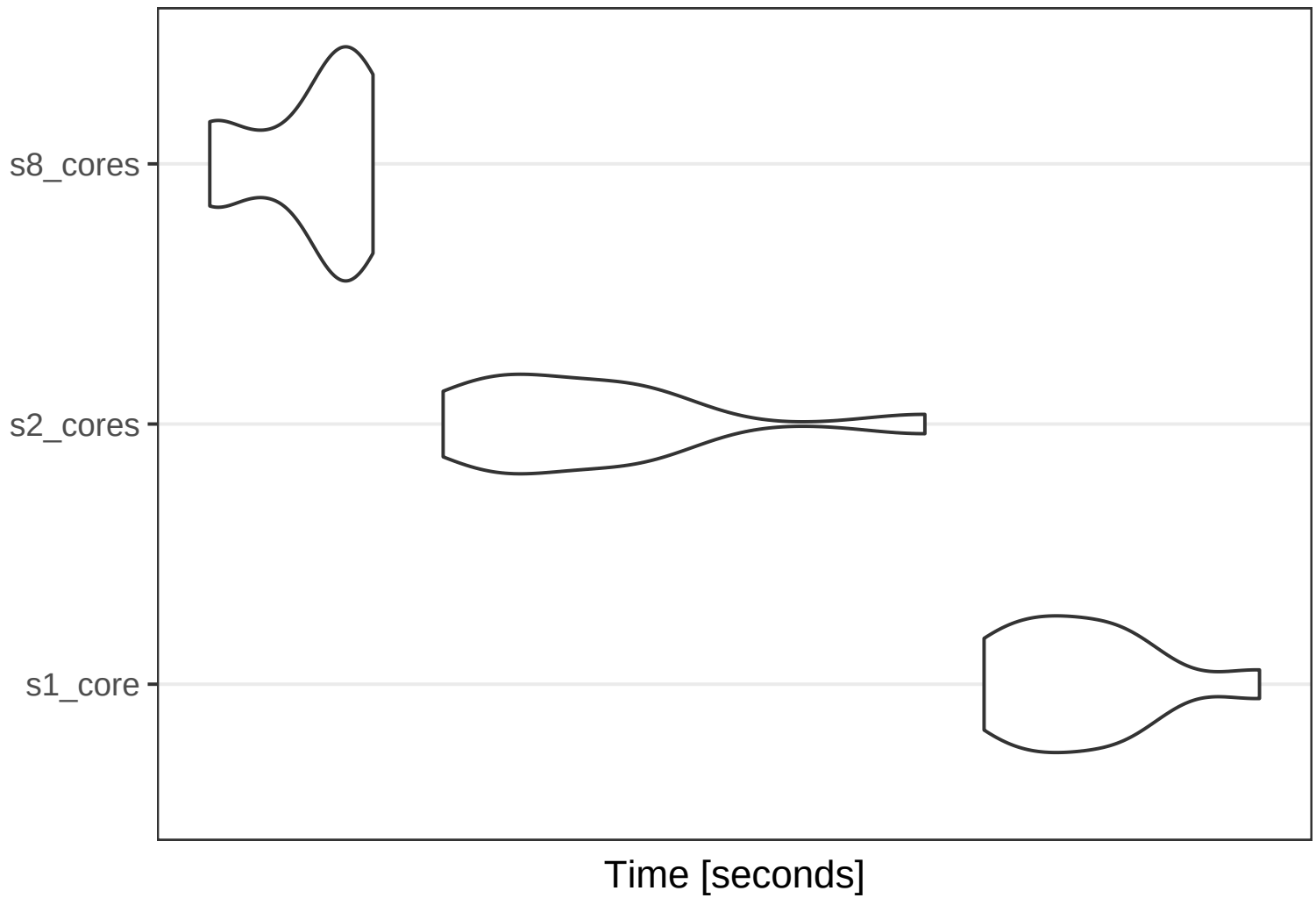
```
one.simu <- function(i) {
  ## draw data
  n <- 1000; p <- 500
  x <- matrix(rnorm(n*p),n,p) ; y <- rnorm(n)
  ## return ridge's coefficients
  train <- 1:floor(n/2)
  test  <- setdiff(1:n,train)
  ridge <- MASS::lm.ridge(y~x+0,lambda=1,subset=train)
  err <- (y[test] - x[test, ] %*% ridge$coef )^2
  return(list(err = mean(err), sd = sd(err)))
}
```

```
head(do.call(rbind, mclapply(1:8, one.simu, mc.cores = cores)), n = 3)
```

```
##       err       sd
## [1,] 13.05205 18.83241
## [2,] 11.55134 16.13871
## [3,] 14.30768 18.50712
```

Forking approach with `parallel::mclapply` (cont'd)

```
library(microbenchmark)
res <- microbenchmark(s1_core  = mclapply(1:8, one.simu, mc.cores = 1),
                      s2_cores = mclapply(1:8, one.simu, mc.cores = 2),
                      s8_cores = mclapply(1:8, one.simu, mc.cores = 8), times = 10)
```



Socket approach with `parallel::parLapply`

Windows users need a bit more code to make it work

A possible option: export from base workspace

```
cl <- makeCluster(4)
clusterExport(cl,"one.simu")
res <- parSapply(cl, 1:8, one.simu) # several parLapply call are possible
stopCluster(cl)
res
```

```
##     [,1]     [,2]     [,3]     [,4]     [,5]     [,6]     [,7]
## err 13.49596 8.664762 11.92576 16.50807 11.66757 11.9488  10.24255
## sd  17.35077 12.70468 17.35847 22.63689 15.63746 16.89484 15.01289
##     [,8]
## err 10.59383
## sd  14.29349
```

Parallel computing with `parallel`: final remarks

- Parallelize pieces of code complex enough
- Do not choose stupidly the number of cores
- Screen outputs are lost in `Rstudio`: use `pbmcapply` (progress bar)

```
pbmcapply::pbmcmapply(1:8, FUN = one.simu, mc.cores = 2)
```

