Benchmarking `rtn()`'s Performance

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This brief document shows some performance benchmarks of **RcppTN**'s `rtn()` compared to other truncated Normal distribution RNG's in R. The other functions considered come from the R packages **truncnorm** and **msm**.

1 Three different RNG's

Broadly speaking, calls to the three different R functions are similar. In the simplest case (no truncation), they even identical return values.

```
library("RcppTN")
library("truncnorm")
library("msm")
library("microbenchmark")

set.seed(1)
rtn() # RcppTN

## [1] -0.6264538

set.seed(1)
rtnorm(n=1) # msm

## [1] -0.6264538

set.seed(1)
rtruncnorm(n=1) # truncnorm

## [1] -0.6264538
```

But, this is not true in general. Differences in return values result from the use of different algorithms and different implementations of the same algorithm. First, consider a standard Normal distribution truncated below 4 and above 4.1. Here, the output from the **RcppTN** package and the **truncnorm** package agree.

```
set.seed(1)
rtn(.mean = 0, .sd = 1, .low = 4, .high = 4.1)
```

```
## [1] 4.026551

set.seed(1)
rtnorm(n=1, mean = 0, sd = 1, lower = 4, upper = 4.1)

## [1] 4.034397

set.seed(1)
rtruncnorm(n=1, mean = 0, sd = 1, a = 4, b = 4.1)

## [1] 4.026551
```

Yet, in the case of truncation below 5 without any truncation from above, the output from the **RcppTN** and the **msm** package agree. Again, this is just a result of how each sampler is implemented using R's base RNG functionality. None of these return values is incorrect, per se, but it is worth noting that the functions do not produce identical output, even if they are all valid RNG's for the same distribution.

```
set.seed(1)
rtn(.mean = 0, .sd = 1, .low = 5, .high = Inf)

## [1] 5.145435

set.seed(1)
rtnorm(n=1, mean = 0, sd = 1, lower = 5, upper = Inf)

## [1] 5.145435

set.seed(1)
rtruncnorm(n=1, mean = 0, sd = 1, a = 5, b = Inf)

## [1] 5.151036
```

2 Compiled Code is faster than Interpreted Code

In setting up a series of conditions under which to compare performance, we will consider drawing samples of size 10, 1,000, and 100,000. And will consider standard Normal distributions restricted to the intervals $[-1, 1]$, $[5, \infty]$, $[-\infty, 10]$, $[4, 7]$, $[4, 4.1]$, $[-\infty, \infty]$, and $[50, 100]$.

```
sizes <- c(1e1, 1e3, 1e5)
lows <- c(-1, 5, -Inf, 4, 4, -Inf, 50)
highs <- c(1, Inf, 10, 7, 4.1, Inf, 100)
```

Both **RcppTN** and **truncnorm** use compiled code for their RNG. However, the RNG in **msm** is written in R. As a result, the performance cost that one would expect manifests in even the a simple case where the standard Normal distribution is truncated below at -1 and above at 1. This case is sufficiently easy that even a naive Accept-Reject sampler works perfectly fine. Yet, the C(++)-based implementations are over 15 times faster in drawing samples of size 1,000

```
s <- sizes[2]

microbenchmark(
    "rtn" = rtn(.mean = rep(0, s),
    .low = rep(lows[1], s),
    .high = rep(highs[1], s),
    .checks = FALSE
    ),
    "rtruncnorm" = rtruncnorm(n = s,
    a = rep(lows[1], s),
    b = rep(highs[1], s)
    ),
    "rtnorm" = rtnorm(n = s,
    lower = rep(lows[1], s),
    upper = rep(highs[1], s)
    ),
    times = 100
    )

## Unit: microseconds
##        expr     min       lq      mean   median        uq      max neval
##         rtn 173.604 181.5450  191.7932 185.6395  197.1090  326.756   100
##  rtruncnorm 176.819 180.8715  219.7301 185.9860  192.0165 3333.559   100
##      rtnorm 711.925 758.1205 1198.7574 816.4585 1241.1935 6134.969   100
##  cld
##   a
##   a
##    b
```

A similarly large performance cost due to writing the RNG in R is seen in a harder case: a standard Normal distribution truncated below at 4 and above at 4.1. The sample size is still 1,000.

