Statistics 1 Unit 4 Team 8

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Exercises 66-80

Exercise 66

```
chi_sq <- function(n, deg){
  nrm <- matrix(rnorm(deg*n), nrow = n)

  apply(nrm, 1, function(x) sum(x^2))
}

sim <- chi_sq(10000, 8)

real <- c(8,16)
sample <- c(mean(sim), var(sim))

data.frame(Real = real,
           Sample = sample,
           Abs.Diff = abs(real - sample),
           Rel.Diff = abs(real-sample)/real,
           row.names = c("Mean", "Variance"))
```

```
##          Real    Sample   Abs.Diff    Rel.Diff
## Mean        8  8.032604 0.03260421 0.004075526
## Variance   16 16.313155 0.31315497 0.019572186
```

Exercise 67

```
rannorm <- function(n, mean = 0, sd = 1){
  singlenumber <- function() {
    repeat {
      U <- runif(1)
      U2 <- sign(runif(1, min = -1)) # value is +/- 1.
      Y <- rexp(1) * U2 # Y is a double exponental r.v.
      if (U < dnorm(Y) / exp(-abs(Y))) break
    }
    Y
  }
  replicate(n, singlenumber()) * sd + mean
}
```

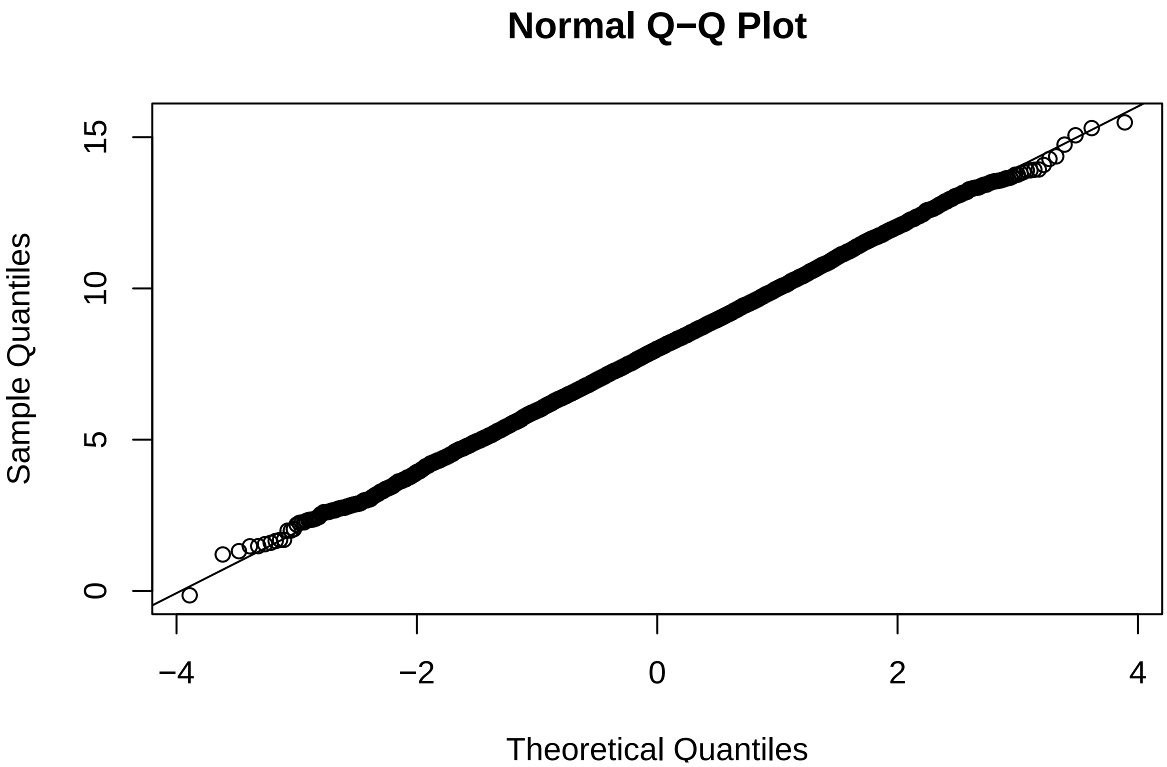
a)

```r
sim <- rannorm(10000, mean = 8, sd = 2)
head(sim)
```

```
## [1] 10.244021  9.631736  7.908165  2.267752  9.980382  8.742088
```

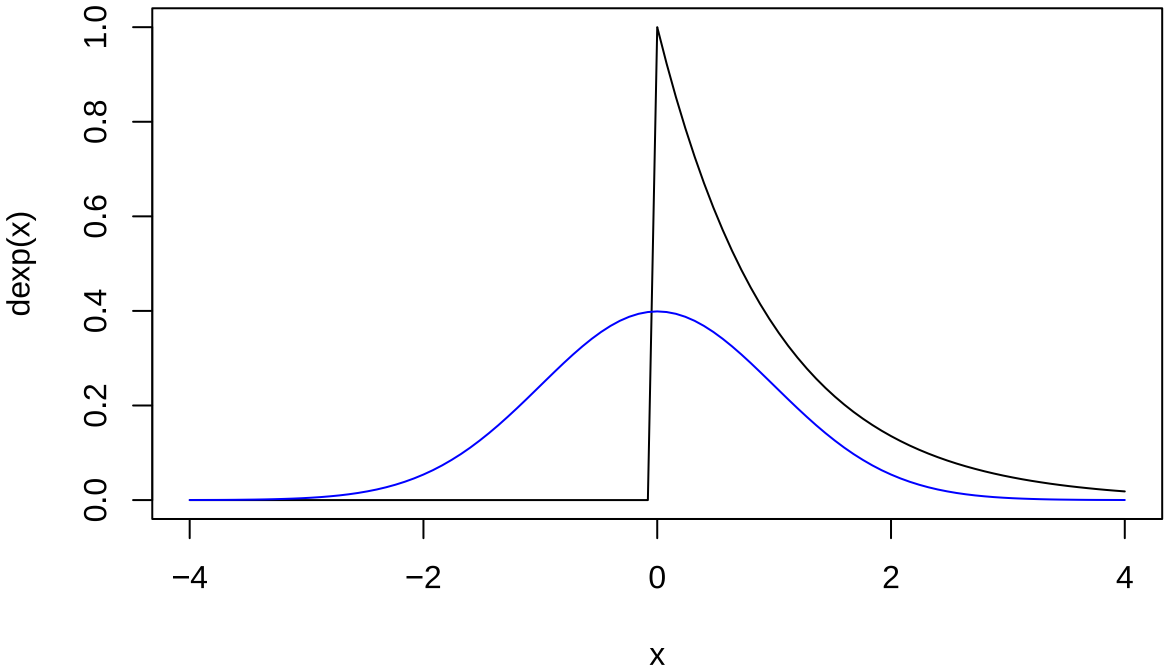
b)

```r
qqnorm(sim)
qqline(sim)
```



c)

