title: “Lab 1” author: “Daniel Herzegh (danhe178) and Richard Friberg (rical803)” date: “2017-09-26” output: pdf_document —

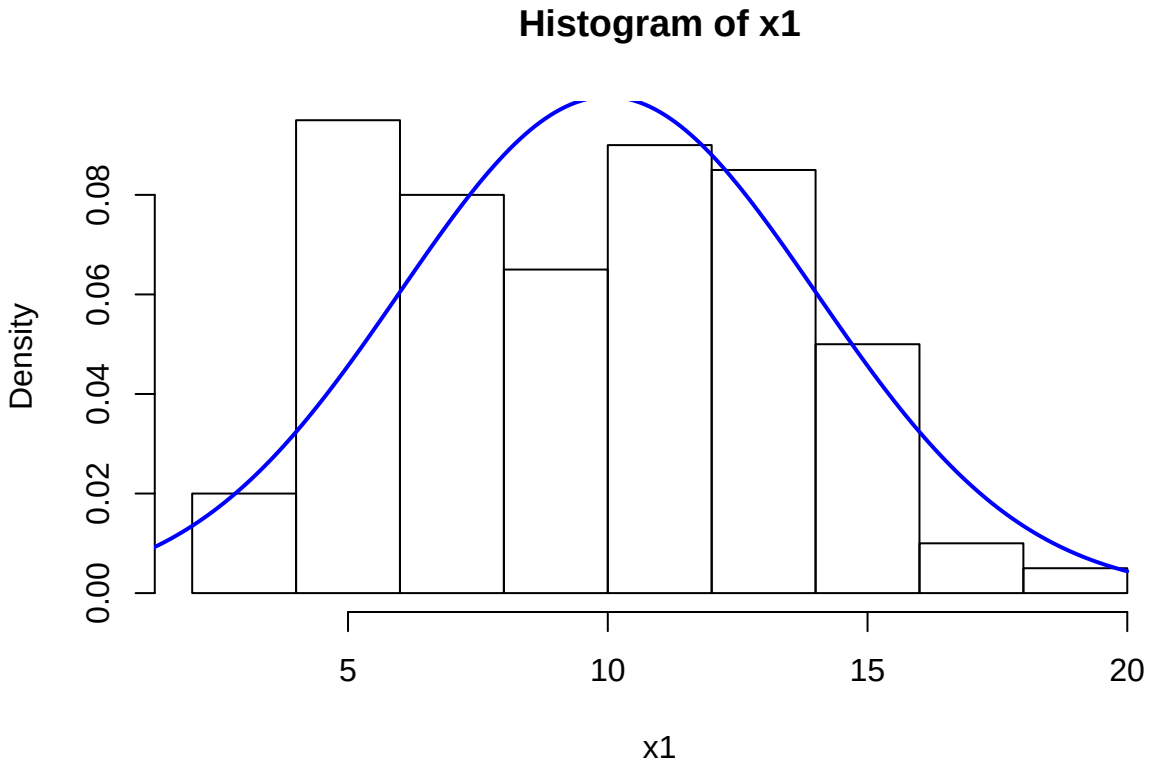
Uppgift 1 Simulering av normalfordelning

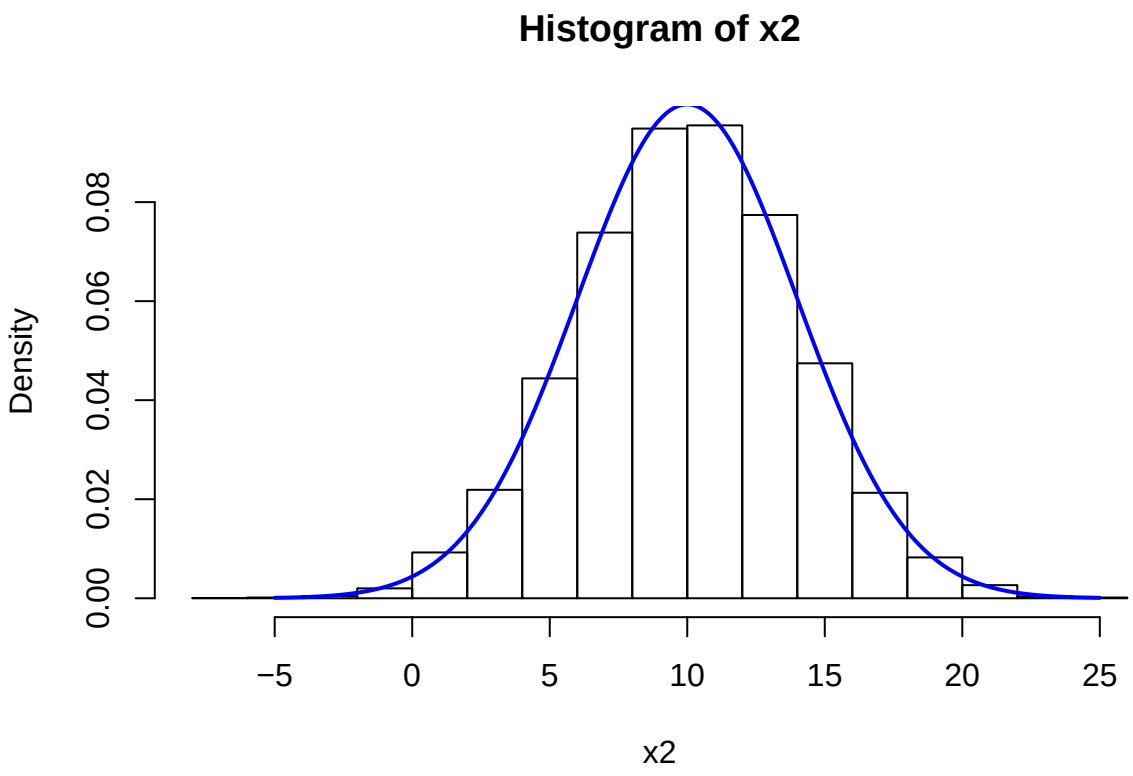
a) Visualisera fördelningarna i två histogram. Visualisera fordelningens pdf i samma graf.

Nedan simuleras normalfördelningen med olika antal dragningar.

```
x1 <- rnorm(100, mean = 10, sd = 4)
x2 <- rnorm(10000, mean = 10, sd = 4)
```

I figurerna nedan visas resultatet av dragningarna som ett histogram tillsammans med tathetsfunktionen.





b) Beskriv skillnaden mellan de olika graferna.

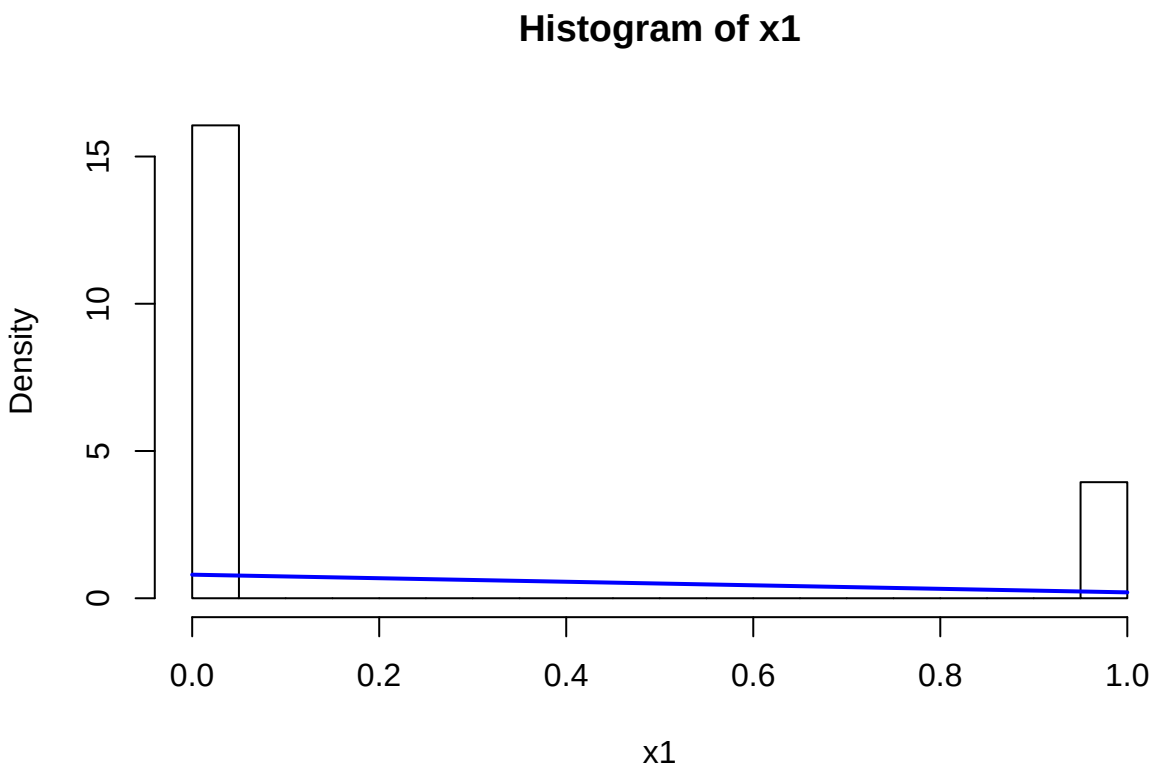
Vi kan tydligare se normalfordelningsformen om vi gor fler dragningar/simuleringar.

Uppgift 2 Simulera och visualisera andra fordelningar

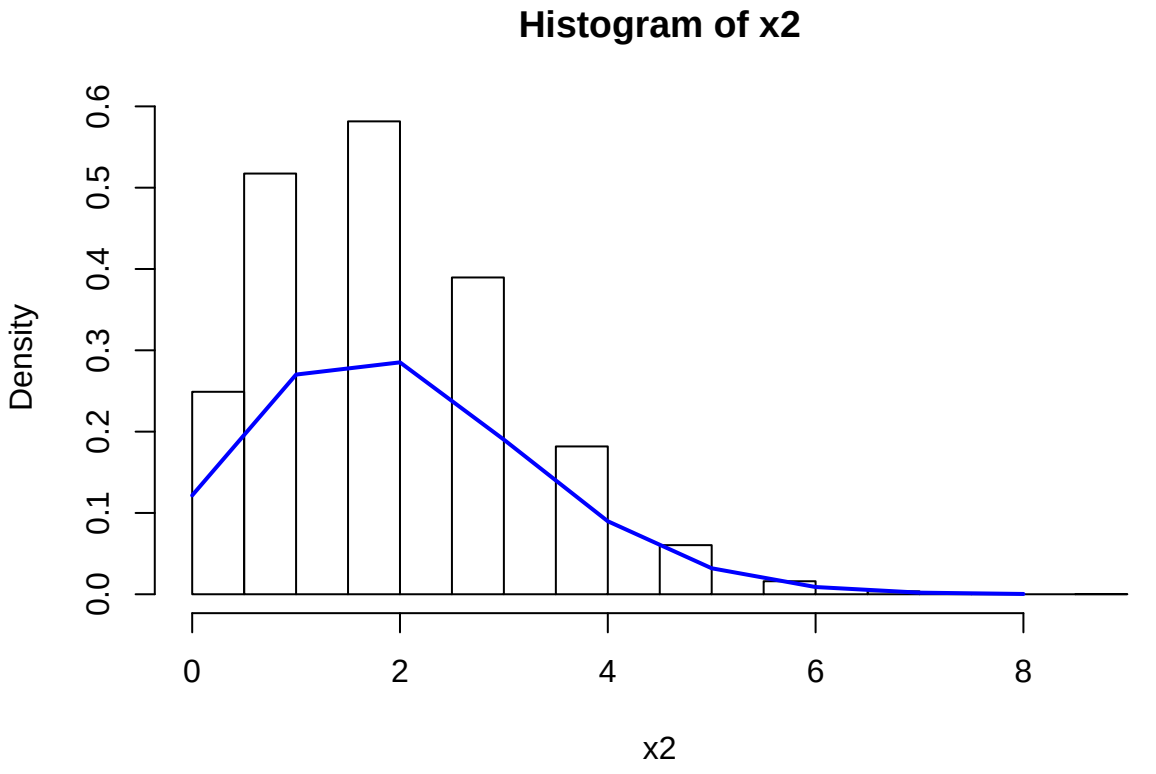
a) Simulera och visualisera foljande fordelningar med 10000 dragningar fran varje fordelning samt fordelningens tathetsfunktioner.

```
x1 <- rbern(10000, 0.2)
x2 <- rbinom(n = 10000, size = 20, prob = 0.1)
x3 <- rbinom(n = 10000, size = 20, prob = 0.5)
x4 <- rgeom(10000, 0.1)
x5 <- rpois(10000, 10)
```

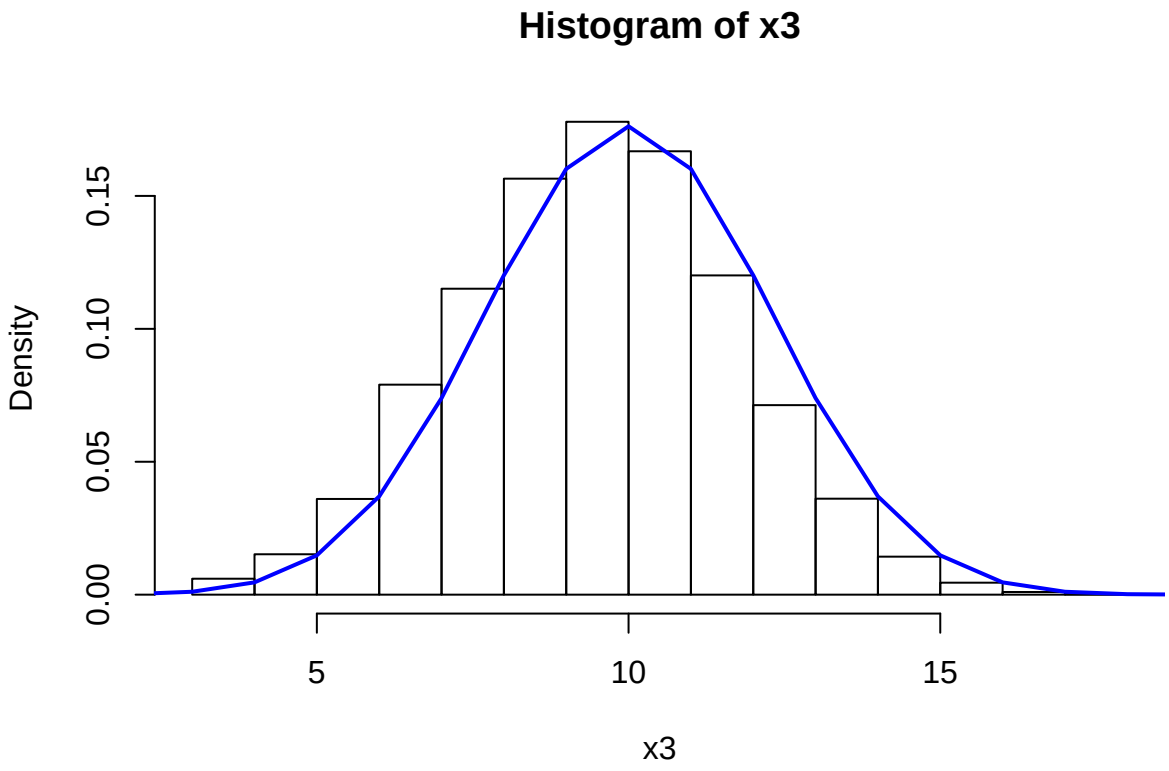
```
hist(x1, probability = TRUE)
xfit <- seq(0, 1, 1)
yfit <- dbern(xfit, 0.2, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```



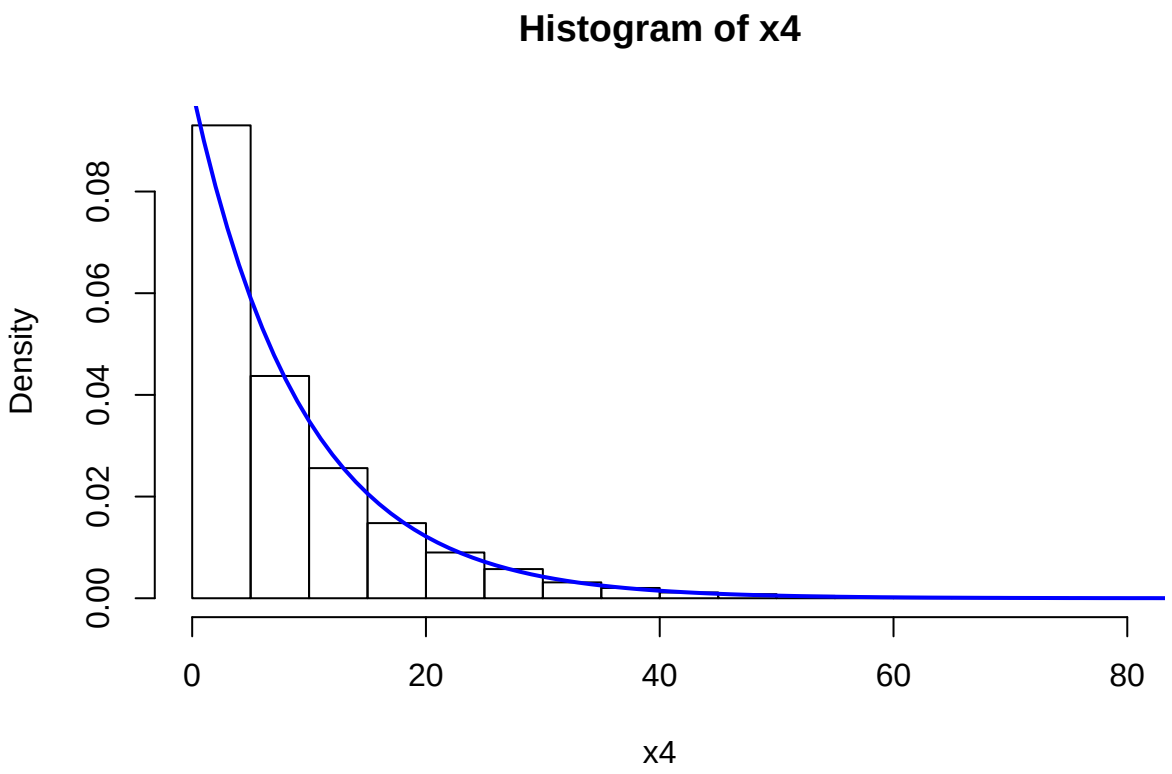

