Homework 3

DATA604 Simulation and Modeling

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March 6, 2016

1

Starting with $X_0 = 1$, write down the entire cycle for $X_i = 11X_{i-1}\ mod(16)$

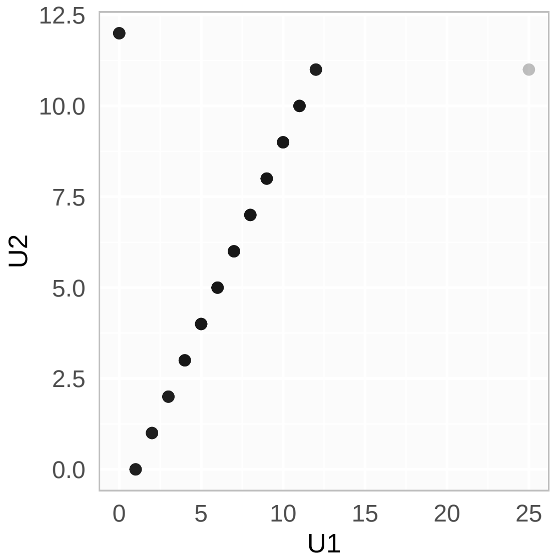
```
fn1 <- function(x0)
{
  df <- data.frame(X=c(), R=c())
  x <- x0
  continue <- TRUE

  while(continue)
  {
    xi <- (11 * x) %% 16
    df <- rbind(df, data.frame(X=x, R=xi))
    x <- xi

    if(xi == x0)
    {
      break
    }
  }

  return(df)
}

res <- fn1(1)
```

X	R
1	11
11	9
9	3
3	1

2

Using the LCG provided below: $X_i = (X_{i-1} + 12) mod(13)$, plot the pairs $(U_1.U_2), (U_2, U_3), \ldots$ and observe the lattice structure obtained. Discuss what you observe.

```
fn2 <- function(x0, max=100)
{
  df <- data.frame(U1=c(), U2=c())
  x <- x0

  for(i in 1:max)
  {
    xi <- (x + 12) %% 13
    df <- rbind(df, data.frame(U1=x, U2=xi))
    x <- xi
  }

  return(df)
}
# Call the function starting at x0=1
res <- fn2(25)
```



The chart above suggests there are only 13 points, but actually the LCG cycle period is 13 and numbers are repeating.

U1	U2
25	11
11	10
10	9
9	8
8	7
7	6
6	5
5	4
4	3
3	2
2	1
1	0
0	12
12	11

3

Implement the pseudo-random number generator:

$$X_i = 16807X_{i-1} \mod(2^{31} - 1)$$

Using the seed 1234567, run the generator for 100,000 observations. Perform a chi-square goodness-of-fit test on the resulting PRN's. Use 20 equal-probability intervals and level $\alpha = 0.05$. Now perform a runs up-and-down test with $\alpha = 0.05$ on the observvations to see if they are independent.

```
fnLCG3 <- function(seed = 1, n = 1)
{
  rands <- rep(NA, n)
  x <- seed
  modVal <- (2^31 - 1)

  for(i in 1:n)
  {
    xi <- (16807 * x) %% (modVal)
    rands[i] <- xi
    x <- xi
  }

  return(rands)
}

n=100000
rn <- fnLCG3(1234567, n)
```

The first 6 generated numbers are shown below:

1422014746
456328559
849987676
681650688
1825340118
1687465831

Chi-Square Test

```
intervals <- 20
maxRn <- max(rn)
minRn <- min(rn)
intWidth <- (maxRn - minRn) / intervals
lwr <- minRn
dfCounts <- data.frame(intID=c(), count=c())
# Bin the data ourselves, I'd guess there
# is an easier way, but this will do.
for(i in 1:intervals)
{
  upr <- lwr + intWidth
  inRange <- rn[lwr <= rn & rn < upr]
  dfCounts <- rbind(dfCounts, data.frame(intID=i, count=length(inRange)))
  # setup for next interval range
  lwr <- upr
}
# Do our own Chi-Squared test
Expected <- (100000 / intervals)
chi2 <- sum((dfCounts$count - Expected)^2 / Expected)
chi2
```

```
## [1] 14.7762
```

```
# Use built-in function to compare
chiTest <- chisq.test(dfCounts$count)
chiTest
```

```
##
```

```
##  Chi-squared test for given probabilities
##
## data:  dfCounts$count
## X-squared = 14.776, df = 19, p-value = 0.7367
```

