Scalable BFAST: R package optimizations and array-based data management

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Topics

Part I: BFAST R package optimizations

Part II: Scalable EO data management with SciDB

Part III: Hands-on with SciDB, Landsat, and BFAST

1. SciDB installation (with Docker)
2. Data ingestion
3. Analysis (practical part)

Online Material

Slides, reports, and tutorial available at:

- https://github.com/appelmar/scalbf-wur/
- https://appelmar.github.io/scalbf-wur/

Overview

- Change detection and monitoring are computationally intensive operations:
  - Example from bfastSpatial package with the TURA dataset [1,2] (148 x 143 pixels and 166 images, approx. 4x4 km, 7 MB) takes around 20 mins on this computer

→ Change detection / monitoring on national scale?

→ Optimize R package and enable scalable distributed processing of large areas

[1] DeVries, B., Verbesselt, J., Kooistra, L., & Herold, M. (2015). Robust monitoring of small-scale forest disturbances in a tropical montane forest using Landsat time series. Remote Sensing of Environment, 161, 107-121.

[2] Dutrieux, L. & DeVries, B. (2014), bfastSpatial: Set of utilities and wrappers to perform change detection on satellite image time-series.

BFAST R package

`bfast()`

Main input:

- time series of response variable
- seasonal model
- **type of fluctuation process**
- maximum number of breaks / minimum segment size between breaks

Main output:

- time, number, and magnitude of changes

`bfastmonitor()`

Main input:

- time series of response variable (and optional regressors)
- start of the monitoring period
- model formula
- **type of monitoring process:** OLS-CUSUM, OLS-MOSUM, RE, ME
- **model for identifying a stable history** (Reverse CUSUM, Bai and Perron, all, …)

Main output:

- change magnitude, change date (if any)

Identifying computational bottlenecks with profiling

- Profiling = executing R expressions and regularly checking which function is currently being evaluated (e.g. every 5 ms)

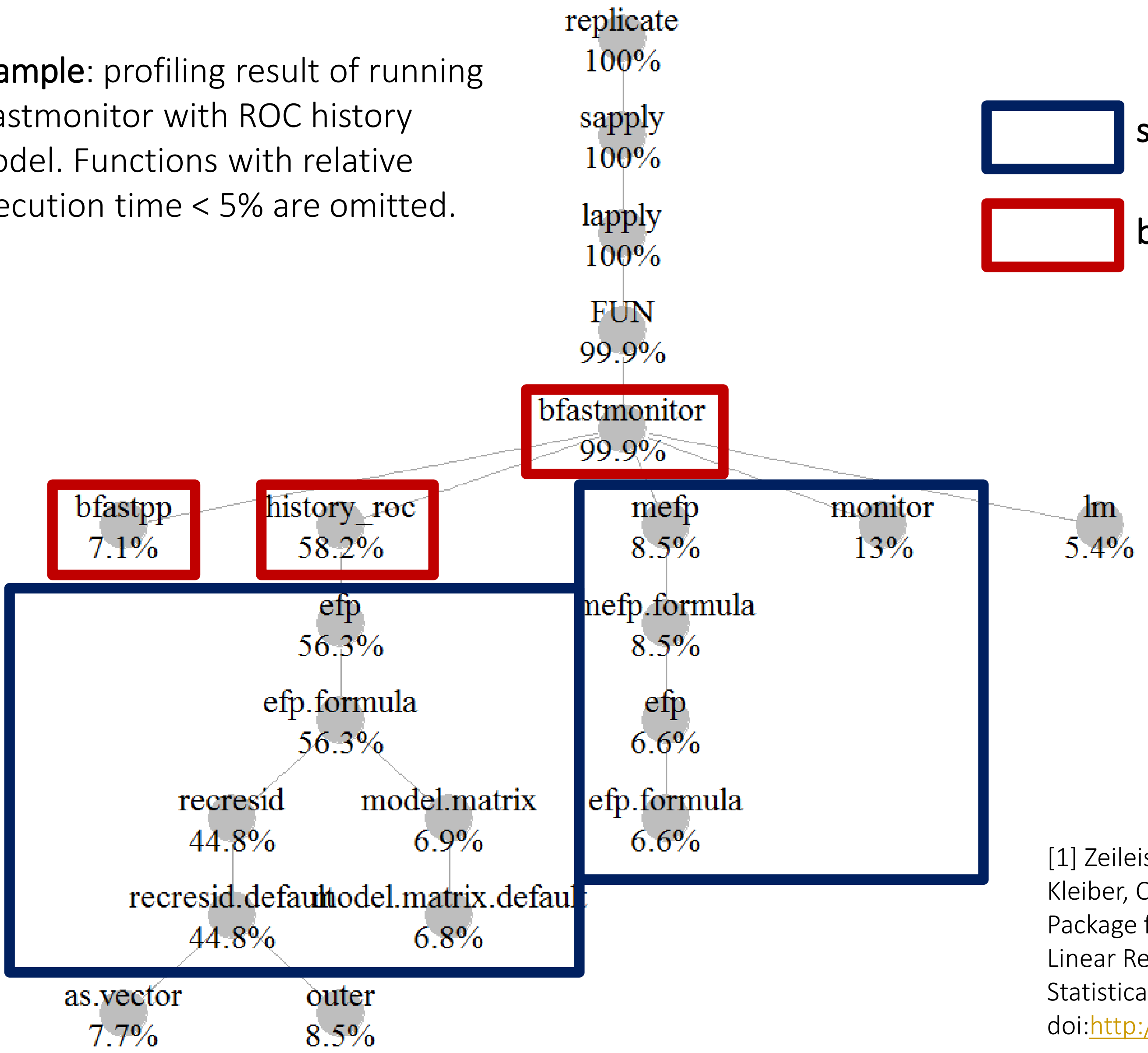
- Counting how often the execution is within a specific function allows to estimates how much of the overall time that function takes