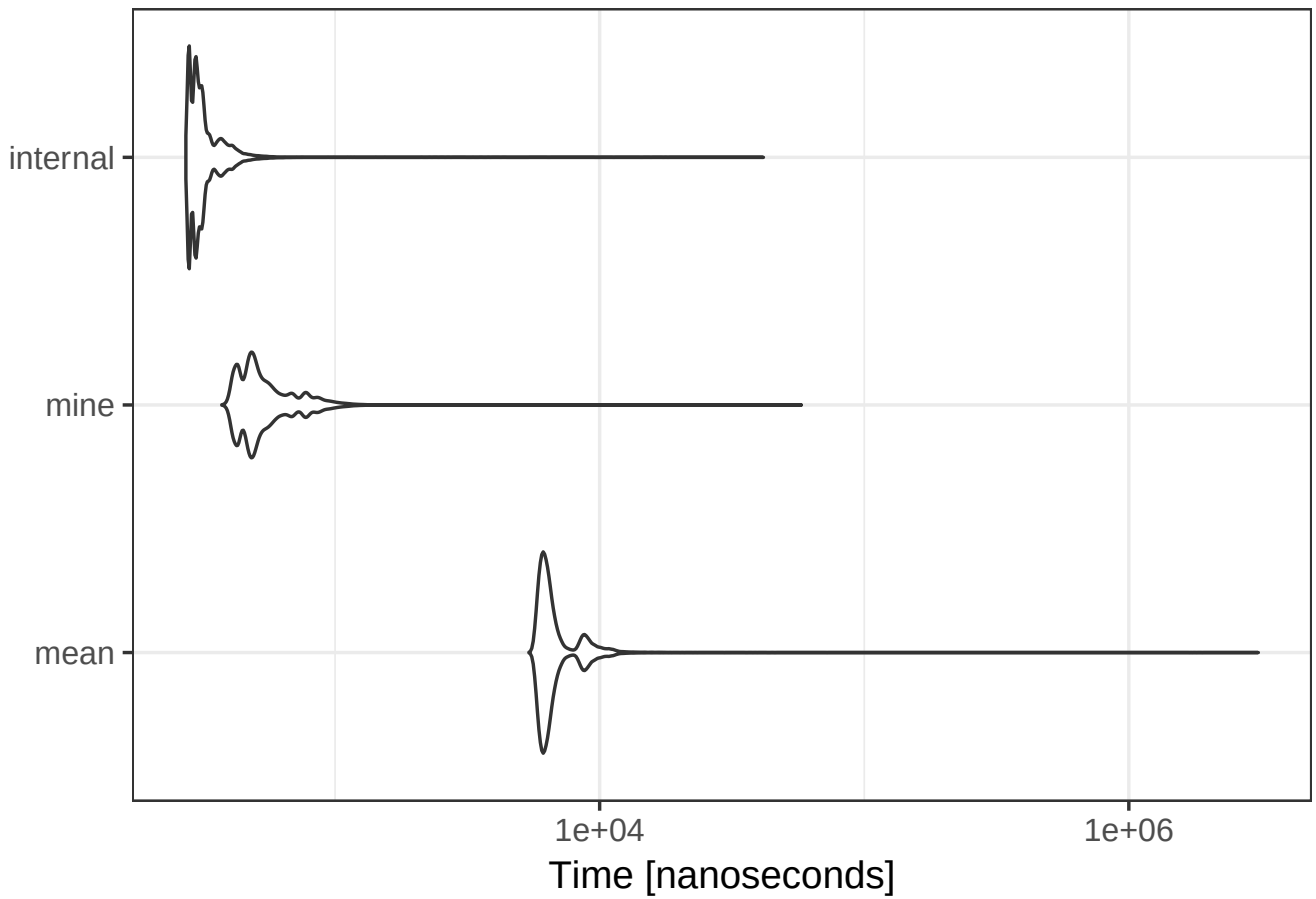
```
##     [,1]     [,2]     [,3]     [,4]     [,5]     [,6]     [,7]
## err 13.30902 9.801744 10.50707 11.04491 10.75684 11.29892 15.66317
## sd  19.76283 14.13212 14.63621 15.87187 13.71803 15.57207 21.81625
##     [,8]
## err 11.09748
## sd  14.70388
```

Outline

Internal function are faster

Function defined internally are sometimes incredibly faster (written in C), but cannot by called in packages submitted to CRAN.

```
x <- rnorm(100)
res <- microbenchmark(mean = mean(x),
                      mine = sum(x)/length(x),
                      internal = .Internal(mean(x)), times = 1e+05)
```

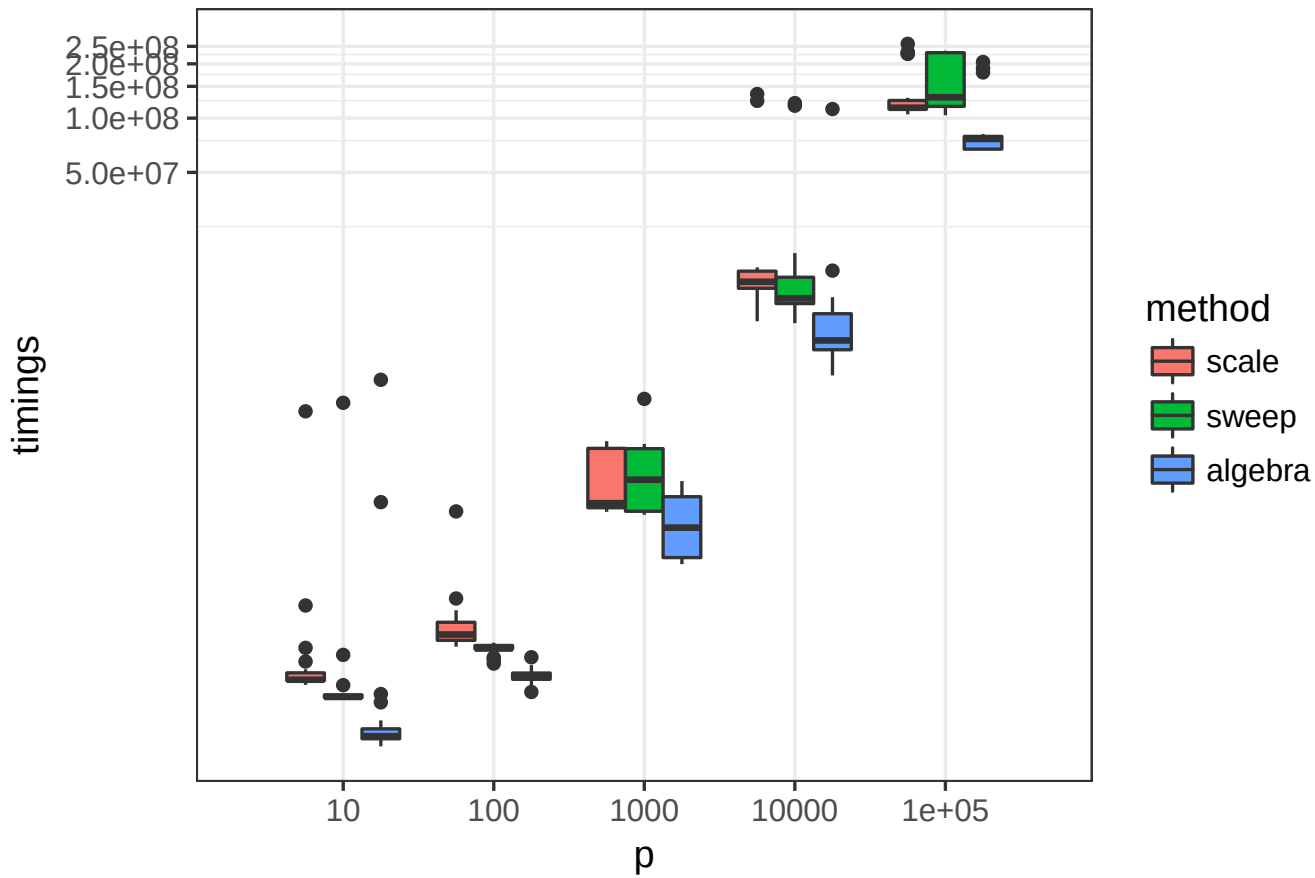


Mind some algebra

Sweep is a general way to apply a statistic on a given dimension of an array.

```
center1 <- function(x) return(scale(x, colMeans(x), FALSE))
center2 <- function(x) return(sweep(x, 2, colMeans(x), "-", check.margin = FALSE))
center3 <- function(x) return(x - outer(rep(1, nrow(x)), colMeans(x)) )

seq.p <- 10^(1:5); n <- 100; times <- 20
```