The p-value = 0.7367029 is not less than $\alpha = 0.05$, therefore we don't reject the null hypothesis that the distrubtion is uniform.

intID	count
1	5069
2	5028
3	5044
4	5087
5	4948
6	4953
7	4937
8	4933
9	4900
10	4957
11	5088
12	4994
13	5076
14	5019
15	5002
16	5067
17	4981
18	4914
19	5062
20	4940

Runs Up-and-Down Test

Using the `tseries` package, we execute the Runs test (Trapletti and Hornik, 2015). First we have to construct the +/- vector. Here we simply convert to boolean.

```r
s <- rep(NA, n - 1)
for(i in 1:n - 1)
{
  s[i] <- rn[i] < rn[i + 1]
}

runsTest <- runs.test(as.factor(s))
runsTest
```

```
##
##  Runs Test
##
## data:  as.factor(s)
## Standard Normal = 105.84, p-value < 2.2e-16
## alternative hypothesis: two.sided
```

Based on the p-value < 0.05, we reject the null hypothesis and conclude there is not evidence to support independence in the psuedo-random numbers.

4.

Give inverse-transforms, composition, and acceptance-rejection algorithms for generating from the following density:

$$f(x) = \begin{cases} \frac{3x^2}{2} & -1 \leq x \leq 1 \\ 0 & otherwise \end{cases}$$

Inverse-Transforms

First find the indefinite integral of the probability density function:

$$F(x) = \int \frac{3x^2}{2} dx = \frac{x^3}{2}$$

Next set $F(x) = R$ and solve for x in terms of R:

