

TMA4300: Exercise 1

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Problem A

A.1

The exponential distribution has a cumulative density function given by

$$F(x) = 1 - e^{-\lambda x},$$

where λ is the rate parameter. By defining $u := F(x)$, x can be expressed as

$$x = -\frac{1}{\lambda} \ln(1 - u) =: F^{-1}(u).$$

This means that we can use the *inversion method* to simulate from the exponential distribution. Let $U \sim \mathcal{U}_{[0,1]}$ and calculate $X = F^{-1}(U)$, then $X \sim \text{Exp}(\lambda)$. A function which simulates from the exponential distribution is given below.

```
sim.exp <- function(rate, n){  
  # Vector of n uniform values  
  u <- runif(n, 0, 1)  
  # Note that (1-U) ~ U, so we can use u instead of 1-u in the returned value.  
  -1/rate * log(u)  
}
```

Next, we need to check if this gives reasonable results by comparing our simulated values to the theoretical knowledge using $\lambda = 0.5$ and $n = 1000$.

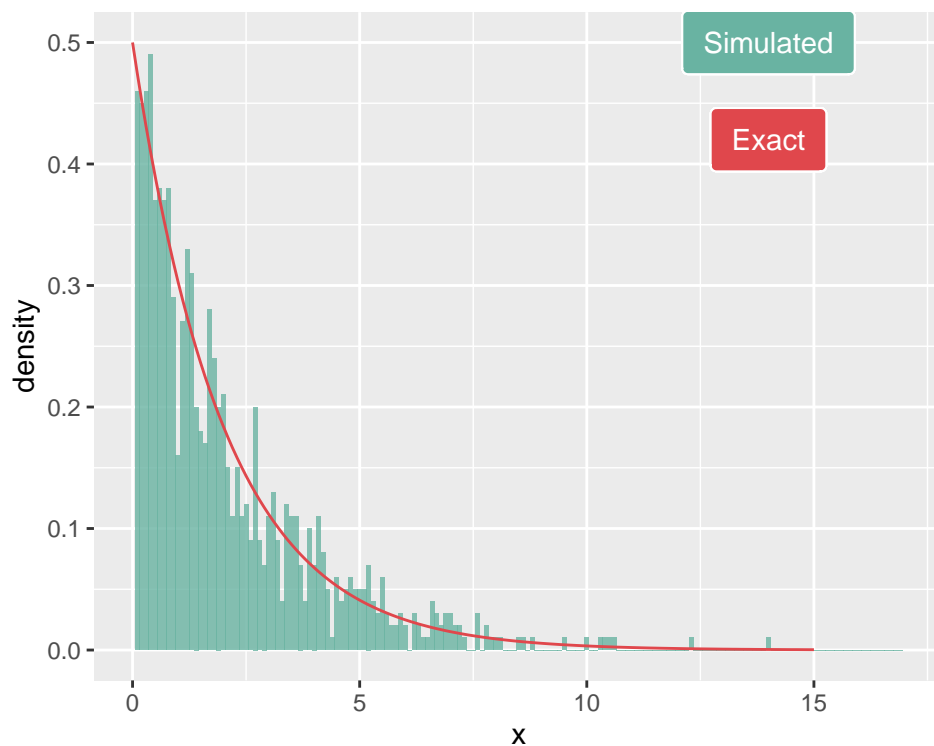
```
rate <- 0.5  
n <- 1000  
sim <- data.frame(x = sim.exp(rate, n))  
x = seq(from = 0, to = 15, by = 0.1)  
exact <- data.frame(x = x, y = rate*exp(-rate*x))  
  
ggplot(sim) +  
  geom_histogram(aes(x = x, y = ..density..),  
                 alpha = 0.8, fill = "#69b3a2", binwidth = 0.1) +  
  geom_line(data = exact, aes(x = x, y = y), color = "#e0474c") +  
  geom_label(  
    label="Simulated",  
    x=14,
```

```

y=0.5,
label.padding = unit(0.55, "lines"), # Rectangle size around label
label.size = 0.35,
color = "white",
fill= "#69b3a2"
) +
geom_label(
  label="Exact",
  x=14,
  y=0.42,
  label.padding = unit(0.55, "lines"), # Rectangle size around label
  label.size = 0.35,
  color = "white",
  fill = "#e0474c"
) +
xlim(0,17)