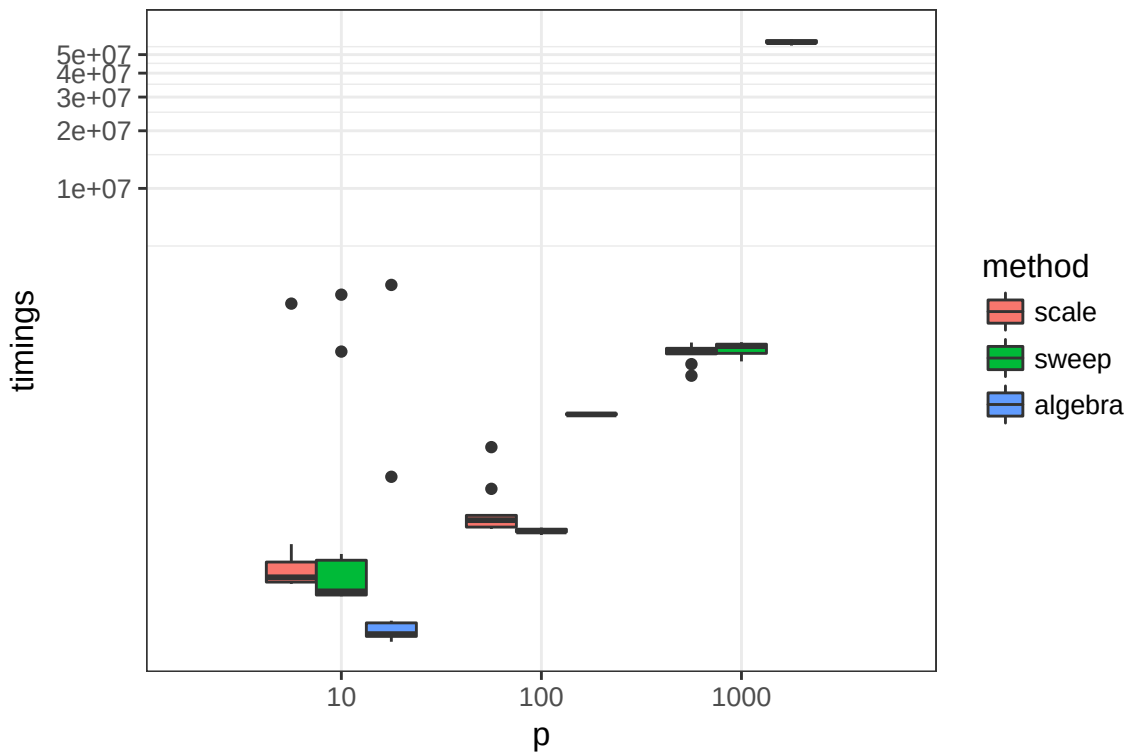


Algebra does not always pay

Example for scaling a matrix

```
scale1 <- function(x) return(scale(x, FALSE, colSums(x^2)))
scale2 <- function(x) return(sweep(x, 2, colSums(x^2), "/", check.margin=FALSE))
scale3 <- function(x) return(x %*% diag(1/colSums(x^2)) )

seq.p <- 10^(1:3); n <- 100; times <- 20
```

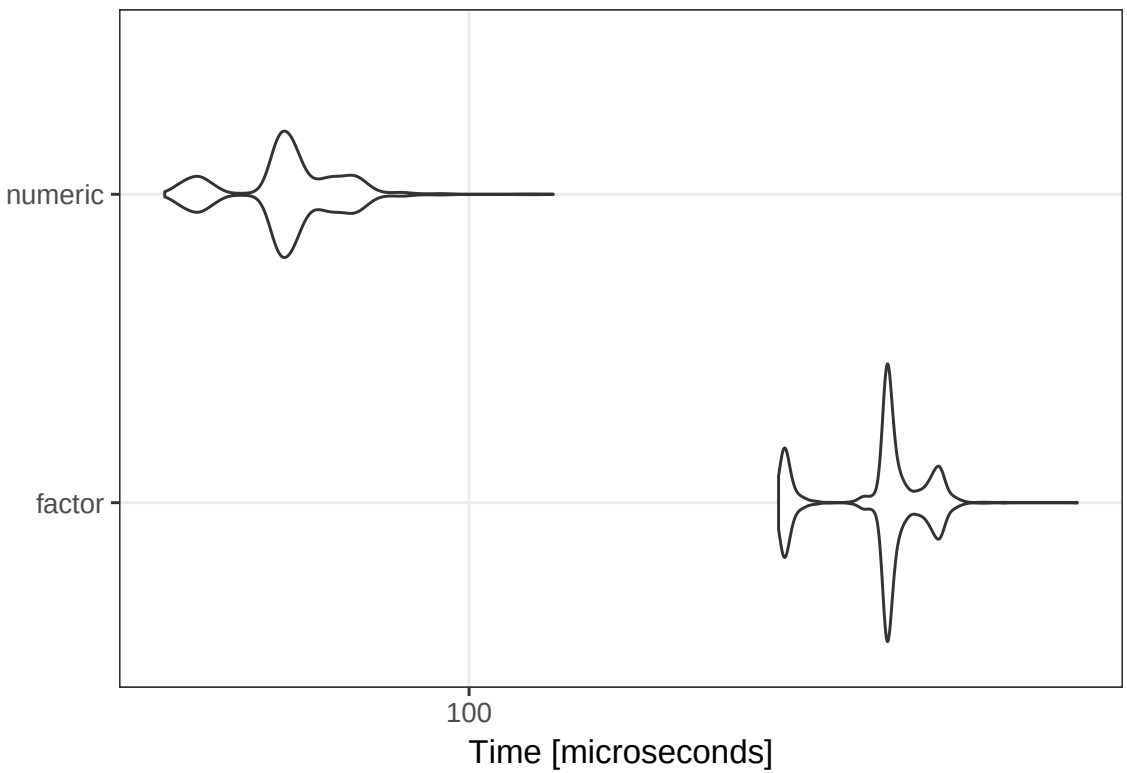


Outline

Factor conversion are slow (`nlevels`)

Do not convert large vector to `factor` if you need to perform just one operation on it.

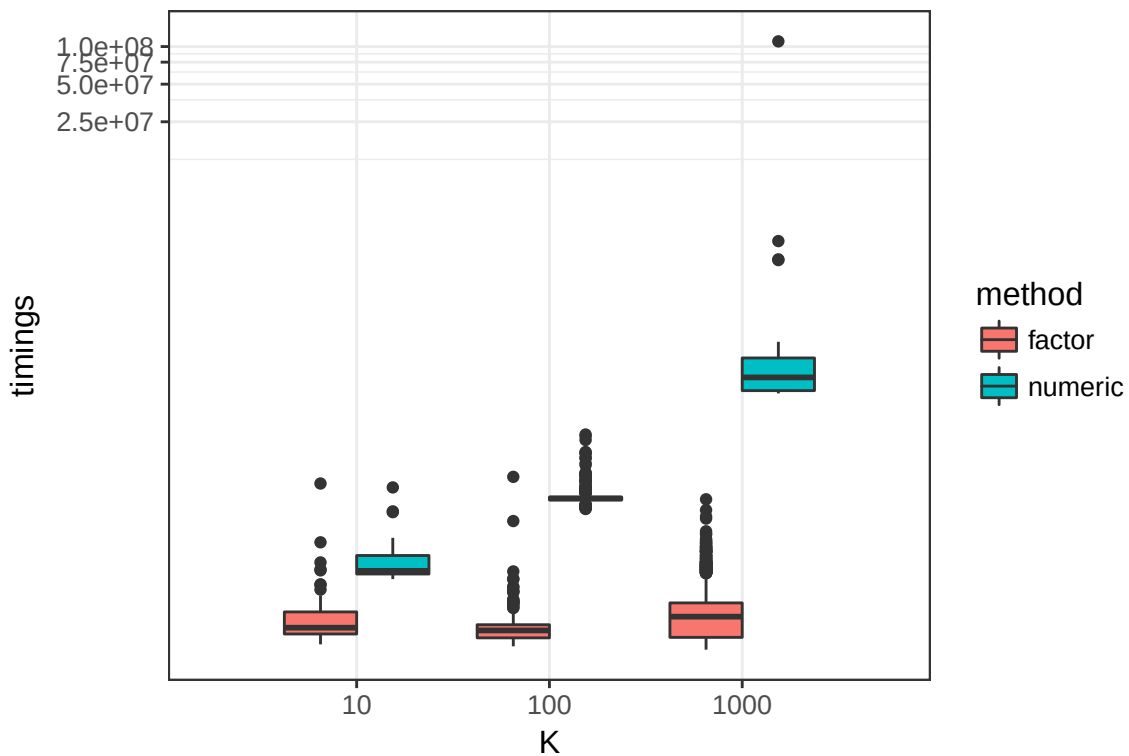
```
n <- 1000; K <- 10
autoplot(microbenchmark(
  factor = nlevels(factor(sample(1:K, n, rep=TRUE))),
  numeric = length(unique(sample(1:K, n, rep=TRUE))), times=1000)
)
```



Operations on factors are fast (e.g. `nlevels`)

Use `factor` if you need repeated operations on the same vector.

