# Statistics for Bioinformatics and eScience - Handin 2

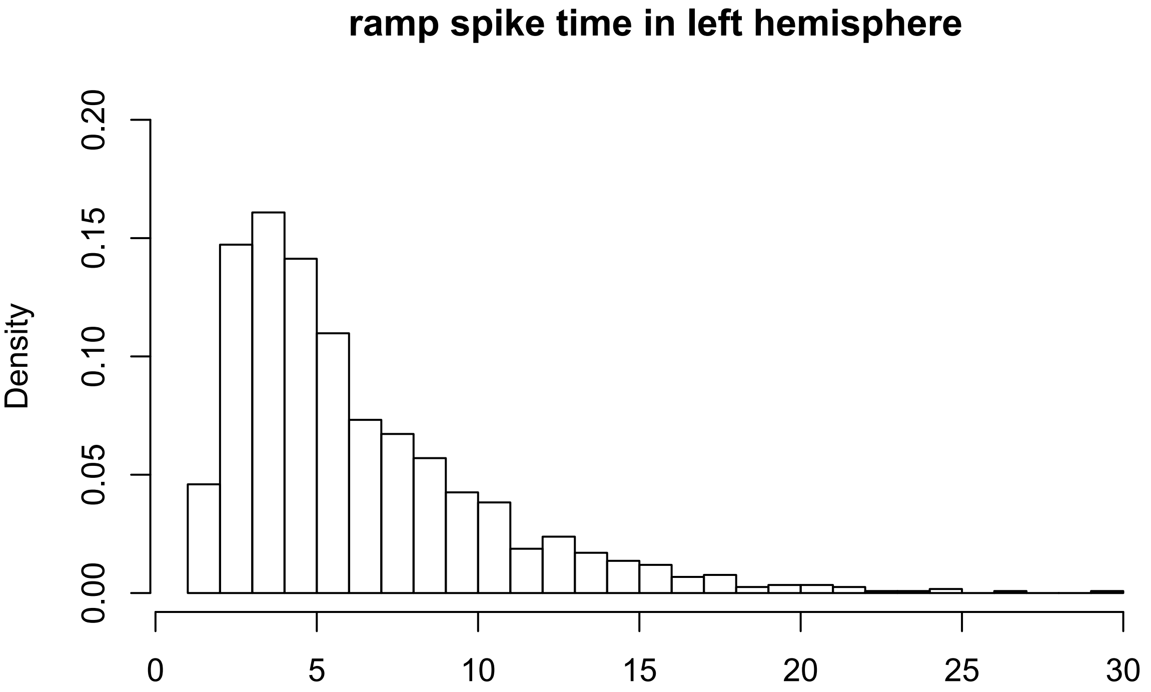
*Group 1*

*12/02/2019*

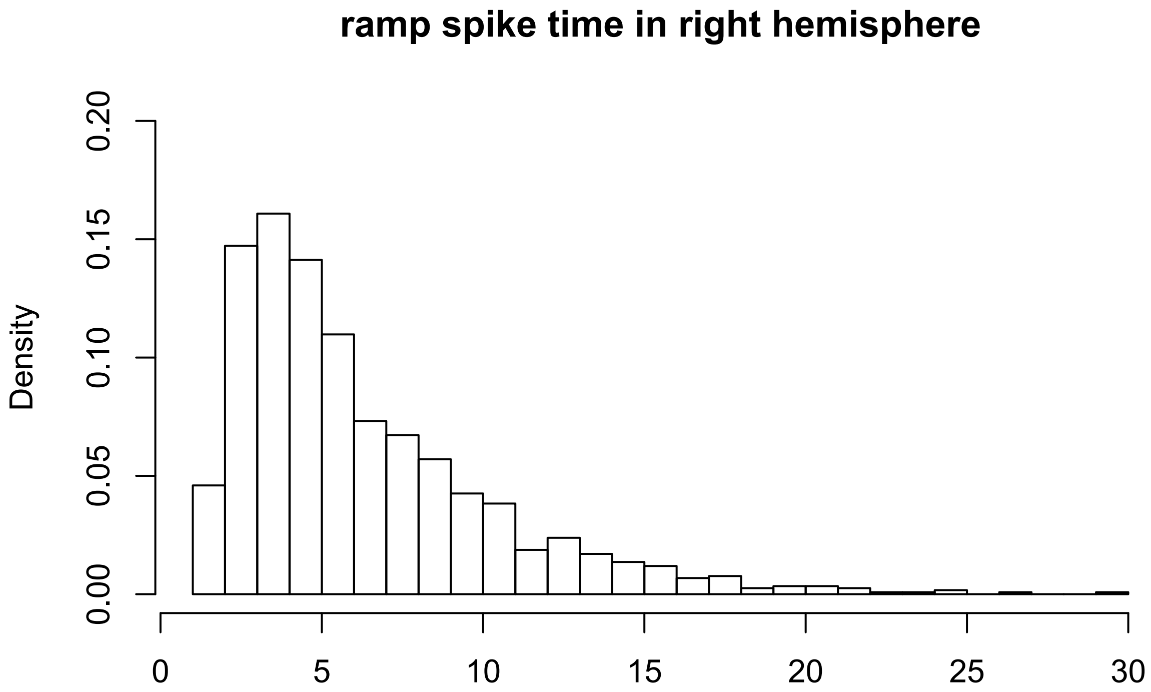
## 1. Brain cell dataset

### 4.1: plot separately histograms for the distribution of the ramp spike time variable in the left and right hemisphere

```r
left_raw <- cells$ef__peak_t_ramp[cells$specimen__hemisphere == "left"]
left <- left_raw[!is.na(left_raw)] # removing NA values again to avoid missing values error

right_raw <- cells$ef__peak_t_ramp[cells$specimen__hemisphere == "right"]
right <- right_raw[!is.na(right_raw)]

hist(left,
     breaks = 40,
     proba = T,
     main = "ramp spike time in left hemisphere", xlab = "", ylim = c(0,0.2))
```