```

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

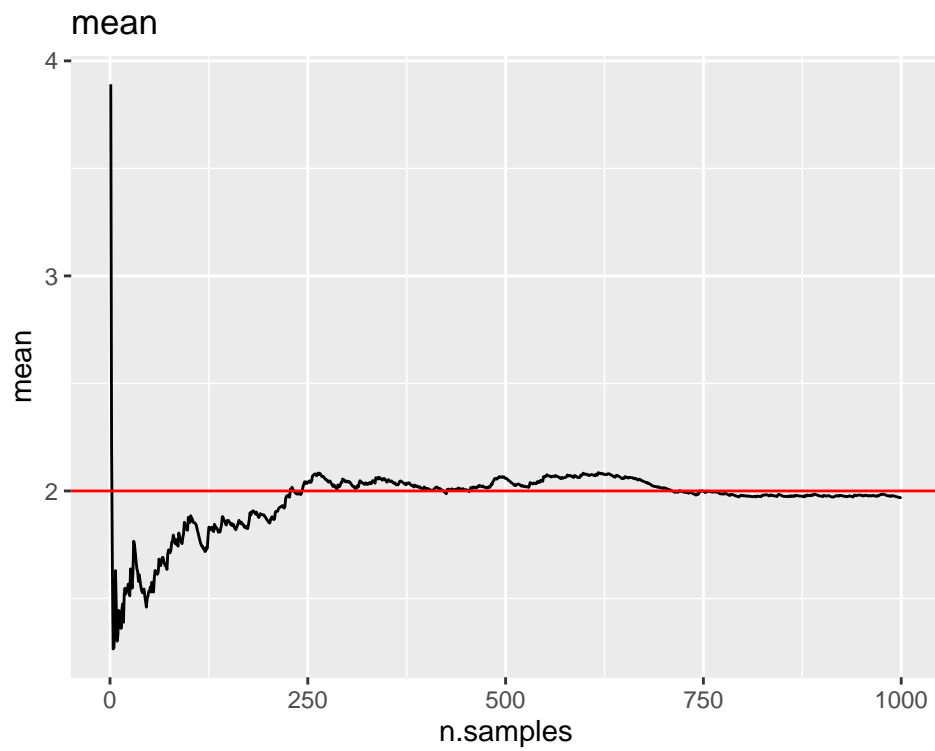


We also compare the estimated mean and variance to first and second central moments of the exponential distribution:

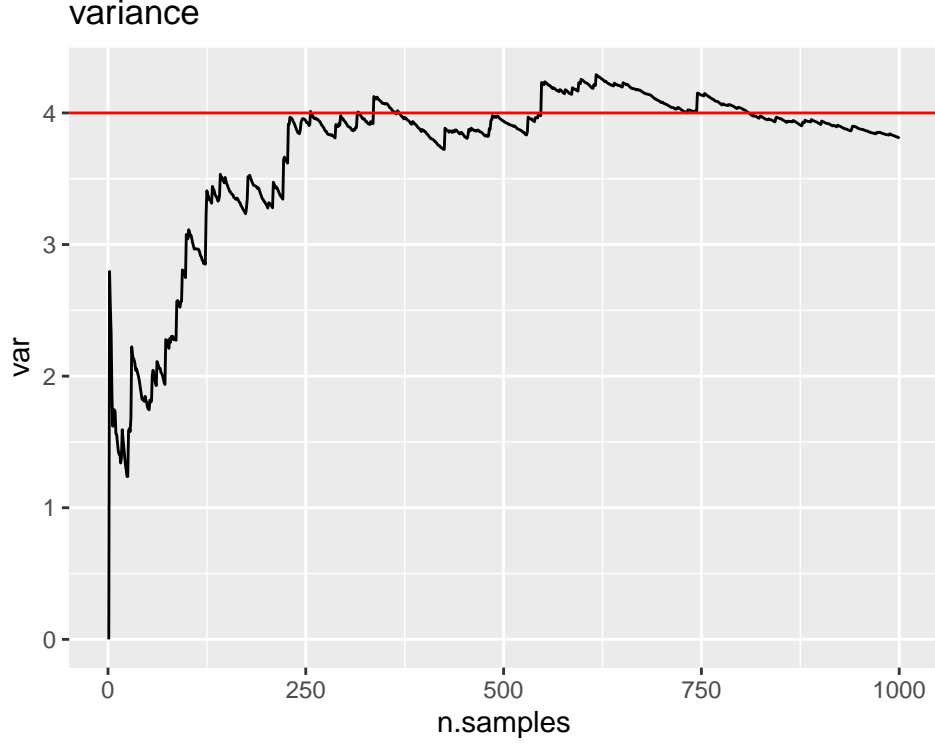
```

# Calculate the cumulative mean
data.frame(n.samples = 1:n,
           mean = cumsum(sim$x)/(1:n)) %>%
  ggplot() + geom_line(aes(n.samples, mean)) +
  geom_hline(yintercept = 1/rate, color = "red") +
  ggtitle("mean")

```



```
# Calculate the cumulative variance
data.frame(n.samples = 1:n,
           mean = cumsum(sim$x)/(1:n),
           mean2 = cumsum(sim$x^2)/(1:n)) %>%
  mutate(var = mean2-mean^2) %>%
  ggplot() + geom_line(aes(n.samples, var)) +
  geom_hline(yintercept = 1/rate^2, color = "red") +
  ggtitle("variance")
```



We observe that the the sampled mean and variance approach the theoretical values as the number of samples grows larger.

A.2

We consider the probability distribution given by

$$g(x) = \begin{cases} cx^{\alpha-1}, & 0 < x < 1 \\ ce^{-x}, & 1 \leq x \\ 0, & \text{otherwise} \end{cases},$$

where c is a normalizing constant and $\alpha \in (0, 1)$.

a)

Normalizing the density using $\int_{-\infty}^{\infty} g(x) dx = c \int_0^1 x^{\alpha-1} dx + c \int_1^{\infty} e^{-x} dx = c(\frac{1}{\alpha} + \frac{1}{e}) = 1$, it follows that the normalizing constant is $c = (\frac{1}{\alpha} + \frac{1}{e})^{-1}$. The cumulative distribution function is given by

$$G(x) = \int_{-\infty}^x g(y) dy = \begin{cases} c \int_0^x y^{\alpha-1} dy, & 0 < x < 1 \\ \frac{c}{\alpha} + c \int_1^x e^{-y} dy, & 1 \leq x \\ 0, & \text{otherwise} \end{cases},$$

which evaluates to

$$G(x) = \begin{cases} \frac{cx^{\alpha}}{\alpha}, & 0 < x < 1 \\ 1 - ce^{-x}, & 1 \leq x \\ 0, & \text{otherwise} \end{cases}.$$

