# Benchmarks for Discrete Fourier Transforms in R

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#### Abstract

The base DFT calculator in R, stats::fft, uses the Mixed-Radix algorithm of Singleton (1969). In this vignette we show how this calculator compares to FFT in the fftw package (Krey et al., 2011), which uses the FFTW algorithm of Frigo and Johnson (2005). For univariate DFT computations, the methods are nearly equivalent with two exceptions which are not mutually exclusive: (A) the series to be transformed is very long, and especially (B) when the series length is not highly composite. In both exceptions the algorithm FFT outperforms fft.

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# 1 Benchmarking function

We use both functions in their default state, and ask them to transform the same univariate random series. Benchmark information comes from the rbenchmark program, and the versatile plyr and reshape2 packages are used to manipulate the information for this presentation; ggplot2 is used for plotting. First we load the libraries needed:

```
rm(list = ls())
library(fftw)
library(rbenchmark)
library(plyr)
library(reshape2)
library(ggplot2)
```

and create a benchmark function:

```
reps <- 10
dftbm <- function(nd, repls = reps) {
    set.seed(1234)
    x <- rnorm(nd, mean = 0, sd = 1)
    bmd <- benchmark(replications = repls, fftw::FFT(x), stats::fft(x))
    bmd$num_dat <- nd
    bmd$relative[is.na(bmd$relative)] <- 1 # NA happens.
    return(bmd)
}</pre>
```

# 2 Highly composite (HC) series

It's well known that DFT algorithms are most efficient for "Highly Composite Numbers" 1, specifically multiples of (2,3,5).

So, we create a vector of series lengths we wish to benchmark

```
(nterms.even \leftarrow round(2^seq.int(from = 4, to = 20, by = 1)))
##
    [1]
              16
                       32
                                64
                                        128
                                                 256
                                                          512
                                                                  1024
                                                                           2048
    [9]
                     8192
                                                      131072 262144
            4096
                             16384
                                      32768
                                               65536
                                                                        524288
## [17] 1048576
```

and use it with lapply and the benchmark function previously defined. These data are further distilled into a usable format with ldply:

<sup>&</sup>lt;sup>1</sup> This is the reason for the stats::nextn function.

```
bench.even <- function() {
    benchdat.e <- plyr::ldply(lapply(X = nterms.even, FUN = dftbm))
}
bench.even()</pre>
```

In order to plot the results, we need to perform some map/reduce operations on the data (Wickham, 2011):

```
pltbench <- function(lentyp=c("even", "odd")){</pre>
  benchdat <- switch(match.arg(lentyp), even=benchdat.e, odd=benchdat.o)</pre>
  stopifnot(exists("benchdat"))
  tests <- unique(benchdat$test)</pre>
  ## subset only information we care about
  allbench.df.drp <- subset(benchdat,</pre>
        select=c(test, num_dat, user.self, sys.self, elapsed, relative))
  ## reduce data.frame with melt
  allbench.df.mlt <- reshape2::melt(allbench.df.drp,</pre>
                                      id.vars=c("test","num_dat"))
  ## calculate the summary information to be plotted:
  tmpd <- plyr::ddply(allbench.df.mlt,</pre>
                        .(variable, num_dat),
                        summarise,
                        summary="medians", # just a name
                        value=ggplot2::mean_cl_normal(value)[1,1])
  ## create copies for each test and map to data.frame
  allmeds <<- plyr::ldply(lapply(X=tests,</pre>
                                   FUN=function(x,df=tmpd){
                                          df$test <- x; return(df)</pre>
  ## plot the benchmark data
  g <- ggplot(data=allbench.df.mlt,</pre>
               aes(x=log10(num_dat),
                   y=log2(value),
                   # 1/sqrt(n) standard errors [assumes N(0,1)]
                   ymin=log2(value*(1-1/sqrt(reps))),
                   ymax=log2(value*(1+1/sqrt(reps))),
                   colour=test,
                   group=test)) +
       scale_colour_discrete(guide="none") +
```

For each row of the figure we plot summary  $curves^2$  so we can easily inter-compare the benchmark data.

# 3 Non highly composite (NHC) series

DFT algorithms can have drastically reduced performance if the series length is not highly composite (NHC). We now test NHC series by adding one to the HC series-length vector (also restricting the total length for sanity's sake):

```
nterms.odd <- nterms.even + 1
nterms.odd <- nterms.odd[nterms.odd < 50000] # painfully long otherwise!</pre>
```

and performing the full set of benchmarks again:

```
bench.odd <- function() {
    benchdat.o <- plyr::ldply(lapply(X = nterms.odd, FUN = dftbm))
}
bench.odd() # FAIR WARNING: this can take a while!!</pre>
```

We can now visualize the results, with the addition of the HC summary curves:

<sup>&</sup>lt;sup>2</sup> Based on this post:

### 4 Conclusion

Figures ?? and ?? compare the DFT calculations for HC and NHC length series. For univariate DFT computations, the methods are nearly equivalent with two exceptions which are not mutually exclusive: (A) the series to be transformed is very long, and especially (B) when the series length is not highly composite. In both exceptions the algorithm FFT outperforms fft. In the case of exception (B), both methods have drastically increased computation times; hence, zero padding should be done to ensure the length does not adversely affect the efficiency of the DFT calculator.