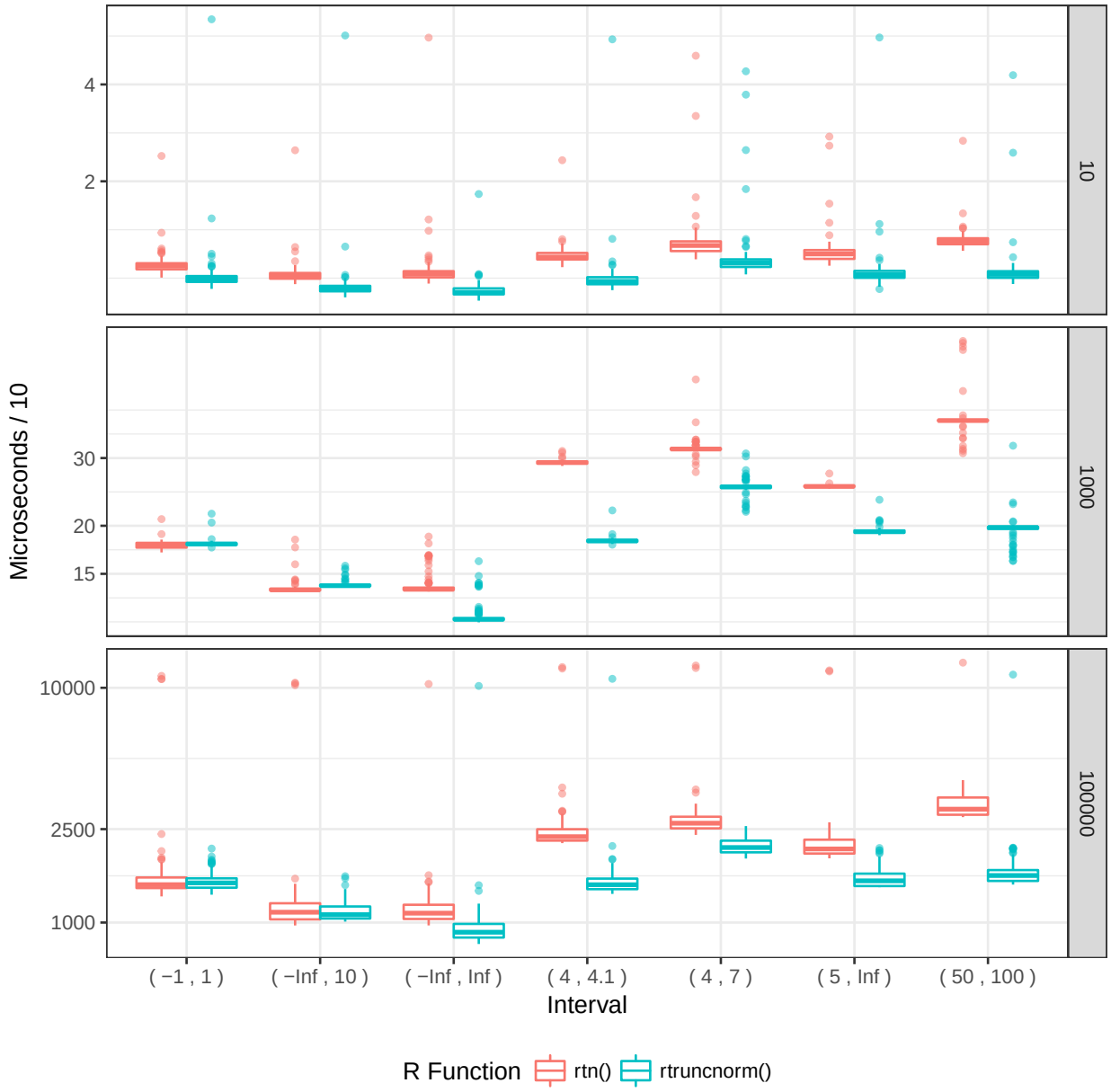
```
microbenchmark(
    "rtn" = rtn(.mean = rep(0, s),
    .low = rep(lows[5], s),
    .high = rep(highs[5], s),
    .checks = FALSE
    ),
    "rtruncnorm" = rtruncnorm(n = s,
    a = rep(lows[5], s),
    b = rep(highs[5], s)
    ),
    "rtnorm" = rtnorm(n = s,
    lower = rep(lows[5], s),
    upper = rep(highs[5], s)
    ),
    times = 100
    )
```

```
## Unit: microseconds
##        expr      min       lq      mean    median       uq      max neval
##         rtn  285.674  292.405  305.0442  295.8135  301.666  900.034   100
##  rtruncnorm  179.643  183.568  214.5034  186.0445  191.822 2767.091   100
##      rtnorm 1115.561 1182.840 1542.7865 1244.7190 1637.740 4571.212   100
##  cld
##   a
##   a
##    b
```

For this reason, the `rtnorm()` function from the **msm** package is excluded from subsequent analysis. Not only is it assumed that it will be the slowest for the different sample sizes and truncation bounds considered, but it will just take too long to build the vignette if it is included.

3 RcppTN vs. truncnorm

The RNG's in **RcppTN** and **truncnorm** are written in **Rcpp**-based C++ and C, respectively. However, they implement different mathematical algorithms. The former uses Robert (1995) and the latter uses Geweke (1991). To compare the R-level performance of the two, the full set of conditions described above is considered.



Results of benchmarking comparing RNG performance for Truncated Normal distributions from ***RcppTN*** *and* ***truncnorm****.*

The motivation for **RcppTN** isn't speed, but the **Rcpp**-based implementation performs quite-well.