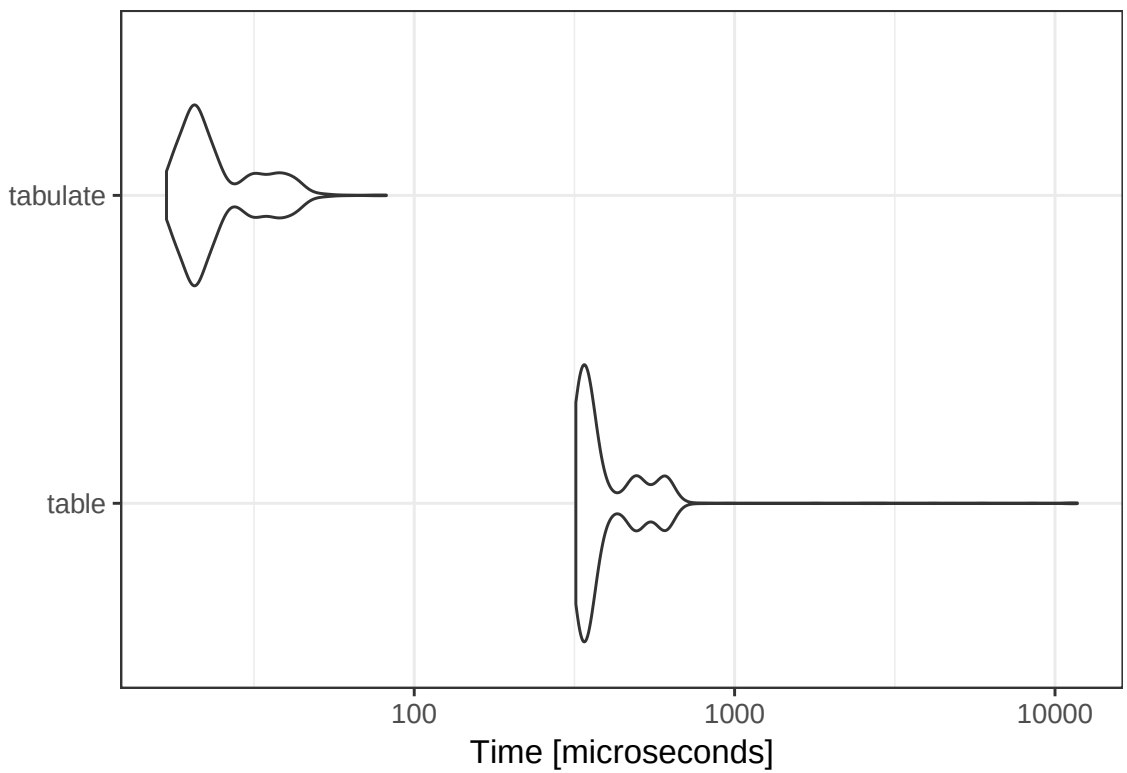
```
nk <- 20
seq.K <- c(10,100,1000)
res <- do.call(rbind, lapply(seq.K, function(K) {
  x1 <- rep(1:K,nk)
  x2 <- factor(x1)
  out <- microbenchmark(factor  = nlevels(x2),
                        numeric = length(unique(x1)), times=1000)
  return(data.frame(method = out$expr, timings = out$time, K = factor(K)))
}))
```



Prefer `tabulate` to `table` whenever you can

`table` is a complex function that should not be use for simple operations like counting the occurrences of integers in a vector.

```
n <- 1000; K <- 10
autoplot(
  microbenchmark(
    table    = table   (sample(1:K, n, rep=TRUE)),
    tabulate = tabulate(sample(1:K, n, rep=TRUE)),
  times=1000)
)
```



R masks the numerical errors

by printing a *convenient* summary of objects

```
7/13
```

```
## [1] 0.5384615
```

```
print(7/13, digits=16)
```

```
## [1] 0.5384615384615384
```

So do not use binary operator to compare floats because

```
.1 == .3/3
```

```
## [1] FALSE
```

```
print(.3/3, digits=16)
```

```
## [1] 0.09999999999999999
```

Try

```
all.equal(.1, .3/3)
```

```
## [1] TRUE
```

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```

Try

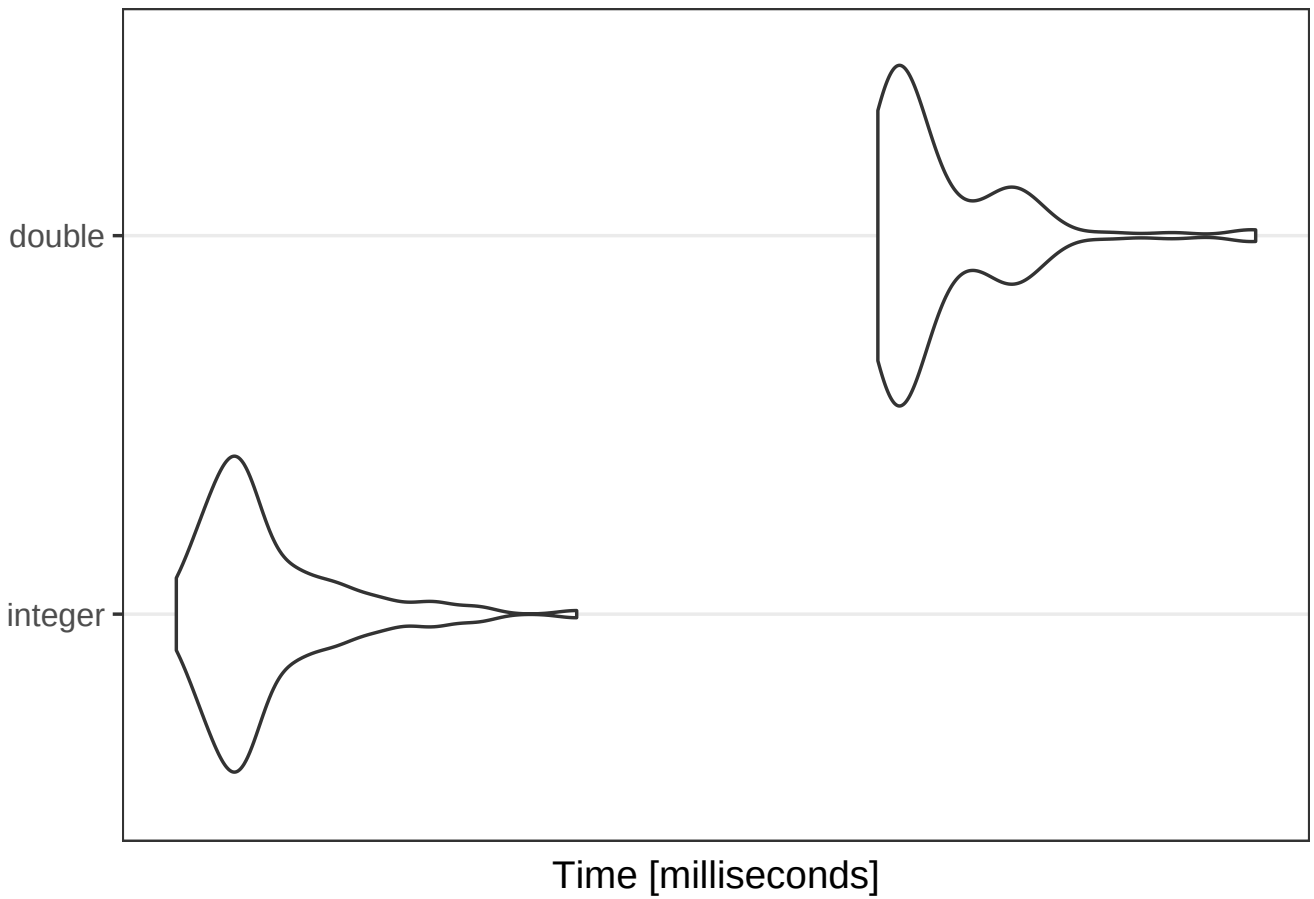
```
all.equal(.1, .3/3)
```

```
## [1] TRUE
```

Variable type matters

Sorting a vector of integers is much faster than a vector of double, but R is so permissive that you might loss the gain if you do not take care:

```
x_int <- sample.int(1e7, 1e7)
x_dbl <- as.numeric(x_int)
res <- microbenchmark(integer = order(x_int),
                      double = order(x_dbl))
```