**Table 1:** A comparison of power spectral density estimators in R, excluding extensions which only estimate raw-periodograms. Normalizations are shown as either "single" or "double" for either single- or double-sided spectra, and "various" if there are multiple, optional normalizations. A (\*) denotes the default for a function having an option for either single or double.

FUNCTION	Namespace	SINE M.T.?	Adaptive?	Norm.	Reference
mtapspec	RSEIS	Yes	No	various	Lees and Park (1995)
pspectrum	rlpSpec	Yes	Yes	single	Parker and Barbour (2013)
spectrum	stats	No	No	double	R Core Team (2012)
spec.mtm	multitaper	Yes	Yes	double	Rahim and Burr (2012)
SDF	sapa	Yes	No	$single^*$	Percival and Walden (1993)

# 5 Session Info

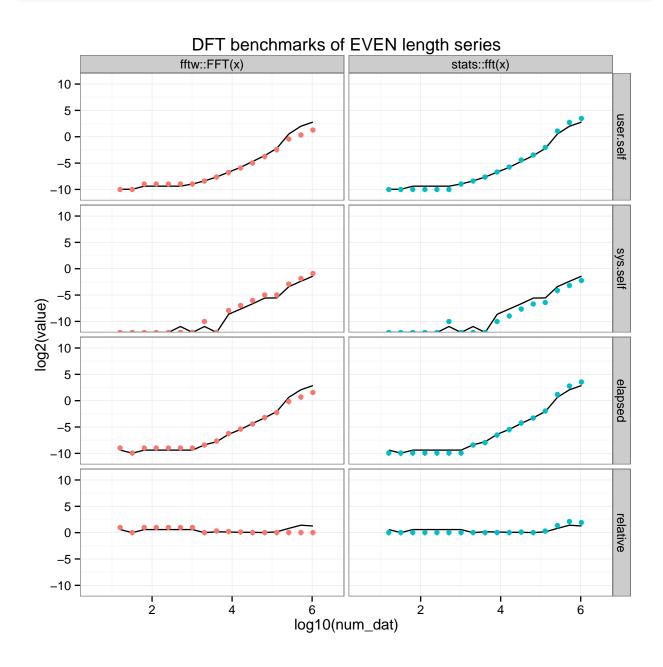
```
## R version 2.15.2 (2012-10-26)
## Platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit)
##
## locale:
## [1] C
##
```

http://geokook.wordpress.com/2012/12/29/row-wise-summary-curves-in-faceted-ggplot2-figures/

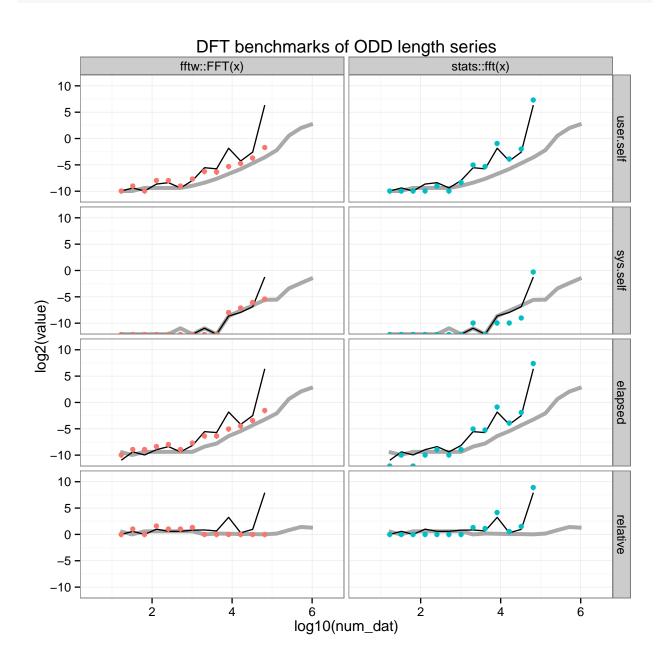
```
## attached base packages:
##
    [1] parallel
                  datasets
                             grDevices grid
                                                  graphics
                                                           tools
                                                                       stats
##
    [8] utils
                  methods
                             base
##
## other attached packages:
## [1] knitr_0.9
##
## loaded via a namespace (and not attached):
## [1] digest_0.6.0
                       evaluate_0.4.3 formatR_0.7
                                                      stringr_0.6.2
```

## References

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- Wickham, H. (2011). The split-apply-combine strategy for data analysis. *Journal of Statistical Software*, 40(1):1–29.



**Figure 1:** DFT benchmark results for HC series lengths.



**Figure 2:** DFT benchmark results for NHC series lengths. We also show the summary curves for the HC results to highlight the drastic degradation in performance.