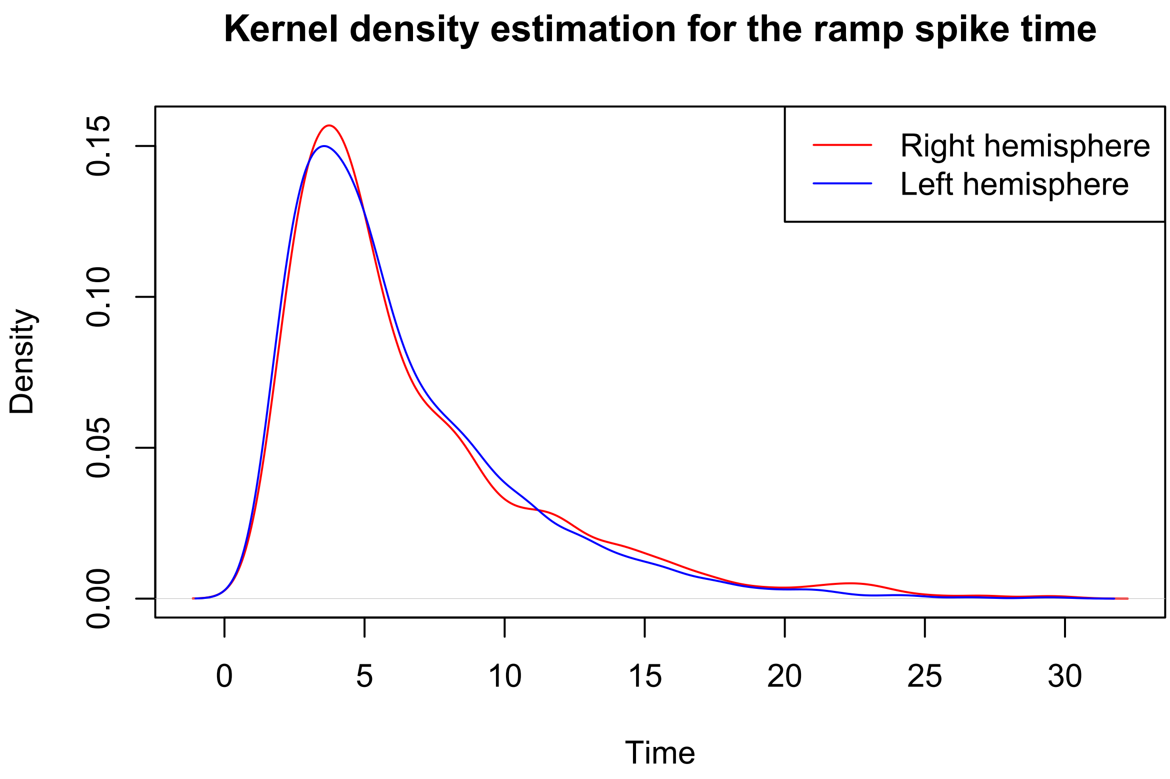


```r
hist(left,
     breaks = 40,
     proba = T,
     main = "ramp spike time in right hemisphere", xlab = "", ylim = c(0,0.2))
```