```
hist(x2, probability = TRUE)
xfit <- seq(0, 8, 1)
yfit <- dbinom(xfit, size = 20, prob = 0.1)
lines(xfit, yfit, col="blue", lwd=2)
```



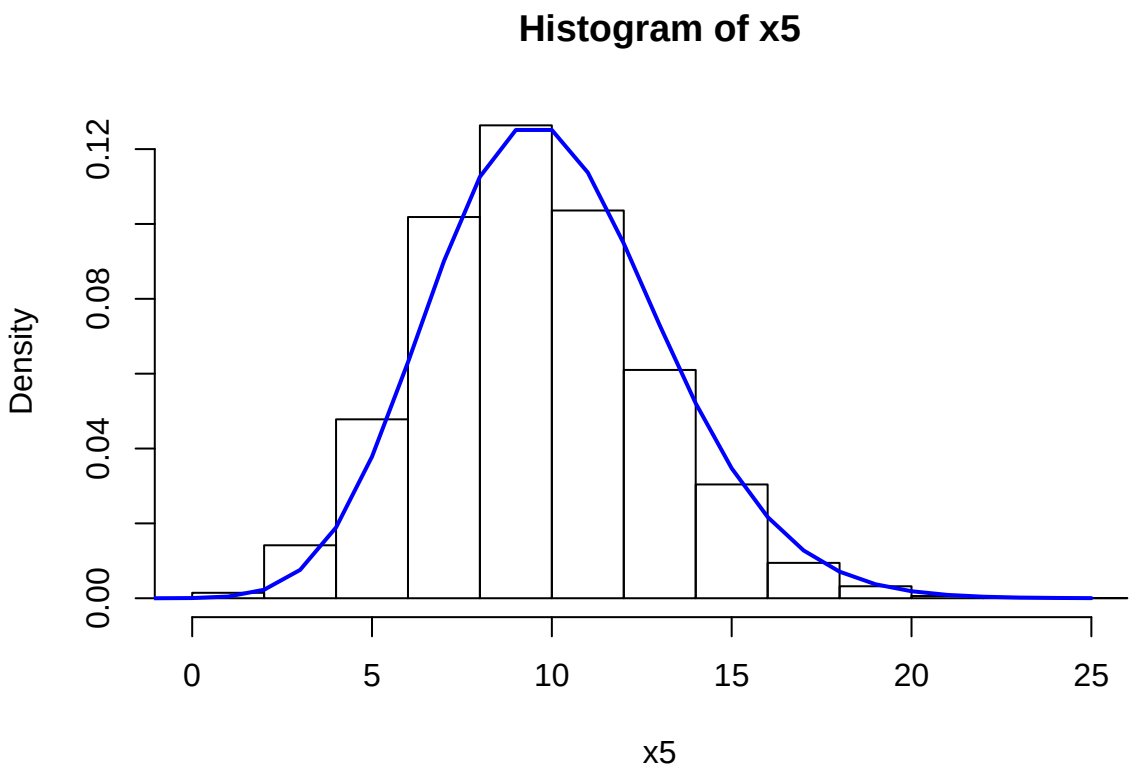
```r
hist(x3, probability = TRUE)
xfit <- seq(0, 20, 1)
yfit <- dbinom(xfit, size = 20, prob = 0.5)
lines(xfit, yfit, col="blue", lwd=2)
```




```r
hist(x4, probability = TRUE)
xfit <- seq(0, 100, 1)
yfit <- dgeom(xfit, prob = 0.1)
lines(xfit, yfit, col="blue", lwd=2)
```

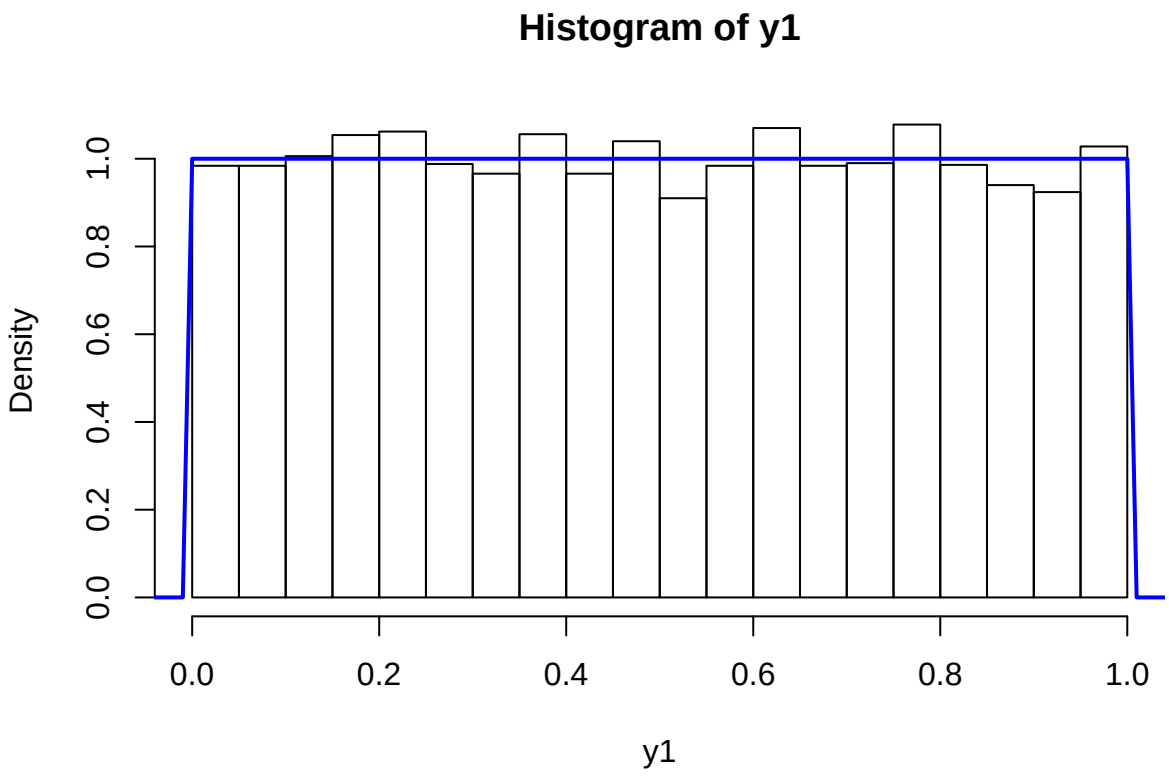



```
hist(x5, probability = TRUE)
xfit <- seq(-5, 25, 1)
yfit <- dpois(xfit, lambda = 10)
lines(xfit, yfit, col="blue", lwd=2)
```

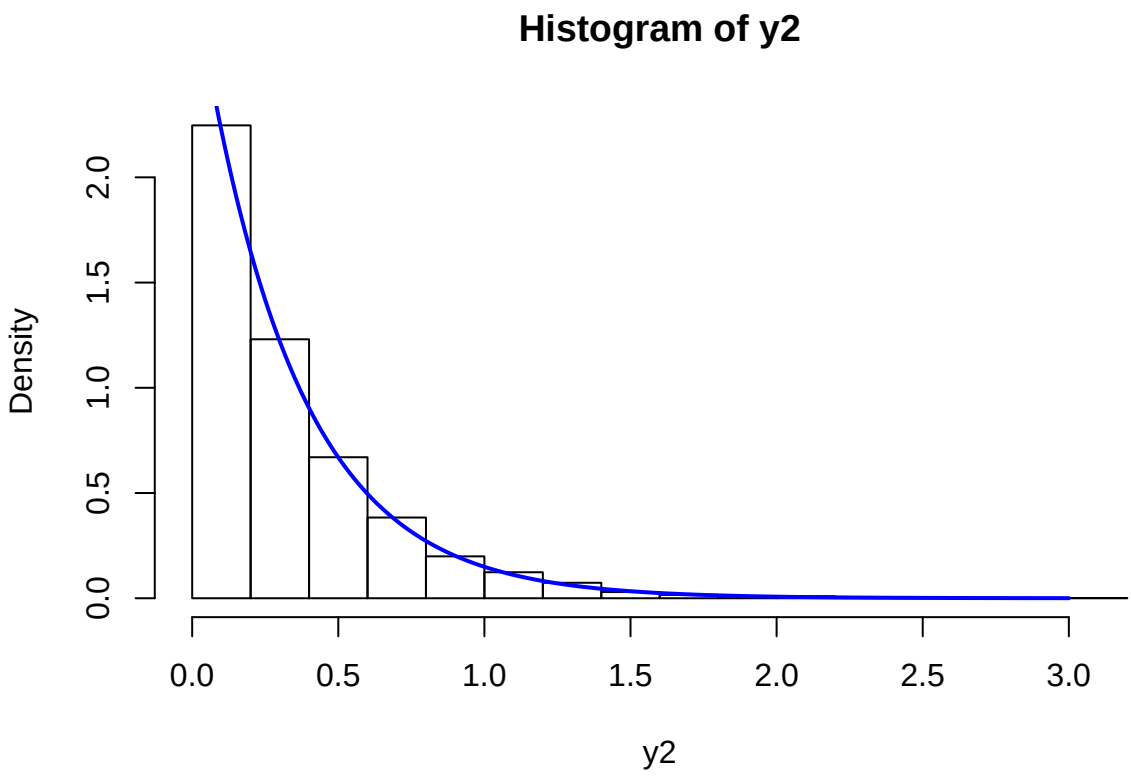


```r
y1 <- runif(10000, min = 0, max = 1)
y2 <- rexp(10000, rate = 3, beta = 1/3)
y3 <- rgamma(10000, shape=2, rate = 1, scale = 1, alpha = 2, beta = 1)
y4 <- rt(10000, 3)
y5 <- rbeta(10000, 0.1, 0.1, 0)
y6 <- rbeta(10000, 1, 1, 0)
y7 <- rbeta(10000, 10, 5, 0)
```

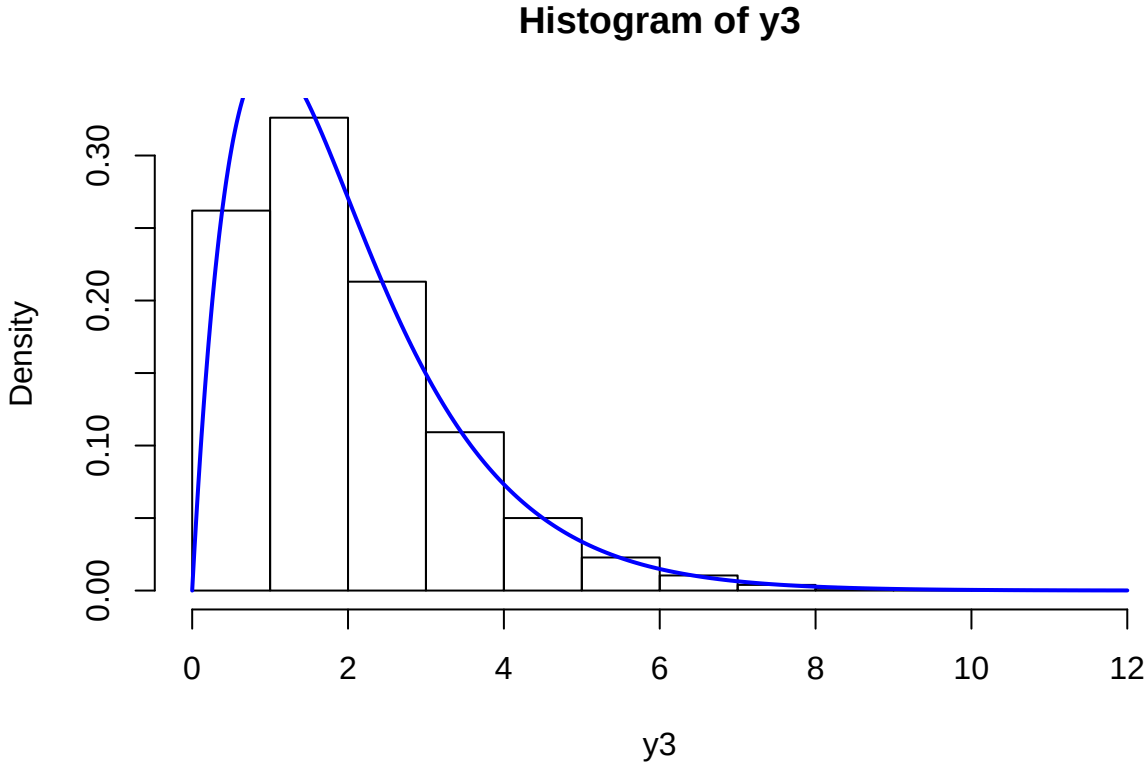
```r
hist(y1, probability = TRUE)
xfit <- seq(-5, 1.1, 0.01)
yfit <- dunif(xfit, min=0, max=1, log=FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```