$$\frac{x^3}{2} = R$$

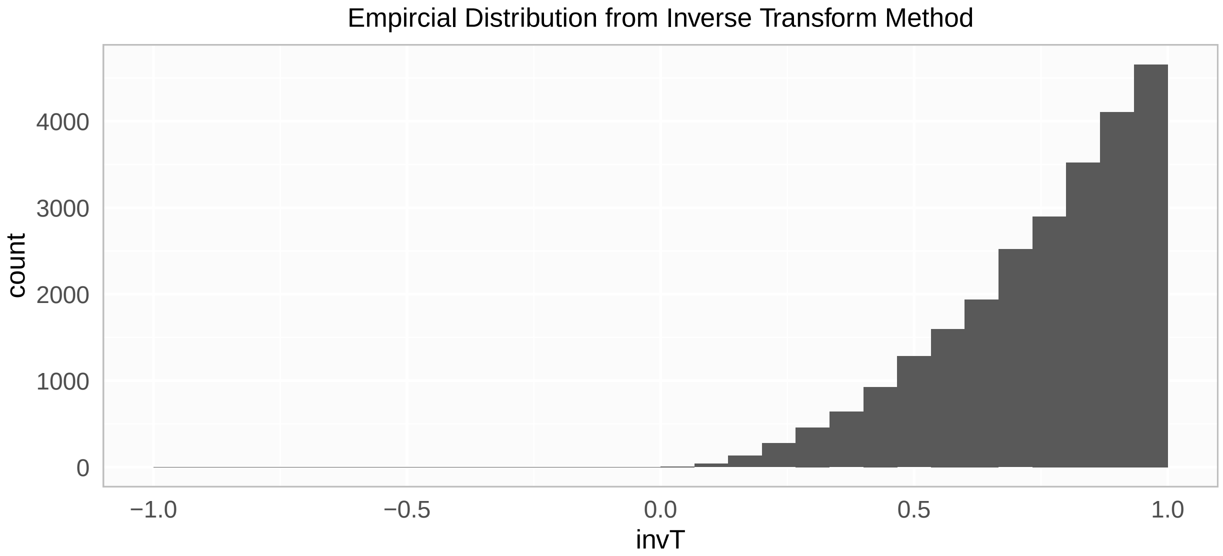
$$x^3 = 2R$$

$$F^-1(x) = \sqrt[3]{2R}$$

```r
# Define a function of the F^-1(X)
invTfn4 <- function(r)
{
  vals <- (2 * r)^(1/3)
  return (vals)
}

# Generate the uniform psuedo-random vars
rVals <- runif(n, -1, 1)
# Convert to the desired distribution using the inverse transform method.
invTVals <- invTfn4(rVals)
```

```
## Warning: Removed 74997 rows containing non-finite values (stat_bin).
```

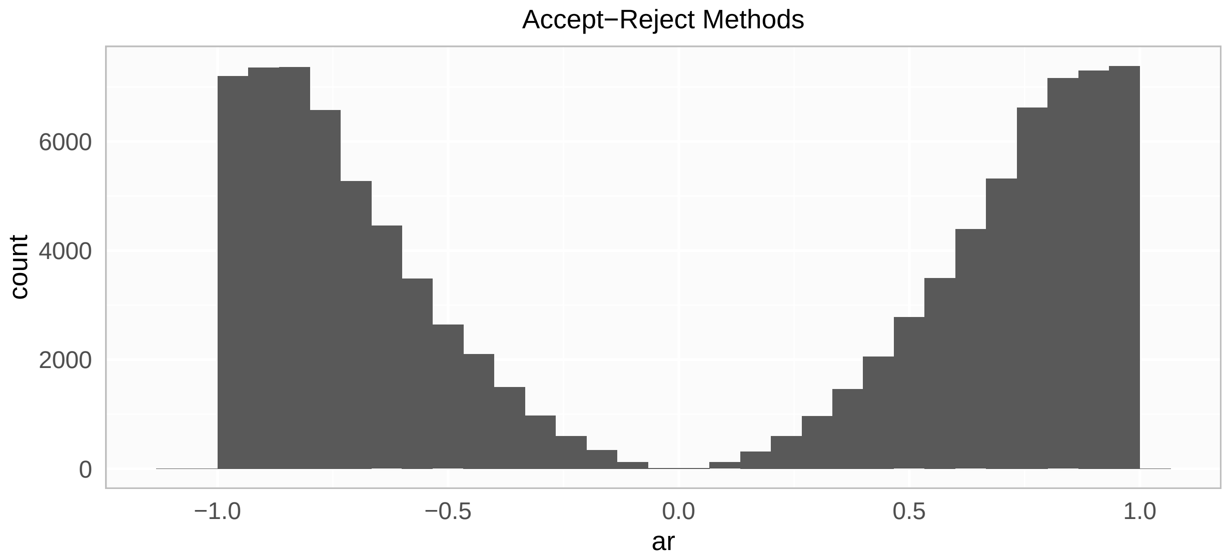
```
## Warning: Removed 2 rows containing missing values (geom_bar).
```