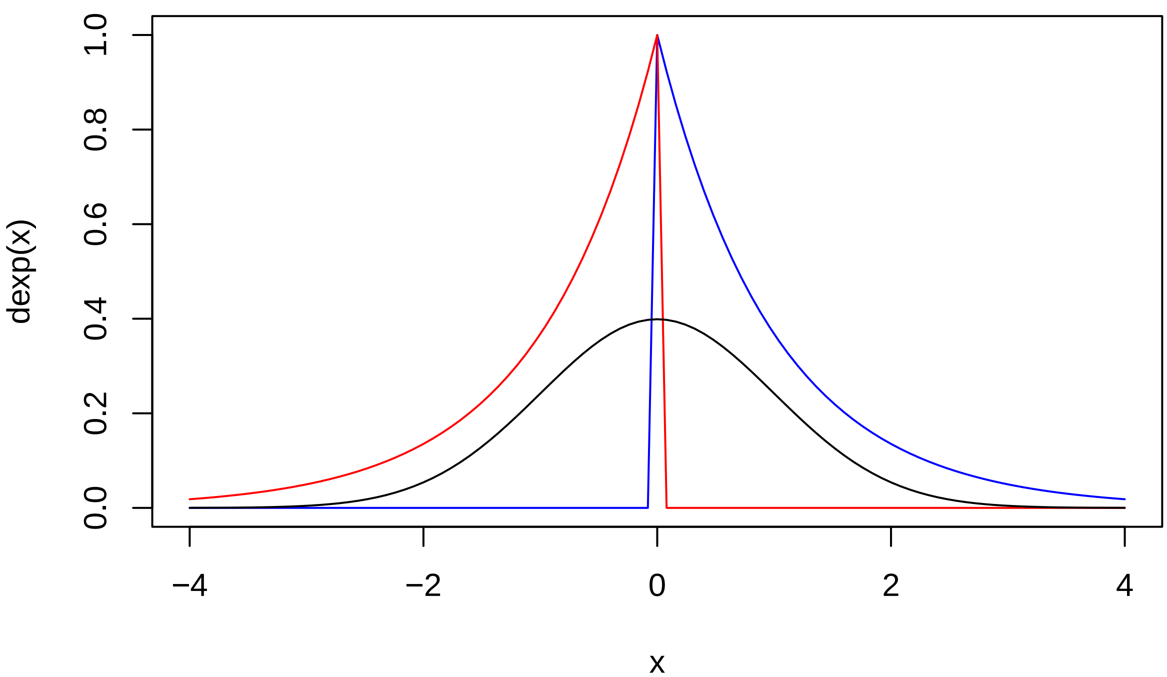
```r
curve(dexp, from = -4, to = 4)
curve(dnorm, from = -4, to = 4, add = T, col = "blue")
```



Note that the exponential distribution works adequately for the rejection method as in bounds the normal distribution above. In the previous graph, it might seem like it does not work given the negative part of the x axis, however it is possible to observe in the code that this is not in fact an issue as we take also negative values into account by multiplying the realization of the exponential by the sign of a random uniform in $[-1, 1]$. In other words, what we have is the following:

```
neg_dexp <- function(x) dexp(-x)

curve(dexp, from = -4, to = 4, col = "blue")
curve(neg_dexp, from = -4, to = 4, col = "red", add = T)
curve(dnorm, from = -4, to = 4, add = T)
```



Exercise 68

```r
# Probabilities
probs <- c(0.2, 0.3, 0.1, 0.15, 0.05, 0.2)

# Inversion
randiscrete1 <- function(n, probs) {
  cumprobs <- cumsum(probs)
  singlenumber <- function() {
    x <- runif(1)
    sum(x > cumprobs)
  }
  replicate(n, singlenumber())
}

# Rejection
randiscrete2 <- function(n, probs) {
  singlenumber <- function() {
    repeat {
      U <- runif(2,
                 min = c(-0.5, 0),
                 max = c(length(probs) - 0.5, max(probs)))
      if(U[2] < probs[round(U[1]) + 1]) break
    }
    return(round(U[1]))
  }
  replicate(n, singlenumber())
}

# Timing execution
n <- 100
t1_100 <- system.time(randiscrete1(n = n, probs = probs))[3]
t2_100 <- system.time(randiscrete2(n = n, probs = probs))[3]

n <- 1000
t1_1000 <- system.time(randiscrete1(n = n, probs = probs))[3]
t2_1000 <- system.time(randiscrete2(n = n, probs = probs))[3]

n <- 10000
t1_10000 <- system.time(randiscrete1(n = n, probs = probs))[3]
t2_10000 <- system.time(randiscrete2(n = n, probs = probs))[3]

data.frame(`n=100` = c(t1_100, t2_100),
           `n=1000` = c(t1_1000, t2_1000),
           `n=10000` = c(t1_10000, t2_10000),
           row.names = c("Inversion", "Rejection"))
```

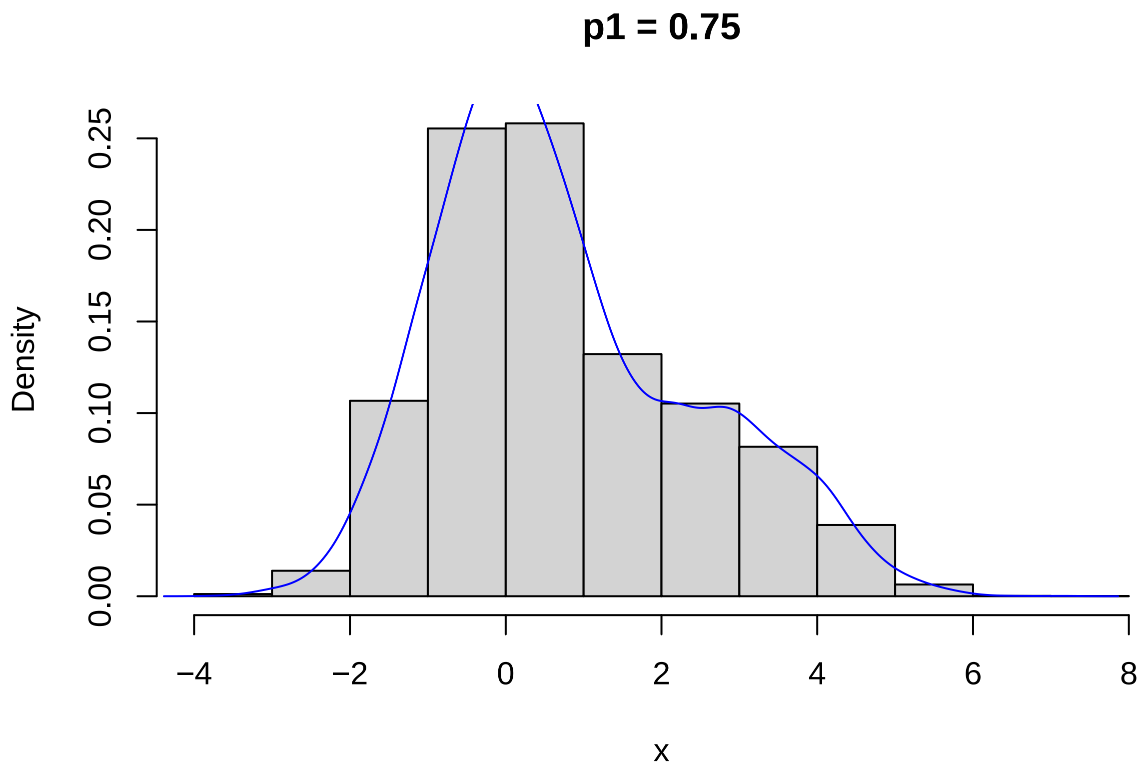
```
##           n.100 n.1000 n.10000
## Inversion 0.001  0.015   0.034
## Rejection 0.012  0.012   0.096
```

It is possible to observe that the inversion method is more time efficient than the rejection method. While for this amounts of simulations the difference might not seem that meaningful, when dealing with larger amounts of needed realizations the additional time generated from the rejection method can stack up and make more complex implementations not as computationally viable.

