CompStat 1

Problem A

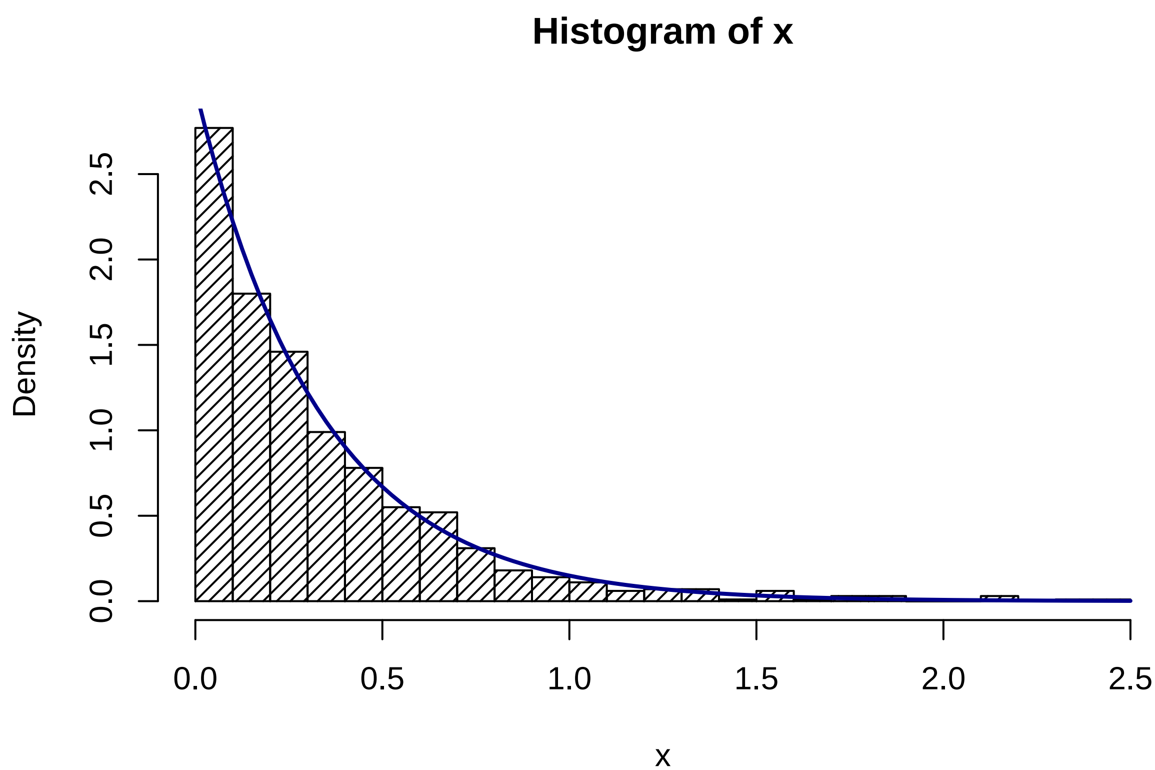
1)

Here using the inversion method, we get:

$$x = F^{-1}(u) = -\frac{1}{\lambda} log(u), \quad u \sim U(0,1).$$

Thus we get xponential samples, by sampling from the uniform distribution, and use the inversion method. Under there is a function that generates a vector of n samples from an exponentially distributed random variable with rate λ.

```r
# Generate samples from exponential distribution
rate <- 3 #Rate parameter
n <- 1000 #Number of samples
generate.exponential <- function(rate, n){
  u <- runif(n)
  x <- - 1/rate * log(u)
  return(x)
}
x <- generate.exponential(rate, n)
hist(x, density=20, breaks = 30, prob=TRUE)
curve(dexp(x, rate=rate), add=TRUE, col="darkblue", lwd=2)
```



2)