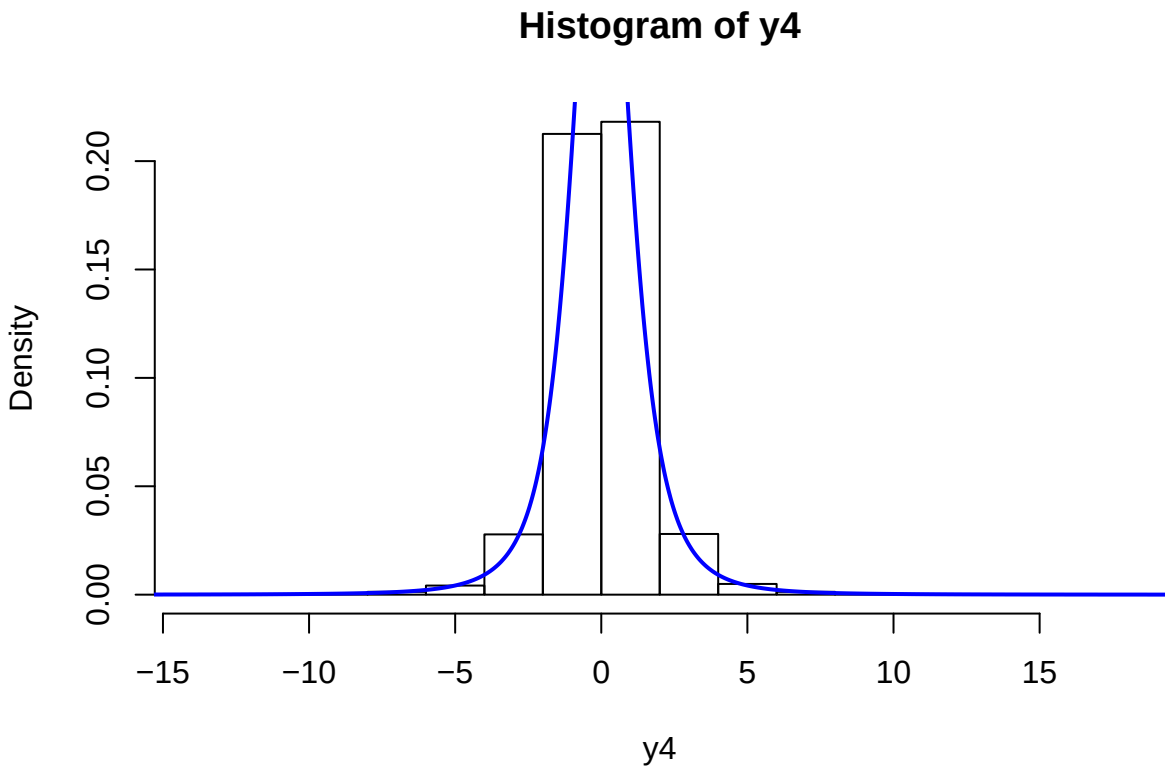

```r
hist(y2, probability = TRUE)
xfit <- seq(0, 3, 0.01)
yfit <- dexp(xfit, rate = 3, beta = 1/3, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```



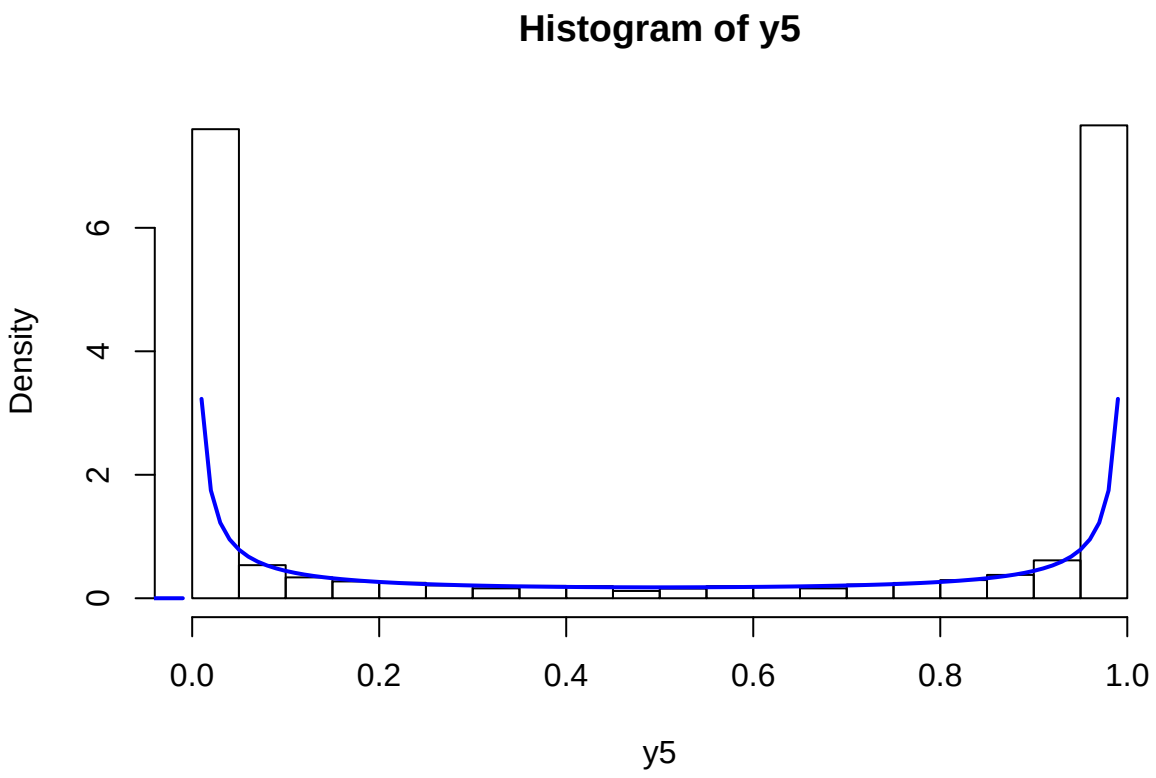

```
hist(y3, probability = TRUE)
xfit <- seq(0, 12, 0.01)
yfit <- dgamma(xfit, 2, 1, 1, 2, 1, log=FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```



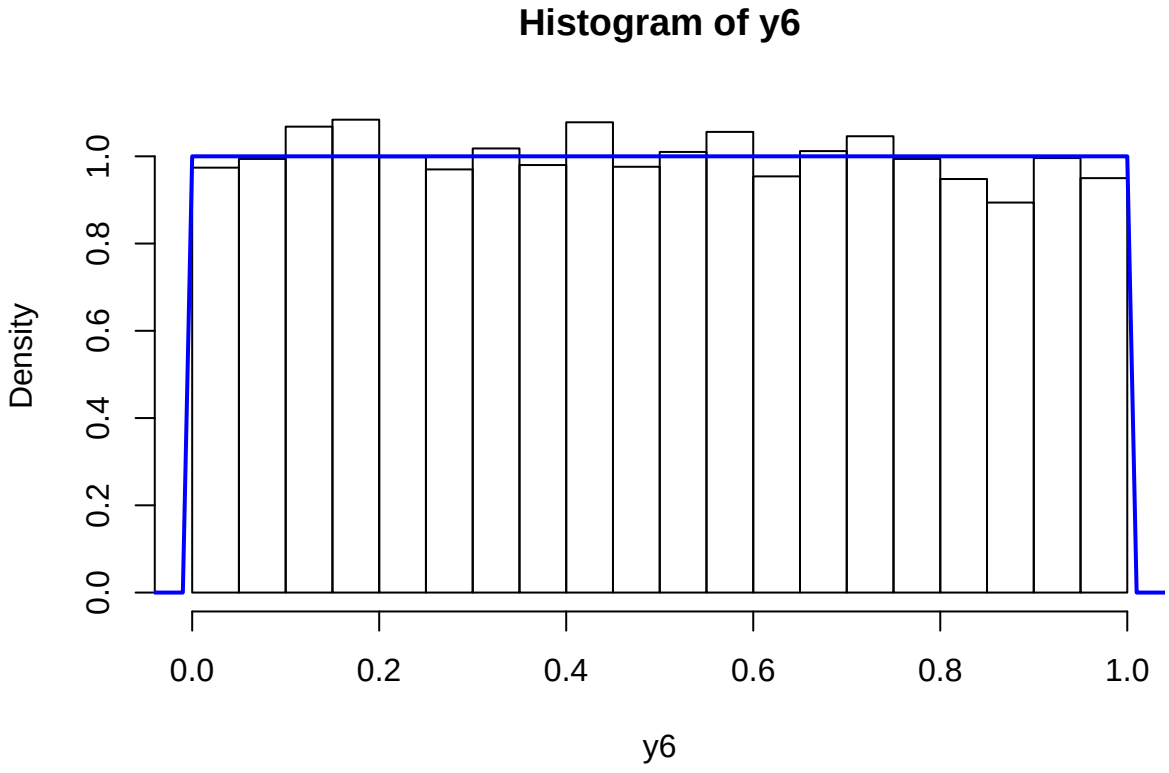
```r
hist(y4, probability = TRUE)
xfit <- seq(-20, 20, 0.01)
yfit <- dt(xfit, 3)
lines(xfit, yfit, col="blue", lwd=2)
```



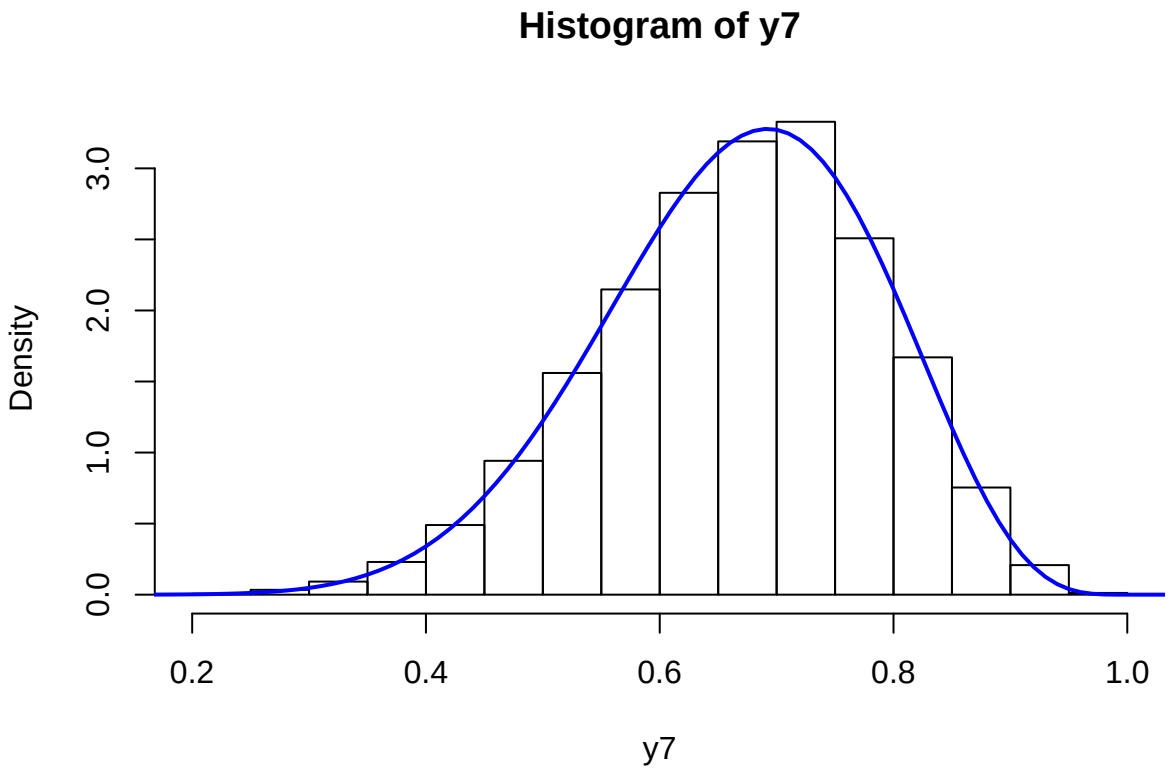

```r
hist(y5, probability = TRUE)
xfit <- seq(-1, 1, 0.01)
yfit <- dbeta(xfit, 0.1, 0.1, 0, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```




```
hist(y6, probability = TRUE)
xfit <- seq(-0.1, 1.1, 0.01)
yfit <- dbeta(xfit, 1, 1, 0, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```



```r
hist(y7, probability = TRUE)
xfit <- seq(-0.1, 1.1, 0.01)
yfit <- dbeta(xfit, 10, 5, 0, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```

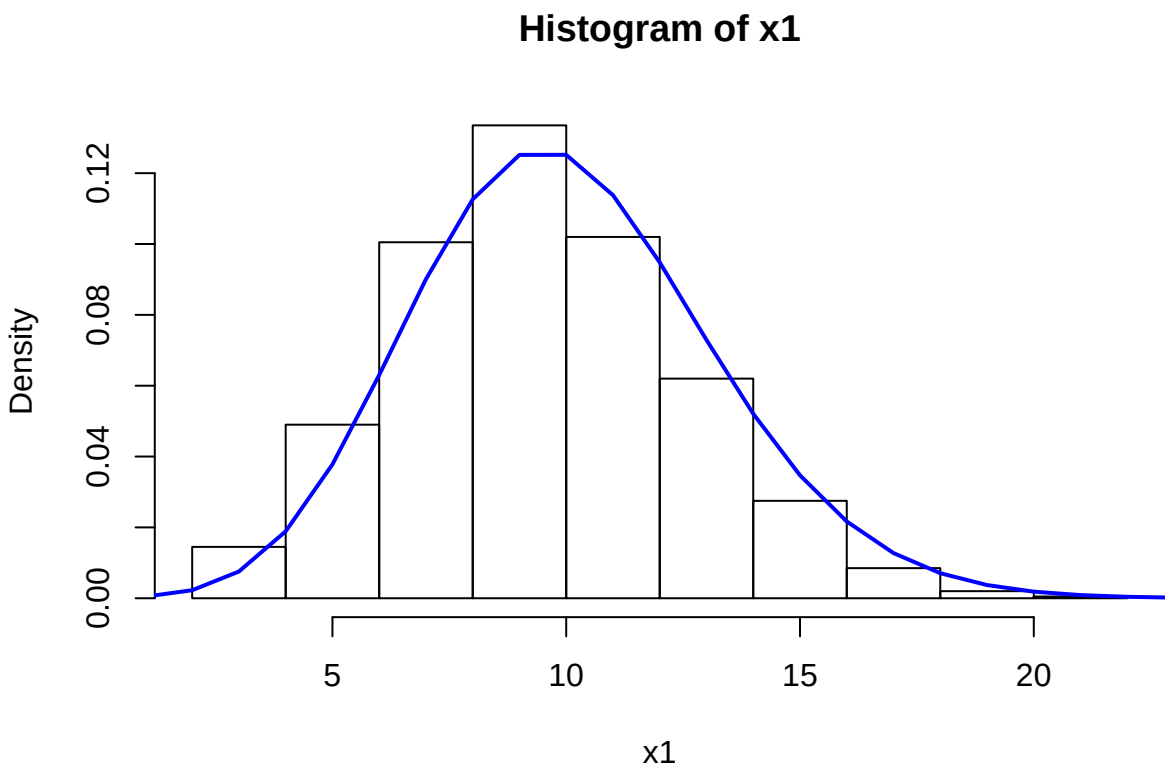


Uppgift 3 Relation mellan fordelningar

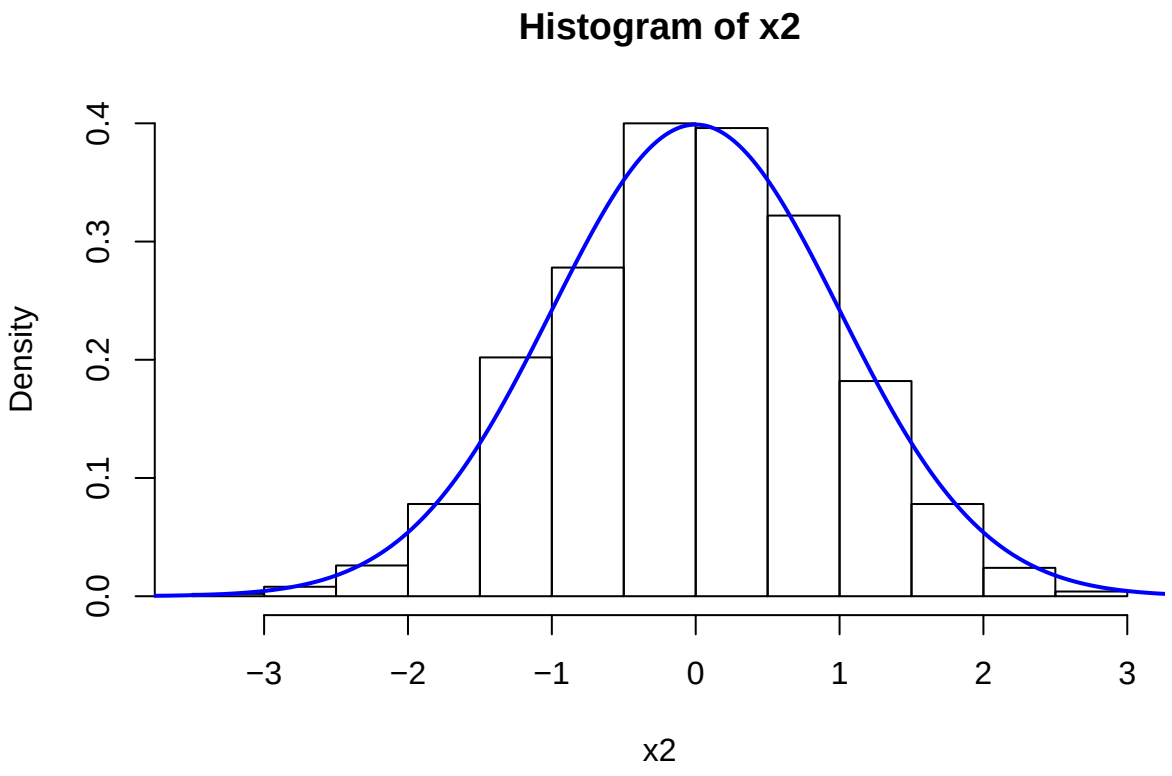
a) Simulera 1000 varden fran respektive fordelning och visualisera fordelningen i ett histogram tillsammans med fordelningens tathetsfunktionen.