- For each sample, the full call stack is available

- Profiling in R: Rprof, lineprof, profr

Profiling: example for bfastmonitor()

Example: profiling result of running bfastmonitor with ROC history model. Functions with relative execution time < 5% are omitted.



replicate 100%

sapply 100%

lapply 100%

FUN 99.9%

bfastmonitor 99.9%

bfastpp 7.1%

history_roc 58.2%

mefp 8.5%

monitor 13%

lm 5.4%

efp 56.3%

efp.formula 56.3%

recresid 44.8%

model.matrix 6.9%

recresid.default 44.8%

model.matrix.default 6.8%

as.vector 7.7%

outer 8.5%

mefp.formula 8.5%

efp 6.6%

efp.formula 6.6%

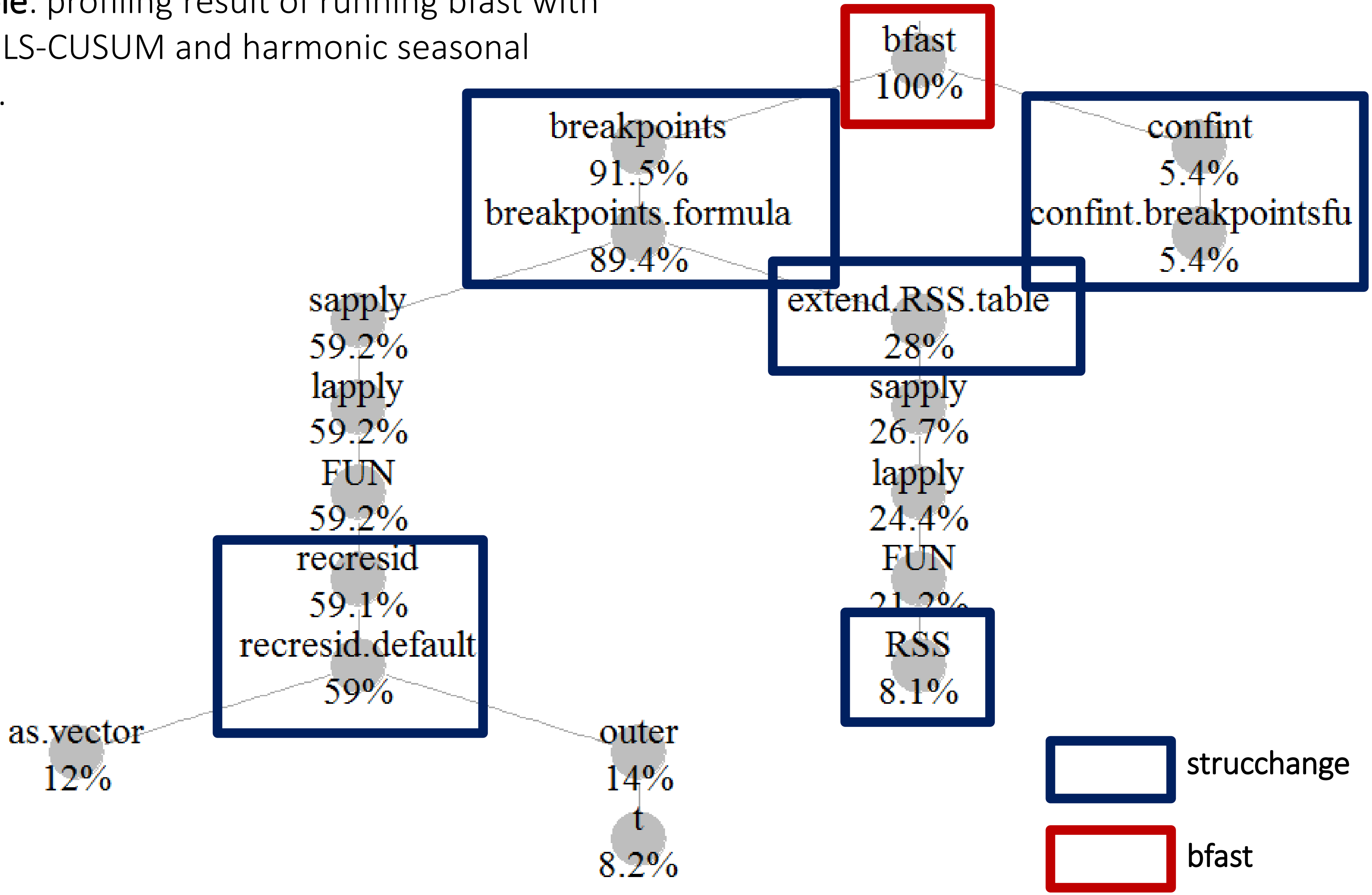
□ strucchange [1]

□ bfast

[1] Zeileis, A., Leisch, F., Hornik, K., & Kleiber, C. (2002). strucchange: An R Package for Testing for Structural Change in Linear Regression Models. Journal of Statistical Software, 7(2), 1 - 38. doi:http://dx.doi.org/10.18637/jss.v007.i02

Profiling: example bfast()

Example: profiling result of running bfast with type OLS-CUSUM and harmonic seasonal model.



Package optimizations (overview)

- Move operations to C++ with Rcpp and RcppArmadillo [1,2] if possible

  → `recresid, extend_rss_table, efp_process_me, efp_process_re`

- Use design matrix and response vector instead of data.frame and formula and `lm.fit()` instead of `lm()`
  - `bfastpp, bfastmonitor, bfast`
  - `breakpoints, efp, mefp, monitor,`

- bfastts: avoid `as.ts(zoo(…))`

[1] Conrad Sanderson and Ryan Curtin. *Armadillo: a template-based C++ library for linear algebra*. Journal of Open Source Software, Vol. 1, pp. 26, 2016.