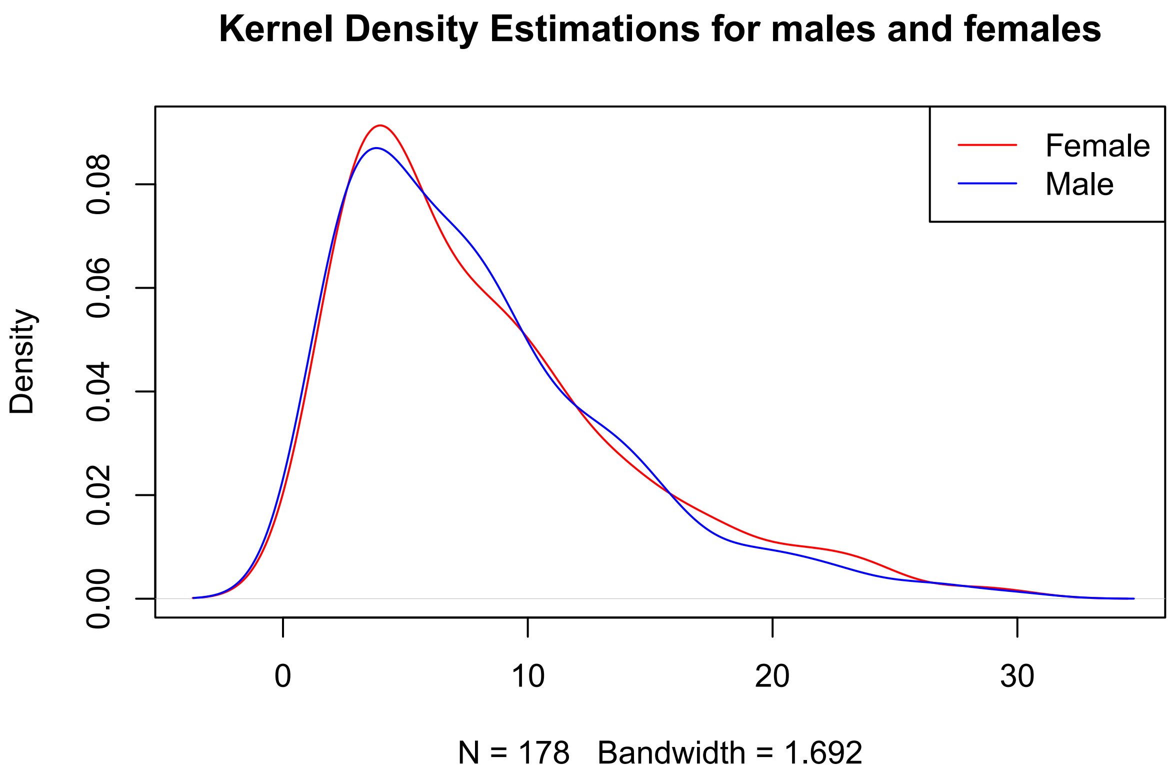
**4.2: plot together kernel density estimations for the ramp spike time variable in the left and right hemisphere.**

```
plot(density(right),
     col = "red",
     main = "Kernel density estimation for the ramp spike time",
     xlab = "Time")
lines(density(left),
      col = "blue")
legend("topright",
       legend = c("Right hemisphere", "Left hemisphere"),
       col = c("red", "blue"),
       lty = 1)
```



**4.3: plot together kernel density estimations for the ramp spike time variable for males and females.**

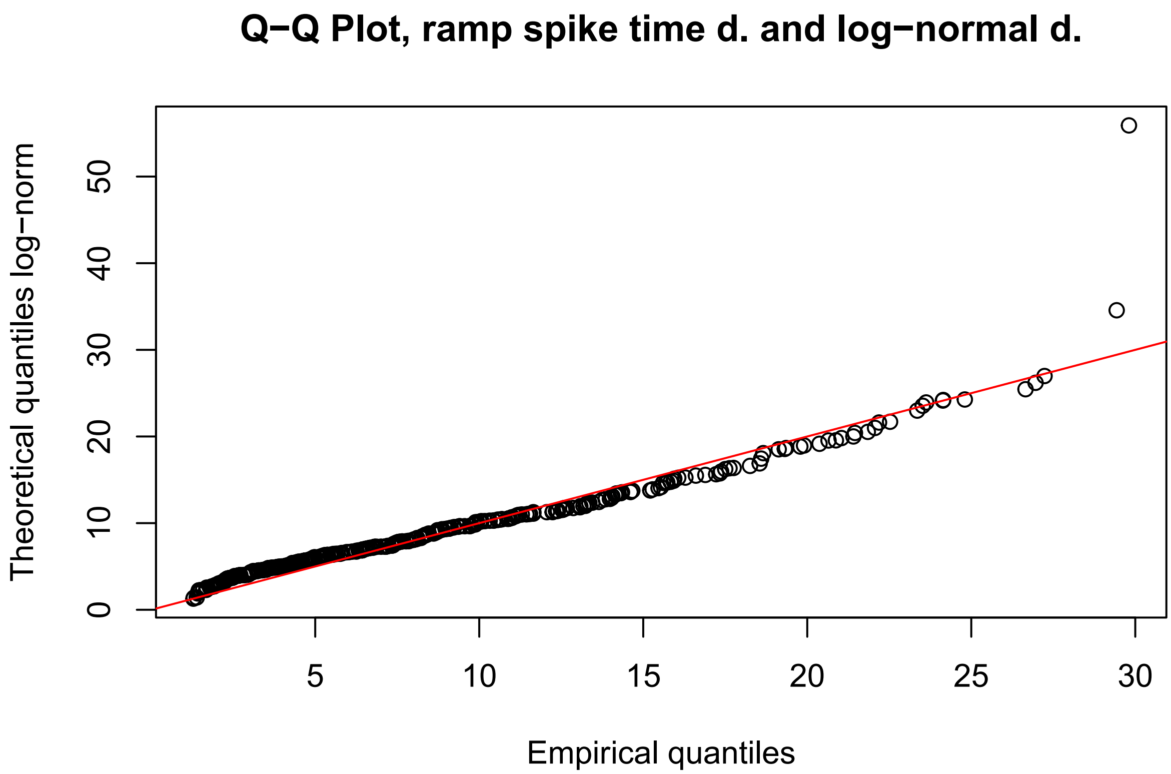
```
female_raw <-
  cells$ef__peak_t_ramp[cells$donor__species == "Homo Sapiens" &
  cells$donor__sex == "Female"]
  female <- female_raw[!is.na(female_raw)]

  male_raw <-
  cells$ef__peak_t_ramp[cells$donor__species == "Homo Sapiens" &
  cells$donor__sex == "Male"]
  male <- male_raw[!is.na(male_raw)]

plot(density(female),
     col = "red",
     main = "Kernel Density Estimations for males and females")
lines(density(male),
      col = "blue")
legend("topright",
       legend = c("Female", "Male"),
       col = c("red", "blue"),
       lty = 1)
```