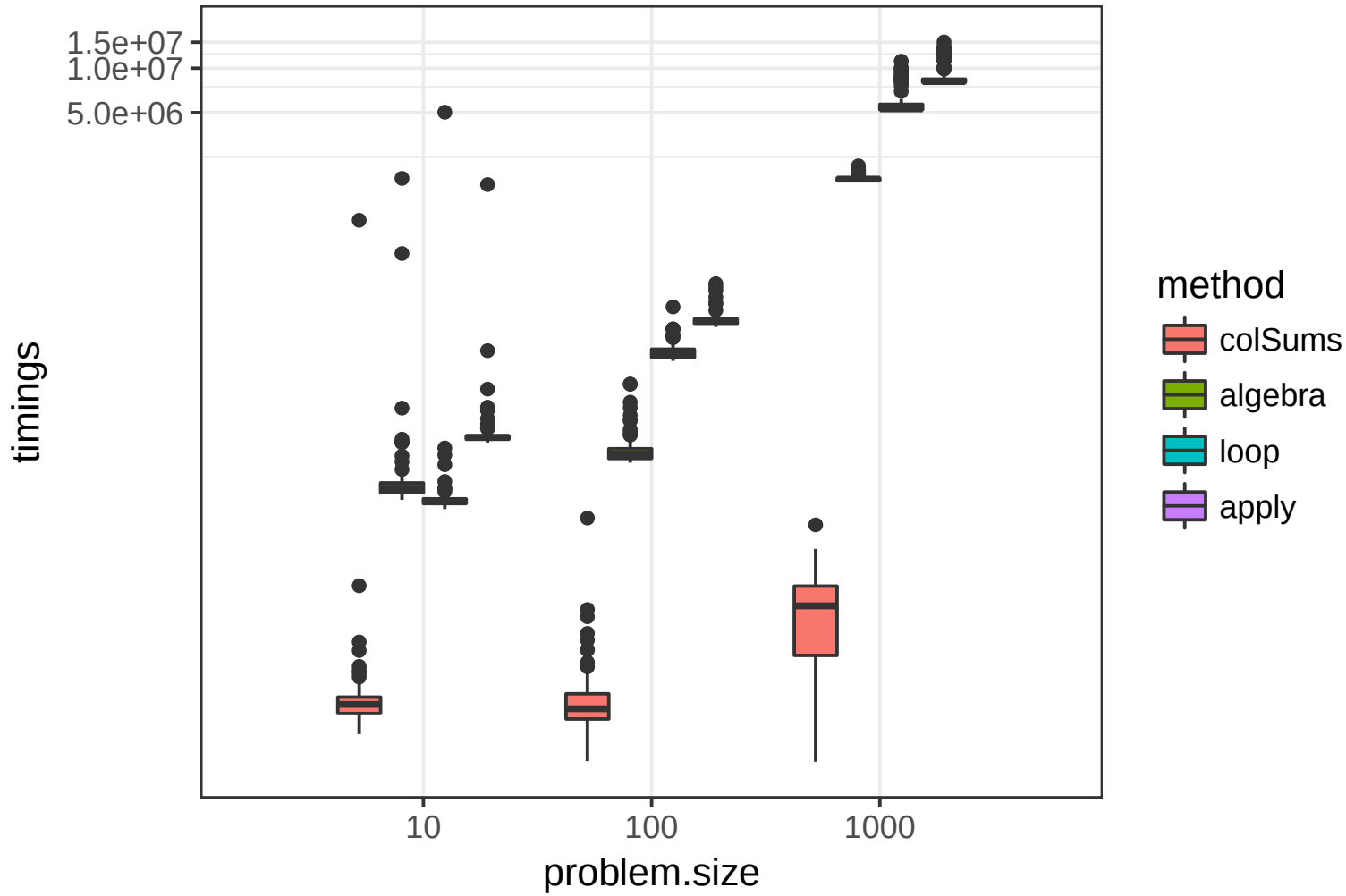
Outline

The row/colSums family I

col/rowSums, col/rowMeans and their extensions in the matrixStats package (rank,max,min, etc.) are very efficient.

```
colSums.default <- function(x) return(colSums)
colSums.algebra <- function(x) return(crossprod(rep(1,nrow(x)), x))
colSums.apply   <- function(x) return(apply(x,2,sum))
colSums.loop    <- function(x) {
  res <- rep(0,ncol(x))
  for (i in 1:ncol(x)) {
    res[i] <- sum(x[,i])
  }
  res
}
```

The row/colSums family II



The secret function `rowsum` I

`rowsum` (not to be confused with `rowSums`) computes sums in a vector split according a grouping variable (work for matrices).

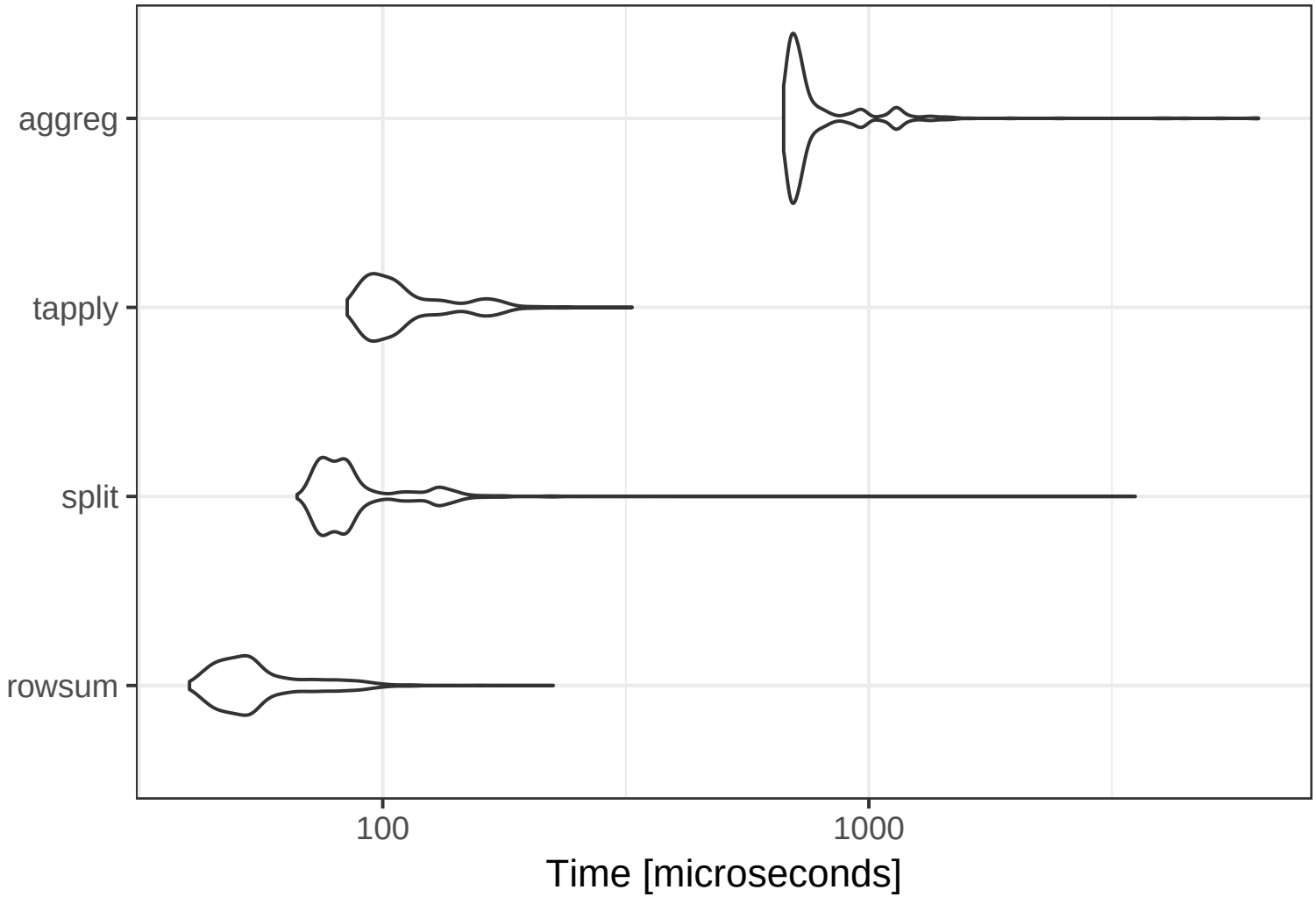
```
vec <- runif(1000)
grp <- sample(1:5, 1000, TRUE)
print(c(rowsum(vec, grp)))
```

```
## [1] 119.25299  92.34115  90.63687 115.88947 105.82181
```