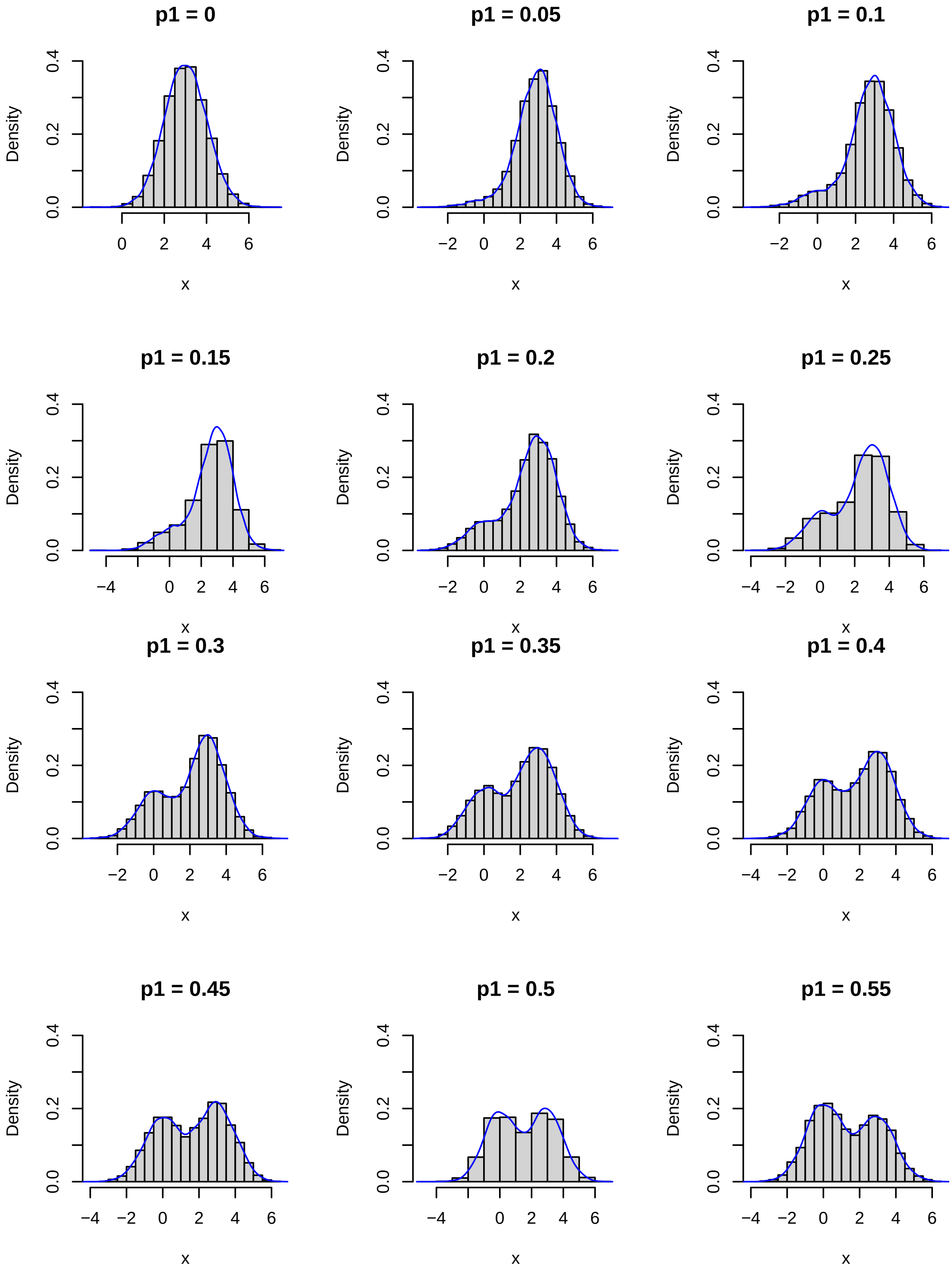
Exercise 69

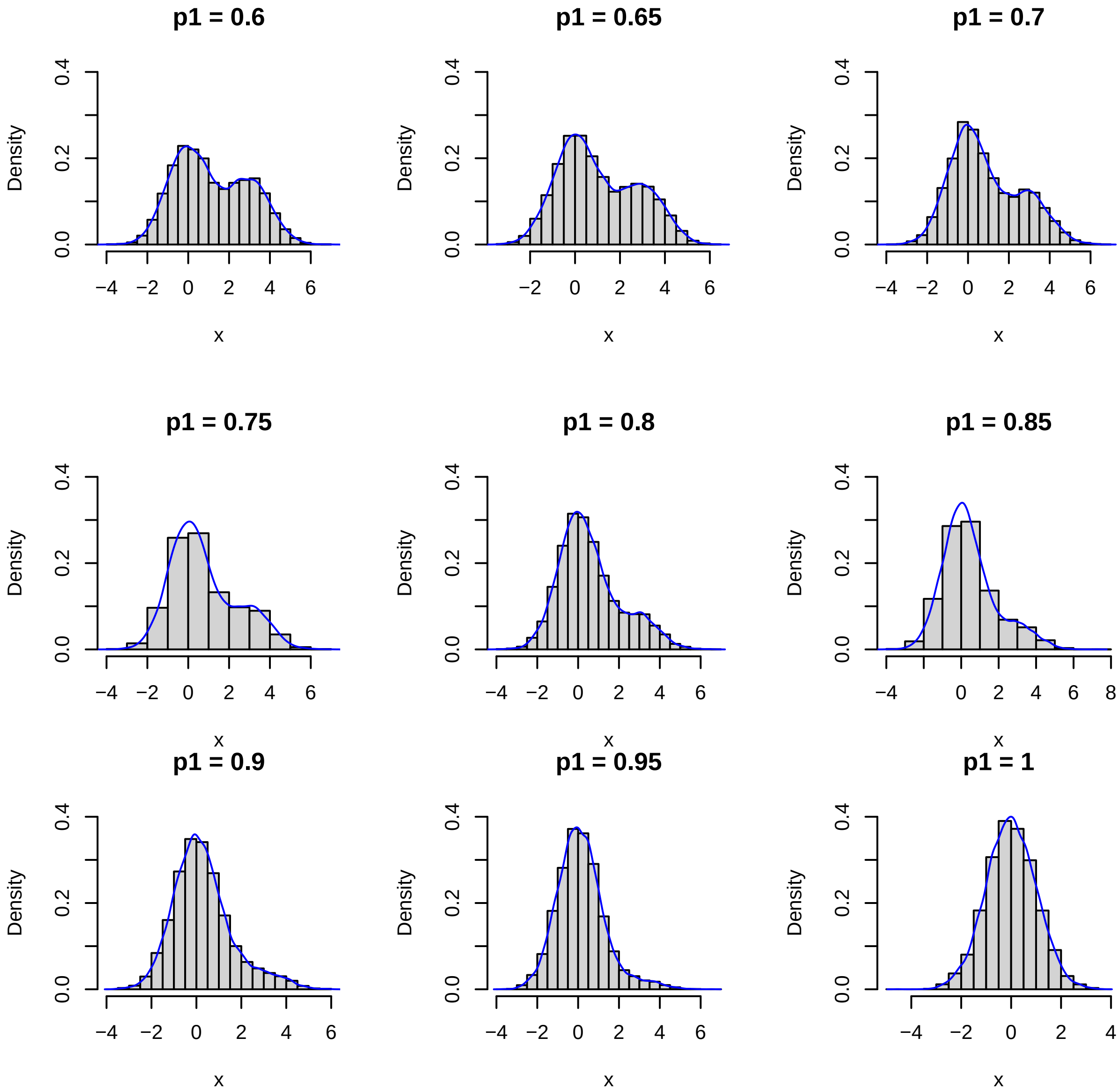
```
normal_mixture <- function(n, mean1, sd1, mean2, sd2, p){
  p1 <- rbinom(n, size = 1, prob = p)
  p1*rnorm(n, mean = mean1, sd = sd1) +
    (1-p1)*rnorm(n, mean = mean2, sd = sd2)
}

sim <- normal_mixture(10000, 0, 1, 3, 1, p = 0.75)
hist(sim, probability = T, main = "p1 = 0.75", xlab = "x")
lines(density(sim), col = "blue")
```




```
par(mfrow = c(2, 3))
p <- seq(from = 0, to = 1, by = 0.05)
for(p1 in p){
  sim <- normal_mixture(10000, 0, 1, 3, 1, p = p1)
  hist(sim,
       probability = T,
       main = paste0("p1 = ", p1),
       xlab = "x",
       ylim = c(0, 0.4))
  lines(density(sim), col = "blue")
}
```