The inverse is the unique function G^{-1} such that $x = G^{-1}(u)$. Since $G(x)$ is piecewise continuous and monotonic, we can calculate the inverses for its constituencies and find appropriate intervals. The intervals are simply found from calculating the corresponding boundary points. In $G(x)$ one of these points is located at $x = 1$, meaning $G(1) = \frac{c}{\alpha}$ will separate two continuous parts in G^{-1} . After solving for u , we end up with the inverse given by

$$G^{-1}(u) = \begin{cases} \left(\frac{\alpha u}{c}\right)^{-\alpha}, & 0 \leq u < \frac{c}{\alpha} \\ -\ln\left(\frac{1-u}{c}\right), & \frac{c}{\alpha} \leq u \end{cases}.$$

b)

Function for generating samples from g :

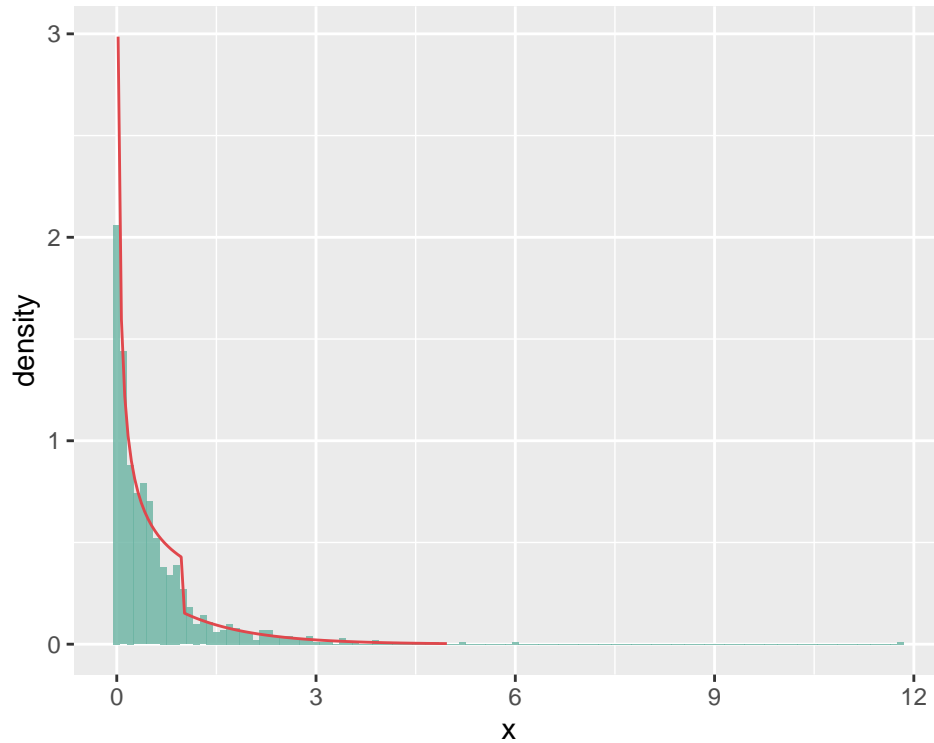
```
sim.g <- function(alpha, n){
  # Normalizing constant
  c <- (1/alpha + exp(-1))^-1
  # Vector of n uniform values
  u <- runif(n, 0, 1)

  (alpha/c * u)^(1/alpha) * (u < c/alpha) - log((1-u)/c) * (c/alpha <= u)
}
```

To test our implementation we use $\alpha = 0.5$ and simulate for $n = 1000$.

```
alpha <- 0.5
n <- 1000
sim <- data.frame(x = sim.g(alpha, n))
x = seq(from = 0.02, to = 5, by = 0.05)
exact <- data.frame(x = x, y = g(alpha, x))

ggplot(sim) +
  geom_histogram(aes(x = x, y = ..density..),
                 alpha = 0.8, fill = "#69b3a2", binwidth = 0.1) +
  geom_line(data = exact, aes(x = x, y = y), color = "#e0474c")
```



From the histogram, we see that we are able to generate samples from g corresponding to the true density. Next we find the theoretical mean and variance and compare with the estimated values. The theoretical mean is given by

$$\mu_g := \int_{-\infty}^{\infty} x g(x) dx = c \int_0^1 x^\alpha dx + c \int_1^{\infty} x e^{-x} dx = \frac{c}{\alpha+1} + \frac{2c}{e}.$$

Similarly, we find the variance

$$\begin{aligned} \text{Var}_g &:= \int_{-\infty}^{\infty} x^2 f(x) dx - \mu_g^2 \\ &= c \int_0^1 x^{\alpha+1} dx + c \int_1^{\infty} x^2 e^{-x} dx - \mu_g^2 \\ &= \frac{c}{\alpha+2} + \frac{5c}{e} - \left(\frac{c}{\alpha+1} + \frac{2c}{e} \right)^2. \end{aligned}$$

Comparing the true mean and variance with estimated values:

```
alpha <- 0.5
c <- (1/alpha + exp(-1))^-1

# 10000 realizations from simulation
sim <- sim.g(alpha, 10000)

# Theoretical mean and variance
mean.g <- c/(alpha+1) + 2*c/exp(1)
var.g <- c/(alpha+2) + 5*c/exp(1) - mean.g^2

# Estimated mean
mean.est <- mean(sim)
```

```
var.est <- var(sim)
```

```
# Comparing means  
c(mean.g, mean.est)
```

```
## [1] 0.5922707 0.5881271
```

```
# Comparing variance  
c(var.g, var.est)
```

```
## [1] 0.5949550 0.5760642
```

We see that our simulation gives approximate correct values for the theoretical mean and variance.