```r
x1 <- rbinom(n = 1000, size = 10000, prob = 0.001)
x2 <- rt(1000, 10000)
```

```r
hist(x1, probability = TRUE)
xfit <- seq(0, 25, 1)
yfit <- dbinom(xfit, size = 10000, prob = 0.001)
lines(xfit, yfit, col="blue", lwd=2)
```




```
hist(x2, probability = TRUE)
xfit <- seq(-4, 4, 0.01)
yfit <- dt(xfit, 10000)
lines(xfit, yfit, col="blue", lwd=2)
```



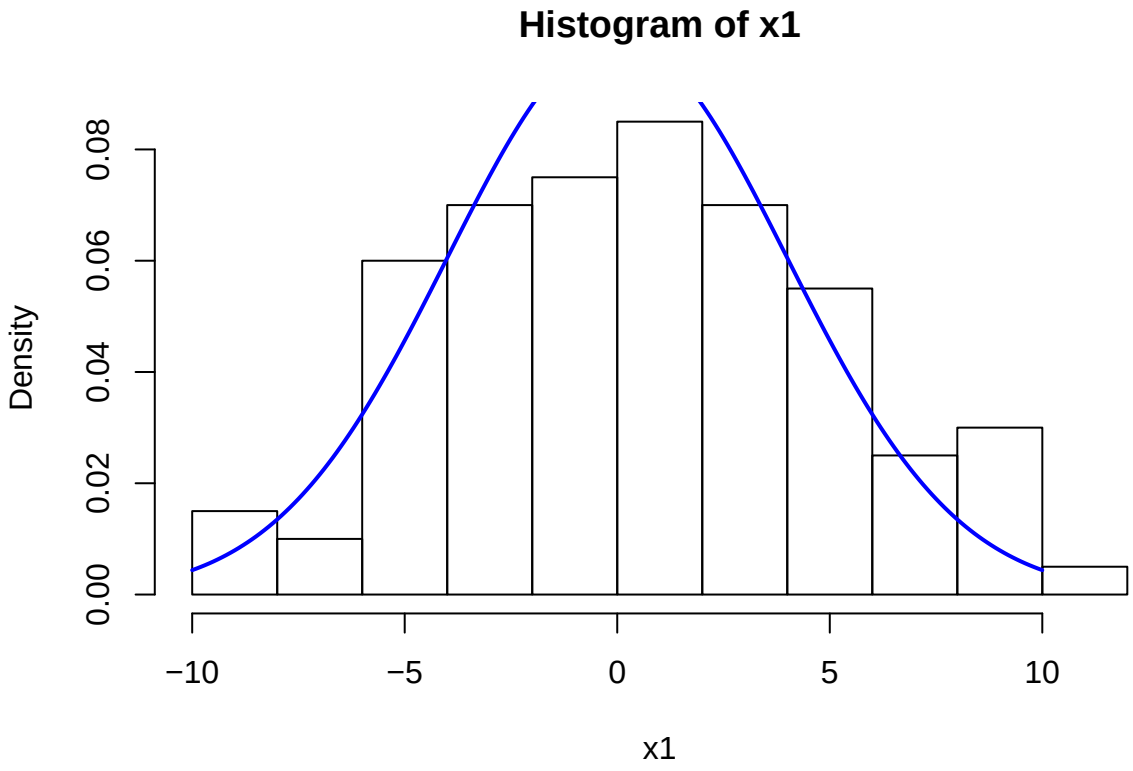
b) Ta reda pa (ex. via Wikipedia) vilken annan fordelning som respektive fordelning borjar konvergera mot.

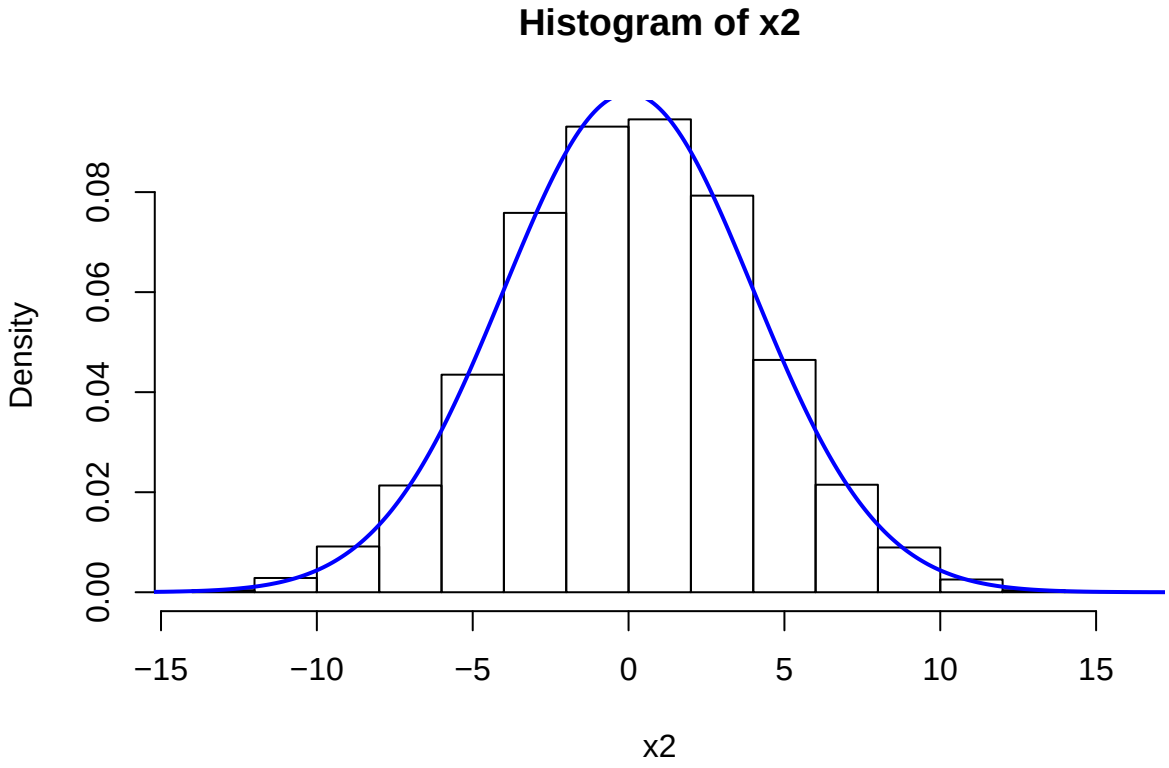
Både Binomialfördelningen och Student-t-fördelningen börjar konvergera mot en normalfördelning med my = 0. #RTK: BINOMIAL GÅR MOT POISSON

c) Simulera dragningar fran dessa fordelningar och jamfor resultatet med de resultat du fick i a).

```
x1 <- rnorm(100, mean = 0, sd = 4)
x2 <- rnorm(10000, mean = 0, sd = 4)
```

I figurerna nedan visas resultatet av dragningarna som ett histogram tillsammans med tathetsfunktionen.



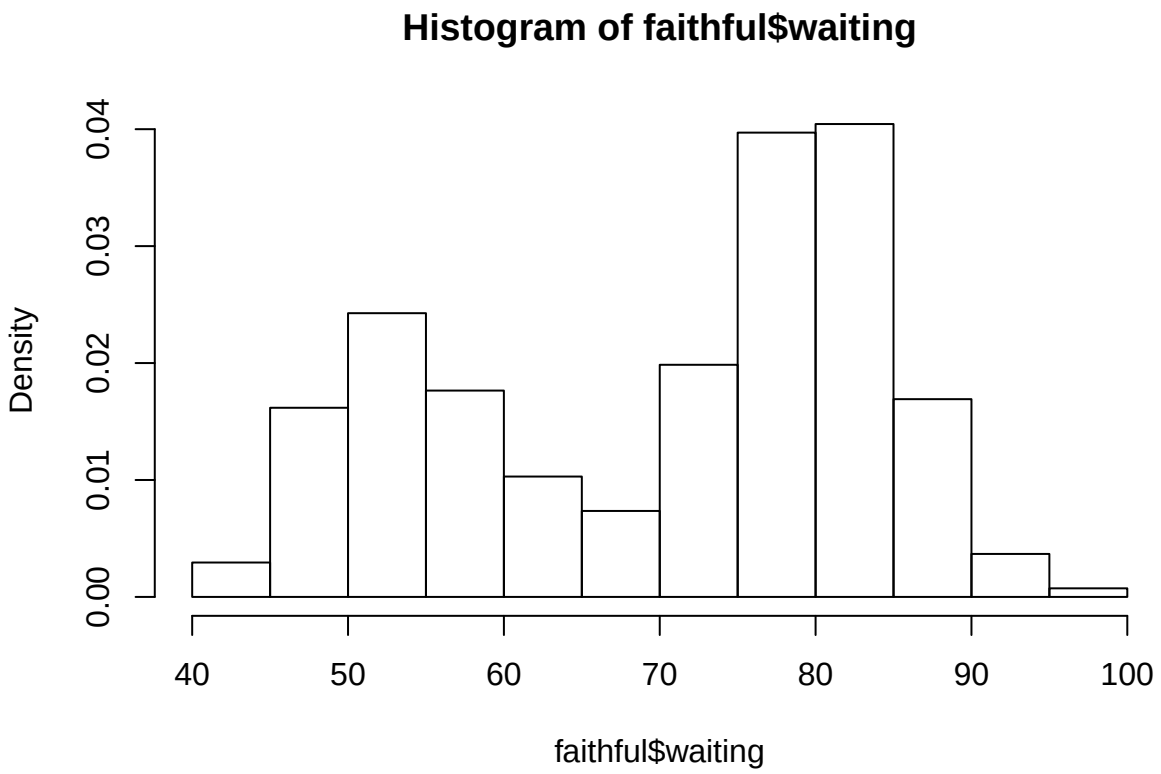


Uppgift 4 Hiearkiska sannolikhetsfördelningar

Vi ska nu simulera en blandad sannolikhetsfördelning (mixture distribution). Börja att läsa in data-materialet faithful i R med data(faithful).

a) Visualisera variabeln waiting i ett histogram.

```
data(faithful)
hist(faithful$waiting, probability = TRUE)
```

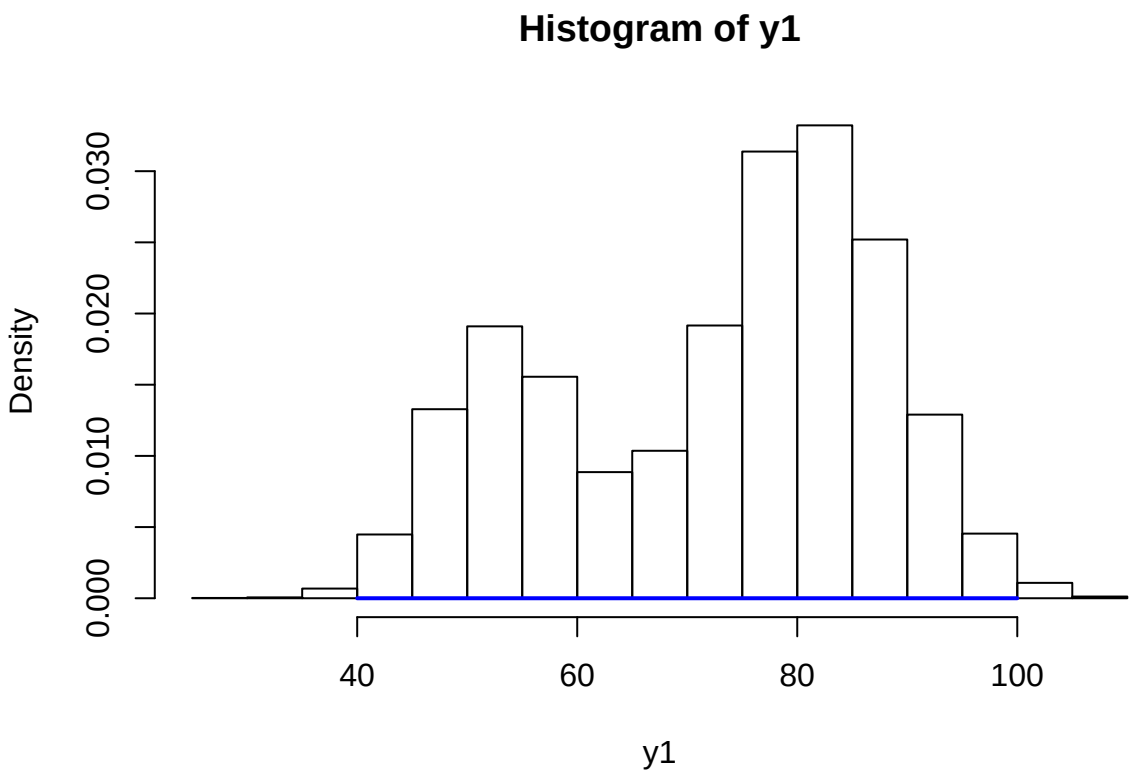


b) Simulera 10000 från följande modell och visualisera fördelningen i ett histogram. Simulera först från X och sedan från Y . Sätt $p = 0.3$, $1 = 15$, $1 = 3$, $2 = 4$ och $2 = 2$.

Xi <- Bernoulli(p)

```
x1 <- rbern(10000, 0.3)
y1 <- numeric(10000)
for(i in 1:10000) {
  y1[i] = x1[i] * rnorm(1, 53, 6) + (1-x1[i]) * rnorm(1, 81,8)
}
```

```
hist(y1, probability = TRUE)
xfit <- seq(40, 100, 1)
yfit <- dbern(xfit, 0.3, log = FALSE)
lines(xfit, yfit, col="blue", lwd=2)
```

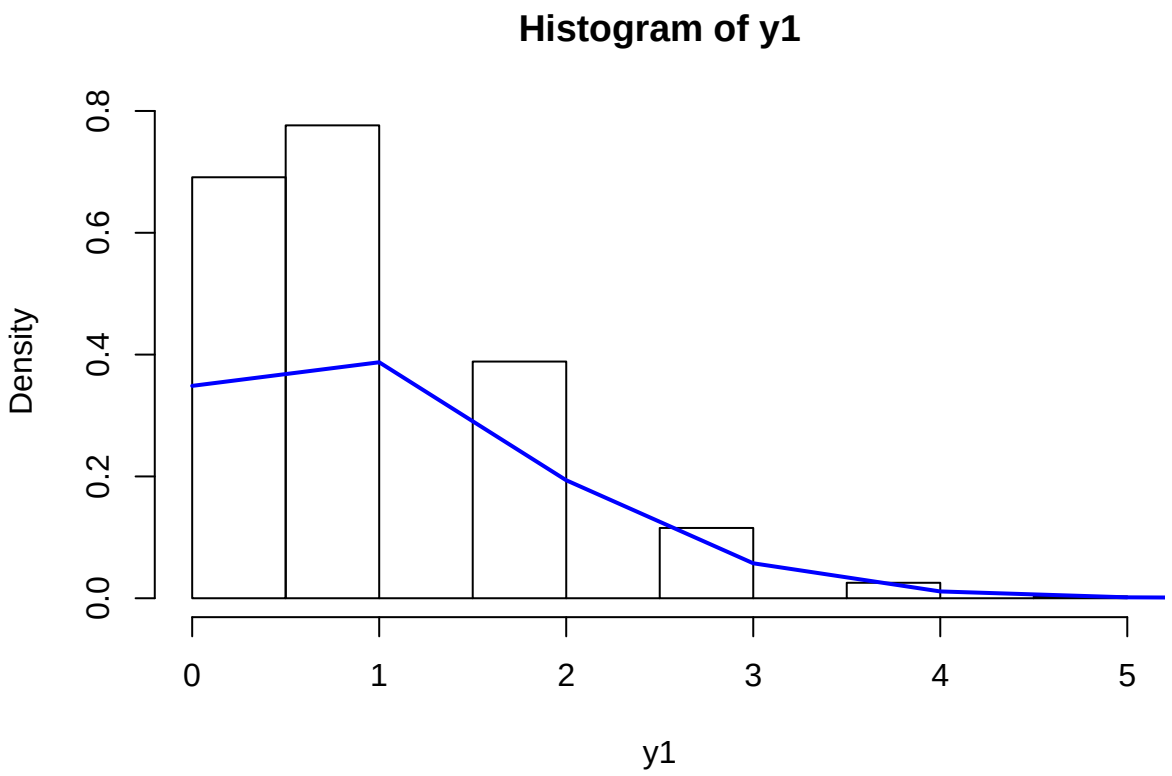


Uppgift 5 Analytisk sannolikhet och approximation med ”Monte Carlo” - metoder

```
x1 <- rnorm(10000, 0, 1)
y1 <- rbinom(10000, 10, 0.1)
```

a)

```
hist(y1, probability = TRUE)
xfit <- seq(0, 10, 1)
yfit <- dbinom(xfit, 10, 0.1)
lines(xfit, yfit, col="blue", lwd=2)
```



b)

1 P(X < 0)

```
pnorm(0, mean = 0, sd = 1)
```

```
## [1] 0.5
```

2 P(1 < X < 1)