### Ex 5

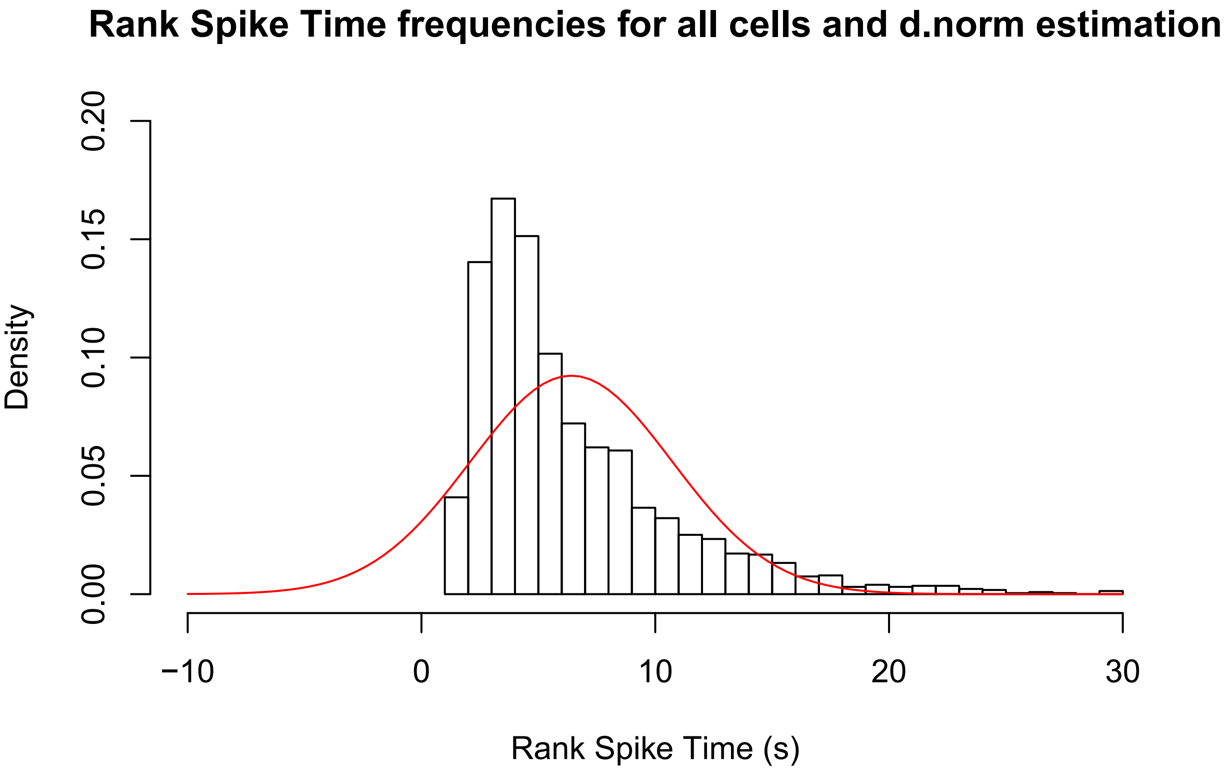
### 5.1: Q-Q plot of ramp spike time distribution for humans, between empirical quantiles and theoretical ones (dlnorm distribution)

```r
humans_raw <- cells$ef__peak_t_ramp[cells$donor__species == "Homo Sapiens"]
humans <- humans_raw[!is.na(humans_raw)]

qqplot(humans,    # qqplot: two "data set" as arg and align quantiles
       rlnorm(ppoints(humans), sdlog = 0.6, meanlog = 2),
       main = "Q-Q Plot, ramp spike time d. and log-normal d.",
       xlab = "Empirical quantiles",
       ylab = "Theoretical quantiles log-norm")
abline(0, 1,
       col = 'red')
```



### 5.2: Plot the Gaussian density on top of the histogram of the ramp spike time with better parameter values

```
allcells <- cells$ef__peak_t_ramp[!is.na(cells$ef__peak_t_ramp)]
hist(allcells,
    breaks = 40,
    ylim = c(0, 0.2),
    xlim = c(-10, 30),
    probability = TRUE,
    main = "Rank Spike Time frequencies for all cells and d.norm estimation",
    xlab = "Rank Spike Time (s)")
curve(dnorm(x, mean = 6.41, sd = 4.32),
      col = "red",
      add = TRUE)
```