[2] Dirk Eddelbuettel, Conrad Sanderson (2014). RcppArmadillo: Accelerating R with high-performance C++ linear algebra. Computational Statistics and Data Analysis, Volume 71, March 2014, pages 1054-1063. URL http://dx.doi.org/10.1016/j.csda.2013.02.005

Moving computations to C++: recursive residuals

Recursive residuals in C++ with RcppArmadillo

```
arma::vec sc_cpp_recresid_arma(const mat& X, const vec& y,  unsigned int
start, unsigned int end, const double& tol, const double& rcond_min) {
  if(!(start > X.n_cols && start <= X.n_rows)) stop("Invalid start");
  if(!(end >= start && end <= X.n_rows)) stop("Invalid end");
  --start;
  --end;
  int n=end;
  int q=start-1;
  int k = X.n_cols;
  vec rval = vec(n-q, fill::zeros);
  vec cur_y = y.subvec(0, q);
  mat cur_X = X.submat(0, 0, q, k-1);
  mat X1;
  colvec cur_coef_full;
  solve(cur_coef_full, cur_X, cur_y, solve_opts::no_approx);
  inv_sympd(X1, trans(cur_X) * cur_X);
  colvec cur_coef = cur_coef_full;
  mat xr = X.row(q+1);
  vec fr = (1 + xr * X1  * trans(xr));
  rval(0) = as_scalar((y(q+1) - xr * cur_coef)/sqrt(fr));
  bool check = true;
  if((q+1) < n)
  {
    for(int r=q+2; r<=n; ++r) {
      X1 -= (X1 * trans(xr) * xr * X1)/as_scalar(fr);
      cur_coef += X1 * trans(xr) * rval(r-q-2) * sqrt(fr);
      if (check) {
        cur_y = y.subvec(0, r-1);
        cur_X = X.submat(0, 0, r-1, k-1);

        solve(cur_coef_full, cur_X, cur_y, solve_opts::no_approx);
        inv_sympd(X1, trans(cur_X) * cur_X);
        bool nona = is_finite( cur_coef) && is_finite( cur_coef_full );
        if(nona && approx_equal(cur_coef_full,cur_coef, "absdiff", tol)) {
          check = false;
        }
        cur_coef = cur_coef_full;
      }
      xr = X.row(r); // This a a row
      fr = (1 + xr * X1  * trans(xr));
      rval(r-q-1) = as_scalar((y(r) - xr * cur_coef)/sqrt(fr));
    }
  }
  return rval;
}
```

```
vec sc_cpp_recresid_arma(const mat&
  X, const vec& y,  ...)
```

```
cur_coef += X1 * trans(xr) *
  rval(r-q-2) * sqrt(fr);
```

Recursive residuals in R

```
recresid.default <- function(x, y, start = ncol(x) + 1, end = nrow(x),
  tol = sqrt(.Machine$double.eps)/ncol(x), ...)
{
  ## checks and data dimensions
  stopifnot(start > ncol(x) & start <= nrow(x))
  stopifnot(end >= start & end <= nrow(x))
  n <- end
  q <- start - 1
  k <- ncol(x)
  rval <- rep(0, n - q)
  y1 <- y[1:q]
  fm <- lm.fit(x[1:q, , drop = FALSE], y1)
  X1 <- .Xinv0(fm)
  betar <- .coef0(fm)
  xr <- as.vector(x[q+1,])
  fr <- as.vector((1 + (t(xr) %*% X1 %*% xr)))
  rval[1] <- (y[q+1] - t(xr) %*% betar)/sqrt(fr)
  check <- TRUE
  if((q+1) < n)
  {
    for(r in ((q+2):n))
    {
      nona <- all(!is.na(fm$coefficients))
      X1 <- X1 - (X1 %*% outer(xr, xr) %*% X1)/fr
      betar <- betar + X1 %*% xr * rval[r-q-1] * sqrt(fr)
      if(check) {
        y1 <- y[1:(r-1)]
        fm <- lm.fit(x[1:(r-1), , drop = FALSE], y1)
        nona <- nona & all(!is.na(betar)) & all(!is.na(fm$coefficients))
        if(nona && isTRUE(all.equal(as.vector(fm$coefficients), as.vector(betar),
tol = tol))) {
          check <- FALSE
        }
        X1 <- .Xinv0(fm)
        betar <- .coef0(fm)
      }
      xr <- as.vector(x[r,])
      fr <- as.vector((1 + (t(xr) %*% X1 %*% xr)))
      rval[r-q] <- (y[r] - sum(xr * betar, na.rm = TRUE))/sqrt(fr)
    }
  }
  return(rval)
}
```

```
betar <- betar + X1 %*% xr *
  rval[r-q-1] * sqrt(fr)
```