```
pnorm(1, mean = 0, sd = 1) - pnorm(-1, mean = 0, sd = 1)
```

```
## [1] 0.6826895
```

3 P(1.96 < X)

```
1 - pnorm(1.96, mean = 0, sd = 1)
```

```
## [1] 0.0249979
```

4 P(0 < Y < 10)

```
pbinom(10, size = 10, prob = 0.1)  - pbinom(0.0, size = 10, prob = 0.1)
```

```
## [1] 0.6513216
```

FEL

5 P(Y = 0)

```
pbinom(0.0, size = 10, prob = 0.1)
```

```
## [1] 0.3486784
```

6 P (0 <= Y <= 10)

```
pbinom(10.0, size = 10, prob = 0.1) - pbinom(0.0, size = 10, prob = 0.1)
```

```
## [1] 0.6513216
```

c)

1 P(X < 0)

```
x1 <- rnorm(10000, 0, 1)
p = ecdf(x1)
p(0.0)
```

```
## [1] 0.5032
```

2 P(1 < X < 1)

```
x2 <- rnorm(10000, 0, 1)
p = ecdf(x2)
p(1.0) - p(-1.0)
```

```
## [1] 0.6756
```

3 P(1.96 < X)

```
x3 <- rnorm(10000, 0, 1)
p = ecdf(x3)
1 - p(1.96)
```

```
## [1] 0.0252
```

4 P(0 < Y < 10)

```
y1 <- rbinom(10000, 10, 0.1)
p = ecdf(y1)
p(10.0) - p(0.0)
```

```
## [1] 0.6473
```

FEL

5 P(Y = 0)

```
y2 <- rbinom(10000, 10, 0.1)
p = ecdf(y2)
p(0.0)
```

```
## [1] 0.3507
```

6 P (0 <= Y <= 10)

```
y3 <- rbinom(10000, 10, 0.1)
p = ecdf(y3)
p(10.0) - p(0.0)
```

```
## [1] 0.6427
```

Uppgift 6 Beräkna (icke-triviala) sannolikheter

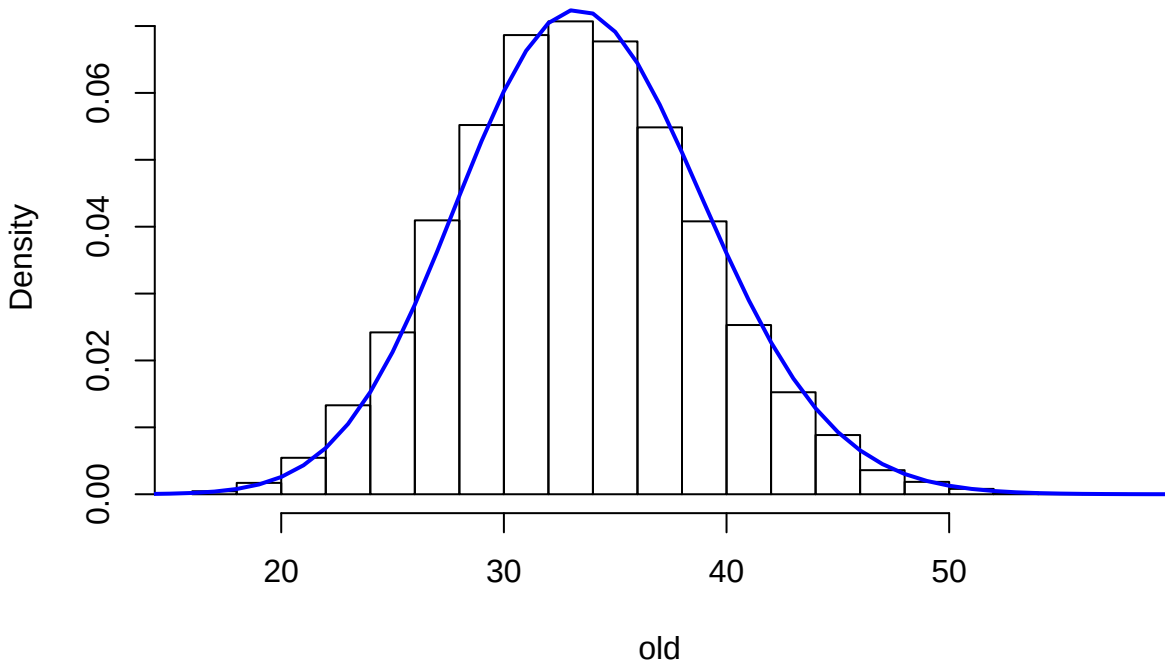
a)

Förväntade antalet fel: Gamla systemet

```
old <- rbinom(10000, size = 337, prob = 0.1)
evold <- mean(old)
print(evold)
```

```
## [1] 33.7695
```

```
hist(old, probability = TRUE)
xfit <- seq(0, 337, 1)
yfit <- dbinom(xfit, 337, 0.1)
lines(xfit, yfit, col="blue", lwd=2)
```



###

Förväntade antalet fel: Nya systemet

```
newprob <- runif(10000, min = 0.02, max = 0.16)
evnewprob <- mean(newprob)
new <- rbinom(10000, size = 337, prob = evnewprob)
evnew <- mean(new)
print(evnew)
```

```
## [1] 30.2416
```

b)

P(färre fel i gamla systemet än nya) = intervallet [0.1, 0.16] / intervallet [0.02, 0.16] = 0.06/0.14 = 0.429

c)

sannolikheten att du kommer få fler än 50 fel i gamla systemet

```
p <- ecdf(old)
print(1-p(50))
```

```
## [1] 0.0024
```

sannolikheten att du kommer få fler än 50 fel i nya systemet

```
p <- ecdf(new)
print(1-p(50))
```

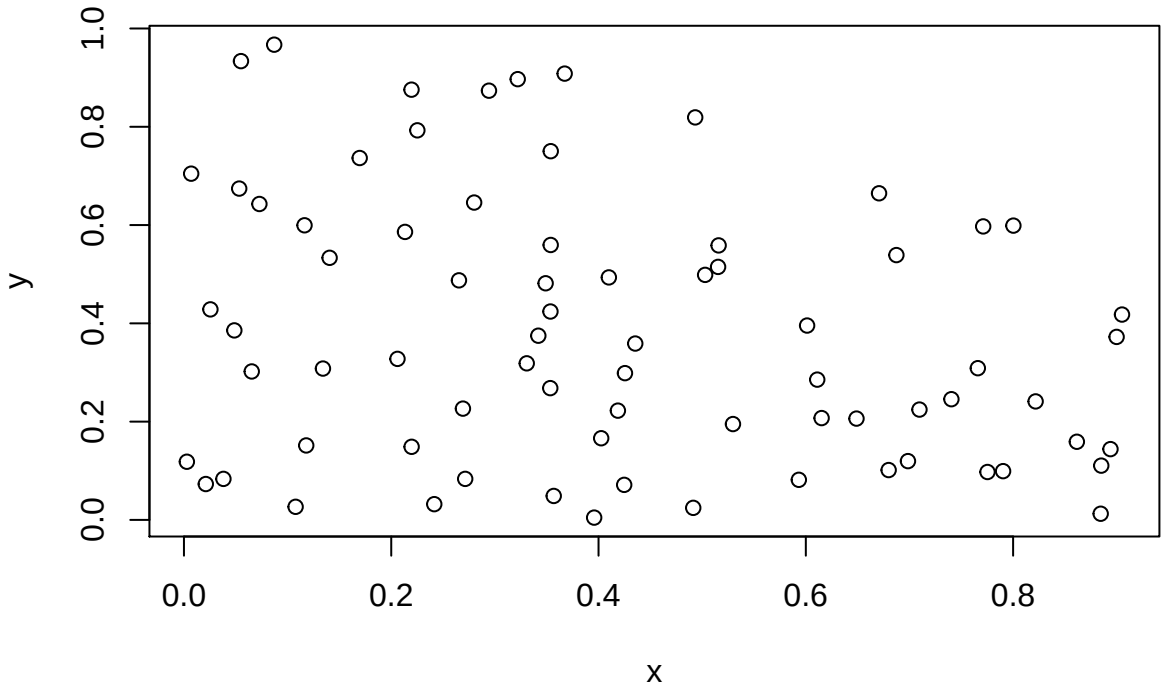
```
## [1] 4e-04
```

Uppgift 7 Monte Carlo metoder för integrering

a)

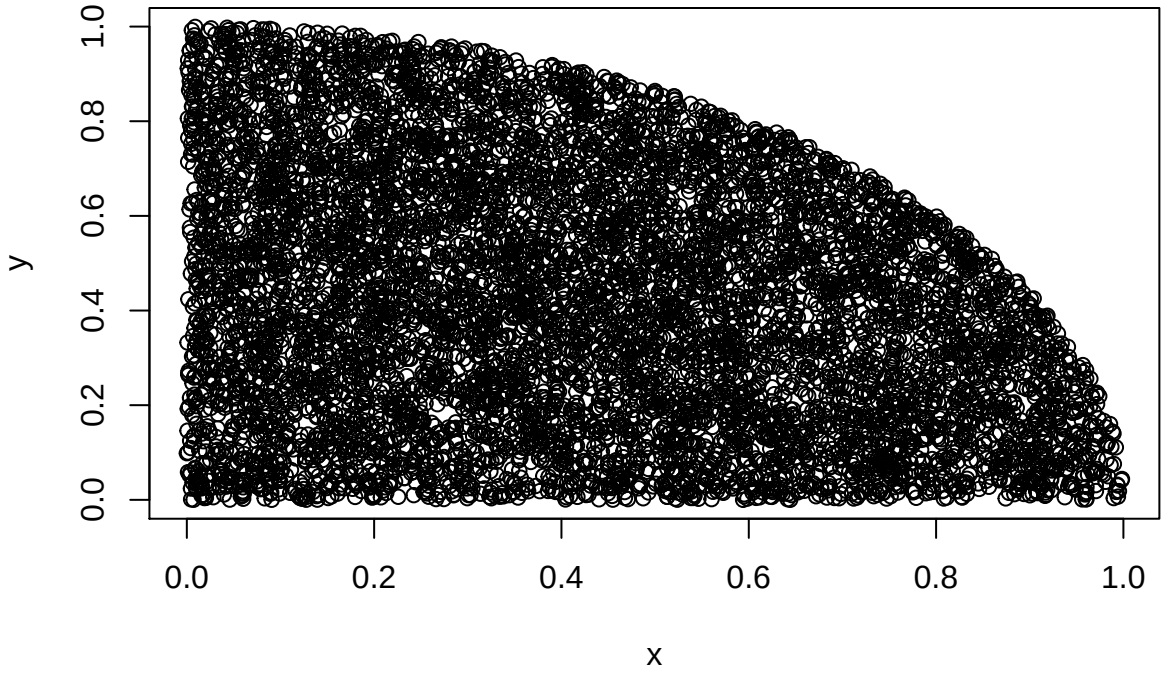
```
montecarlocalcpi <- function(n) {

x <- runif(n, min = 0.0, max = 1.0)
y <- runif(n, min = 0.0, max = 1.0)

i <- 1
while (i <= length(x)) {
  eq <- (x[i]*x[i]+y[i]*y[i])**(1/2)
  if (eq > 1) {
    x <- x[-i]
    y <- y[-i]
  }
  else {
    i <- i + 1
  }
}

z <- length(x)

plot(x, y)

const <- 4 * z/n

return(const)
}
```

```
montecarlocalcpi(100)
```




```
## [1] 2.96
```

```
montecarlocalcpi(10000)
```




```
## [1] 3.0904
```

```
#montecarlocalcpi(100000)
```

```
#montecarlocalcpi(1000000)
```

b)

Vi försöker approximera pi, vilket verkar gå ganska väl både sett till talet man får fram samt den grafiska kvartscirkeln.

c)

Approximationen blir exaktare, men beräkningen tar mycket längre tid.

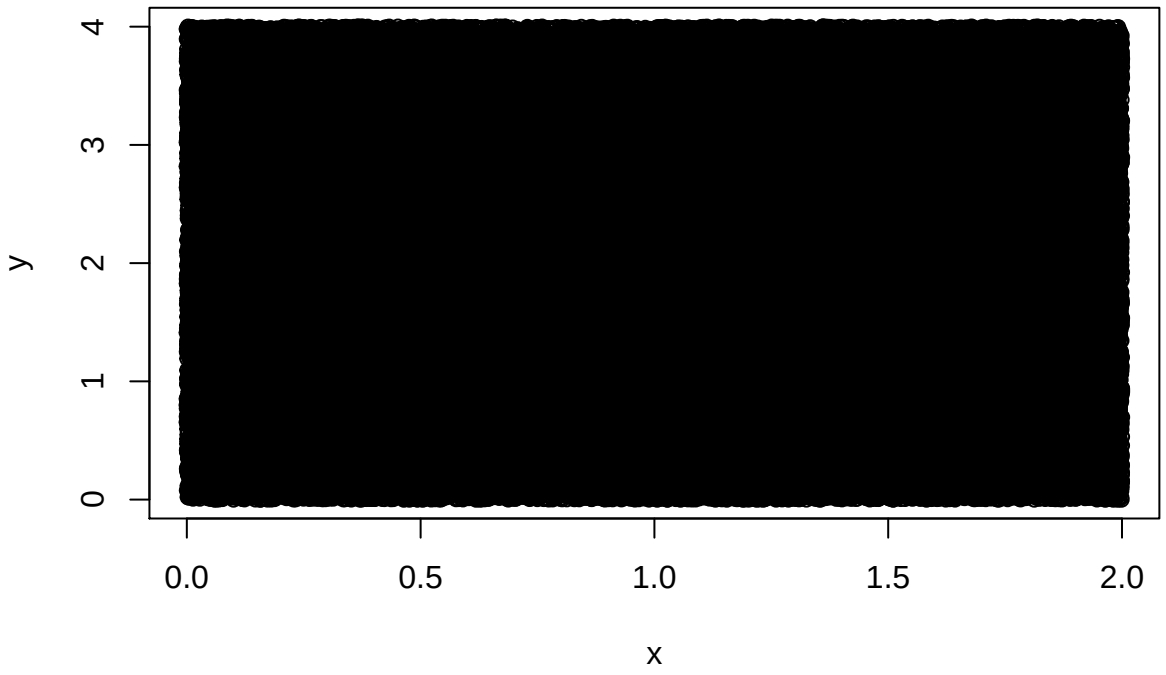
d)

```
x2 <- function(n) {
  return(n*n)
}
integrate(x2, lower = 0, upper = 2)
```

```
## 2.666667 with absolute error < 3e-14
```

e)