There are many possibilities to perform the required task:

```
res <- microbenchmark(
 rowsum = rowsum(vec, grp),
 split  = sapply(split(vec, grp), sum),
 tapply = tapply(vec, grp, sum),
 aggreg = aggregate(vec, list(grp), sum),
times = 1000)
```

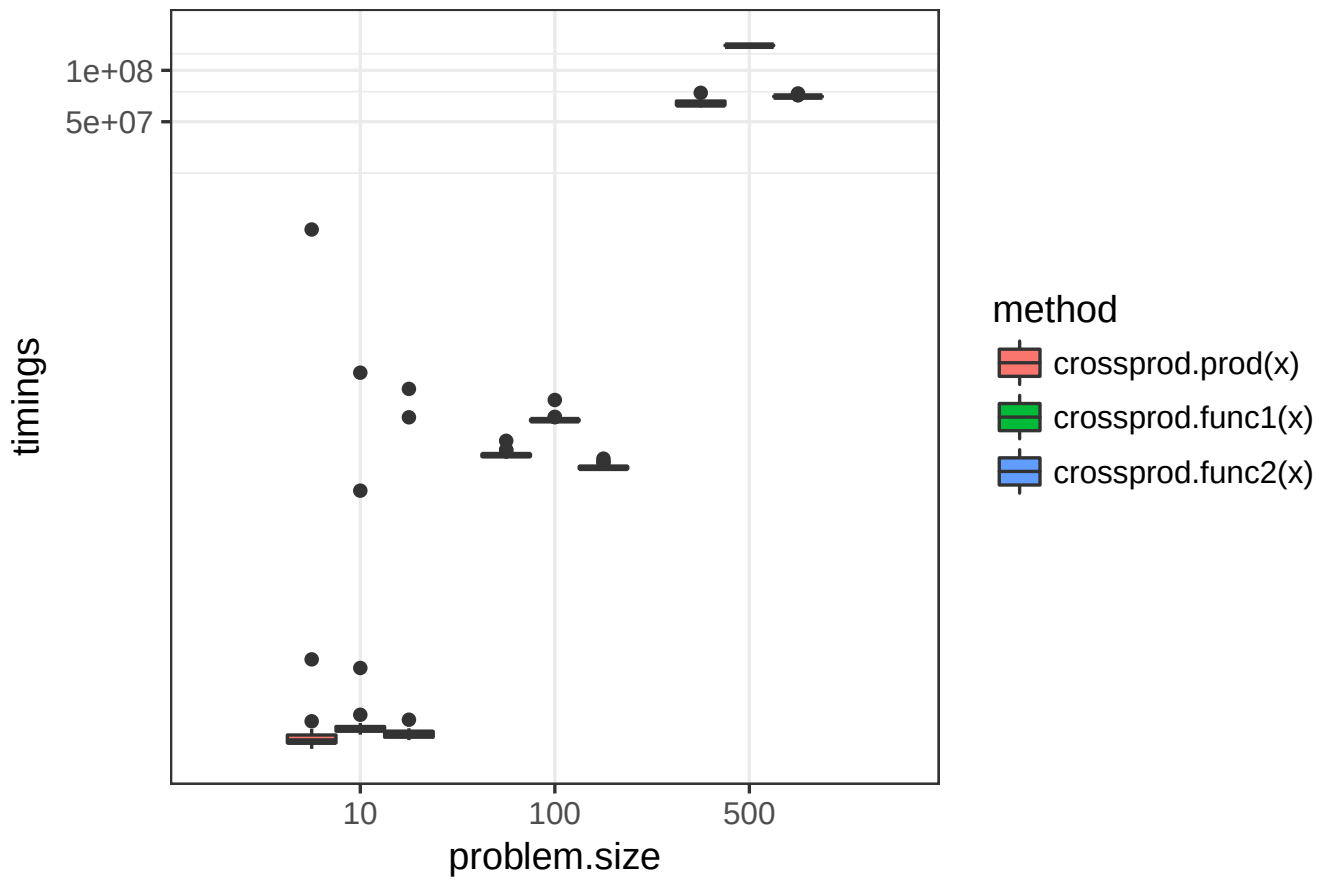
The secret function `rowsum` II



Dedicated function: cross-product

Generally (a bit) fastest than \% * \% !

```
crossprod.prod <- function(x) return(t(x) %*% x)
crossprod.func1 <- function(x) return(crossprod(x,x))
crossprod.func2 <- function(x) return(crossprod(x))
```



Dedicated function: inverting a PD matrices I

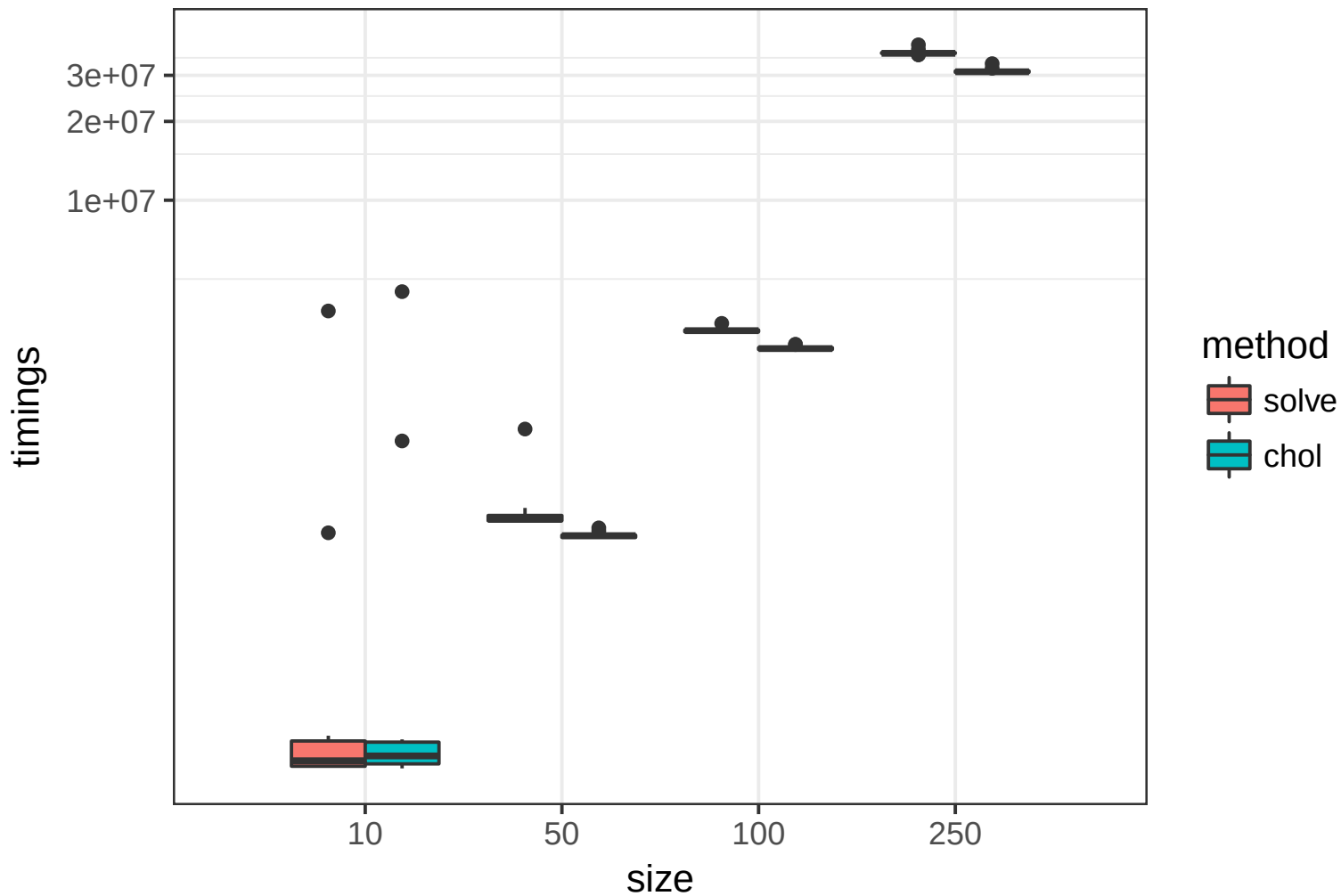
Use a Cholesky factorization

```
use.chol <- function(n,p) {
  x <- matrix(rnorm(n*p),n,p)
  xtx <- crossprod(x)
  return(chol2inv(chol(xtx)))
}

use.solve <- function(n,p) {
  x <- matrix(rnorm(n*p),n,p)
  xtx <- crossprod(x)
  return(solve(xtx))
}

bench.p.fixed <- function(p, times) {
  res <- microbenchmark(solve = use.solve(2*p,p),
                        chol  = use.chol (2*p,p), times=times)
  return(data.frame(method  = res$expr,
                    timings = res$time,
                    size    = rep(as.character(p),times)))
}
```