A.3

a)

To find the value of c , we integrate the density over the entire domain and equate the result to 1:

$$1 = \int_{-\infty}^{\infty} f(x)dx = c \int_{-\infty}^{\infty} \frac{e^{\alpha x}}{(1 + e^{\alpha x})^2} dx.$$

To progress from here, we introduce the substitution, $v = e^{\alpha x}$, which gives

$$1 = \frac{c}{\alpha} \int_0^{\infty} \frac{dv}{(1 + v)^2} = \frac{c}{\alpha} \left(-\frac{1}{1 + v} \right) \Big|_0^{\infty} = \frac{c}{\alpha}.$$

Consequently, $c = \alpha$.

b)

The CDF is defined as follows,

$$\begin{aligned} F(x) &= \int_{-\infty}^x f(z)dz = \int_0^{\exp(\alpha x)} \frac{dv}{(1 + v)^2} \\ &= 1 - \frac{1}{1 + \exp(\alpha x)} = \frac{\exp(\alpha x)}{1 + \exp(\alpha x)}, \end{aligned}$$

where we have used the same substitution as earlier, namely $v = e^{\alpha z}$. We notice that $F(x)$ is the Sigmoid function, which has the well known logit-function as its inverse. I.e.,

$$F^{-1}(x) = \frac{1}{\alpha} \ln \left(\frac{x}{1 - x} \right).$$

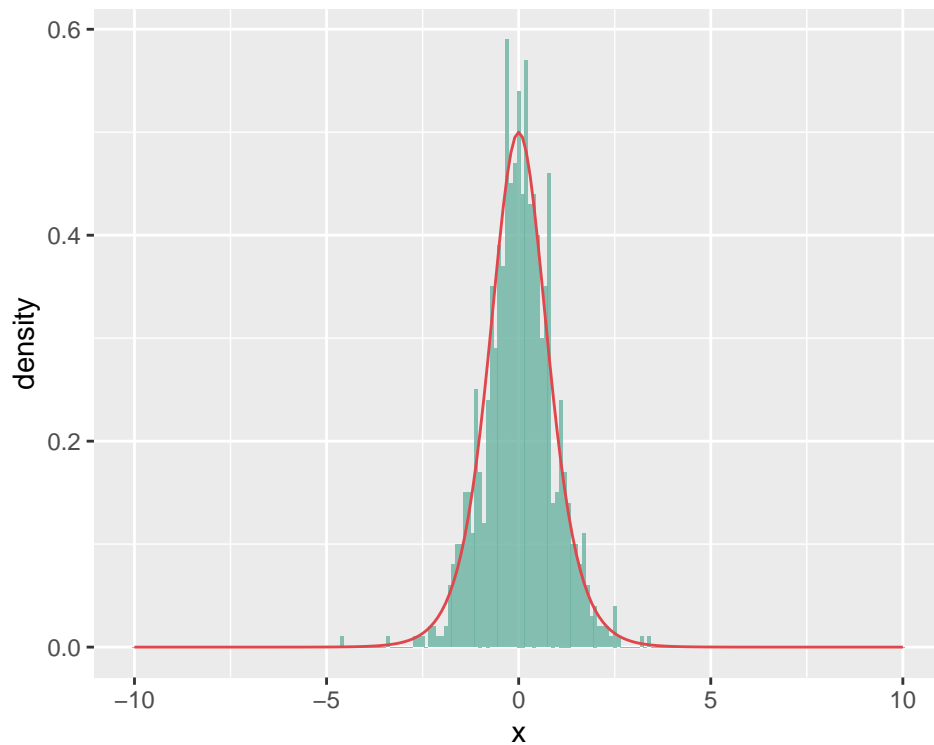
c)

Since we have an analytic expression for the inverse, we can again use the *inversion method* to sample from f . The sampling-function is given below.

```
sim.sigm <- function(alpha, n){
  u <- runif(n,0,1)
  1/alpha * log(u/(1-u))
}
```

```
alpha <- 2
n <- 1000
sim <- data.frame(x = sim.sigm(alpha, n))
x = seq(from = -10, to = 10, by = 0.1)
exact <- data.frame(x = x, y = alpha*exp(alpha*x)/(1 + exp(alpha*x))^2)

ggplot(sim) +
  geom_histogram(aes(x = x, y = ..density..),
                 alpha = 0.8, fill = "#69b3a2", binwidth = 0.1) +
  geom_line(data = exact, aes(x = x, y = y), color = "#e0474c")
```



To compare the simulated values with the theoretical mean and variance, we first need to compute the expression of these moments. **Think maybe the mean is undefined??**

A.4

Below is our implementation of the Box-Muller algorithm.

```
box.mul <- function(n){
  odd <- FALSE
  if(n %% 2 != 0){
    odd <- TRUE
  }
```



```

  n <- n + 1
}

x1 <- 2*pi * runif(n/2, 0, 1)
x2 <- sim.exp(0.5, n/2)

y1 <- sqrt(x2)*cos(x1)
y2 <- sqrt(x2)*sin(x1)

concat <- c(y1,y2)
if(odd){
  return(head(concat, -1))
}
else{
  return(concat)
}
}