```
montecarlocalc <- function(n) {

x <- runif(n, min = 0.0, max = 2.0)
y <- runif(n, min = 0.0, max = 4.0)

plot(x,y)

return(mean(y < x**2)*8)
}

montecarlocalc(100000)
```




```
## [1] 2.66656
```

Uppgift 8 Stora talens lag

```
binomfunc <- function(n) {
  x <- rbinom(n, size = 10, prob = 0.2)
  return(x)
}

gammafunc <- function(n) {
  y <- rgamma(n, shape = 2, rate = 2)
  return(y)
}
```

a)

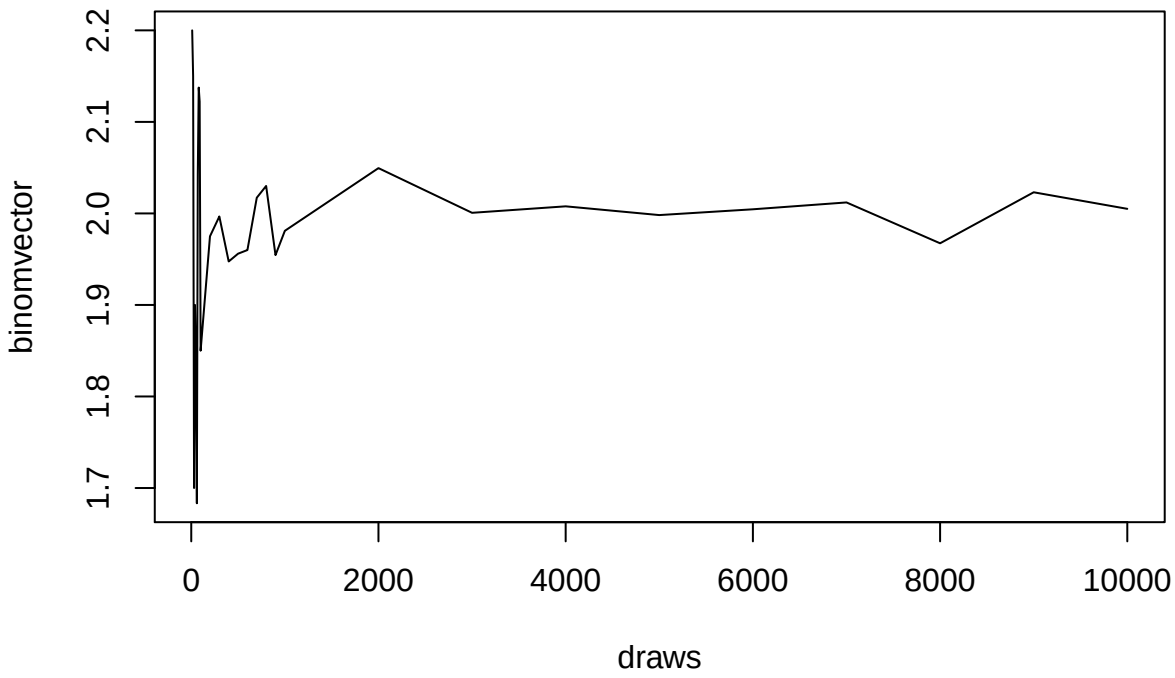
E[X] = size * prob = 10 * 0.2 = 2

E[Y] = shape / rate = 2 / 2 = 1 #RTK: alpha / beta alltså: 2 / (1/2) = 2 * 2 = 4

b)

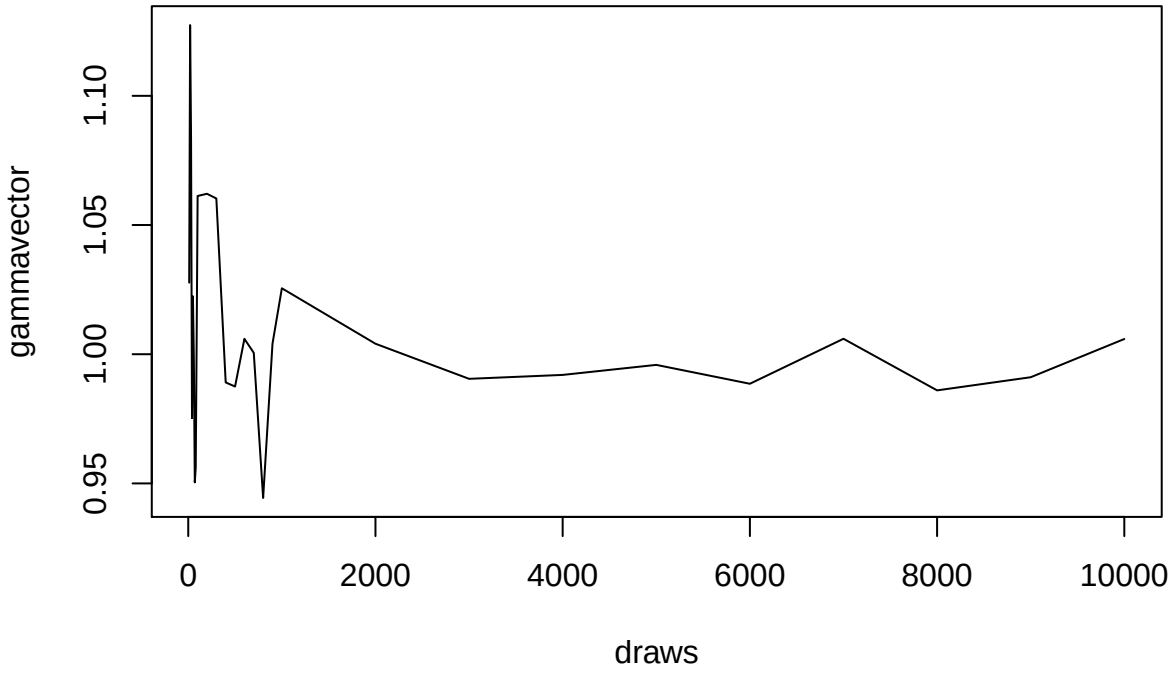
```
binomvector <- c()
draws <- c()

n <- 0
while (n < 10000) {
  if(n < 100) {
```

```
    n <- n + 10
  }
  else if (n < 1000) {
    n <- n + 100
  }
  else if (n < 10000) {
    n <- n + 1000
  }
  x <- mean(binomfunc(n))
  binomvector <- c(binomvector, x)
  draws <- c(draws, n)
}

plot(draws, binomvector, type = "l")
```




```
gammavector <- c()
draws <- c()

n <- 0
while (n < 10000) {
  if(n < 100) {
    n <- n + 10
  }
  else if (n < 1000) {
    n <- n + 100
  }
  else if (n < 10000) {
    n <- n + 1000
  }
  x <- mean(gammafunc(n))
  gammavector <- c(gammavector, x)
```

```
  draws <- c(draws, n)
}

plot(draws, gammavector, type = "l")
```



Uppgift 9 Väntevärde och varians

```
exponentialfunc <- function(n) {
 x <- rexp(n, rate = 10)
 return(x)
}

poissonfunc <- function(n) {
  y <- rpois(n, lambda = 3)
  return(y)
}
```

a)

E[X] = 1/rate = 1/10 = 0.1

Var[X] = $1/\text{rate}^2$ = 1/100 = 0.01

E[Y] = lambda = 3

Var[Y] = lambda = 3

b)

```
# Beräknar E(X)
mean(exponentialfunc(10000))
```

```
## [1] 0.09990761
```

```
# Beräknar Var(X)
var(exponentialfunc(10000))
```

```
## [1] 0.01035301
```

```
# Beräknar E(Y)
mean(poissonfunc(10000))
```

```
## [1] 3.0053
```

```
# Beräknar Var(Y)
var(poissonfunc(10000))
```

```
## [1] 3.014371
```

c)

1. $E(3) = 3$
2. $E(3 * X + 2) = 3 * E(X) + 2 = 3 * 0.1 + 2 = 2.3$
3. $E(X + Y) = E(X) + E(Y) = 0.1 + 3 = 3.1$
4. $E(X * Y) = E(X) * E(Y) = 0.1 * 3 = 0.3$
5. $E(3 * X + 2 * Y - 3) = 3 * E(X) + 2 * E(Y) - 3 = 3 * 0.1 + 2 * 3 - 3 = 3.3$
6. $Var(2 * X - 5) = 2^2 * Var(X) = 4 * 0.01 = 0.04$
7. $Var(X + Y) = Var(X) + Var(Y) = 0.01 + 3 = 3.01$

d)

```
x <- exponentialfunc(10000)
y <- poissonfunc(10000)

#1
mean(3)
```

```
## [1] 3
```

```
#2
mean(3*x+2)
```

```
## [1] 2.2979
```

```r
#3
mean(x+y)
```

```
## [1] 3.1115
```

```r
#4
mean(x*y)
```

```
## [1] 0.299553
```

```r
#5
mean(3*x+2*y-3)
```

```
## [1] 3.3223
```

```r
#6
var(2*x-5)
```

```
## [1] 0.03891135
```

```r
#7
var(x+y)
```

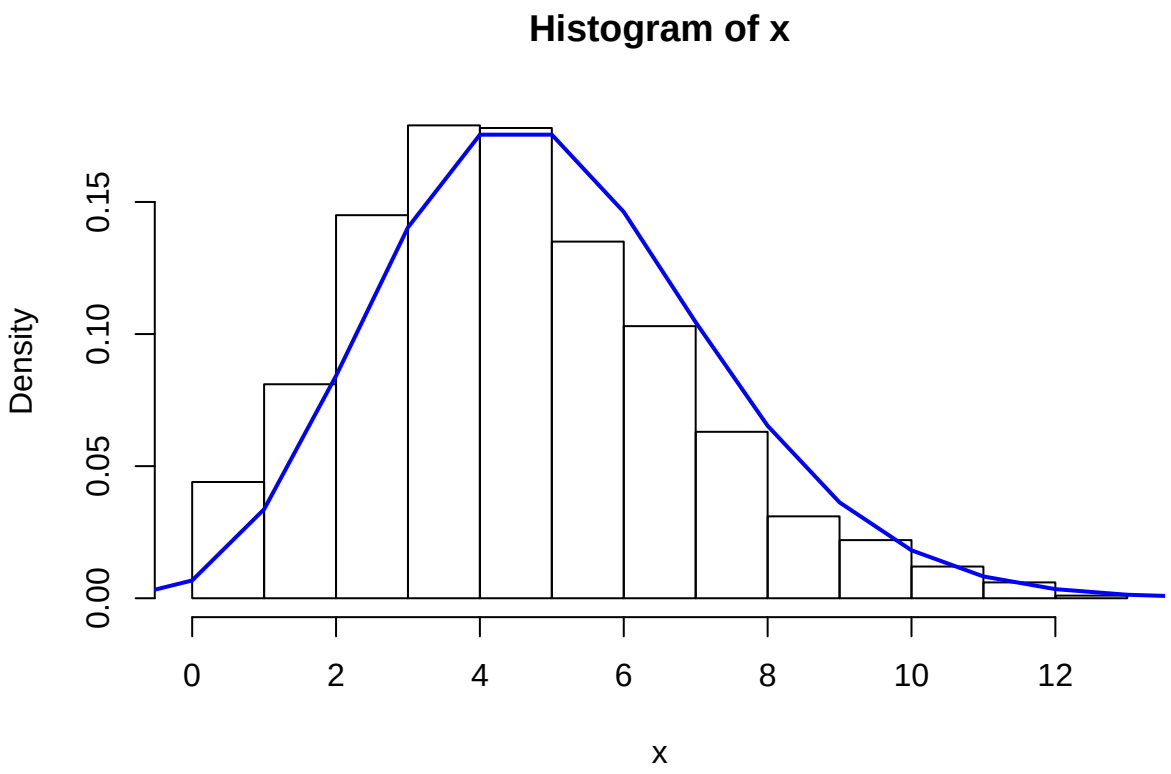
```
## [1] 2.99416
```

Uppgift 10 Centrala gränsvärdessatsen

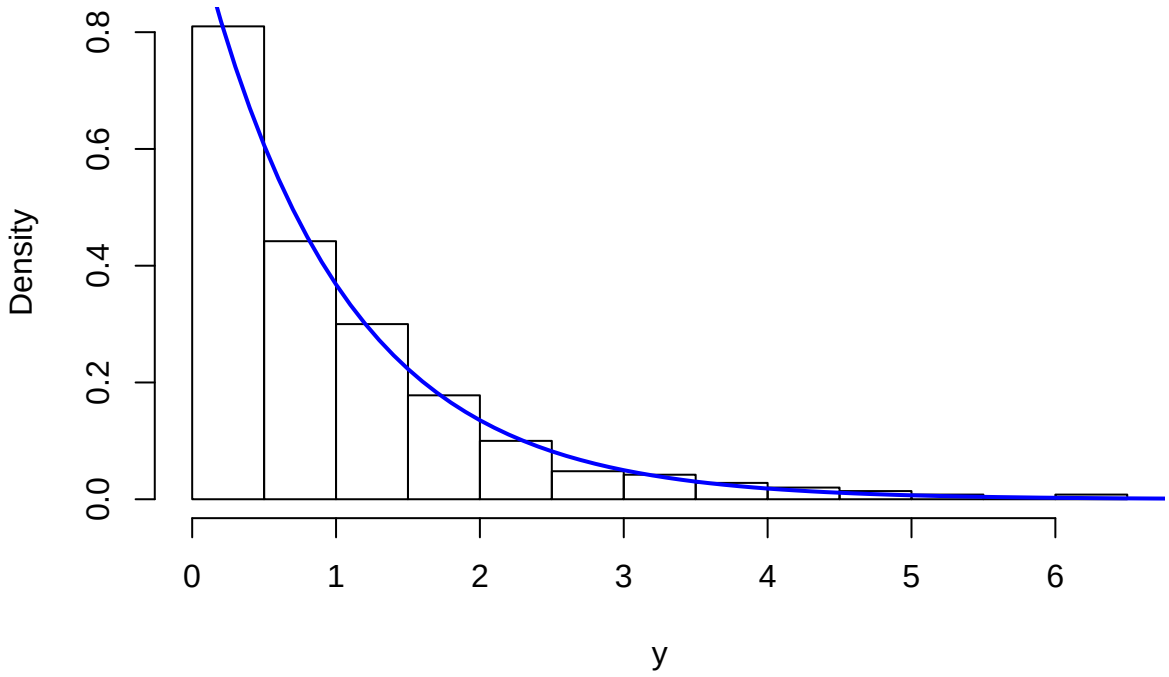
```r
poissonfunc <- function(n) {
  x <- rpois(n, lambda = 5)
  return(x)
}

exponentialfunc <- function(n) {
 y <- rexp(n, rate = 1)
 return(y)
}

binomfunc <- function(n) {
  z <- rbinom(n, size = 10, prob = 0.01)
  return(z)
}
```

a)

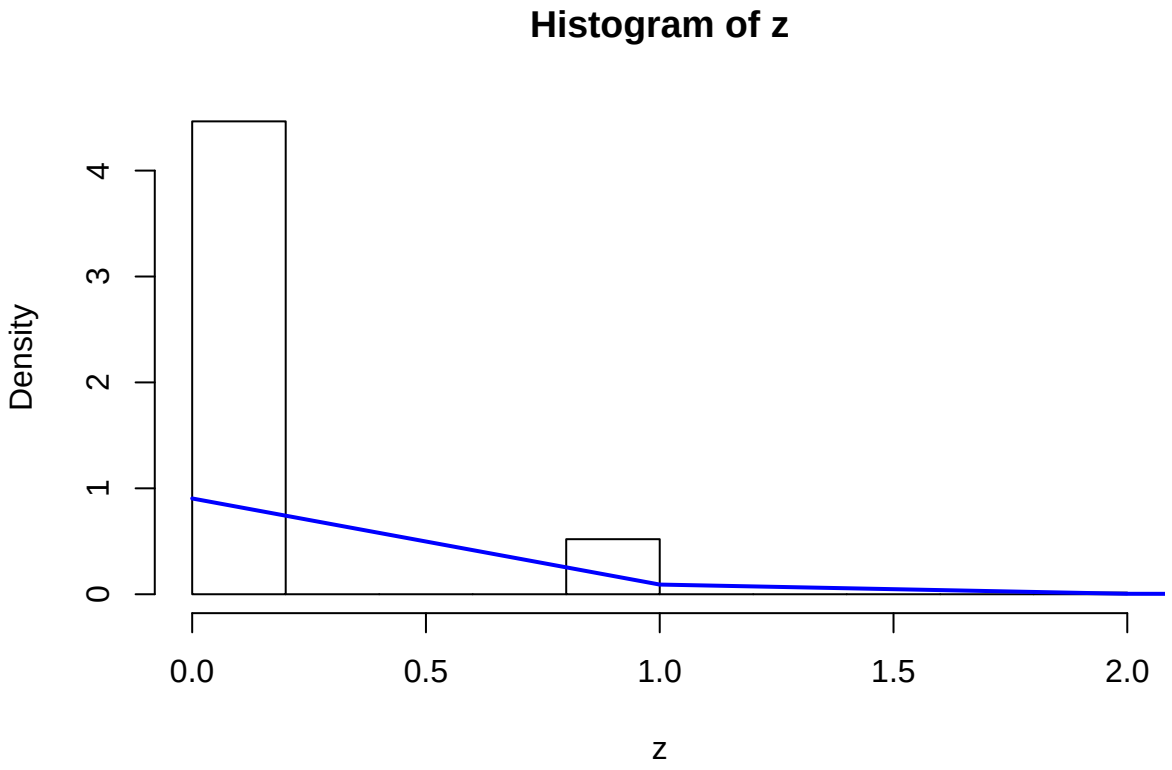
```r
x <- poissonfunc(1000)
hist(x, probability = TRUE)
xfit <- seq(-5, 15, 1)
yfit <- dpois(xfit, lambda = 5)
lines(xfit, yfit, col="blue", lwd=2)
```