Dedicated function: inverting a PD matrices II

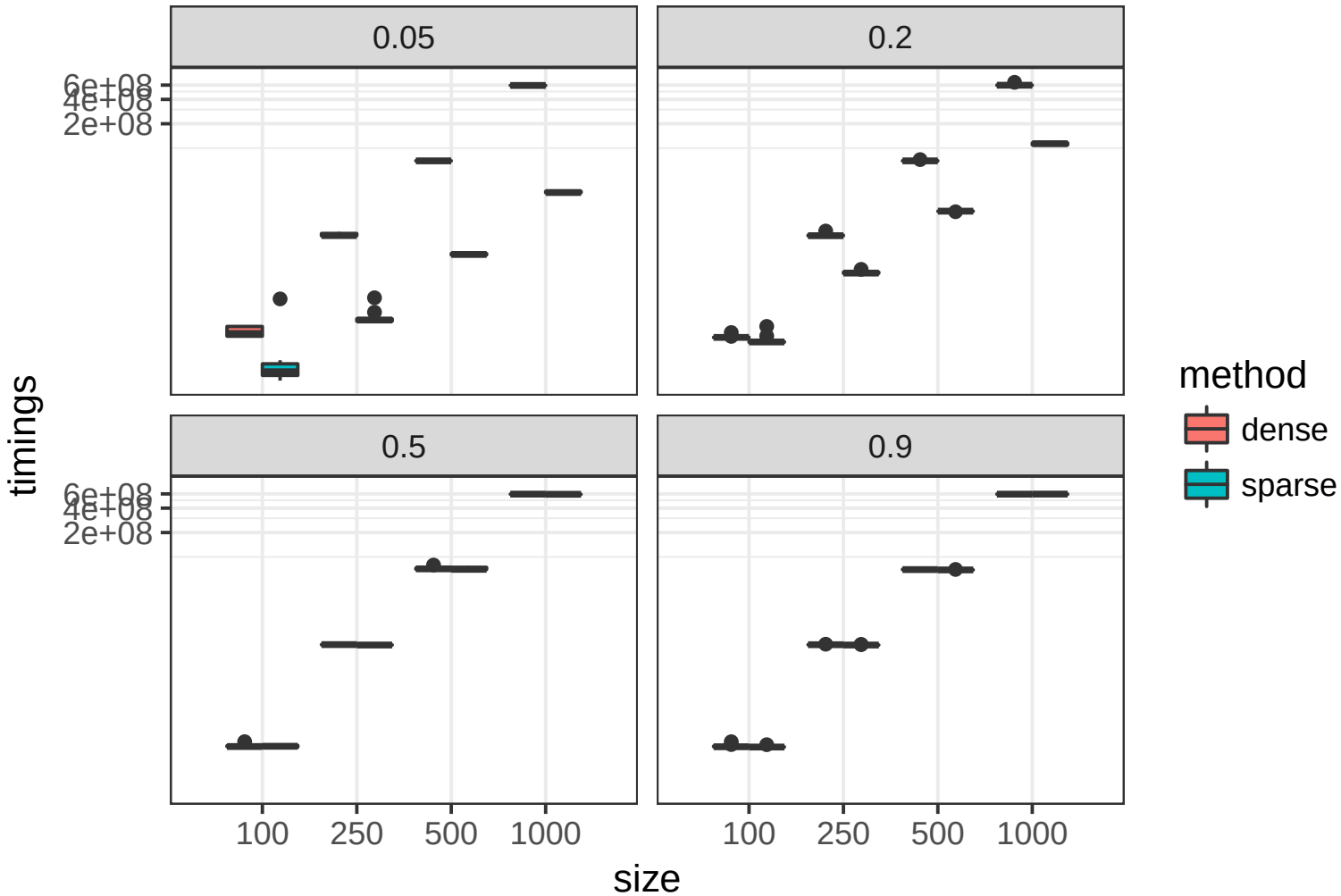


The Matrix package I

Propose a collection of functions for of matrix algebra adapted to the type of matrix at hand (sparse, diagonal, triangular, block diagonal, etc.)

```
library(Matrix)
bench.par.fixed <- function(par) {
    n <- par$n; density <- par$density
    data <- sample(c(0,1),n**2,rep=TRUE,prob=c(1-density,density))
    x.dense  <- matrix(data,n,n)
    x.sparse <- Matrix(data,n,n)
    res <- microbenchmark(dense  = crossprod(x.dense) ,
                          sparse = crossprod(x.sparse), times=10)
    return(data.frame(method  = res$expr,
                      timings = res$time,
                      size    = n       ,
                      density = density ))
}
```

The Matrix package II



Outline

Interfacing C++ with R is *really* easy I

For a vector $\mathbf{x} = (x_1, \ldots, x_n)$, consider the simple task of computing