Moving computations to C++: recursive residuals

- fits linear models in the first few iterations, until recursive model parameter updates are stable

- for ill-conditioned systems (e.g. dummy variables), R‘s `lm.fit` is used, otherwise Armadillo‘s `solve`

- speedup varies with length of time series, number of explanatory variables, and stability of the system, mostly around 15-20 on this machine

- changes have effect on performance of both bfast and bfastmonitor (unless `history = „all“`)

bfastpp

```
bfastpp(data, order = 3,
  lag = NULL, slag = NULL, na.action = na.omit,
  stl = c("none", "trend", "seasonal", "both"),
  formula = NULL)
```

- Derives variables that occur in the formula only

- Instead of a data.frame, modified output is a list with elements
  - `y`: response vector
  - `X`: design matrix
  - `t`: vector of dates (same as `time(data)`)

Avoiding formulas and data.frames

S3 methods for matrix input:

- `breakpoints, efp, mefp, monitor`

```
breakpoints.formula(formula, h = 0.15, breaks = NULL,
    data = list(), hpc = c("none", "foreach"), ...)
```

⬇

```
breakpoints.matrix(X, y, h = 0.15, breaks = NULL,
    hpc = c("none", "foreach"), ...)
```

Matrix methods

- avoid `model.frame()` and `model.matrix()`
- use `lm.fit()` instead of `lm()`

bfastts modifications

- `bfastts()` not directly called from `bfast()` or `bfastmonitor()` but often used before (e.g. in `bfmSpatial()`)
- takes up to 30% of computation time of bfastSpatial example with the TURA dataset
- modification does not use zoo
- around 2 -3 times faster

Using package modifications

1. Install strucchange and bfast from github (Rtools needed for Windows)

```
library(devtools)
install_github("appelmar/strucchange")
install_github("appelmar/bfast")
```