```
y <- exponentialfunc(1000)
hist(y, probability = TRUE)
xfit <- seq(0, 10, 0.1)
yfit <- dexp(xfit, 1)
lines(xfit, yfit, col="blue", lwd=2)
```



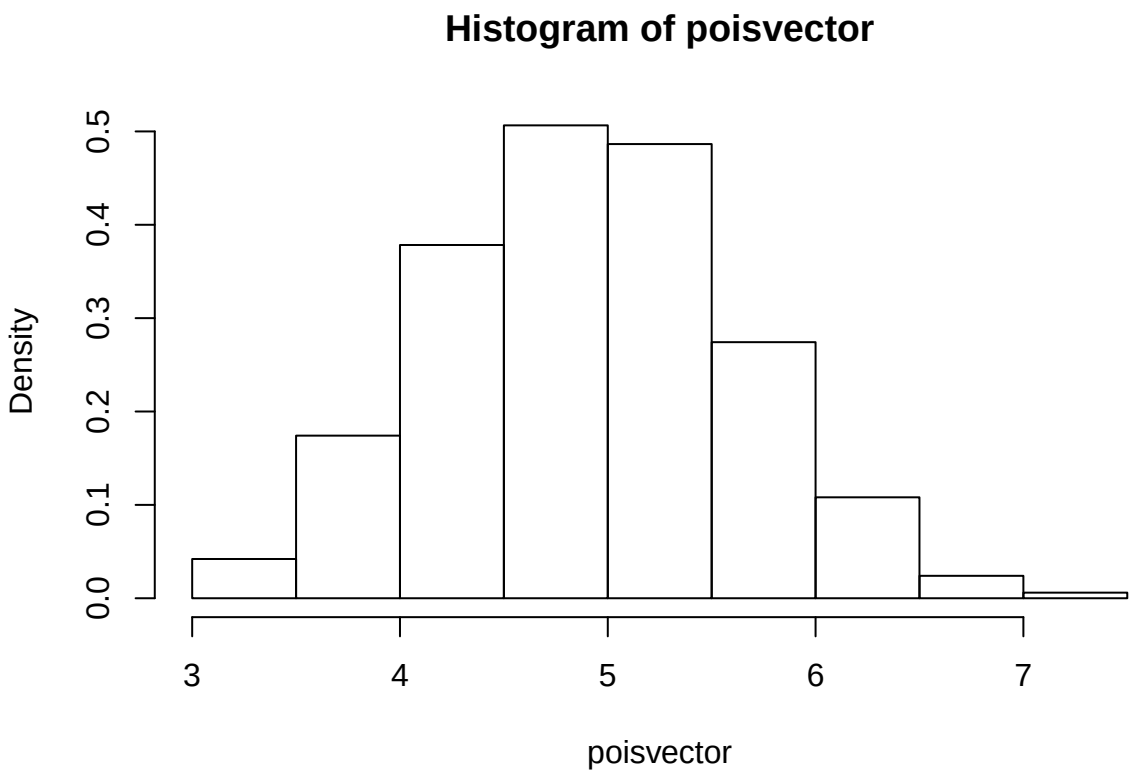

```
z <- binomfunc(1000)
hist(z, probability = TRUE)
xfit <- seq(0, 3, 1)
yfit <- dbinom(xfit, size = 10, prob = 0.01)
lines(xfit, yfit, col="blue", lwd=2)
```



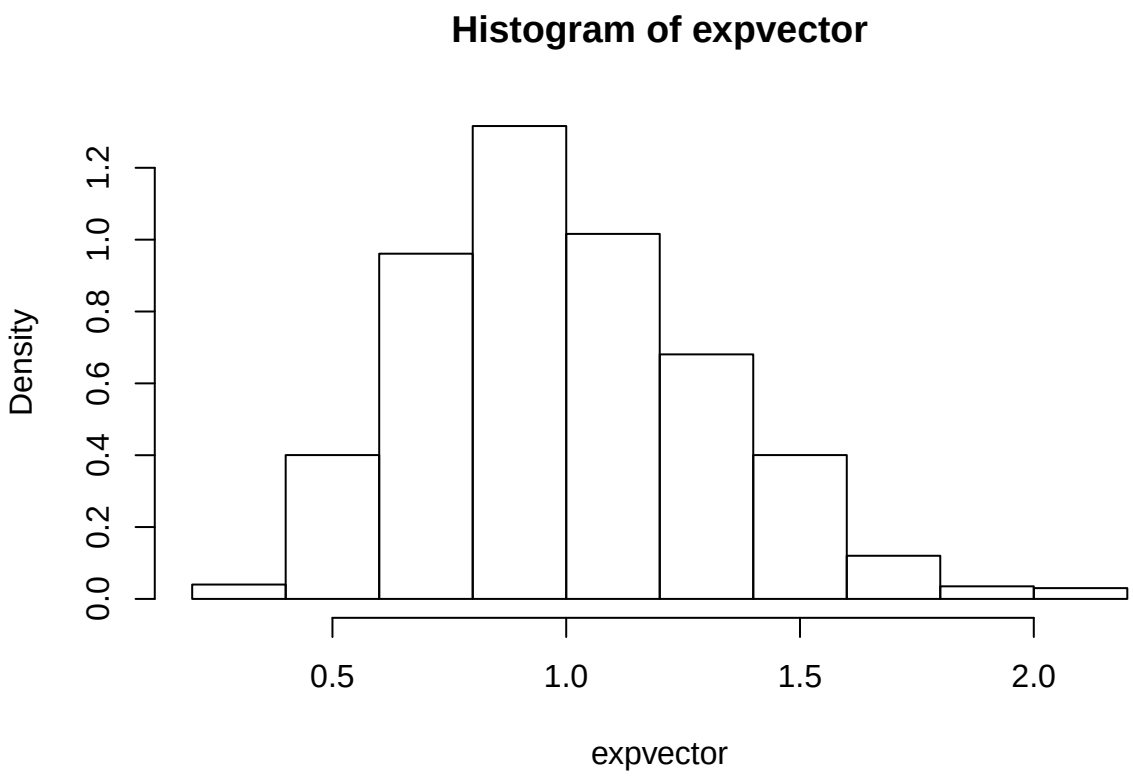
b)

```
poisvector <- c()
expvector <- c()
i = 1
while (i < 1000) {
  poisvector <- c(poisvector, mean(poissonfunc(10)))
  expvector <- c(expvector, mean(exponentialfunc(10)))
  i <- i + 1
}
```

```
hist(poisvector, probability = TRUE)
```



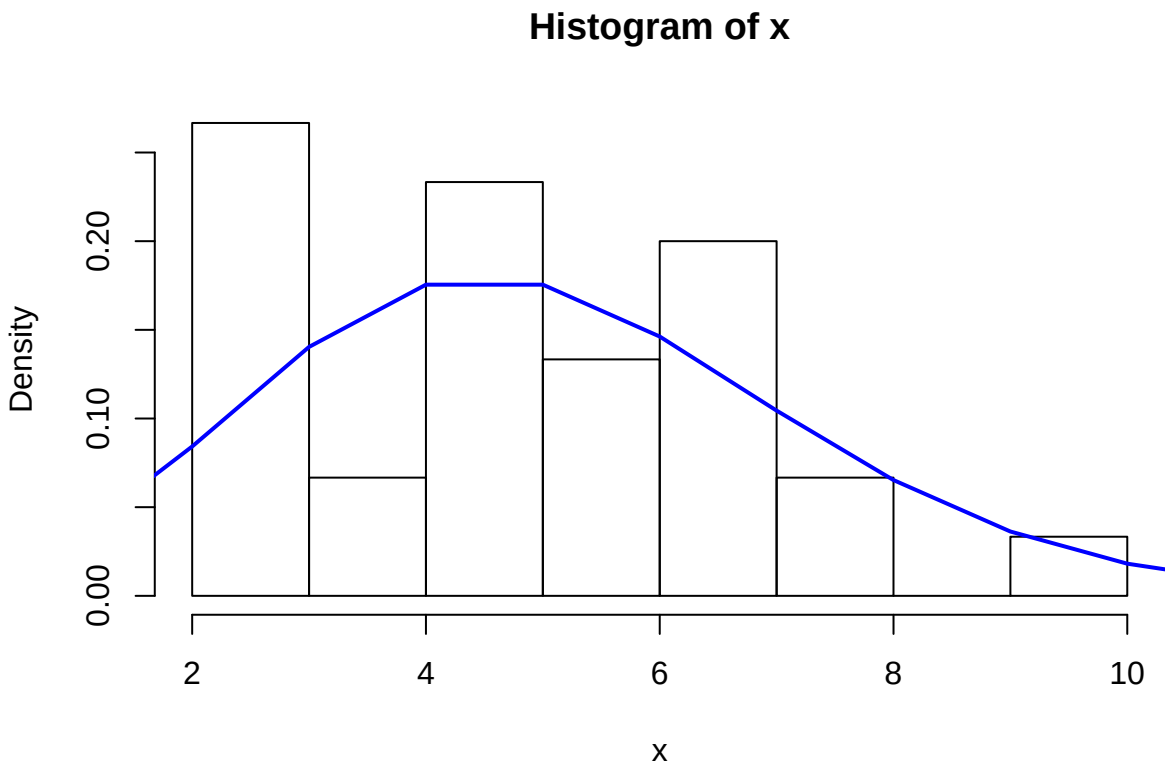

```
hist(expvector, probability = TRUE)
```



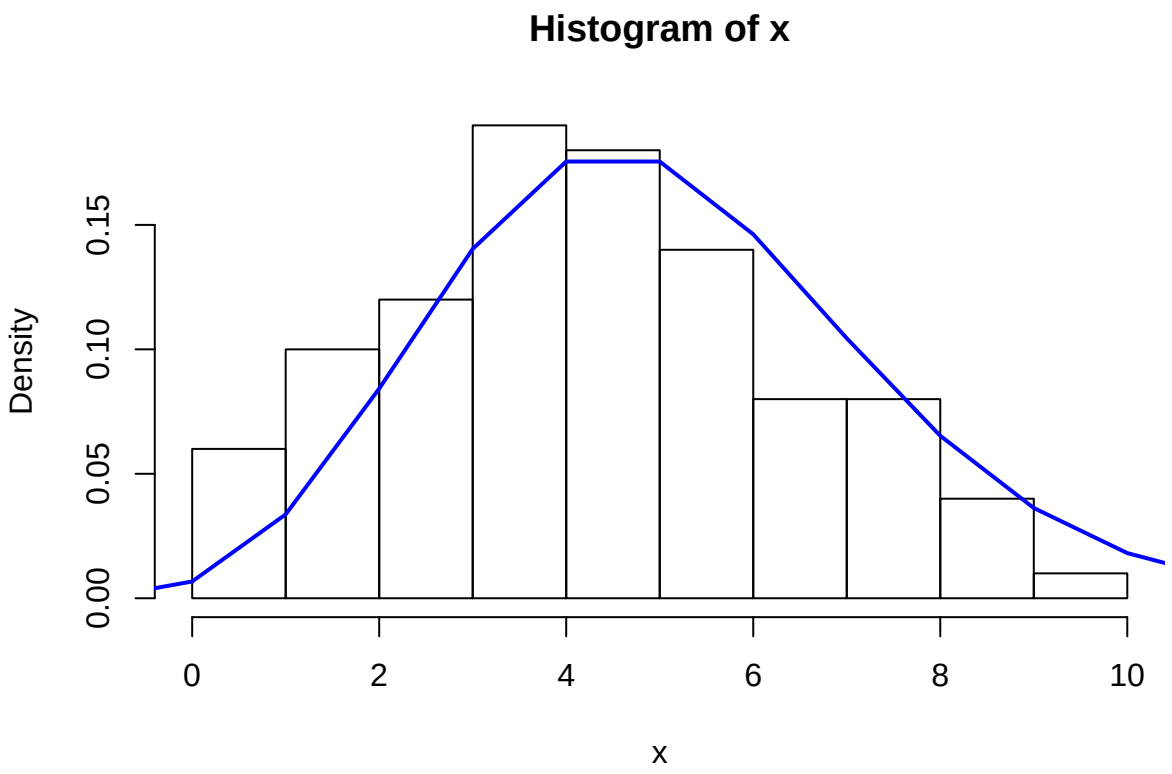
c)

Poisson

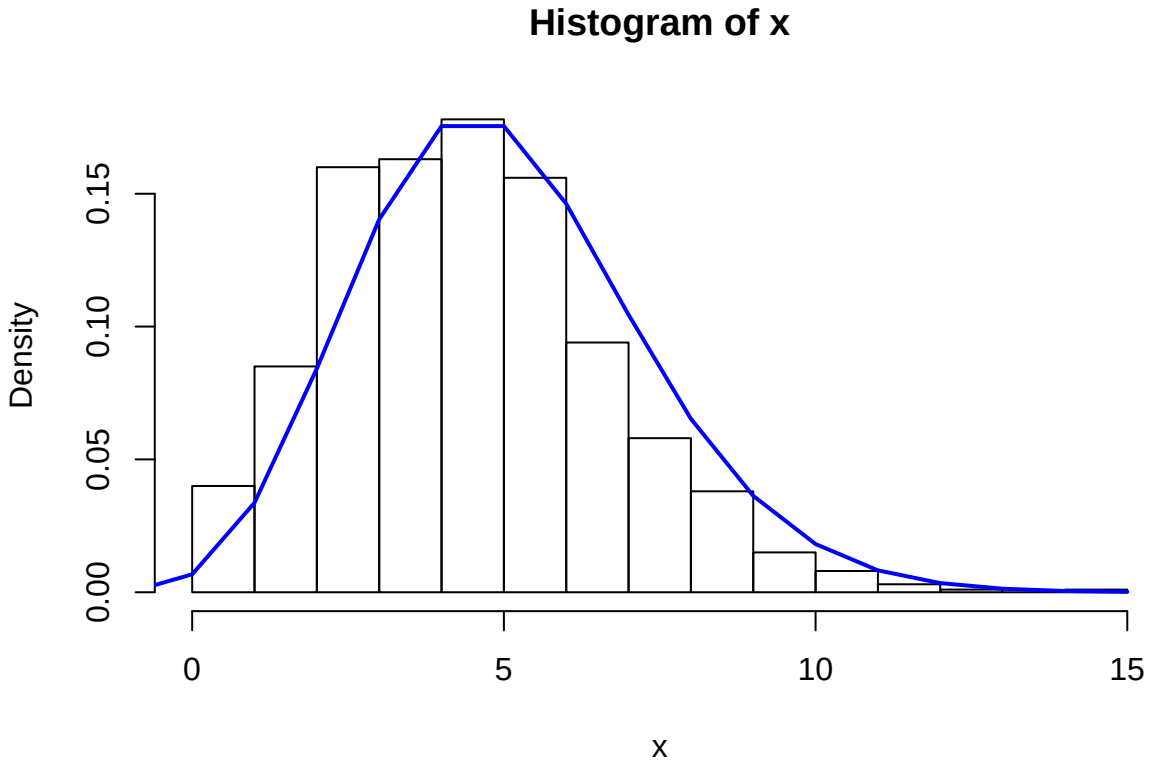
```
x <- poissonfunc(30)
hist(x, probability = TRUE)
xfit <- seq(-5, 15, 1)
yfit <- dpois(xfit, lambda = 5)
lines(xfit, yfit, col="blue", lwd=2)
```




```
x <- poissonfunc(100)
hist(x, probability = TRUE)
xfit <- seq(-5, 15, 1)
yfit <- dpois(xfit, lambda = 5)
lines(xfit, yfit, col="blue", lwd=2)
```

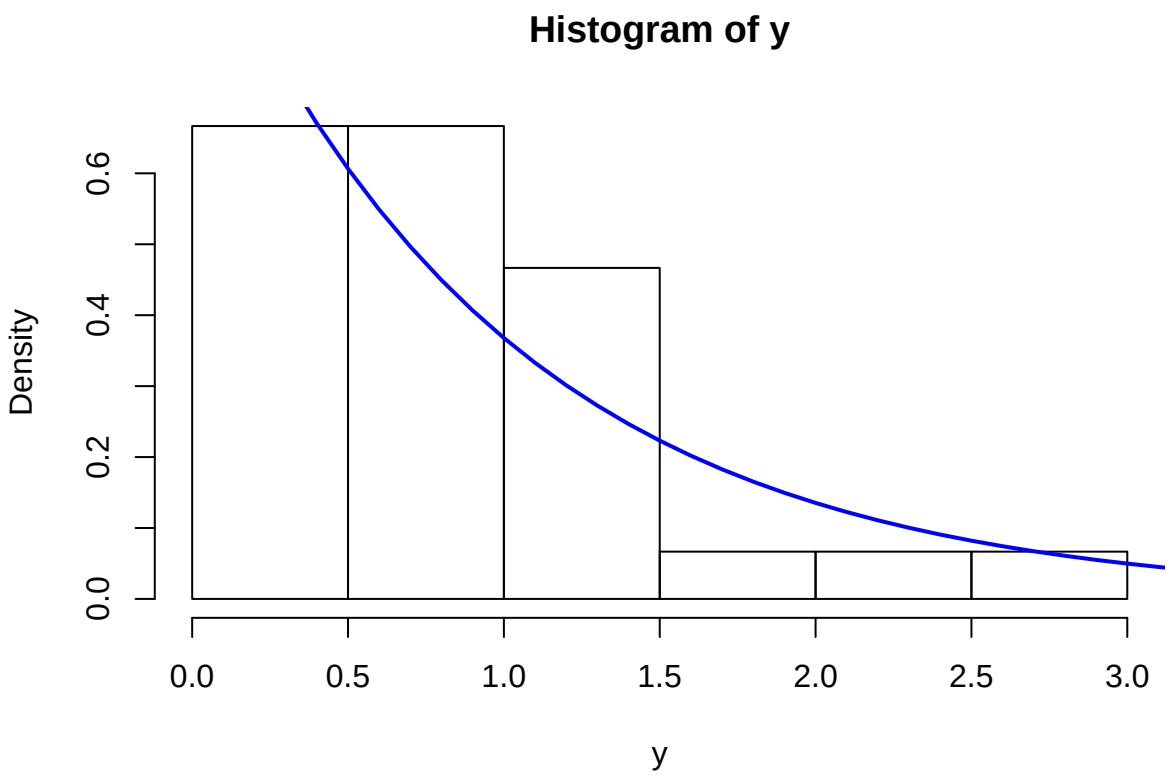