Acceptance-Rejection Method

```r
# Helper function for the Accept/Reject approach
myRARmethod <- function(fun, min, max)
{
  M <- 2
  accepted <- FALSE
  while(!accepted)
  {
    # Get a random value from uniform distrubtion (g(x) for us)
    r <- runif(1, min, max)

    # Sample x from g(x) and u from U(0,1) (the uniform distribution over the unit interval)
    u <- runif(1, 0, 1)
    gx <- dunif(r, min, max)

    # Check whether or not u<f(x)/Mg(x).
    if(u < fun(r) / (M * gx))
    {
      accepted = TRUE
    }
  }

  return(r)
}

# Define a function for the PDF
Arfn4 <- function(x)
{
  if(-1 <=x && x <= 1)
  {
    val <- (3 * x^2) / 2
  }
  else
  {
    val = 0
  }
  return (val)
}

# Loop to generate the values
rarVals <- rep(NA, n)
for(i in 1:n)
{
  rarVals[i] <- myRARmethod(Arfn4, -1, 1)
}
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Composition

Hmm. . . .

5

Implement, test and compare different methods to generate from a N(0,1) distribution.

$$f(x) = \frac{1}{\sqrt{2\pi}} e^{\frac{-x^2}{2}}$$

Inverse Transform Method

$$F(X) = \int \frac{1}{\sqrt{2\pi}} e^{\frac{-x^2}{2}} dx$$

It turns out the `qnorm` function is the inverse normal CDF function, so we'll use it.

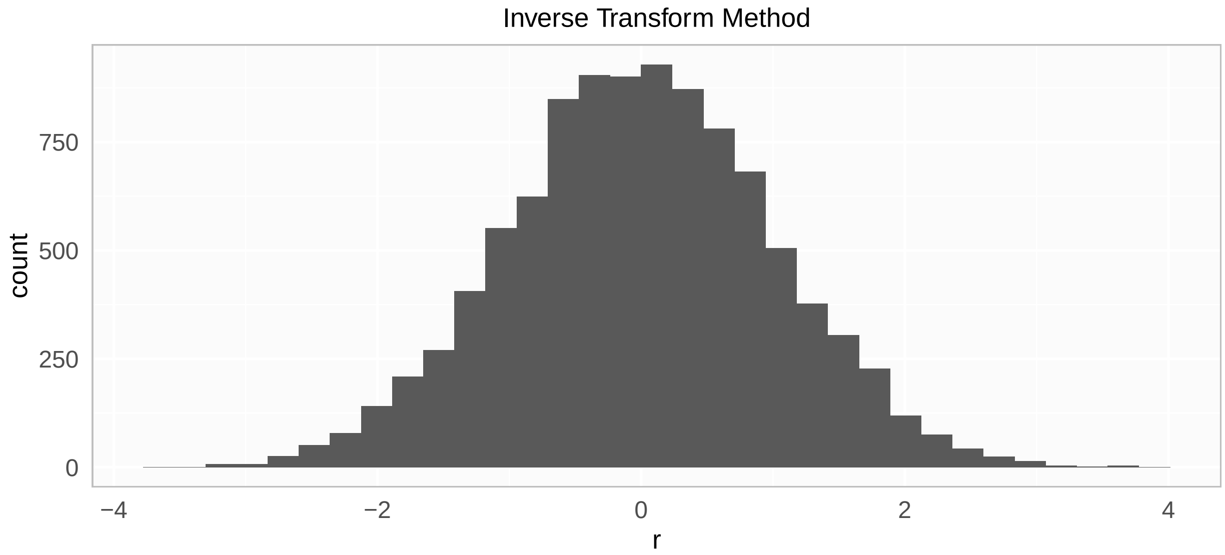
```
normrandit <- function()
{
  u <- runif(1)
  return (qnorm(u))
}

itstats <- function(n)
{
  vals <- rep(NA, n)
  for(i in 1:n)
  {
    vals[i] <- normrandit()
  }

  return(list(values=vals, mean=mean(vals), sd=sd(vals)))
}

res <- itstats(10000)
res$mean
```

```
## [1] -0.005543553
```

```
res$sd
```

```
## [1] 1.003801
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Box-Muller Method

```
normrandbm <- function()
{
  u2 <- runif(2)

  v1 <- (-2 * log(u2[1]))^(1/2) * cos(2 * pi * u2[2])
  v2 <- (-2 * log(u2[1]))^(1/2) * sin(2 * pi * u2[2])

  return (c(v1, v2))
}

bmstats <- function(n)
{
  vals <- rep(NA, n)
  for(i in seq(1, n, by=2))
  {
    rs <- normrandbm()
    vals[i] <- rs[1]
    vals[i + 1] <- rs[2]
  }

  return(list(values=vals, mean=mean(vals), sd=sd(vals)))
}

resBm <- bmstats(10000)
length(resBm[[1]])
```