```

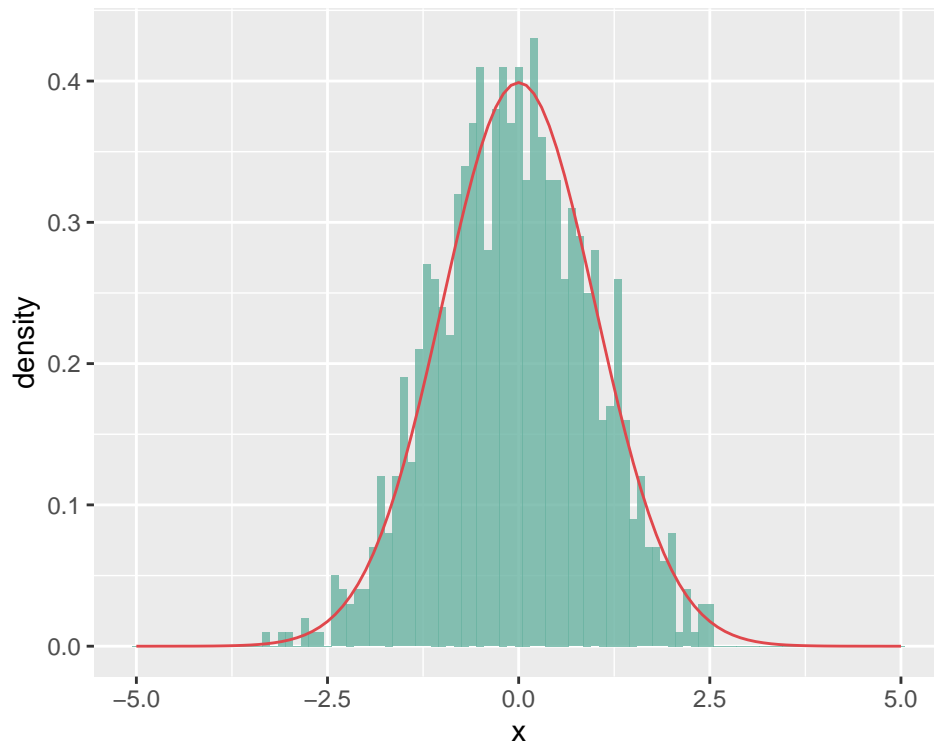
As usual, we compare the results of a simulation against the theoretical distribution.

```

n <- 1000
sim.box.mul <- data.frame(x = box.mul(n))
x = seq(from = -5, to = 5, by = 0.1)
exact <- data.frame(x = x, y = 1/sqrt(2*pi)*exp(-1/2*x^2))

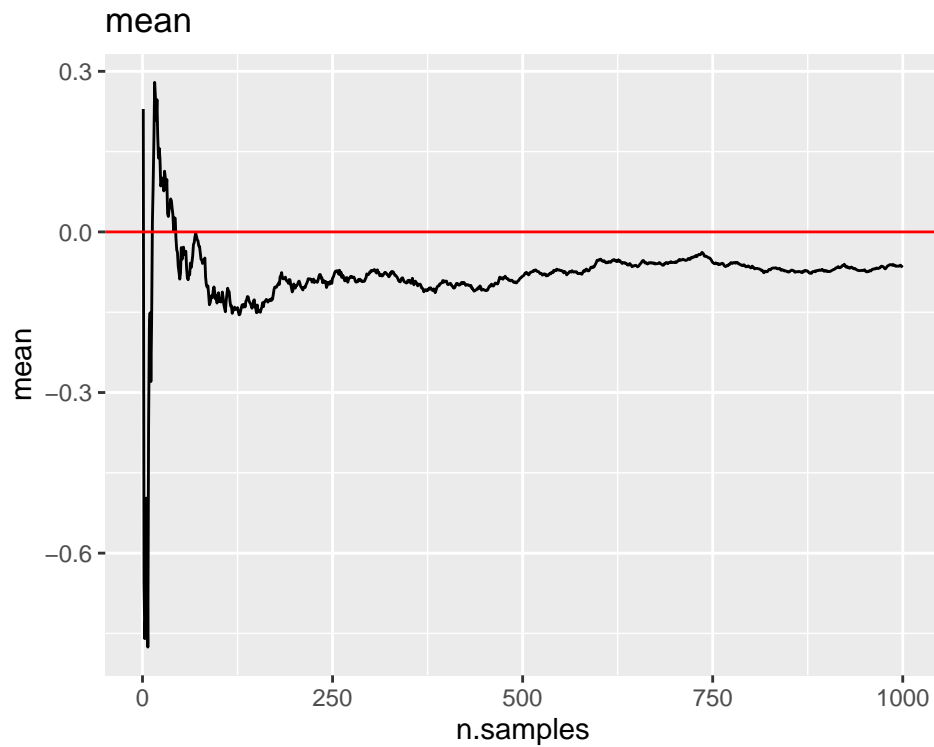
ggplot(sim.box.mul) +
  geom_histogram(aes(x = x, y = ..density..),
                 alpha = 0.8, fill = "#69b3a2", binwidth = 0.1) +
  geom_line(data = exact, aes(x = x, y = y), color = "#e0474c")