2. Load the package and enable modifications

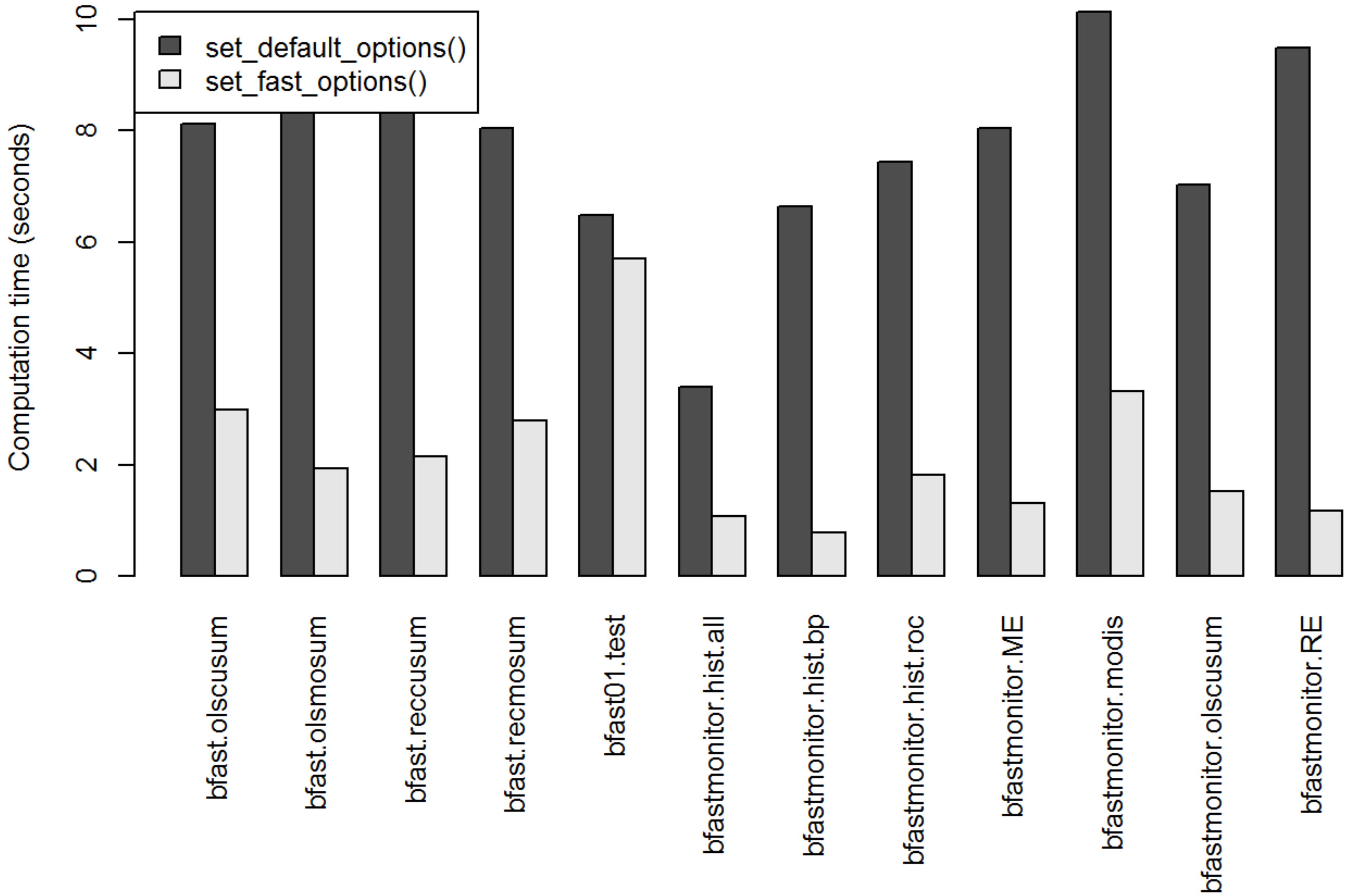
```
library(bfast)
set_fast_options()    # use modifications
...
set_default_options() # use default implementation
...
```

see https://github.com/appelmar/bfast

Package Options

Package option	Description
`strucchange.use_armadillo`	Defines whether or not C++ functions should be used if available
`strucchange.armadillo_rcond_min`	For ill-conditioned systems in the recursive residual computation, the minimum reciprocal conditioning number to use armadillo solve instead of column pivoting QR from R
`bfast.prefer_matrix_methods`	Defines whether or not bfastpp generates a data frame or a matrix
`bfast.use_bfastts_modifications`	Defines whether or not bfastts modifications should be used