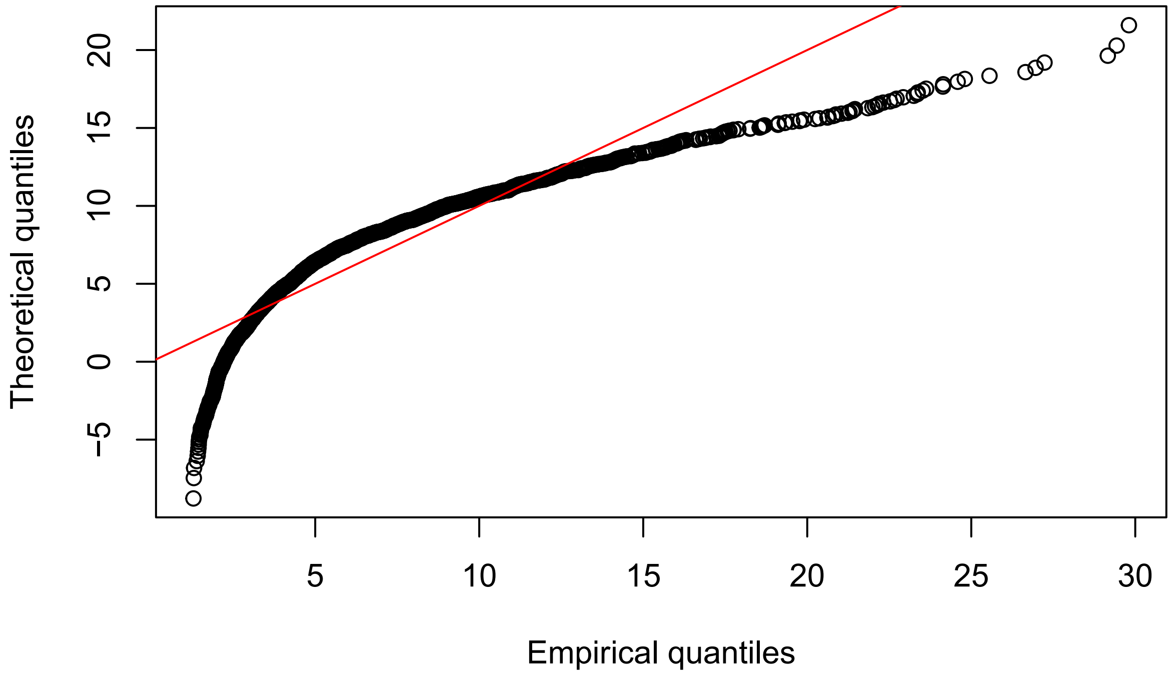


>

Our data daesnt have a left tail and the peak of the histogram is much larger than the curve of the norm distribution.

### 5.3: Q-Q plot for the ramp spike time against the Gaussian distribution with these new parameter values

```
theoretical_spike_q <- qnorm(ppoints(allcells), sd = 4.32, mean = 6.41)
plot(sort(allcells), theoretical_spike_q,
     xlab = "Empirical quantiles",
     ylab = "Theoretical quantiles")
abline(0, 1,
       col = "red")
```



We can visually observe that our data don't follow a Gaussian distribution since several quantiles in the tails don't match in the diagonal.

## 2. Empirical mean and variance

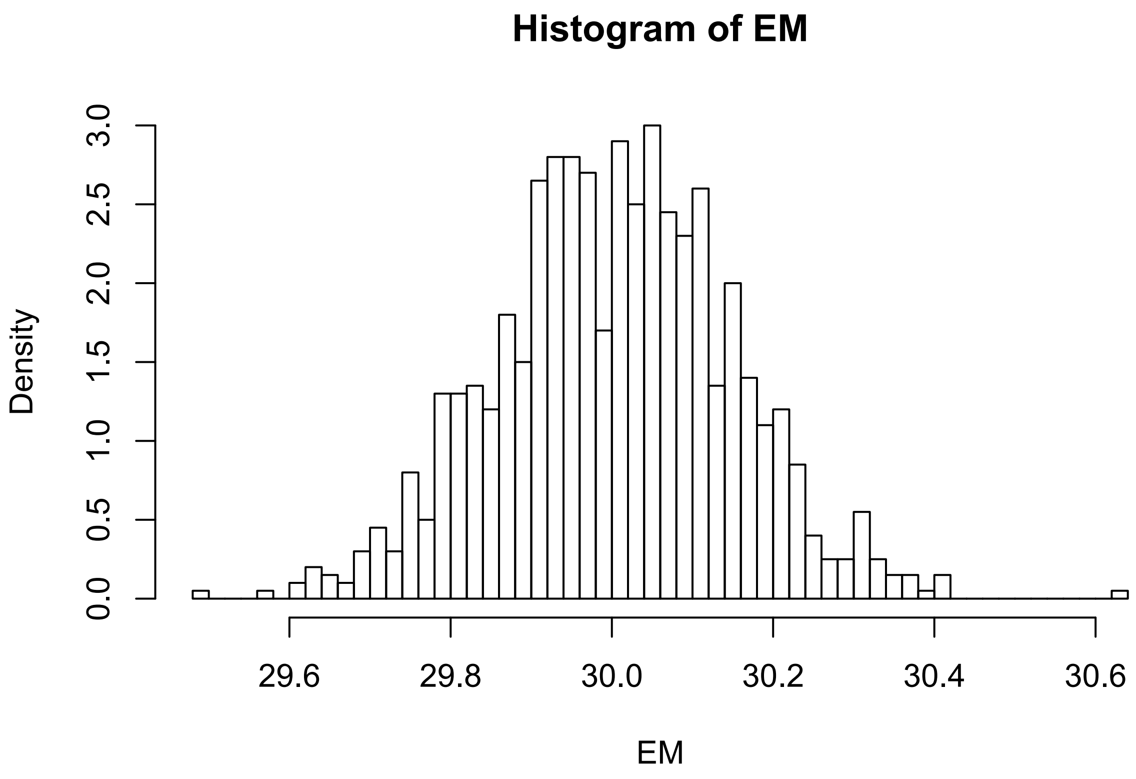
### 6.1: Sample n values of X ~ Bi(parameter size = 100, prob = 0.3) for n = 10, 100, 1000, 1000.

```
n = 100       # n. of experiments (size or i.e. nb of coin tosses)
p = 0.3       # p. of success (i.e. head)
EM = c()
EV = c()
Esd = c()
rep = c()
for (x in c(10, 100, 1000, 10000)){      # x = nb of sampling repetitions
  sample <- rbinom(x, size = n, prob = p)
  EM <- c(EM, mean(sample))                # empirical mean
  EV <- c(EV, var(sample))                 # empirical variance
  Esd <- c(Esd, sd(sample))                # empirical standard deviation
  rep <- c(rep, x)                         # n. of sampling repetition
}
mean <-  n * p                         # true or theoretical mean
var <-  n * p * (1-p)                  # true or theoretical variance
sd <-  sqrt(var)                       # true or theoretical standard deviation

data.frame(EM, mean, EV, var, Esd, sd,
           row.names = rep)
```

```
##             EM mean       EV var      Esd        sd
## 10    31.7000   30 16.67778  21 4.083844 4.582576
## 100   30.1700   30 25.07182  21 5.007177 4.582576
## 1000  29.6420   30 19.52536  21 4.418751 4.582576
## 10000 30.0292   30 21.11006  21 4.594568 4.582576
```