p1 = 0
p1 = 0.05
p1 = 0.1
p1 = 0.15
p1 = 0.2
p1 = 0.25
p1 = 0.3
p1 = 0.35
p1 = 0.4
p1 = 0.45
p1 = 0.5
p1 = 0.55
Density
x



While pure bimodality (i.e. both maxima share the same density) seems to be present only in the case when $p_1 = p_2 = 0.5$, it is possible to start appreciating the emergence of local maxima clearly starting from when $p_1 = 0.2$ until $p_1 = 0.8$. Therefore we conjecture the presence of bimodal behavior whenever $p_1 \in [0.2, 0.8]$. When p_1 gets closer to 0 or 1, then the mixture appears less bimodal as only one of the two normal distributions takes up practically all of the mixture's density. This same intuition justifies the first sentence, given that when $p_1 = 0.5$ then we have an equal participation of both distributions in the mixture, resulting in each one's modes to be equally important. Note that this is true since because only the location parameter changes between the individual normal distributions, what we have is a mixture between a distribution and a shift of itself along the x-axis. This pure bimodal nature would not be attained at $p_1 = 0.5$ if the standard deviations were different among both individual normals, as this would scale the distribution.

Exercise 70

```
exp_gamma_mix <- function(n, r, beta){
  rexp(n, rgamma(n, r, beta))
}
```

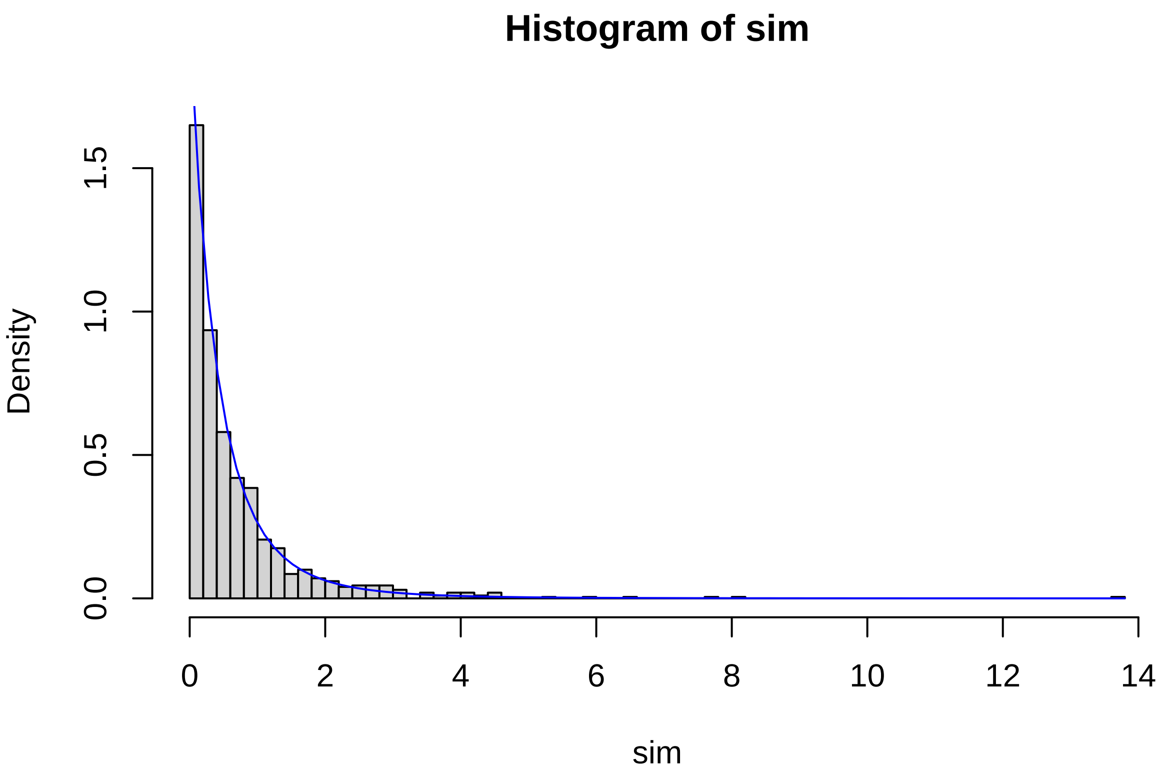
```r
sim <- exp_gamma_mix(1000, 4, 2)
```

Now, before plotting we need the Pareto density, which we can find by differentiating the distribution's cdf. For $x \geq 0$ we have:

$$
\begin{aligned}
\frac{d}{dx}F(x) &= \frac{d}{dx}\left[1 - \left(\frac{\beta}{\beta + x}\right)^r\right] \\
&= -\frac{d}{dx}\left(\frac{\beta + x}{\beta}\right)^{-r} \\
&= r \cdot \left(\frac{\beta + x}{\beta}\right)^{-r-1} \cdot \frac{1}{\beta} \\
&= \frac{r \cdot \beta^r}{(\beta + x)^{r+1}}
\end{aligned}
$$

```r
dpareto <- function(x, r = 4, beta = 2){
  (r*beta^r)/(beta+x)^(r+1)
}

hist(sim, probability = T, breaks = 50)
curve(dpareto, add = T, col = "blue")
```



By plotting the density histogram of the continuous mixture and the density function of the Pareto distribution with the corresponding parameters, it is possible to observe that the mixture does seem to follow the Pareto distribution.