```
x <- poissonfunc(1000)
hist(x, probability = TRUE)
xfit <- seq(-5, 15, 1)
yfit <- dpois(xfit, lambda = 5)
lines(xfit, yfit, col="blue", lwd=2)
```

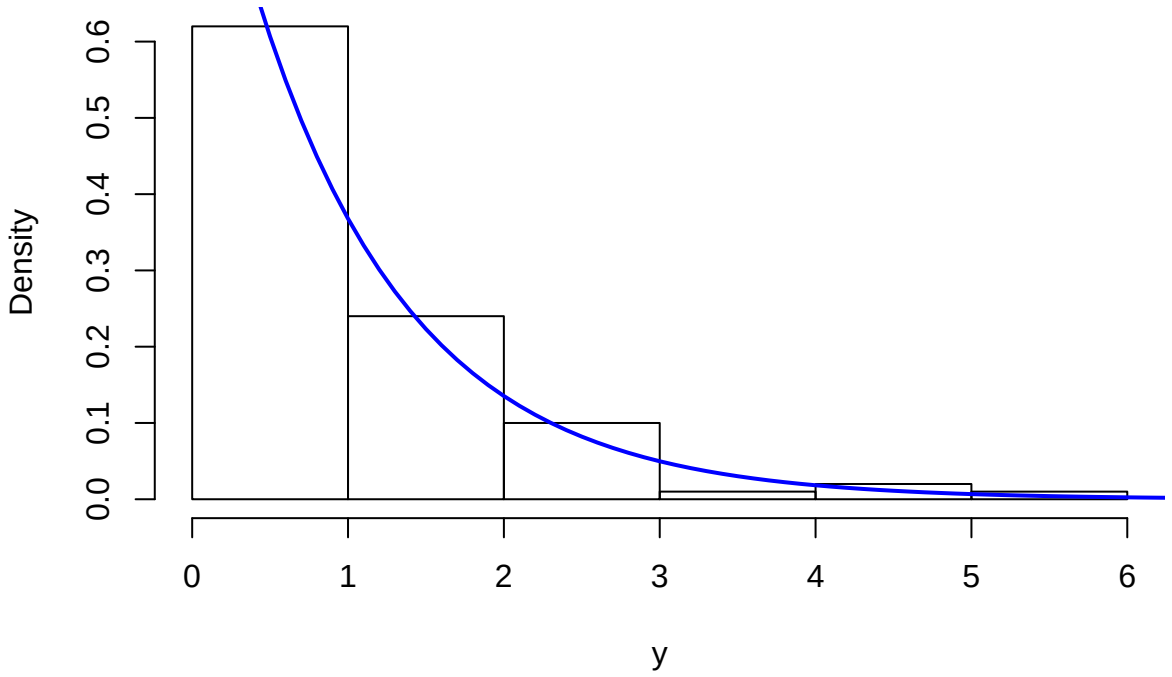


Exponential

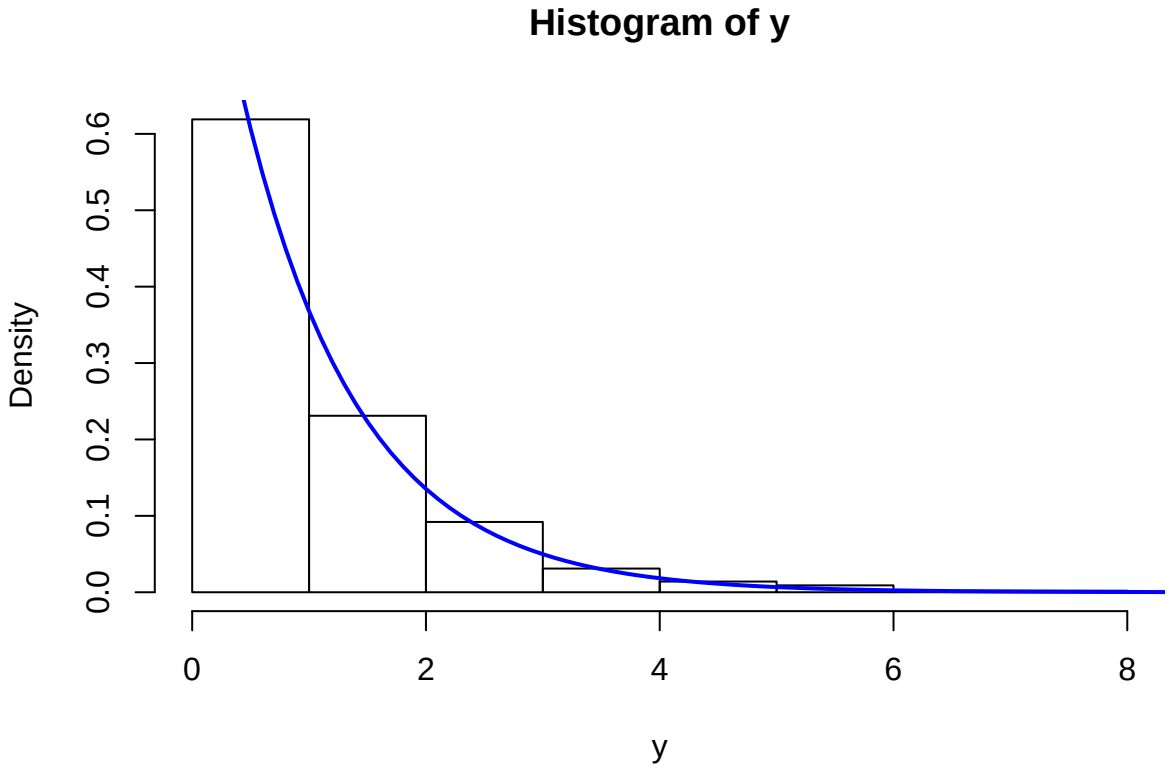
```
y <- exponentialfunc(30)
hist(y, probability = TRUE)
xfit <- seq(0, 10, 0.1)
yfit <- dexp(xfit, 1)
lines(xfit, yfit, col="blue", lwd=2)
```




```
y <- exponentialfunc(100)
hist(y, probability = TRUE)
xfit <- seq(0, 10, 0.1)
yfit <- dexp(xfit, 1)
lines(xfit, yfit, col="blue", lwd=2)
```

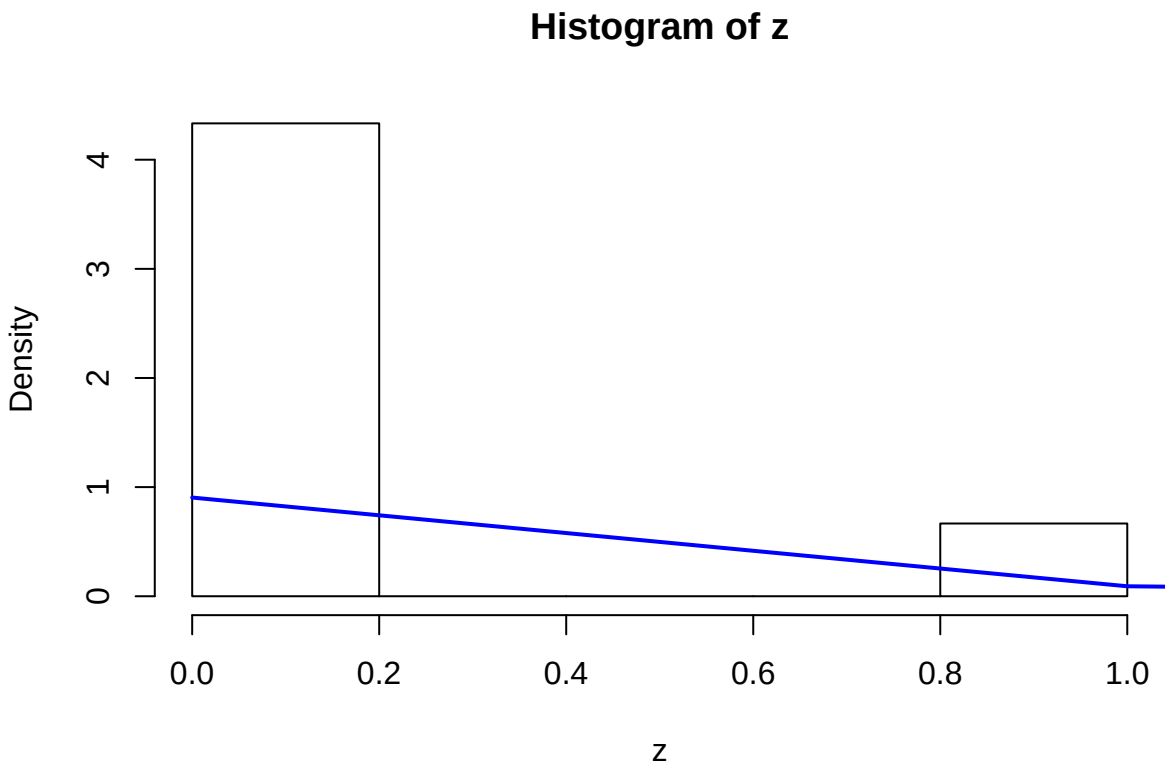



```
y <- exponentialfunc(1000)
hist(y, probability = TRUE)
xfit <- seq(0, 10, 0.1)
yfit <- dexp(xfit, 1)
lines(xfit, yfit, col="blue", lwd=2)
```

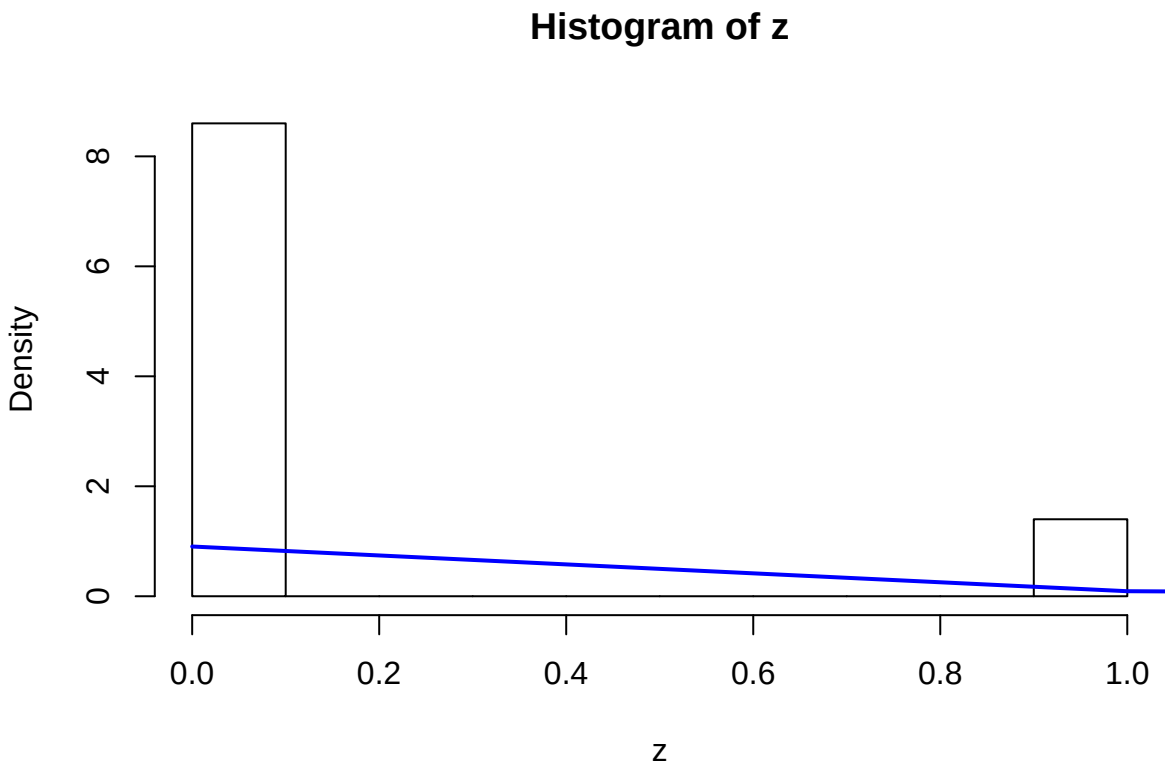


Binomial

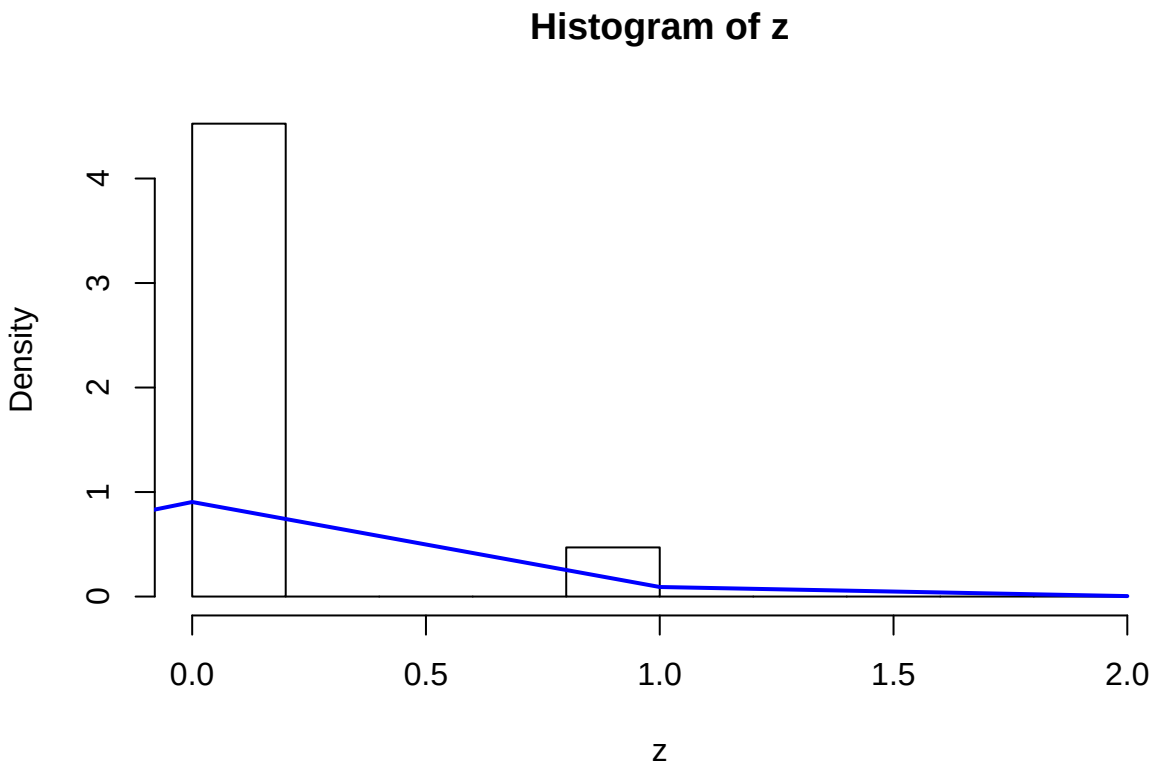
```
z <- binomfunc(30)
hist(z, probability = TRUE)
xfit <- seq(0, 3, 1)
yfit <- dbinom(xfit, size = 10, prob = 0.01)
lines(xfit, yfit, col="blue", lwd=2)
```




```
z <- binomfunc(100)
hist(z, probability = TRUE)
xfit <- seq(0, 3, 1)
yfit <- dbinom(xfit, size = 10, prob = 0.01)
lines(xfit, yfit, col="blue", lwd=2)
```



```r
z <- binomfunc(1000)
hist(z, probability = TRUE)
xfit <- seq(-2, 2, 1)
yfit <- dbinom(xfit, size = 10, prob = 0.01)
lines(xfit, yfit, col="blue", lwd=2)
```



Medelvärdena konvergerar mot en normalfördelning. Då väntevärdena för Y och Z är nära 0 får vi att histogrammen för de bara visar ena halvan av en normalfördelning och inte på ett lika tydligt sätt närmar sig normalfördelningen som X gör. Därmed ser det ut som att X konvergerar snabbast mot normalfördelningen.