The cdf $G(x)$ of $g(x)$ and its inverse G^{-1} are

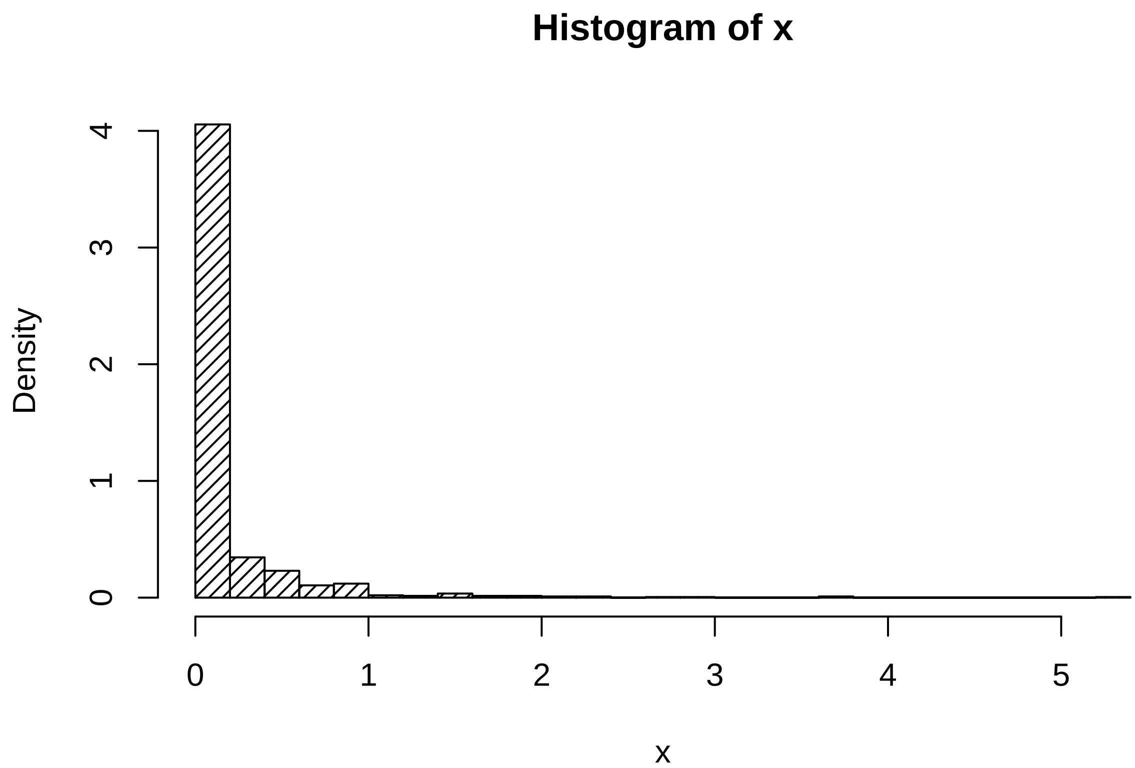
$$G(x) \quad = \quad \begin{cases} \int_0^1 cx^{\alpha-1}dx & , \ 0 < x \leq 1 \\ \int_1^{\infty} ce^{x}dx & , \ 1 \leq x \\ 0 & , \ x \leq 0 \end{cases} \qquad = \begin{cases} c(\alpha-1)x^{\alpha} & , \ 0 < x \leq 1 \\ c(e^{-1} - e^{-x}) & , \ 1 \leq x \\ 0 & , \ x \leq 0 \end{cases}$$

$$G^{-1}(u) = \begin{cases} \left(\frac{u}{c(\alpha-1)}\right)^{\frac{1}{\alpha}} & , \text{ SJEKK GRENSER } 0 < (\frac{u}{\alpha-1})^{\frac{1}{\alpha}} \leq 1 \\ -\log(e^{-1} - \frac{u}{c}) & , 1 \leq -\log(e^{-1} - \frac{u}{c}) \\ 0 & , u \leq 0 \end{cases}$$

Writing a function that returns g-samples.

```
# Generate samples from g(X)
rate <- 3 #Rate parameter
n <- 1000 #Number of samples
alpha <- 0.1
generate.samples.g<- function(alpha, n){
  c <- alpha*exp(1)/(alpha+exp(1))
  u <- runif(n, 0,1)
  x <- c()
  for (i in 1:n){
    if (u[i] < c/(alpha)){
      x <- c(x, (u[i]*(alpha)/c)^(1/alpha))
    }
    else{
      x <- c(x, 1-log(exp(1)/c*(1-u[i])))
    }

  }
  return(x)
}
x <- generate.samples.g(alpha, n)
hist(x, density=20, breaks = 20, prob=TRUE)
```