Exercise 71

To solve this exercise, we first need to be able to generate samples from the two-dimensional t-Student distribution. We use the function from exercise 43 (previous homework) to do this:

```
rmvnorm <- function(n, m, Sigma){
  X <- matrix(rnorm(n*nrow(Sigma)), nrow = nrow(Sigma), ncol = n)

  A <- t(chol(Sigma))

  t(A %*% X + m)

}

rmvt <- function(n, nu, m, Sigma){

  AZ <- rmvnorm(n, 0, Sigma)

  W <- nu/rchisq(n, df = nu)

  sim <- t( apply(sqrt(W)*AZ, 1, function(Xi) Xi+m))

  sim
}

B <- 3000
nu <- 3
n <- 90
m <- c(0,0)
Sigma <- matrix(c(1,0.5,0.5,1), nrow = 2)

samples <- lapply(1:B, function(i) rmvt(n, nu, m, Sigma))
```

We now calculate the estimates for ρ using both methods:

```
rhos <- do.call(rbind, lapply(samples, function(X){
  c(DIRECT = cor(X[,1], X[,2]),
    KENDALL = sin(pi/2 * cor(X[,1], X[,2], method = "kendall")))
}))

head(rhos)
```

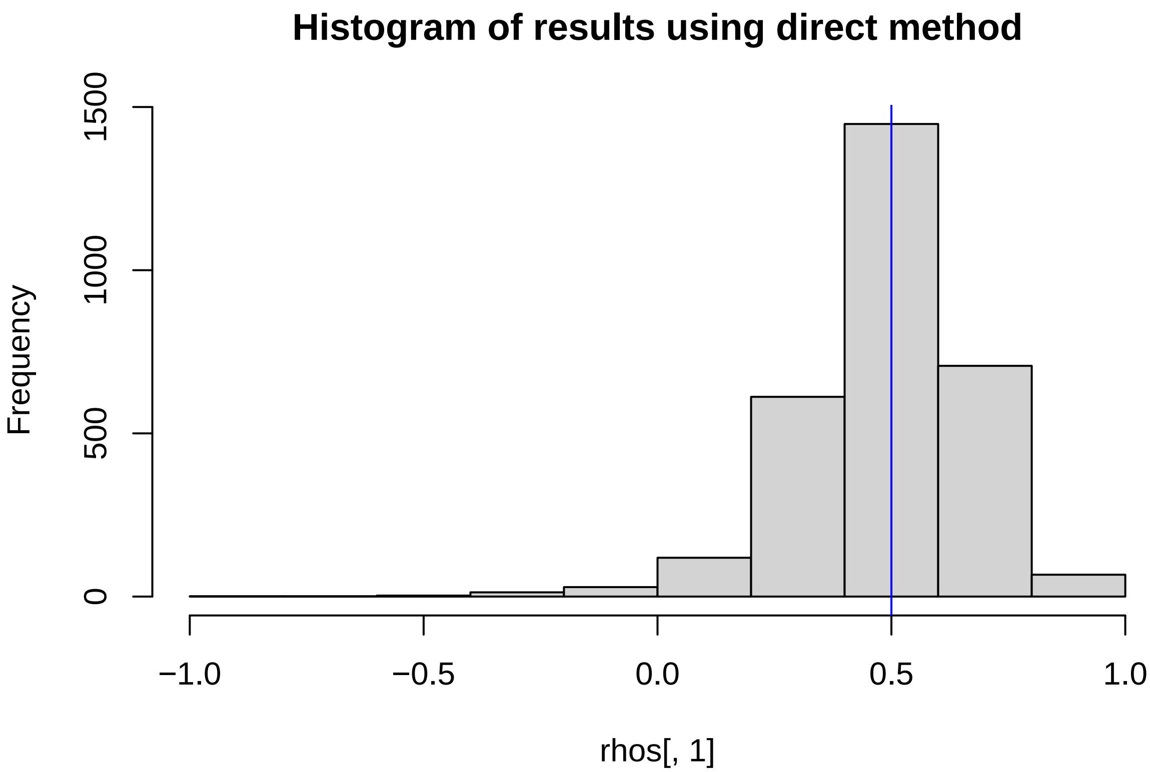
```
##         DIRECT   KENDALL
## [1,] 0.8759968 0.4993205
## [2,] 0.5543451 0.4870378
## [3,] 0.3995728 0.4235067
## [4,] 0.5580510 0.3804176
## [5,] 0.6060562 0.6526483
## [6,] 0.5146216 0.5013580
```

```
rbind(apply(rhos, 2, summary), sd = apply(rhos, 2, sd))
```

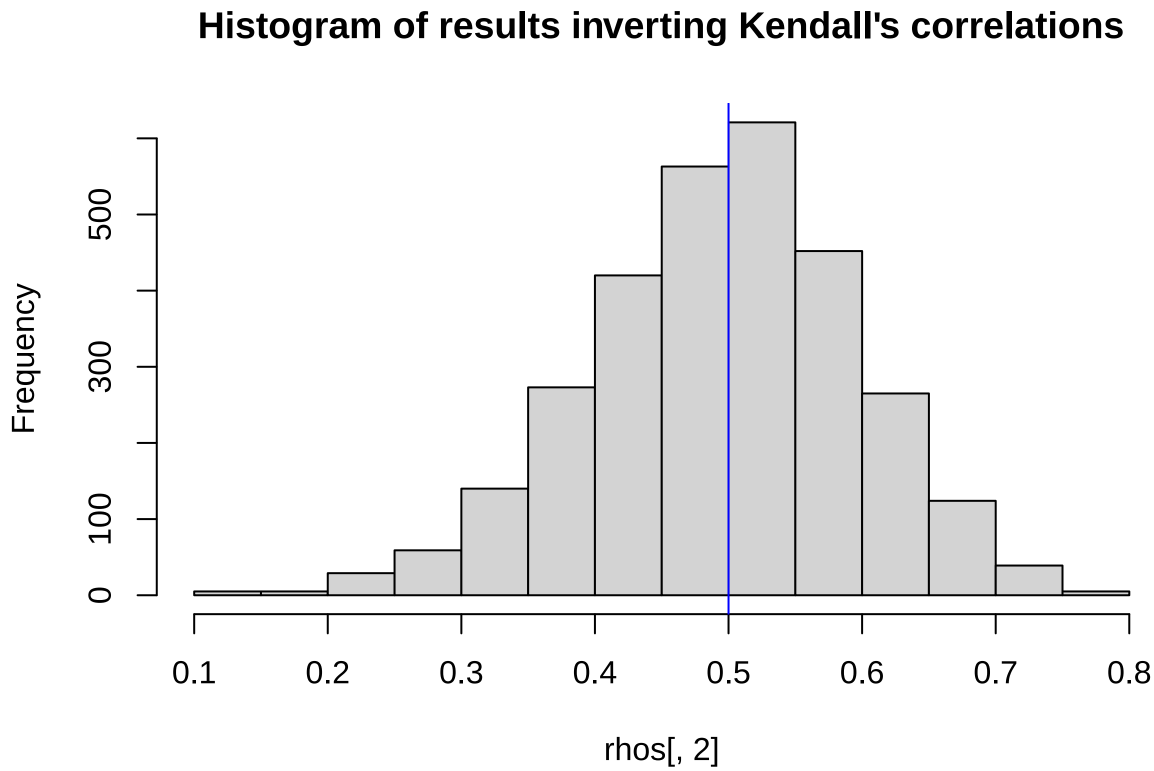
```
##             DIRECT   KENDALL
## Min.    -0.8434684 0.1154436
## 1st Qu.  0.3963591 0.4297144
## Median   0.5044006 0.5006792
```

```
## Mean      0.4877251 0.4952065
## 3rd Qu.  0.6036371 0.5650317
## Max.      0.9813804 0.7992252
## sd        0.1802387 0.1004536
```

```r
hist(rhos[,1], main = "Histogram of results using direct method")
abline(v = 0.5, col = "blue")
```




```r
hist(rhos[,2], main = "Histogram of results inverting Kendall's correlations")
abline(v = 0.5, col = "blue")
```