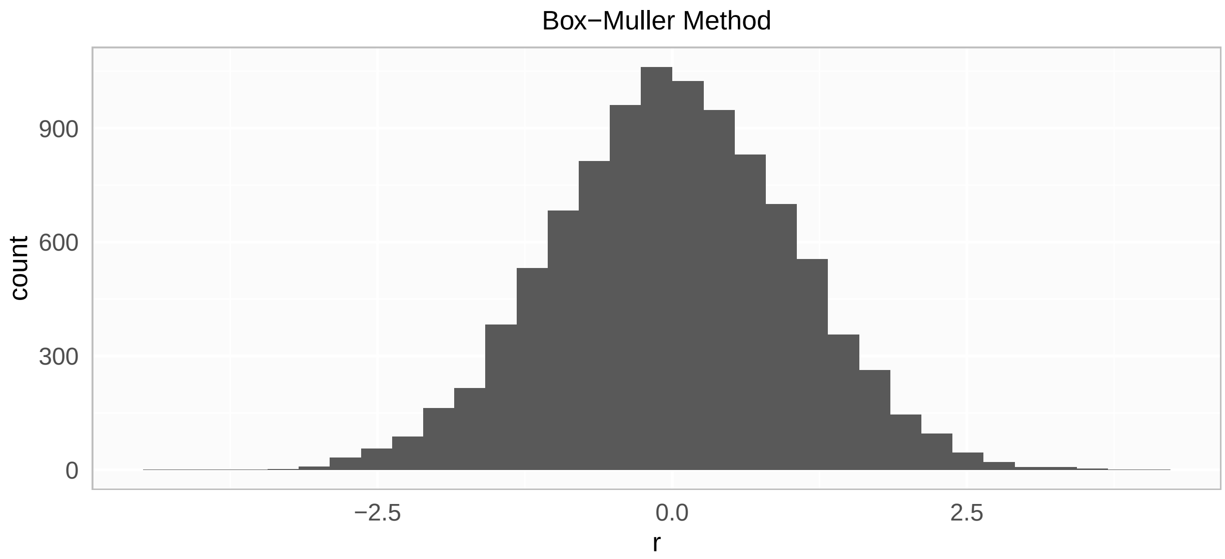
```
## [1] 10000
```

```
# Mean
resBm$mean
```

```
## [1] 0.00486827
```

```
# SD
resBm$sd
```

```
## [1] 1.009415
```



Accept Reject Method

```
normrandar <- function()
{
  continue <- TRUE
  while(continue)
  {
    u2 <- runif(2)
    eu2 <-  - log(u2)

    if(eu2[2] >= ( (eu2[1] - 1)^2 / 2) )
    {
      break
    }
  }

  sign <- runif(1)
  if(sign > 0.5)
  {
    eu2[1] <- eu2[1] * -1
  }

  return(eu2[1])
}

arstats <- function(n)
{
```

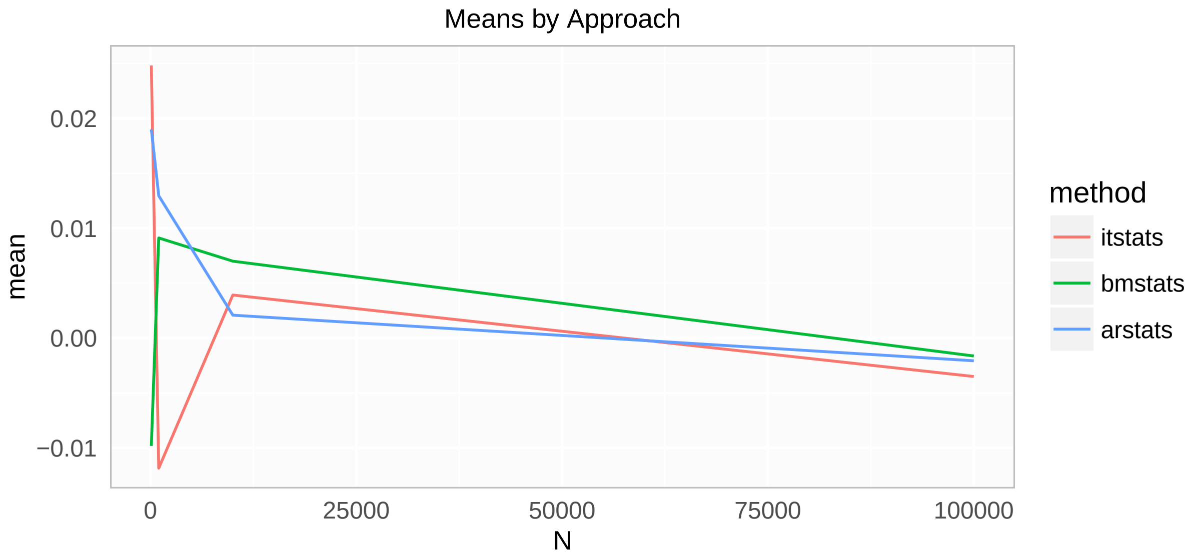
```r
  vals <- rep(NA, n)
  for(i in seq(1, n))
  {
    rs <- normrandar()
    vals[i] <- rs
    #vals[i + 1] <- rs[2]
  }

  return(list(values=vals, mean=mean(vals), sd=sd(vals)))
}
```