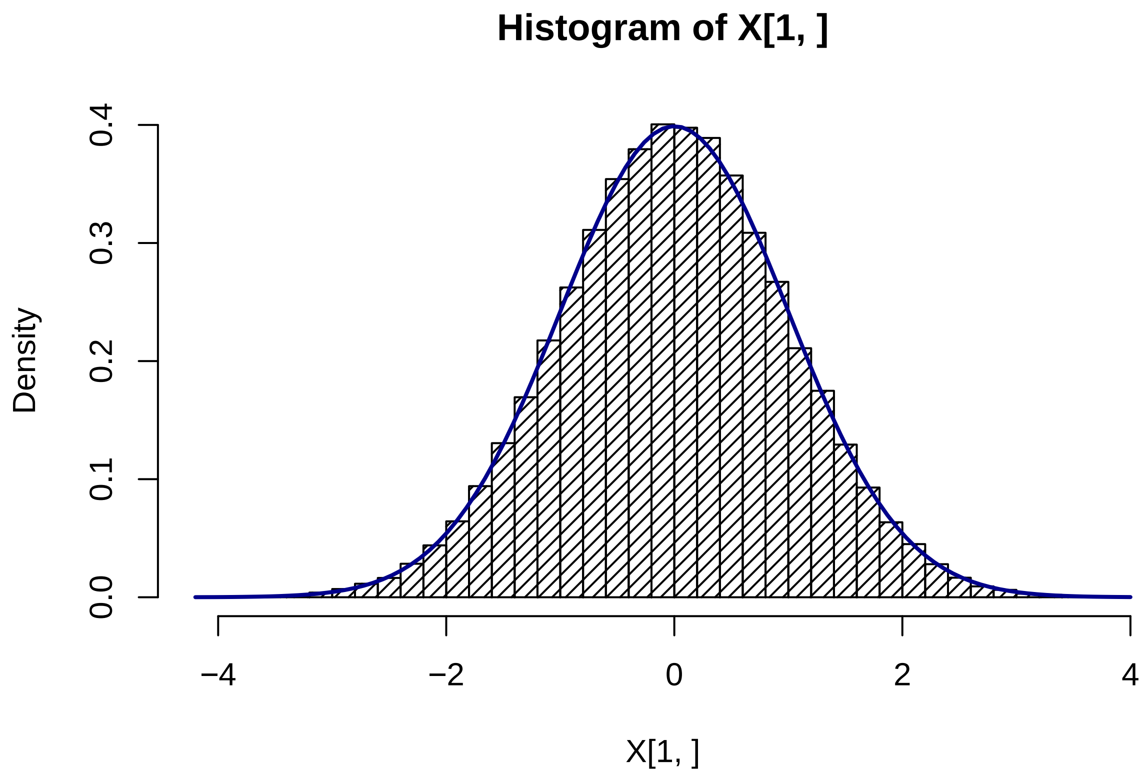


The histogram is used to check that generate.samples.g returns the correct value. As we see here, ...

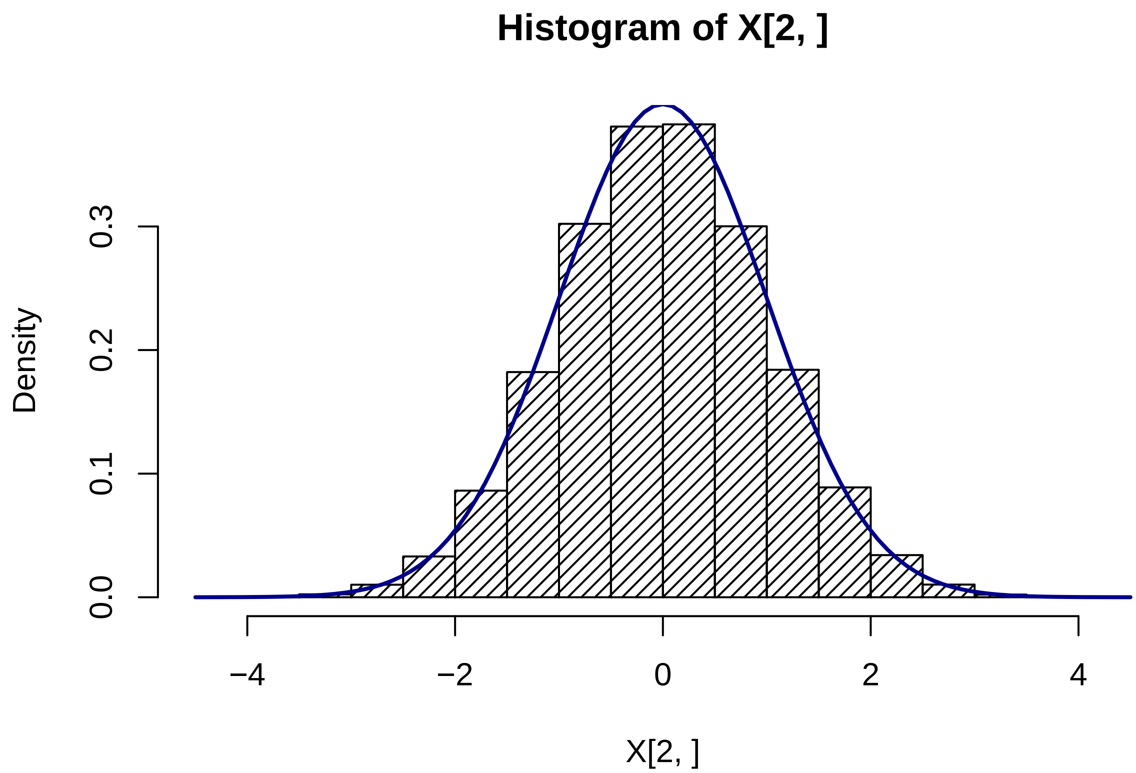
3)