### 6.2: Write a function to repeat the sampling and estimation for n = 1000 and plot.

```
samp_est_f <- function(nb_rep){
  nb_trials = 100
  p = 0.3
  EM = c()
  EV = c()
  Esd = c()
  for (i in 1:1000){
    sample <- rbinom(nb_rep, size = nb_trials, prob = p)
    EM <- c(EM, mean(sample))   # that's an easy way to "append" values to a vector
  }

  hist(EM,
       probability = TRUE,
       breaks = 50)           # histogram of the distribution of the empirical means

  data = list()               # list to store the output of the function

  data$EM <- EM                # means distributions for 6.4
  data$sample <- sample        # the last sample generated
  data$rep <- nb_rep           # n. of repetition
  data$var_EM <- var(EM)       # (emp.) variance of empirical/sample means
  data$sd_EM <- sd(EM)         # (emp.) standard deviation of the empirical/sample means

  cat("rep:", data$rep, # cat() to print numbers and strings in the same line
      ", var_EM:", data$var_EM,
      ", sd_EM:", data$sd_EM)
  return(data)
}

data <- samp_est_f(1000)
```



```
## rep: 1000 , var_EM: 0.0214498 , sd_EM: 0.1464575
```

### 6.3: Compute the standard error of the mean

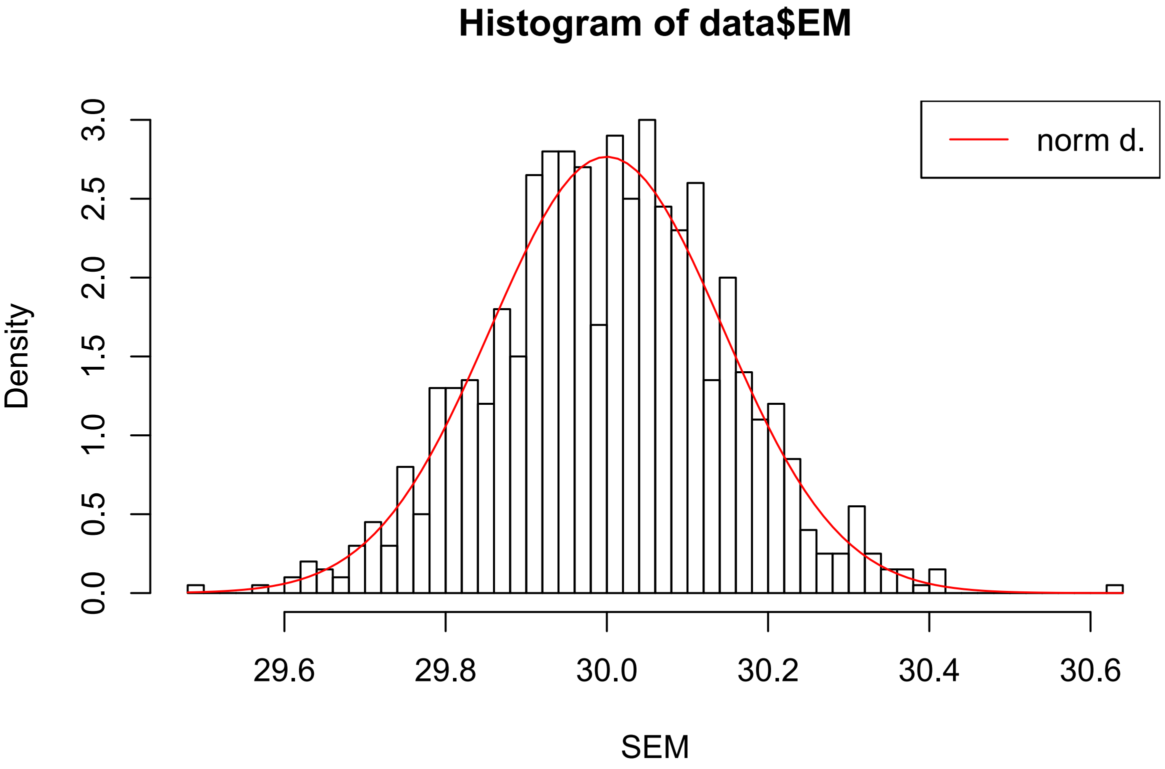
```
SEM_f <- function(x){
  SEM <- (sd(data$sample) / sqrt(length(data$sample) - 1))
  return(SEM)
}
data$SEM <- SEM_f(1000)
cat("sd_EM:", data$sd_EM, ", SEM:", data$SEM)
```

```
## sd_EM: 0.1464575 , SEM: 0.1442269
```

```
# SEM = ESTIMATOR of the error between the sample means and the population mean
# sd_EM = standard deviation of the sample means
```