```

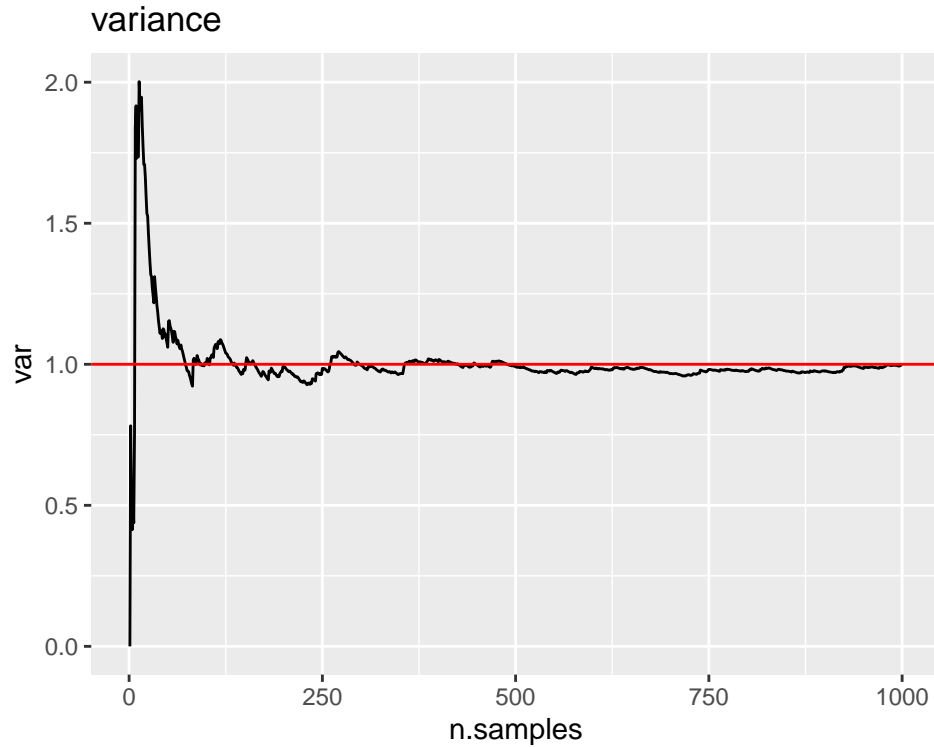


Finally, we compare the mean and variance resulting from the simulation with the theoretical values.

```
# mean
data.frame(n.samples = 1:n,
           mean = cumsum(sim.box.mul$x)/(1:n)) %>%
  ggplot() + geom_line(aes(n.samples, mean)) +
  geom_hline(yintercept = 0, color = "red") +
  ggtitle("mean")
```



```
# variance
data.frame(n.samples = 1:n,
           mean = cumsum(sim.box.mul$x)/(1:n),
           mean2 = cumsum(sim.box.mul$x^2)/(1:n)) %>%
  mutate(var = mean2 - mean^2) %>%
  ggplot() + geom_line(aes(n.samples, var)) +
  geom_hline(yintercept = 1, color = "red") +
  ggtitle("variance")
```



A.5

Let $N_d(\mu, \Sigma)$ be a d -variate normal distribution with mean μ and covariance Σ . This is our target distribution. To simulate from it, let $x \sim N_d(0, I_d)$ be a standard d -variate normal distribution. Then it follows that

$$y = \mu + Ax \implies y \sim N(\mu, AA^T),$$

where A is a $d \times d$ matrix. Since the covariance matrix Σ is both symmetric and positive-definite, we can write $\Sigma = AA^T$ using the Cholesky decomposition. Thus, for a given μ and Σ , we are able to simulate from this distribution after simulating from $N_d(0, I_d)$.

Reusing our implementation of the Box-Muller algorithm from A.4, a function for generating realizations from the target is shown below:

```
sim.mvnorm <- function(mu, Sigma, n){
  # Returns n realizations from a d-variate normal distribution
  d <- length(mu)

  # Get n d-variate standard normal realizations using the Box-Muller algorithm
  x <- array(box.mul(n*d), dim=c(d,n))

  # Cholesky decomposition of Sigma
  A <- t(chol(Sigma)) # Transposes to get a lower triangular matrix

  mu + A %*% x
}
```

To test our implementation, we generate a bivariate normal distribution:

```

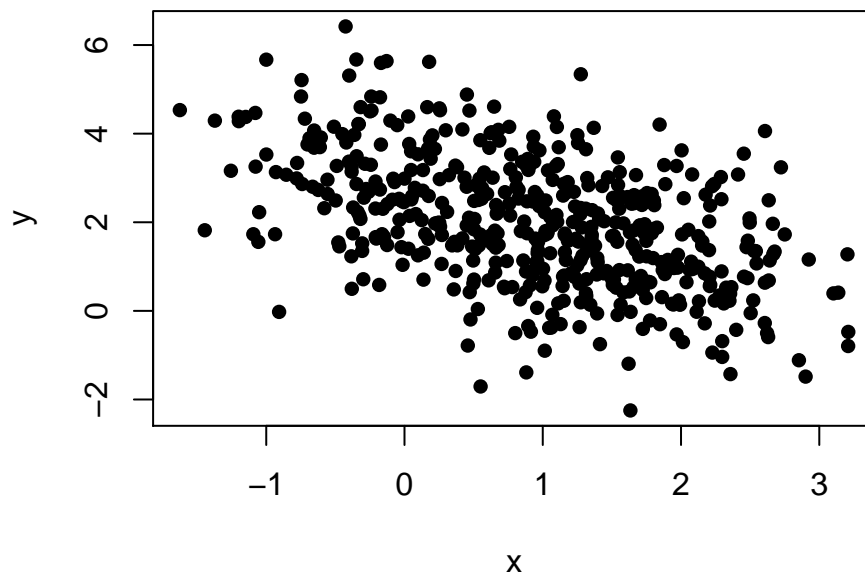
# Bivariate example
mu <- c(1,2)
Sigma <- matrix(c(1, -.7, -.7, 2), 2)

# Simulate 10000 realizations
y <- sim.mvnorm(mu, Sigma, 10000)

# Plot first 500 points
plot(y[1,1:500], y[2,1:500], main="Bivariate normal distribution", xlab="x", ylab="y", pch=16)

```

Bivariate normal distribution



Comparing the true mean and covariance with estimated values:

```

# Estimate mean
mu.est <- rowMeans(y)
mu.est

## [1] 0.9843779 2.0141289

# Estimate covariance matrix
Sigma.est <- cov(t(y))
Sigma.est

##           [,1]      [,2]
## [1,]  1.0307664 -0.7399571
## [2,] -0.7399571  2.0673293

```

From the printout in R, we see that the estimated values are close to the true values $\mu = \begin{pmatrix} 1 \\ 2 \end{pmatrix}$ and $\Sigma = \begin{pmatrix} 1 & -0.7 \\ -0.7 & 2 \end{pmatrix}$. This means that our function works properly.