The function generate.normal uses Box-Muller to generate an n-vector of independent samples from the standard normal distribution.

```
# Generate samples from normal distribution with Box-Muller
n <- 100000 #Number of samples
generate.normal <- function(n){
  u1 <- runif(n)
  u2 <- runif(n)
  x1 <- sqrt(-2*log(u1))*cos(2*pi*u2)
  x2 <- sqrt(-2*log(u1))*sin(2*pi*u2)
  X <- rbind(x1, x2)
  return (X)
}
X <- generate.normal(n)
hist(X[1,], density=20, breaks = 30, prob=TRUE)
curve(dnorm, add=TRUE, col="darkblue", lwd=2)
```




```r
hist(X[2,], density=20, breaks = 30, prob=TRUE)
curve(dnorm, add=TRUE, col="darkblue", lwd=2)
```




```
## Expected mean:  0 0

## Expected variance:

##      [,1] [,2]
## [1,]    1    0
## [2,]    0    1

## Sample mean:  -0.002035135 0.003967926

## Sample variance:

##               x1            x2
## x1  0.9918405330 -0.0001817515
## x2 -0.0001817515  1.0036317956
```

As we see, the observed mean and variance is fairly close to the moments of the standard normal distribution, which are zero and one. The empirical covariance $Cov(x_1, x_2)$ is also close to zero, as expected.

4)

Writing function generate.d.normal that generates samples from a d-variate normal distribution with mean vector μ and covariance matrix Σ.

```r
# Generate n samples from d variate normal distribution
n <- 10000 #Number of samples
mu <- c(0,0)
sigma <- cbind(c(1,0.5),c(0.5,1))
generate.d.normal <- function(n, mu, sigma){
  A <- chol(sigma)
```

```
  d <- length(mu)
  X <- generate.normal(n*d)
  x <- matrix(X[1,], nrow=d, ncol=n)
  Z <- mu+t(A)%*%x
}
```

```
## Expected mean:  0 0

## Expected variance:

##      [,1] [,2]
## [1,]  1.0  0.5
## [2,]  0.5  1.0

## Sample mean:  0.003011486 -0.006952729

## Sample variance:

##           [,1]      [,2]
## [1,] 1.0063622 0.5169991
## [2,] 0.5169991 1.0153525
```

As we see, $\tilde{\mu}$ is close to ER MU KUN 2-VARIAT?