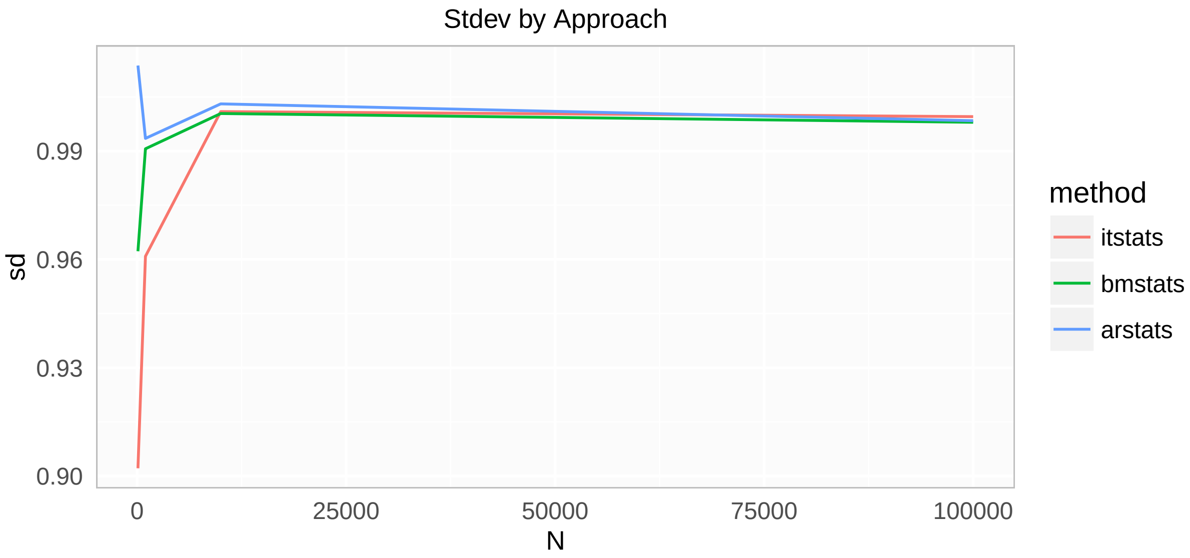
Compare

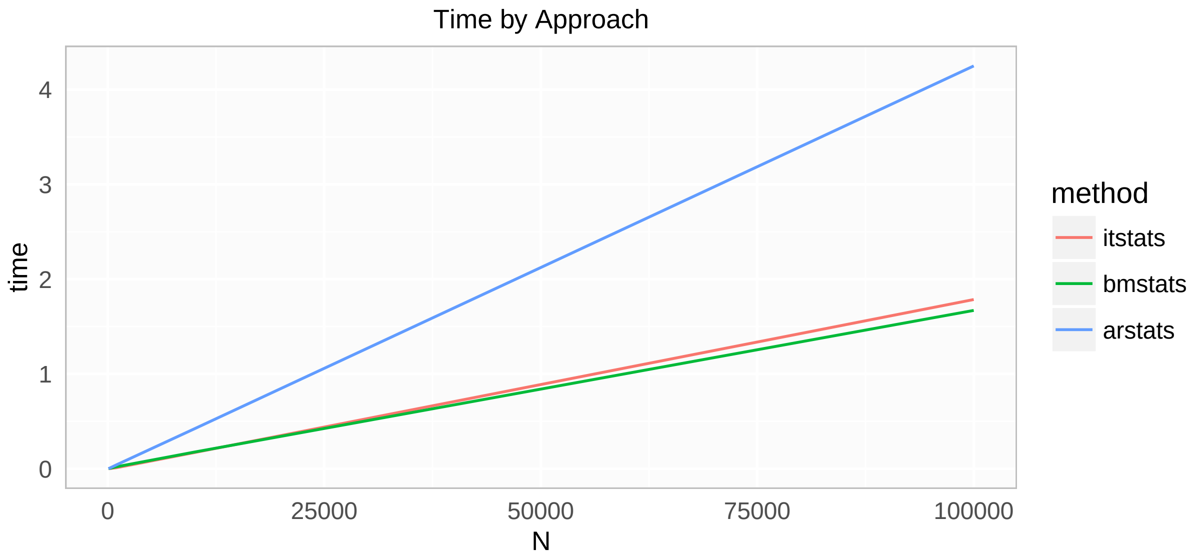
```r
dfCompare <- data.frame(method=c(), N=c(), mean=c(), sd=c(), time=c())

perfTest <- function(fun)
{
  dfResult <- data.frame(method=c(), N=c(), mean=c(), sd=c(), time=c())
  Ns <- c(100, 1000, 10000, 100000)
  it <- 2

  for(n in Ns)
  {
    m <- rep(NA, it)
    s <- rep(NA, it)
    t <- rep(NA, it)
    for(i in 1:it)
    {
      st <- system.time({ret <-  fun(n)})
      #print(st)
      m[i] <- ret$mean
      s[i] <- ret$sd
      t[i] <- st[[3]]
    }

    dfResult <- rbind(dfResult, data.frame(method=deparse(substitute(fun)),
                                           N=n,
                                           mean=mean(m),
                                           sd=mean(s),
                                           time=mean(t)))
  }

  return (dfResult)
}
# Force less use of scientific notation
# http://stackoverflow.com/questions/9397664/force-r-not-to-use-exponential-notation-e-g-e10
options("scipen"=100, "digits"=5)

dfCompare <- rbind(dfCompare, perfTest(itstats))
dfCompare <- rbind(dfCompare, perfTest(bmstats))
dfCompare <- rbind(dfCompare, perfTest(arstats))
```

method	N	mean	sd	time
itstats	100	0.02481	0.90215	0.000