$$y_k = \sum_{i=1}^{k} \log(x_i), \quad k = 1, \ldots, n.$$

One can easily integrate some C++ version of this code with Rcpp.

```
library(Rcpp)
rcpp <- cppFunction('NumericVector rcpp(NumericVector x) {
  using namespace Rcpp;

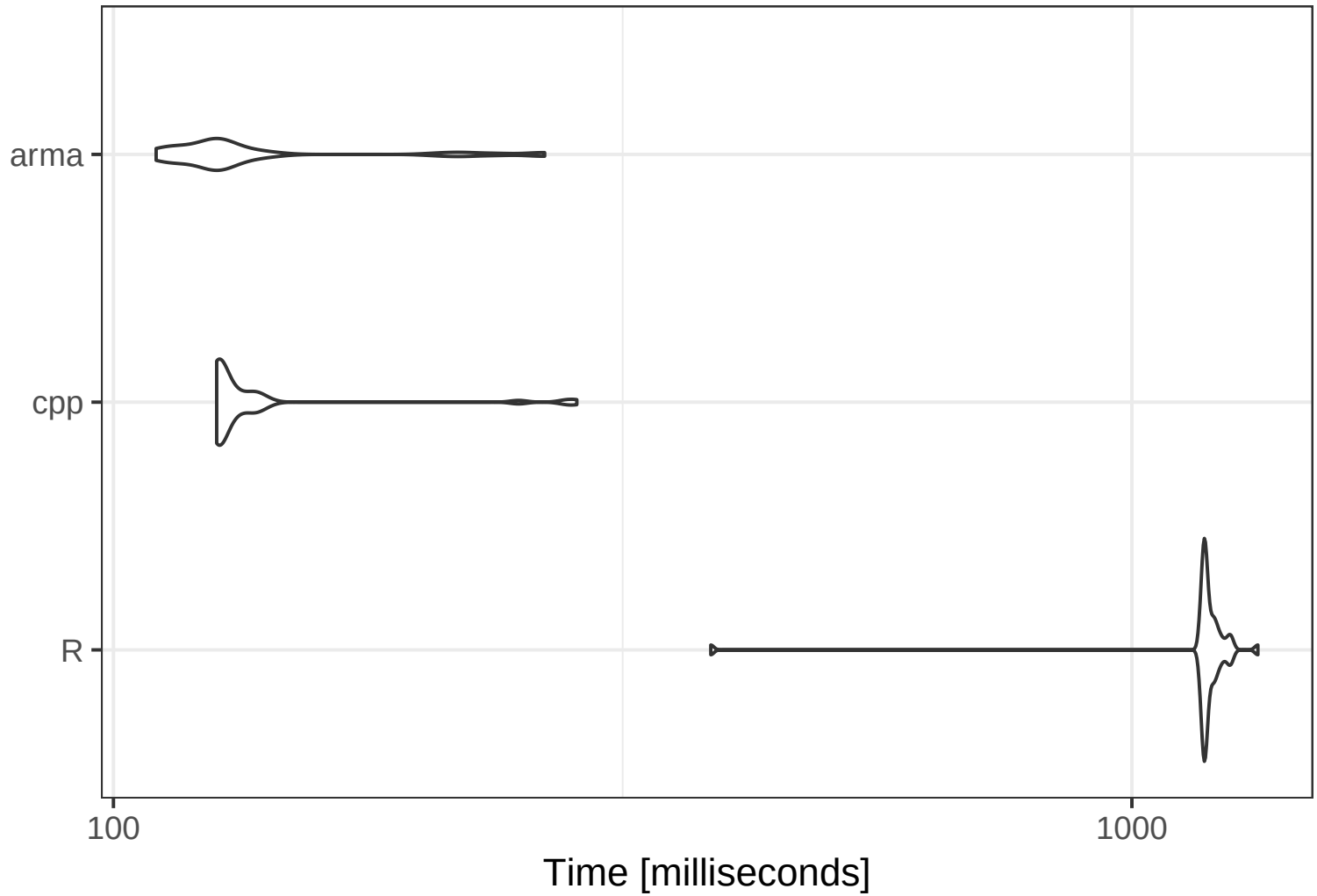
  int n = x.size() ;
  NumericVector res(x) ;
  res(0) = log(x(0));
  for (int i=1; i<n; i++) {
    res(i) = res(i-1) + log(x(i)) ;
  }
  return(wrap(res)) ;
}')
```

Interfacing C++ with R is *really* easy II

```
library(RcppArmadillo)
Arma <- cppFunction(depends = "RcppArmadillo", 'NumericVector Arma(NumericVector x) {
  using namespace Rcpp;
  using namespace arma;
  return(wrap(cumsum(log(as<vec>(x))))) ;
}')
```

```
x <-  runif(1e7, 1,2)
res <- microbenchmark(R = cumsum(log(x)), cpp = rcpp(x), arma = Arma(x), times = 40)
print(autoplot(res))
```

Interfacing C++ with R is *really* easy III



Interfacing C++ with R is *really* easy I

Example that couples C++ + algebraic tricks

Let $\mathbf{T}$ be an $n \times n$ lower triangular matrix with nonzero elements equal to one. We need fast computation of

$$\text{vec}(\mathbf{T}\mathbf{B}\mathbf{T}^\top) = (\mathbf{T} \otimes \mathbf{T}) \times \text{vec}(\mathbf{B}).$$

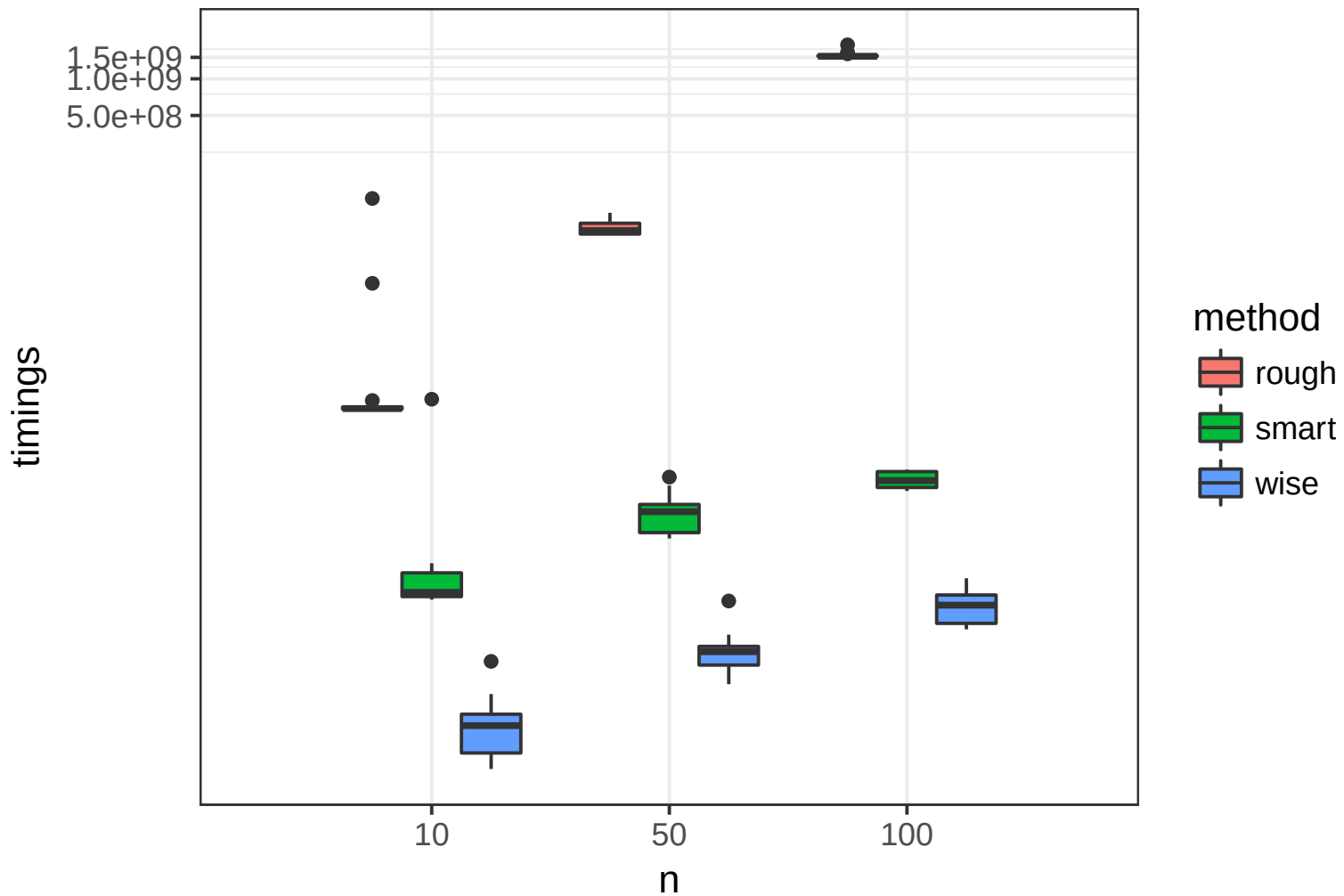
```
library(Matrix); library(inline); library(RcppArmadillo)

prod.rough <- function(B) {
    n <- ncol(B); T <- bandSparse(n,k=(-n+1):0)
    return(kronecker(T,T) %*% as.vector(B))}

prod.smart <- function(B) {
    return(as.vector(apply(apply(B,1,cumsum),1,cumsum)))}

prod.wise <- cxxfunction(signature(B="matrix"),'
  using namespace Rcpp;
  using namespace arma;
  return(wrap(vectorise(cumsum(cumsum(as<mat>(B),0),1)))) ;
'   , plugin="RcppArmadillo")
```

Interfacing C++ with R is *really* easy II



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