Results: speedup



see https://appelmar.github.io/scalbf-wur/reports/report.benchmark.html

Example: bfastSpatial with tura dataset

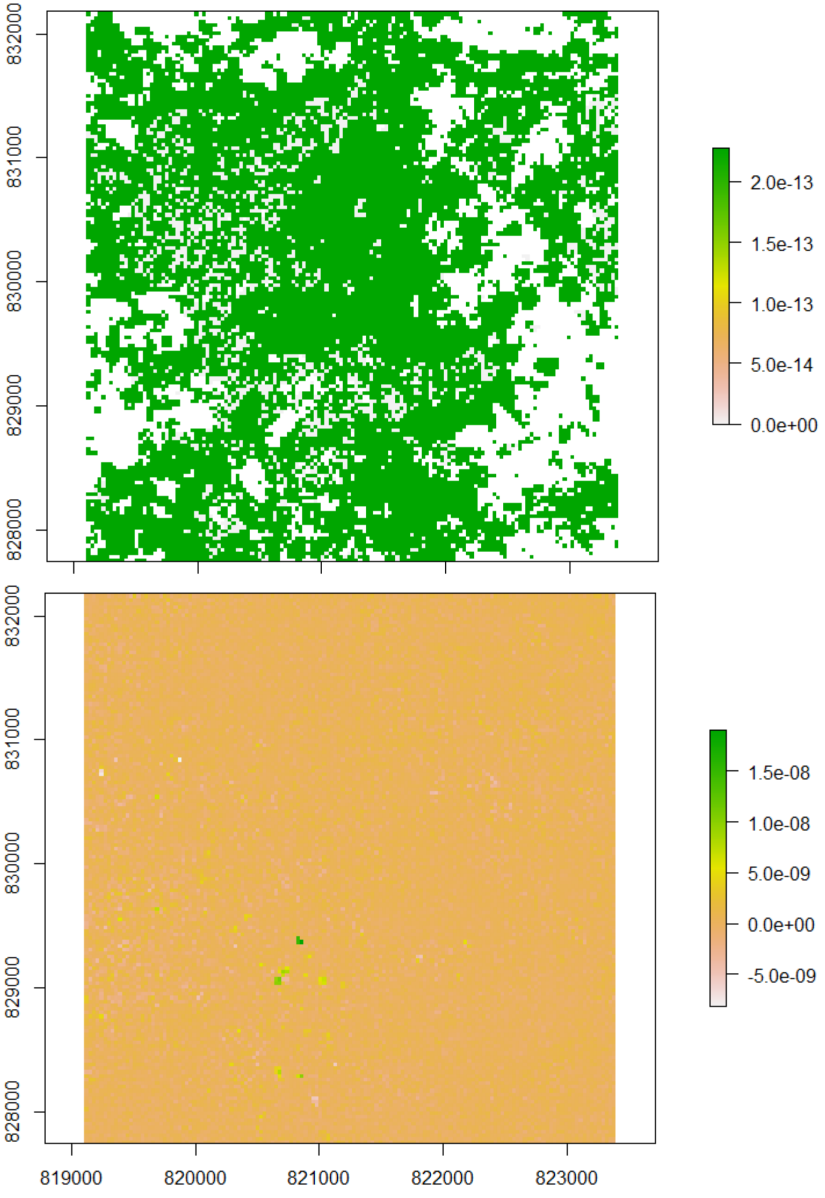
```
library(bfastSpatial)
data(tura)

set_default_options()
system.time(bfm.tura.new <-
    bfmSpatial(tura, start=c(2009, 1),
    history = "ROC")) # 1318.52 s

set_fast_options()
system.time(bfm.tura.new <-
    bfmSpatial(tura, start=c(2009, 1),
    history = "ROC")) # 288.75 s


plot(bfm.tura.new$breakpoint -
     bfm.tura.reference$breakpoint)
plot(bfm.tura.new$magnitude -
     bfm.tura.reference$magnitude)
```

http://appelmar.github.io/scalbf-wur/examples/example02-tura.R



Package reports

The package comes with some R Markdown reports to test, benchmark, and profile the modifications.

```
library(rmarkdown)

render(system.file("reports/report.test.Rmd",
    package = "bfast"),output_file = "report.test.html")

render(system.file("reports/report.benchmark.Rmd",
    package = "bfast"),output_file = "report.benchmark.html")

render(system.file("reports/report.profiling.Rmd",
    package = "bfast"),output_file = "report.profiling.html")
```

Examples:

- https://appelmar.github.io/scalbf-wur/reports/report.test.html
- https://appelmar.github.io/scalbf-wur/reports/report.benchmark.html
- https://appelmar.github.io/scalbf-wur/reports/report.profiling.html

Summary and conclusions

- speedup of bfastmonitor and bfast varies between 2 and 10, depending on computations

- There is no single computational bottleneck, probably difficult to employ e.g. GPUs

- Strongest speedup in bfastmonitor with `(type="RE"`, Bai and Perron history `(history = "BP")`

- Optimizations also work with bfastSpatial even with parallelization

- bfast and strucchange now need to be compiled and linked to Rcpp and RcppArmadillo respectively

Thank you

Questions?