Problem B

```
#Function f(x)
function.f <- function(x, alpha){
  if (x>0){
    return (x^(alpha-1)*exp(-x)/gamma(alpha))
  }
  else{
    return(0)
  }
}

#Function g(x)
function.g <- function(x, alpha){
  c = alpha*exp(1)/(alpha+exp(1))
  if (x>0 && x<1){
    return (c*x^(alpha-1))
  }
  else if(x >= 1){
    return(c*exp(-x))
  }
  else{
    return(0)
  }
}

# Generate n samples from d variate normal distribution
n <- 10000 #Number of samples
alpha <- 0.3
rejection.sampling <- function(n, alpha){
  c <- (alpha+exp(1))/(gamma(alpha)*alpha*exp(1))
  samples <- c()
```

```r
  for (i in 1:n){
    repeat{
      x <- generate.samples.g(alpha, 1)
      acceptance.prob <- function.f(x, alpha)/(c*function.g(x, alpha))
      if(runif(1) <= acceptance.prob){
        samples <- c(samples, x)
        break
      }
    }
  }
  return (samples)
}
```

```
## Expected mean:  0.3
```

```
## Expected variance:  0.3
```

```
## Sample mean:  0.2955176
```

```
## Sample variance:  0.2994871
```

```r
# An analytic log(gamma(x, alpha))-function
log.gamma <- function(x, alpha){
  return((alpha-1)*log(x)-x)
}
# Ratio-of-uniforms method
n <- 10000
alpha <- 30
ratio.of.uniforms <- function(n, alpha){
  sample.counter <- 0
  b.minus <- 0
  log.b.plus <- (alpha+1)/2*(log(alpha+1)-1)
  log.a <- (alpha-1)/2*(log(alpha-1)-1)
  samples <- c()
  for(i in 1:n){
    repeat{
      sample.counter <- sample.counter + 1
      log.x1 <- -generate.exponential(1, rate=1) + log.a
      log.x2 <- -generate.exponential(1, rate=1) + log.b.plus
      log.y <- log.x2 - log.x1
      y <- exp(log.y)
      if (2*log.x1 <= log.gamma(y, alpha)){
        samples <- c(samples, y)
        break
      }
    }
  }
  cat("Rejection ratio: ", (sample.counter-n)/n , "\n")
  return (samples)
}
```

```
## Rejection ratio:  3.4284
```

```
## [1] "Expected: "
```

```
## Mean:  30
```

```
## Variance:  30
```

```
## [1] "Observed: "
## Mean:  30.04637
## Variance:  30.19518
```

```
n = 10000
alpha = 0.1
beta = 2
sample.gamma <- function(n, alpha, beta){
  if(alpha < 1){
    return(rejection.sampling(n, alpha)/beta)
  }
  else if (alpha == 1){
    return(generate.exponential(1, n)/beta)
  }
  else if (alpha > 1){
    return(ratio.of.uniforms(n, alpha)/beta)
  }
  else{
    return(0)
  }
}
```

```
## [1] "Expected: "
## Mean:  0.05
## Variance:  0.025
## [1] "Observed: "
## Mean:  0.04812905
## Variance:  0.02237744
```

Problem C

1)

Claim: Given independent variables $z_k \sim \text{gamma}(\alpha_k, \beta = 1)$ for $k = 1, ..., K$, define $x_k = z_k \cdot (\sum_{k=1}^{K} z_k)^{-1}$ for $k = 1, ..., K$. Then vector $(x_1, ..., x_K)$ has the Dirichlet distrution with parameter vector $\alpha = (\alpha_1, ..., \alpha_K)$. Demonstration: Consider vector $x = (x_1, ..., x_{K-1})$ with x_k as before and vairable $v = \sum_{k=1}^{K} z_k$. Express the transformation

$$Z_k = X_k \cdot V \;\text{ for }\; k = 1, ..., K-1 \;\;;\;\; Z_K = V \cdot X_K = V(1 - X_1 - ... - X_{K-1})$$

X, V now has joint distribution $f_{X,V} = |J| \cdot f_Z(z) = |J| \cdot \prod_{k=1}^{K} e^{-z_k} z_k^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)}$

$$f_{X,V} = |J| \cdot f_Z(z) = |J| \cdot \prod_{k=1}^{K} e^{-z_k} z_k^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)}$$

with

$$J = \begin{bmatrix} V & 0 & \dots & X_1 \\ 0 & V & \dots & \vdots \\ \vdots & \vdots & \ddots & X_{K-1} \\ -V & \dots & -V & X_K \end{bmatrix} \sim \begin{bmatrix} V & 0 & \dots & X_1 \\ 0 & V & \dots & \vdots \\ \vdots & \vdots & \ddots & X_{K-1} \\ 0 & 0 & 0 & 1 \end{bmatrix} \implies |J| = V^{K-1}$$

Here we have used row reduction on the bottom row, along with the fact that $X_K = \sum_{k=1}^{K-1} X_k$ and determinant rule for triangular matrices.