It is possible to see that in this case, the method that inverts Kendall's τ correlations achieves a closer mean value to the real value of $\rho = 0.5$ with a significantly lower standard deviation than the direct method. This means that in this particular case, inverse Kendall's τ correlations method is better.

Now in the case of $d > 2$, it should still be possible to use the inverse Kendall's τ correlations method by taking pairwise combinations of each dimension of the realized t-Student. However, this means that for any $d > 2$, we would need to run the same method used here $\frac{d(d-1)}{2}$ times. This would already be computationally slower and potentially more memory demanding than R's implementation of cor used in the direct method.

Exercise 72

Let's start by proving the hint. Before that, notice that since $N(t) \sim Poi(\lambda t)$, then $E[N(t)] = \lambda t$ and $Var[N(t)] = \lambda t$. Also, since $Y_i \sim Gamma(\alpha, \beta)$ then $E[Y_i] = \frac{\alpha}{\beta}$ and $Var[Y_i] = \frac{\alpha}{\beta^2}$.

Now, using the law of total expectation, we have that:

$$
\begin{aligned}
E[X(t)] &= E\left[\sum_{i=1}^{N(t)} Y_i\right] \\
&= E\left[E\left[\sum_{i=1}^{N(t)} Y_i | N(t) = N\right]\right] \\
&\text{Because of iid of } Y_i \\
&= E[N(t)E[Y_1]] \\
&\text{Because of independence between } Y_i, N \\
&= E[N(t)]E[Y_1] \\
&= \lambda t \frac{\alpha}{\beta}
\end{aligned}
$$

Similarly, using the law of total variance:

$$
\begin{aligned}
Var[X(t)] &= Var\left[\sum_{i=1}^{N(t)} Y_i\right] \\
&= E\left[Var\left[\sum_{i=1}^{N(t)} Y_i | N(t) = N\right]\right] + Var\left[E\left[\sum_{i=1}^{N(t)} Y_i | N(t) = N\right]\right] \\
&= E\left[N(t)Var[Y_i]\right] + Var[N(t)E[Y_i]] \\
&= E[N(t)]Var[Y_i] + E[Y_i]^2 Var[N(t)] \\
&= \lambda t[E[Y_i^2] - E[Y_i]^2] + \lambda t E[Y_i]^2 \\
&= \lambda t E[Y_i^2]
\end{aligned}
$$

Now

$$
Var[Y_i] = E[Y_i^2] - E[Y_i]^2 = \frac{\alpha}{\beta}
$$

Therefore, recalling that $E[Y_i] = \frac{\alpha}{\beta}$ we have that $E[Y_i^2] = \frac{\alpha^2+\alpha}{\beta^2}$

Finally, we get that:

$$
E[X(t)] = \lambda t \frac{\alpha}{\beta}
$$

$$
Var[X(t)] = \lambda t \frac{\alpha^2 + \alpha}{\beta^2}
$$

We use this to simulate the process:

```r
compPoisson <- function(n, t, lambda, alpha, beta){

  single_process <- function(t, lambda, alpha, beta){
    sum(rgamma(rpois(1, lambda*t), alpha, beta))
  }

  sim <- replicate(n, single_process(t, lambda, alpha, beta))

  sample <- c(mean(sim), var(sim))
  real <- c(lambda*t*alpha/beta, lambda*t*(alpha^2 + alpha)/beta^2)

  return( list(PARAMS = c(n = n, t = t, lambda = lambda, alpha = alpha, beta = beta),
               RESULTS = data.frame(SAMPLE = sample,
                                    REAL = real,
                                    ABS.DIFF = abs(sample - real),
                                    REL.DIFF = abs(sample - real)/real)) )
}
```

We proceed now to test with different parameters:

```r
compPoisson(n = 10000, t = 10, lambda = 0.5, alpha = 1, beta = 1)
```

```
## $PARAMS
##      n      t lambda  alpha   beta
##  1e+04  1e+01  5e-01  1e+00  1e+00
##
```

```
## $RESULTS
##     SAMPLE REAL   ABS.DIFF    REL.DIFF
## 1 5.032222    5 0.03222159 0.006444319
## 2 9.833376   10 0.16662405 0.016662405
```

```r
compPoisson(n = 10000, t = 10, lambda = 2, alpha = 15, beta = 0.2)
```

```
## $PARAMS
##       n       t  lambda   alpha    beta
## 10000.0    10.0     2.0    15.0     0.2
##
## $RESULTS
##       SAMPLE   REAL   ABS.DIFF    REL.DIFF
## 1   1504.391   1500   4.391206 0.002927471
## 2 120441.730 120000 441.729843 0.003681082
```

```r
compPoisson(n = 10000, t = 10, lambda = 0.7, alpha = 3, beta = 4)
```

```
## $PARAMS
##      n      t lambda  alpha   beta
##  1e+04  1e+01  7e-01  3e+00  4e+00
##
## $RESULTS
##     SAMPLE REAL   ABS.DIFF    REL.DIFF
## 1 5.223480 5.25 0.02652000 0.005051429
## 2 5.206022 5.25 0.04397835 0.008376828
```

```r
compPoisson(n = 10000, t = 10, lambda = 3, alpha = 5, beta = 0.01)
```

```
## $PARAMS
##      n      t lambda  alpha   beta
##  1e+04  1e+01  3e+00  5e+00  1e-02
##
## $RESULTS
##       SAMPLE    REAL    ABS.DIFF    REL.DIFF
## 1   14955.08   15000    44.92431 0.002994954
## 2 9075104.23 9000000 75104.22563 0.008344914
```

```r
compPoisson(n = 10000, t = 10, lambda = 0.85, alpha = 8, beta = 3)
```

```
## $PARAMS
##       n       t  lambda   alpha    beta
## 1.0e+04 1.0e+01 8.5e-01 8.0e+00 3.0e+00
##
## $RESULTS
##     SAMPLE     REAL   ABS.DIFF    REL.DIFF
## 1 22.61811 22.66667 0.04855333 0.002142058
## 2 66.17521 68.00000 1.82478599 0.026835088
```

We observe that in all cases the estimated sample values of mean and variance are close to the theoretical ones calculated beforehand.