itstats	1000	-0.01185	0.96086	0.010
itstats	10000	0.00391	1.00094	0.170
itstats	100000	-0.00350	0.99954	1.785

method	N	mean	sd	time
bmstats	100	-0.00982	0.96226	0.000
bmstats	1000	0.00911	0.99064	0.020
bmstats	10000	0.00700	1.00040	0.175
bmstats	100000	-0.00163	0.99798	1.670
arstats	100	0.01899	1.01370	0.000
arstats	1000	0.01295	0.99351	0.040
arstats	10000	0.00208	1.00308	0.420
arstats	100000	-0.00207	0.99842	4.250







For me, the Box-Muller approach takes the least time with Inverse Transform close behind. Also, I found that preallocating the vector in the stats method had a significant effect on performance. If the vector is not fully allocated, the time for the 100K samples jumps to 30+ seconds.

Million Sample Histograms

```
m <- 1000000
itMil <- itstats(m)
bmMil <- bmstats(m)
arMil <- arstats(m)
dfAll <- rbind(cbind(method="itstats", itMil))
dfAll <- rbind(cbind(method="bmstats", bmMil))
dfAll <- rbind(cbind(method="arstats", arMil))

g58 <- ggplot(dfAll) + geom_histogram(aes(x=r)) + myTheme + facet_wrap(~method)
g58
```

References

Trapletti, A. and K. Hornik. tseries: Time Series Analysis and Computational Finance. R package version 0.10-34. 2015. URL: http://CRAN.R-project.org/package=tseries.