Problem B

B.1

(a)

B.2

(a)

We repeat that

$$f^*(x) = \begin{cases} x^{\alpha-1}e^{-x}, & x > 0, \\ 0, & \text{otherwise.} \end{cases}$$

To find $a = \sqrt{\sup_{x \geq 0} f^*(x)}$, we first note that $f^*(x=0) = 0$ and only consider

$$\sup_{x>0} f^*(x),$$

which amounts to solving

$$\begin{aligned} \frac{d}{dx} f^*(x) &= 0 \\ \iff (\alpha - 1)x^{\alpha-2}e^{-x} - x^{\alpha-1}e^{-x} &= 0 \\ \iff x = \alpha - 1 > 0, \end{aligned}$$

which clearly is a global maximum. Consequently,

$$a = \sqrt{\alpha - 1}.$$

Analogously, to find $b_+ = \sqrt{\sup_{x \geq 0} x^2 f^*(x)} = \sqrt{\sup_{x \geq 0} g(x)}$, we note that $g(z=0) = 0$ and only consider $\sup_{x>0} g(x)$, which amounts to solving

$$\begin{aligned} \frac{d}{dx} g(x) &= 0 \\ \iff (\alpha + 1)x^{\alpha}e^{-x} - x^{\alpha+1}e^{-x} &= 0, \\ \iff x = \alpha + 1 > 0, \end{aligned}$$

which clearly is a global maximum for $x \geq 0$. Consequently,

$$b_+ = \sqrt{\alpha + 1}.$$

Finally, $b_- = -\sqrt{\sup_{x \leq 0} x^2 f^*(x)} = -\sqrt{0} = 0$.

(b)

```

rou.gamma <- function(n, alpha){
  a <- sqrt(alpha - 1)
  b.minus <- 0
  b.plus <- sqrt(alpha + 1)

  count <- 0
  tries <- 0
  result <- rep(0,n)

  while(count < n){
    x1 <- a*runif(1, 0, 1)
    x2 <- b.minus + b.plus*runif(1, 0, 1)

    if(log(x1) <= 0.5*((alpha - 1)*log(x2/x1) - x2/x1)){
      result[count + 1] = x2/x1
      count <- count + 1
    }
    tries = tries + 1
  }
  return(list("sim" = result, "tries" = tries))
}

```

First, we check that the simulation algorithm gives reasonable results:

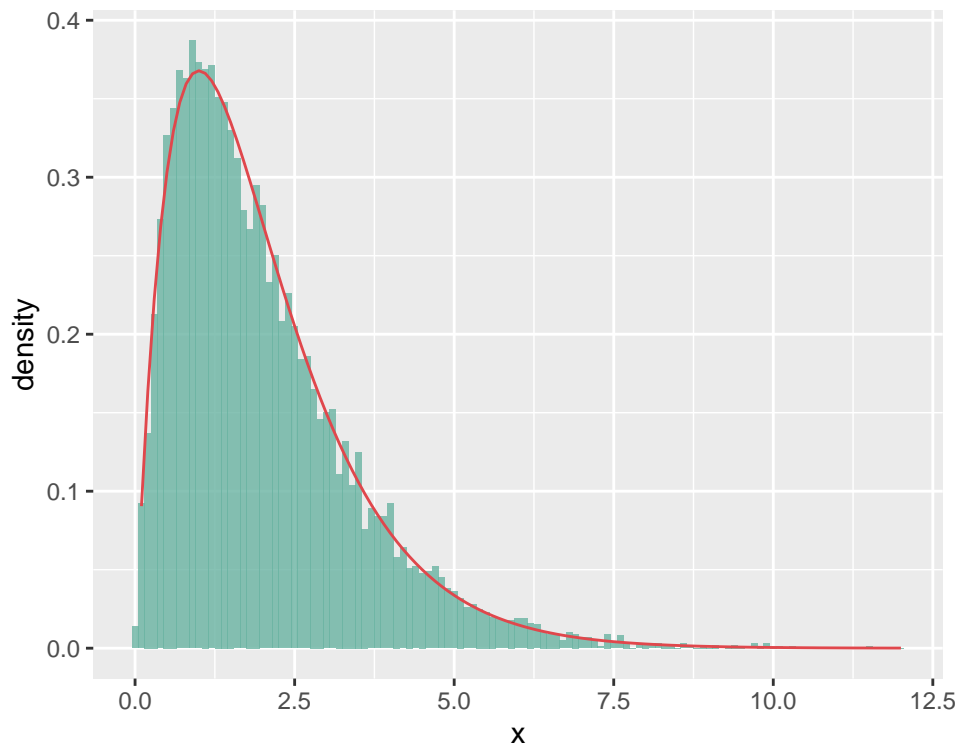
```

n <- 10000
alpha <- 2

sim.gamma <- rou.gamma(n, alpha)
x = seq(from = 0.1, to = 12, by = 0.1)
exact <- data.frame(x = x, y = 1/gamma(alpha) * x^(alpha - 1) * exp(-x))

ggplot(data.frame(x = sim.gamma$sim)) +
  geom_histogram(aes(x = x, y = ..density..),
                 alpha = 0.8, fill = "#69b3a2", binwidth = 0.1) +
  geom_line(data = exact, aes(x = x, y = y), color = "#e0474c")

```



```
sim.gamma$tries
```

```
## [1] 34615
```

```
library(pracma)
```

```
##
```

```
## Attaching package: 'pracma'
```