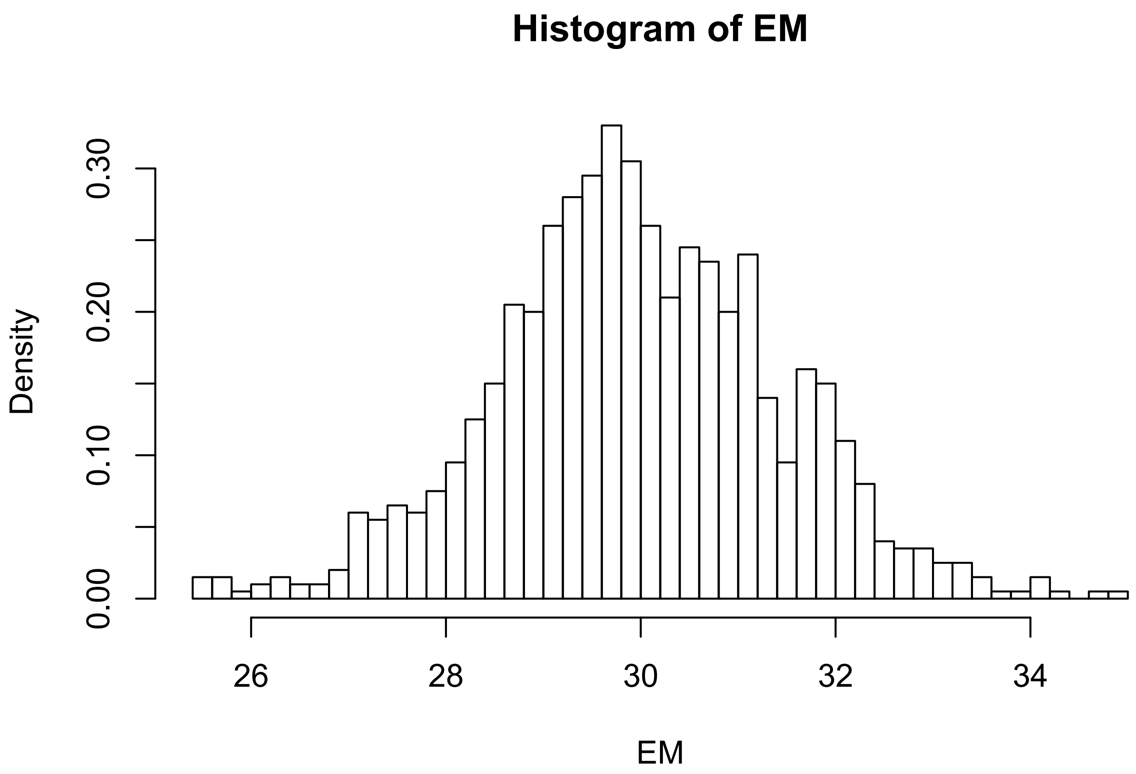
### 6.4: draw the density of Gaussian distribution with parameters mean $= 100 \times 0.3$ and sd equal to the sem

```
plot_f <- function(x){
  hist(data$EM,
       probability = TRUE,
       breaks = 50,
       xlab = "SEM")
  curve(dnorm(x, mean = 100 * 0.3, sd = data$SEM),
        col = "red",
        add = TRUE)
  legend("topright",
         legend = "norm d.",
         col = "red",
         lty = 1)
}
plot_f(1000)
```



**check the result for different values of x:**

```
data_10 <- samp_est_f(10)
```



```
## rep: 10 , var_EM: 2.140837 , sd_EM: 1.46316
```