Exercise 73

a)

Notice that the real value of the integral is given by:

$$\int_1^3 x^2 dx = \frac{x^3}{3}\bigg|_1^3 = \frac{26}{3}$$

Using Montecarlo simulation, take $g(x) = x^2$ and $f(x) = \frac{1}{3-1}$ for $1 \leq x \leq 3$ and 0 otherwise. That is, we sample from a $\mathcal{U}(1,3)$ distribution. We get:

```
real <- 26/3
sim <- (3-1)*mean(runif(10000, min = 1, max = 3)^2)

data.frame(Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real)
```

```
##       Real Monte.Carlo   Abs.Diff    Rel.Diff
## 1 8.666667    8.679198 0.01253091 0.001445874
```

b)

The real value of the integral is given by

$$\int_0^\pi sin(x)dx = -cos(x)|_0^\pi = 2$$

Similar to part a) take $g(x) = sin(x)$ and $f(x) = \frac{1}{\pi-0}$ for $0 \leq x \leq \pi$ and 0 otherwise. In this case we sample from a $\mathcal{U}(0,\pi)$ distribution. We get:

```
real <- 2
sim <- (pi-0)*mean(sin(runif(10000, min = 0, max = pi)))

data.frame(Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real)
```

```
##   Real Monte.Carlo    Abs.Diff    Rel.Diff
## 1    2     2.00388 0.003880029 0.001940015
```

c)

To see the real value of the third integral, it is enough to notice that $f(x) = e^{-x}$ is the density function of an exponential random variable with parameter 1. That means the value of the integral is 1, due to the exponential's support. However, we can also calculate it using integration by parts, taking $u = 1$ and $dv = e^{-x}$. Then $du = 0$ and $v = -e^{-x}$. Thus:

$$\int_0^\infty e^{-x}dx = -e^{-x}\big|_0^\infty - 0 = 0 - (-1) = 1$$

In this case, notice we cannot sample from a uniform that has infinity as upper limit. Therefore, we will instead use the fact stated above that $f(x) = e^{-x}$ is the density function of an exponential random variable with parameter 1, and sample from this distribution. In this case, $g(x) = \mathbb{1}_{x\geq 0}$. However, this will be redundant in our case given by definition the exponential random variable only generates non-negative numbers. Therefore, we can use Montecarlo as follows:

```r
real <- 1
sim <- mean(rexp(10000, 1))

data.frame(Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real)
```

```
##   Real Monte.Carlo    Abs.Diff    Rel.Diff
## 1    1    1.005588 0.005588177 0.005588177
```

d)

In this case, the value of the integral has simplified close form, therefore numerical approximations are used to determine its approximate value. In this case, we take WolfraAlpha's value as real, given by:

$$\int_0^3 sin(e^x)dx \approx 0.606124$$

Similar to parts a) and b), we take $g(x) = sin(e^x)$ and $f(x) = \frac{1}{3-0}$ for $0 \leq x \leq 3$ and 0 otherwise. In this case we sample from a $\mathcal{U}(0,3)$ distribution. We get:

```r
real <- 0.606124
sim <- (3-0)*mean(sin(exp(runif(10000, min = 0, max = 3))))

data.frame(Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real)
```

```
##       Real Monte.Carlo   Abs.Diff   Rel.Diff
## 1 0.606124   0.6414693 0.03534533 0.05831369
```

e)

For the final integral, notice that the function we wish to integrate corresponds to the density of a standard normal distribution. Also, notice that:

$$\int_0^2 \frac{1}{\sqrt{2\pi}} e^{-x^2/2}dx = \int_{-\infty}^2 \frac{1}{\sqrt{2\pi}} e^{-x^2/2}dx - \int_{-\infty}^0 \frac{1}{\sqrt{2\pi}} e^{-x^2/2}dx = \Phi(2) - \Phi(0) \approx 0.4772499$$

Similar to previous exercises, we take $g(x) = e^{-x^2/2}$ and $f(x) = \frac{1}{2-0}$ for $0 \leq x \leq 2$ and 0 otherwise. Again, we sample from a $\mathcal{U}(0,2)$ distribution. Notice that we take out the constant $\frac{1}{\sqrt{2\pi}}$

```r
real <- pnorm(2)-pnorm(0)
sim <- 1/sqrt(2*pi) * (2-0)*mean(exp( -runif(10000, min = 0, max = 2)^2 / 2 ))

data.frame(Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real)
```

```
##        Real Monte.Carlo     Abs.Diff    Rel.Diff
## 1 0.4772499   0.4779446 0.0006947718 0.001455782
```

Exercise 74

First, let's caculate the real value of the integral. Similar to the previous exercise, we can do integration by parts taking $u = 1$ and $dv = e^{-x}$. Then $du = 0$ and $v = -e^{-x}$. Thus:

$$\int_0^{0.5} e^{-x} dx = -e^{-x}\Big|_0^{0.5} - 0 = -\frac{1}{\sqrt{e}} + 1 \approx 0.3934693$$

We start by sampling from a uniform distribution. Like in the previous exercise, we take $g(x) = e^{-x}$ and $f(x) = \frac{1}{0.5-0}$ for $0 \leq x \leq 0.5$ and 0 otherwise. In this case we sample from a $\mathcal{U}(0, 0.5)$ distribution. We get:

```
real <- -1/sqrt(exp(1)) + 1
sim <- (0.5-0)*mean(exp(-runif(10000, min = 0, max = 0.5)))
mc_var <- var(exp(-runif(10000, min = 0, max = 0.5)))/10000

data.frame(Sampling = "Uniform",
           Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real,
           Var = mc_var)
```

```
##   Sampling      Real Monte.Carlo     Abs.Diff   Rel.Diff         Var
## 1  Uniform 0.3934693   0.3941624 0.0006930452 0.00176137 1.28624e-06
```

Next, we can use the fact that $f(x) = e^{-x}$ is the density function of an exponential random variable with parameter 1, and sample from this distribution. In this case, $g(x) = \mathbb{1}_{0.5 \geq x \geq 0}$.

```
real <- -1/sqrt(exp(1)) + 1
x <- rexp(10000, 1)
sim <- mean((x >= 0) & (x <= 0.5))
mc_var <- var((x >= 0) & (x <= 0.5))/10000

data.frame(Sampling = "Exponential",
           Real = real,
           Monte.Carlo = sim,
           Abs.Diff = abs(real-sim),
           Rel.Diff = abs(real-sim)/real,
           Var = mc_var)
```

```
##      Sampling      Real Monte.Carlo     Abs.Diff    Rel.Diff          Var
## 1 Exponential 0.3934693      0.3942 0.0007306597 0.001856967 2.388302e-05
```

It is possible to see that both methods approximate the integral fairly well. However, the first method (sampling from an uniform distribution) has a lower variance and difference values than the second one. This happens because by sampling from a uniform distribution that already falls wothin the integration limits, all realizations of the random variable are used to calculate the mean. This means that if we take n realizations, all n are effectively useful and provide information to make the approximation better. However, if we sample from an exponential distribution as in the second part, we need to use an indicator to guarantee that the points fall within the integration limits. This means we are essentially throwing away information whenever a realization lies outside our desired interval, which reduces accuracy and increases variance.