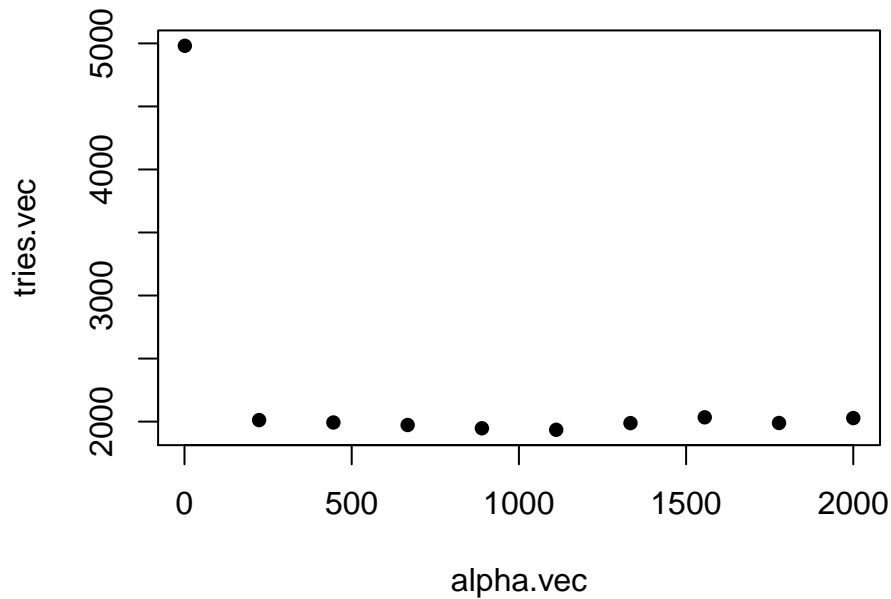
```
## The following object is masked from 'package:purrr':
```

```
##
```

```
## cross
```

```
n <- 1000
alpha.vec <- seq(1.01, 2000, length.out = 10)
tries.vec <- rep(0, 10)
for(i in 1:length(alpha.vec)){
  alpha <- alpha.vec[i]
  sim.gamma <- rou.gamma(n, alpha)
  tries.vec[i] = sim.gamma$tries
}
```

```
plot(alpha.vec, tries.vec, pch = 16)
abline(h = 3, col="blue")
```



The number of necessary tries is highest for low values of α , i.e. $\ln \alpha < 2$, while it stabilizes after that. This indicates that C_f constitutes a smaller proportion of $[0, a] \times [b_-, b_+]$. mer tolkning?? Tror det er feil. Tror antall tries skal øke med alpha.

B.3

We recall that the gamma distribution has probability density function (PDF)

$$f(x) = \frac{\beta^\alpha}{\Gamma(\alpha)} x^{\alpha-1} e^{-\beta x}.$$

We use Marsaglia and Tsang's method to generate from the gamma distribution:

```
sim.gamma <- function(n, alpha, beta){
  d <- alpha - 1/3
  c <- 1/sqrt(9*d)
  count <- 0
  result <- rep(0, n)
  while(count < n){
    z <- box.mul(1)
    u <- runif(1, 0, 1)
    v <- (1 + c*z)^3
    if(z > -1/c && log(u) < 0.5*z^2 + d - d*v + d*log(v)){
      result[count + 1] = d*v
      count <- count + 1
    }
  }
  return(1/beta * result)
}
```

Check that it works god:...

B.4

We repeat that $X \sim \text{Gamma}(\alpha, 1)$ and $Y \sim \text{Gamma}(\beta, 1)$, and note that their joint density is $f_{X,Y}(x, y) = f_X(x)f_Y(y)$, since they are independent. Next, we define $Z = \frac{X}{X+Y}$ and also introduce $V = X + Y$. Then, $X = ZV$ and $Y = V(1 - Z)$, and, by the transformation formula, the joint density of Z and V is

$$\begin{aligned} f_{Z,V}(z, v) &= f_{X,Y}(zv, v(1-z)) \cdot \left| \begin{vmatrix} v & z \\ -v & 1-z \end{vmatrix} \right| \\ &= (\Gamma(\alpha)\Gamma(\beta))^{-1} \cdot (zv)^{\alpha-1} e^{-zv} \cdot (v(1-z))^{\beta-1} e^{-v(1-z)} \cdot [v(1-z) + vz] \\ &= (\Gamma(\alpha)\Gamma(\beta))^{-1} \cdot z^{\alpha-1} (1-z)^{\beta-1} \cdot v^{[\alpha+\beta]-1} \cdot e^{-v}. \end{aligned}$$

Thus, the marginal distribution of Z is given as

$$\begin{aligned} \int_0^\infty f_{Z,V}(z, v) dv &= \Gamma(\alpha)\Gamma(\beta)^{-1} \cdot z^{\alpha-1} (1-z)^{\beta-1} \int_0^\infty v^{[\alpha+\beta]-1} \cdot e^{-v} dv \\ &= \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} z^{\alpha-1} (1-z)^{\beta-1}, \end{aligned}$$

which is what we wanted show.

Problem C

C.1

We observe that $\theta = \Pr\{X > 4\} = \int_4^\infty f_X(x) = \int_{-\infty}^\infty \mathbb{I}(x > 4) f_X(x)$. Then, by the method of Monte Carlo (MC) integration, an estimate of θ is

$$\hat{\theta} = \frac{1}{n} \sum_{i=1}^n \mathbb{I}(X > 4).$$

Here, n is the number of samples, \mathbb{I} is the indicator function and $X \sim \mathcal{N}(0, 1)$.