Isolate the v-part of $f_{X,V}$ and integrate with respect to v, yielding the marginal distribution f_X.

$$f_{X,V} = v^{K-1} \prod_{k=1}^{K} e^{-x_k v} (x_k v)^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)} = v^{\sum \alpha - 1} e^{-v} \prod_{k=1}^{K} x_k^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)}$$

$$f_X(x) = \prod_{k=1}^{K} x_k^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)} \cdot \int_0^\infty v^{\sum \alpha_k - 1} e^{-v} dv$$

$$f_X(x) = \Big(\prod_{k=1}^{K} x_k^{\alpha_k - 1} \cdot \frac{1}{\Gamma(\alpha_k)} \Big) \cdot \Gamma\big(\sum_{k=1}^{K} \alpha_k \big) = \frac{\Gamma\big(\sum_{k=1}^{K} \alpha_k \big)}{\Pi_{k=1}^{K} \Gamma(\alpha_k)} \prod_{K=1}^{K-1} x_k^{\alpha_k - 1} \cdot \Big(1 - \sum_{k=1}^{K-1} x_k \Big)^{\alpha_K - 1}$$

where the integral resolves from the fact that the Gamma distribution with shape $\sum_{k=1}^{K} \alpha_k$ and rate one integrates to one. We again used that $X_K = 1 - \sum_{k=1}^{K-1}$. ## 2)

```r
# Here, the user can manually change the alpha vector
# in order to draw a sample from any chosen Dirichlet distribution.
alphas.from.user=c(1.34534,0.9345,0.6356,20,14,5,2)

gammas.in.dirichlet <- function(alpha){
  n=length(alpha)
  gammas <- c()
  for(i in 1:n){
    gammas <- c(gammas, sample.gamma(1,alpha[i],1))
  }
  return(gammas)
}

generate.dirichlet <- function(alpha){  # Creates Dirichlet distributed vector
  g<-gammas.in.dirichlet(alpha)         # with the K chosen alphas
  print(g)                              # as K-variate parameter vector.
  v<-sum(g)
  z=g/v
  return(z)
}
dirich.var<-generate.dirichlet(alphas.from.user)
```

```
## Rejection ratio:  0
## Rejection ratio:  7
## Rejection ratio:  0
## Rejection ratio:  2
## Rejection ratio:  0
## [1]  4.0961793  0.4742495  0.6237241 13.1510243 10.4634409  9.2752036
## [7]  1.2745050
```

```
dirich.var              # The elements in the Dirichlet distribution
```

```
## [1] 0.10407402 0.01204954 0.01584732 0.33413576 0.26585076 0.23566052
## [7] 0.03238209
```

```
print(sum(dirich.var)) # The sum of the elements in the Dirichlet distribution
```

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

In the code, the normalising of the Dirichlet distributed vector x occurs after the gammas z have been sampled, so $||x||_1$ is always one, which is equal to the joint expected value of x's elements.

Problem D

1)

Given a prior Beta(1, 1), which is equal to the uniform distribution on (0, 1), and a mulitnomial density function:

$$f(\boldsymbol{y}|\theta) \propto (2+\theta)^{y_1}(1-\theta)^{y_2+y_3}\theta^{y_4},$$

we have that the posterior is distributed with:

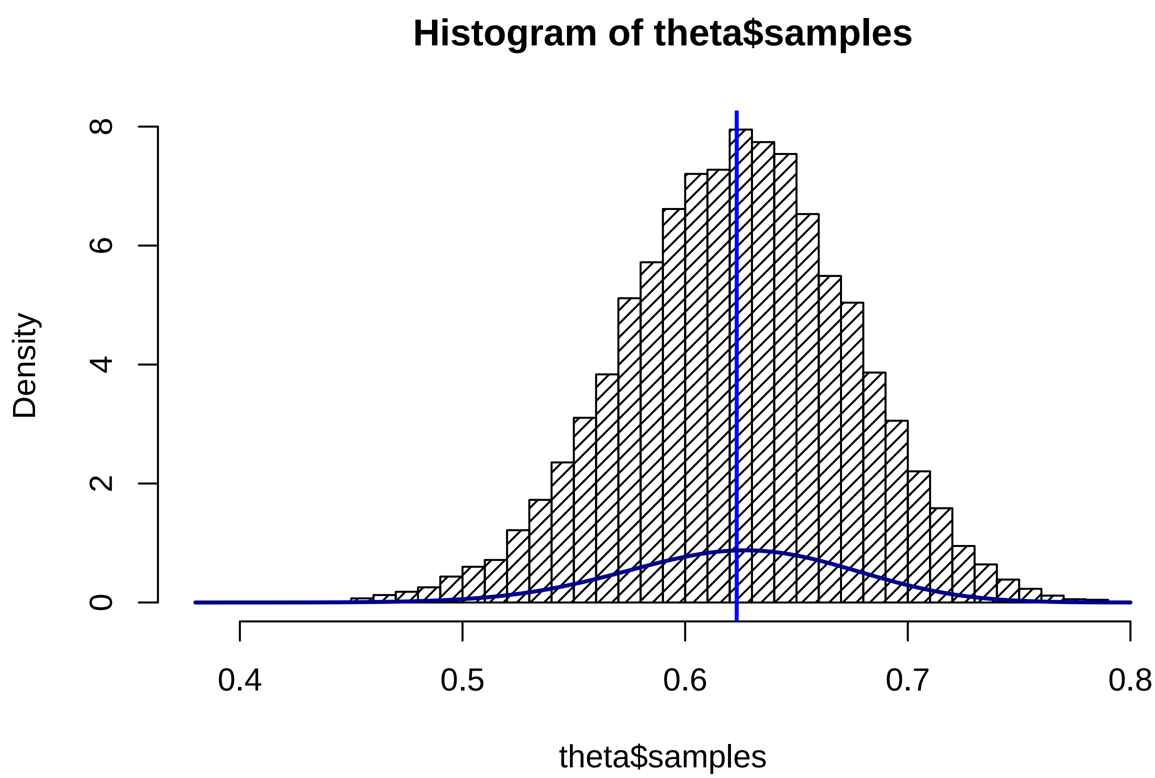
$$f(\theta, \boldsymbol{y}|) \propto (2+\theta)^{y_1}(1-\theta)^{y_2+y_3}\theta^{y_4}, \quad \theta \in (0,1).$$