Exercise 75

We first introduce the portfolio composition and default probabilities:

```r
nAssets <- c(AA = 10,
             A = 25,
             BBB = 96)

pd <- c(AA = 0.0001,
        A = 0.0005,
        BBB = 0.0025)
```

We now create a function to simulate one year of the portfolio multiple times, using bernoulli random variables, where we assume independence between defaults and that a "success" (i.e. a realization of 1 by the Bernoulli) represents a default. This way, we can generate one Bernoulli realization by asset according to its respective default probability, and repeat this multiple times.

```r
port_sim <- function(n, assets, probs){
  do.call(rbind, lapply(1:n, function(i){
    c(AA = sum(rbinom(n = assets[1], size = 1, prob = probs[1])),
      A = sum(rbinom(n = assets[2], size = 1, prob = probs[2])),
      BBB = sum(rbinom(n = assets[3], size = 1, prob = probs[3]))
    )
  }))
}
```

```r
set.seed(1802) # For reproducibility and interpretations
sim <- port_sim(1e5, nAssets, pd)

head(sim)
```

```
##      AA A BBB
## [1,]  0 0   1
## [2,]  0 0   0
## [3,]  0 0   1
## [4,]  0 0   2
## [5,]  0 0   0
## [6,]  0 0   1
```

```r
apply(sim, 2, sum)
```

```
##    AA     A   BBB
##   105  1297 23904
```

In $100,000$ simulations, it is possible to observe that there were only 105 defaults total for AA, $1,297$ for A and $23,904$ for BBB. If we look at it in a simulation-by-simulation basis, we get the following results:

```r
rbind(apply(sim, 2, summary), sd = apply(sim, 2, sd))
```

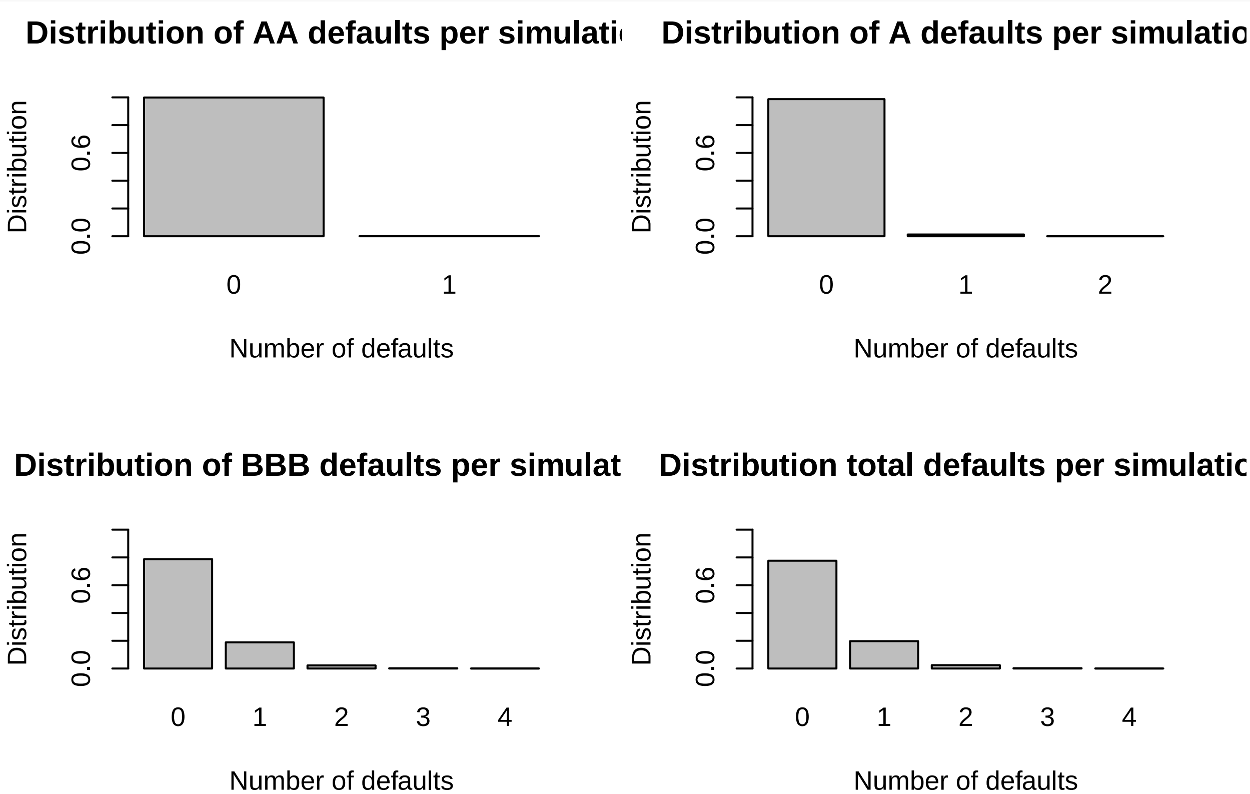
```
##                 AA         A       BBB
## Min.    0.00000000 0.0000000 0.0000000
## 1st Qu. 0.00000000 0.0000000 0.0000000
## Median  0.00000000 0.0000000 0.0000000
## Mean    0.00105000 0.0129700 0.2390400
## 3rd Qu. 0.00000000 0.0000000 0.0000000
## Max.    1.00000000 2.0000000 4.0000000
## sd      0.03238685 0.1140259 0.4893488
```

This shows that, indeed, the AA obligors are the safest, with a maximum value of 1 default per simulation in the sample, which means the 105 reported above all happened in different simulations. Following the AA come the A obligors with a maximum value of 2 defaults per simulation in the sample, and finally the

BBB with a maximum of 4. It is important to note that all of them have a mean value less than 1 default per simulation. However, there is indeed more volatility as the credit rating decreases (which makes sense intuitively but is confirmed by the numbers), as demonstrated by the increasing standard deviation with decrease of rating.

We now look at the default distributions via histograms:

```
par(mfrow = c(2,2))
barplot(table(sim[,1])/1e5,
        main = "Distribution of AA defaults per simulation",
        ylim = c(0, 1),
        xlab = "Number of defaults",
        ylab = "Distribution")
barplot(table(sim[,2])/1e5,
        main = "Distribution of A defaults per simulation",
        ylim = c(0, 1),
        xlab = "Number of defaults",
        ylab = "Distribution")
barplot(table(sim[,3])/1e5,
        main = "Distribution of BBB defaults per simulation",
        ylim = c(0, 1),
        xlab = "Number of defaults",
        ylab = "Distribution")
barplot(table(apply(sim, 1, sum))/1e5,
        main = "Distribution total defaults per simulation",
        ylim = c(0, 1),
        xlab = "Number of defaults",
        ylab = "Distribution")
```



Since some of the values are too small to be legible, we include a table of values as well. Note that the values are in percentages:

```r
data.frame( AA = c(table(sim[,1])/1e5, 0, 0, 0)*100,
            A = c(table(sim[,2])/1e5, 0, 0)*100,
            BBB = c(table(sim[,3])/1e5)*100,
            TOTAL = c(table(apply(sim, 1, sum))/1e5)*100)
```

```
##       AA      A    BBB  TOTAL
## 0 99.895 98.713 78.743 77.630
## 1  0.105  1.277 18.828 19.696
## 2  0.000  0.010  2.224  2.428
## 3  0.000  0.000  0.192  0.230
## 4  0.000  0.000  0.013  0.016
```