We also have the values for $\boldsymbol{y}$: $y_1 = 125$, $y_2 = 18$, $y_3 = 20$, $y_4 = 34$. Thus we can use a rejection sample method, where we sample thetas from the prior, computes the acceptance probability, and then reject/include a random number into sample. To find the constant c, we have optimized over the posterior distribution. This will not be the real c value, but c times the proportional constant of the posterior distribution and the multinomial distribution. There is however no need to find this constant as when dividing the posterior by c, it would cancel.

```
# Rejection sampling
n <- 20000 #Number of samples
posterior.f <- function(theta){
  y <- c(125, 18, 20, 34)
  return ((2+theta)^y[1]*(1-theta)^(y[2]+y[3])*theta^y[4])

}
rejection.sampling.multinomial <- function(n){
  sample.counter <- 0
  c <- optimize(posterior.f, c(0, 1), maximum=TRUE)$objective
  samples <- c()
  for(i in 1:n){
    repeat{
      sample.counter <- sample.counter + 1
      theta <- runif(1)
      acceptance.prob <- posterior.f(theta)/c
      u <- runif(1)
      if (u <= acceptance.prob){
        samples <- c(samples, theta)
        break
      }
    }
  }
  li <- list("samples" = samples, "number.samples" = sample.counter)
  return (li)
```

```
}
theta <- rejection.sampling.multinomial(n)
```




```
## Theta sample mean 0.6231598
```

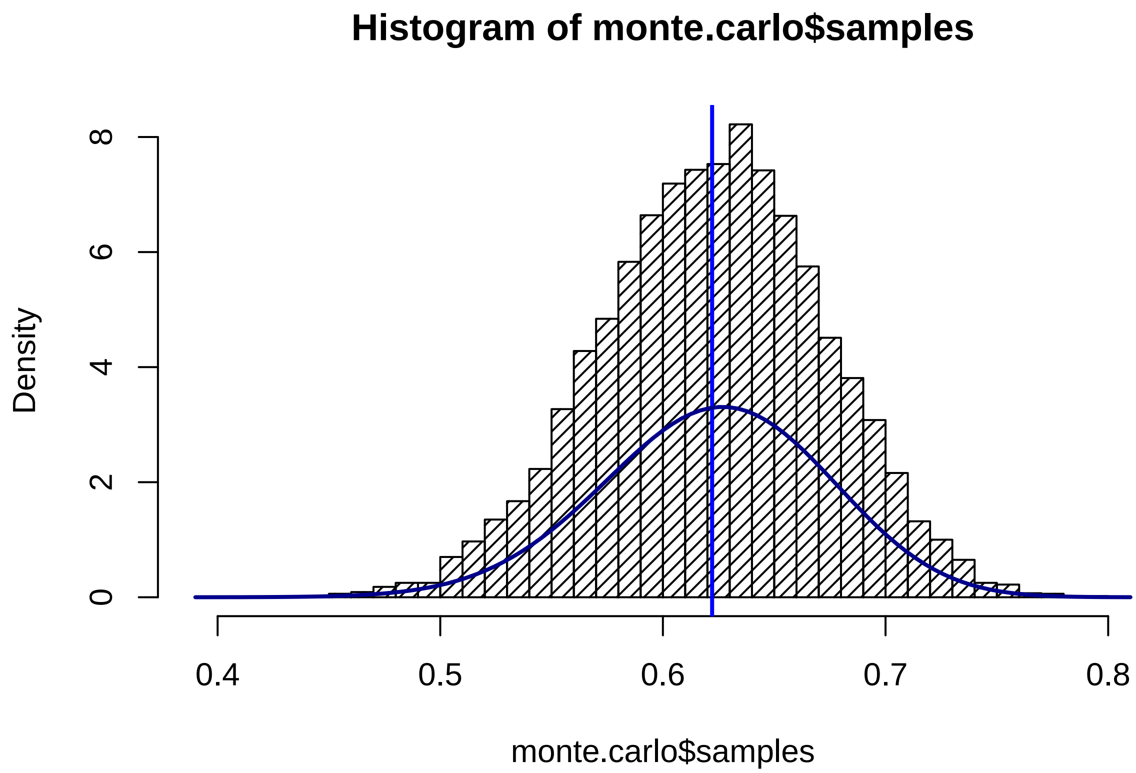
Here is a plot over the density of the sampled θ's as well as the sampled mean. As we can see the sample mean of θ is circa 0.623, which may suggest that the prior was not right (as we would expect mean close to 0.5 from a uniform (0, 1) distribution).

2)

Here we have

```
monte.carlo.integration <- function(){
  m <- 10000 # Number of samples
  samples <- rejection.sampling.multinomial(m)$samples
  mu <- sum(samples)/m
  li <- list("observed_mean" = mu, "samples" = samples)
  return (li)
}
monte.carlo <- monte.carlo.integration()

hist(monte.carlo$samples, density=20, breaks = 30, prob=TRUE)
abline(v = mean(monte.carlo$samples), col = "blue", lwd = 2)
curve(posterior.f(x)/mean(posterior.f(x)), add=TRUE, col="darkblue", lwd=2)
```




```
numerical.integration <- function(theta){
  return (theta*posterior.f(theta))
}
Analytic_mean <- integrate(numerical.integration, lower=0,upper=1)$value/integrate(posterior.f, lower=0
```

```
## Observed mean:  0.622108
```

```
## Analytic mean:  0.6228061
```

3)

Sampling using the rejection algorithm leads to a number of rejected samples. In this case we have counted the ratio as we sampled, marked as observed, as well as found the analytic solution which will be:

$$c^{-1} = \int_0^1 \frac{f(x)}{c} dx.$$

Using the built in optimize and integrate function, we get the integral, which will be the ratio $\frac{\text{Total samples}}{\text{Accepted samples}}$:

```
## Observed:  7.80875
```

```
## Analytic:  7.799308
```

As we see we have a observed ratio close to the analytic ratio.

4)

We have the samples from earlier which are sampled with the prior Beta(1, 1): $x_1, ..., x_n \sim g(x)$. However we can change this by using importance sampling:

$$w_i = \frac{f(x_i)}{g(xi)}$$

Here $f(x) \sim Beta(1, 5)$. Since the density function will stay the same, all the elements will cancel, and we will get weights:

$$w_i = \frac{\text{Beta(1, 5)}}{\text{Beta(1, 1)}} = \text{Beta(1, 5)} = (1-\theta)^4.$$

Thus the importance sampling algorithm will be for this case:

$$\tilde{\mu}_{IS} = \frac{\sum h(\theta_i) w(\theta_i)}{\sum w(\theta_i)} = \frac{\sum \theta_i w(\theta_i)}{\sum w(\theta_i)}, \quad w(\theta_i) = (1-\theta_i)^4$$

Running this algorithm as code gives a estimator $\tilde{\mu}_{IS}$ for the new mean.

```
beta.distribution <- function(x, alpha, beta){
  return(x^(alpha-1)*(1-x)^(beta-1)/beta(alpha, beta))
}
importance.sampling <- function(n){
  samples <- rejection.sampling.multinomial(n)$samples
  w = (1-samples)^4
  mu.is <- sum(samples*w)/sum(w)
  return(mu.is)
}

importance.sampling(20000)
```

```
## [1] 0.5953001
```

Here we see from the print out, that the importance sampling shifts the observed mean from 0.623 to 0.596.