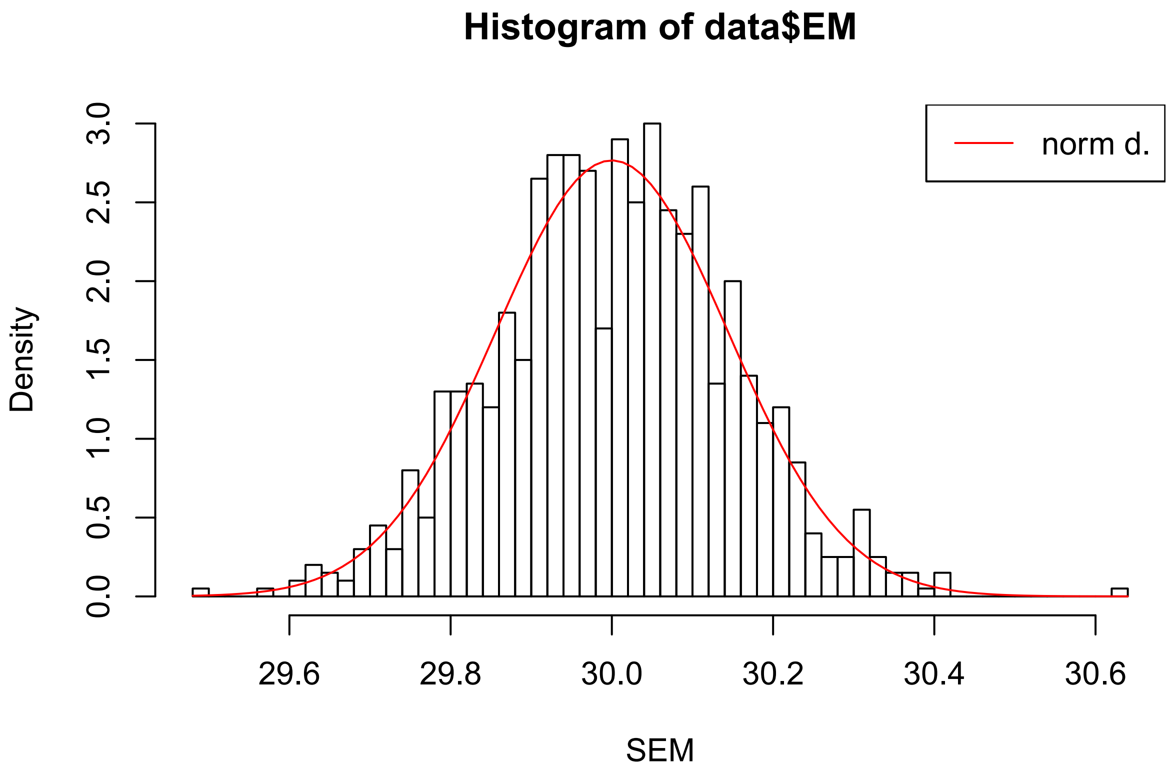
```
data_10$SEM <- SEM_f(10)
cat("rep:", data_10$rep,
    ", var_EM:", data_10$var_EM,
    ", sd_EM:", data_10$sd_EM)
```

```
## rep: 10 , var_EM: 2.140837 , sd_EM: 1.46316
```

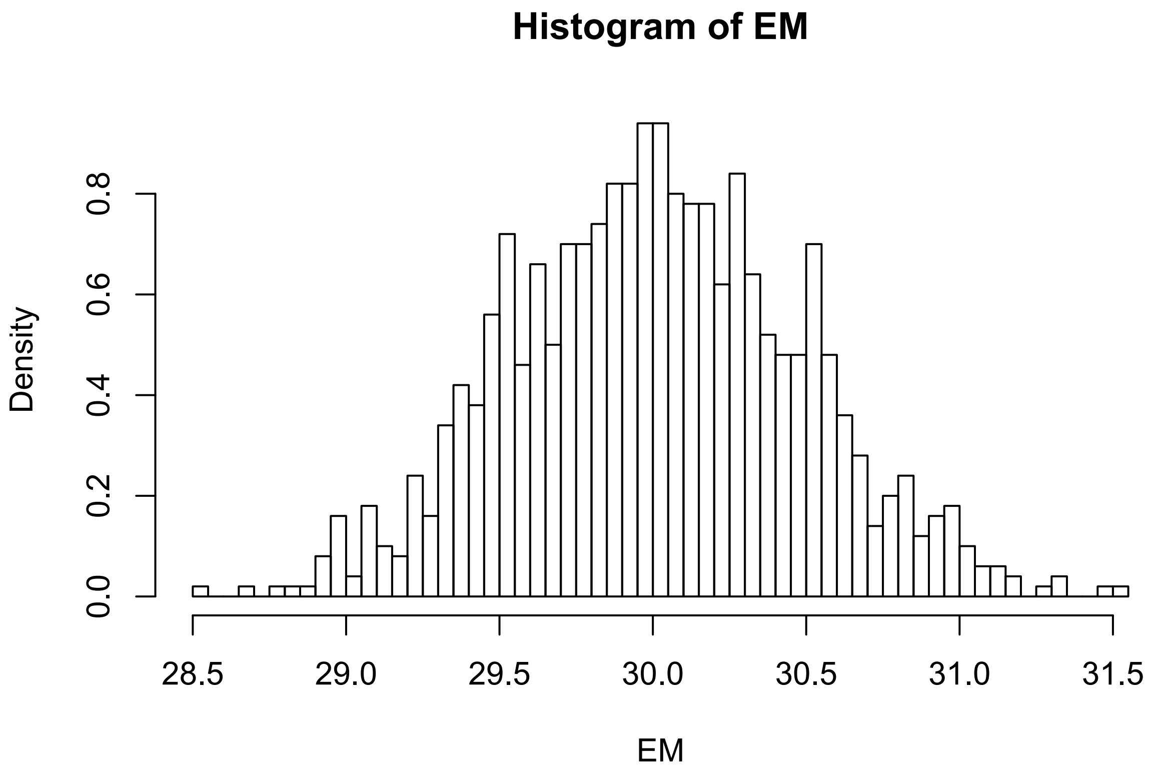
```
cat("sd_EM:", data_10$sd_EM, ", SEM:", data_10$SEM)
```

```
## sd_EM: 1.46316 , SEM: 0.1442269
```

```
plot_f(10)
```



```
data_100 <- samp_est_f(100)
```



```
## rep: 100 , var_EM: 0.2215541 , sd_EM: 0.4706954
```

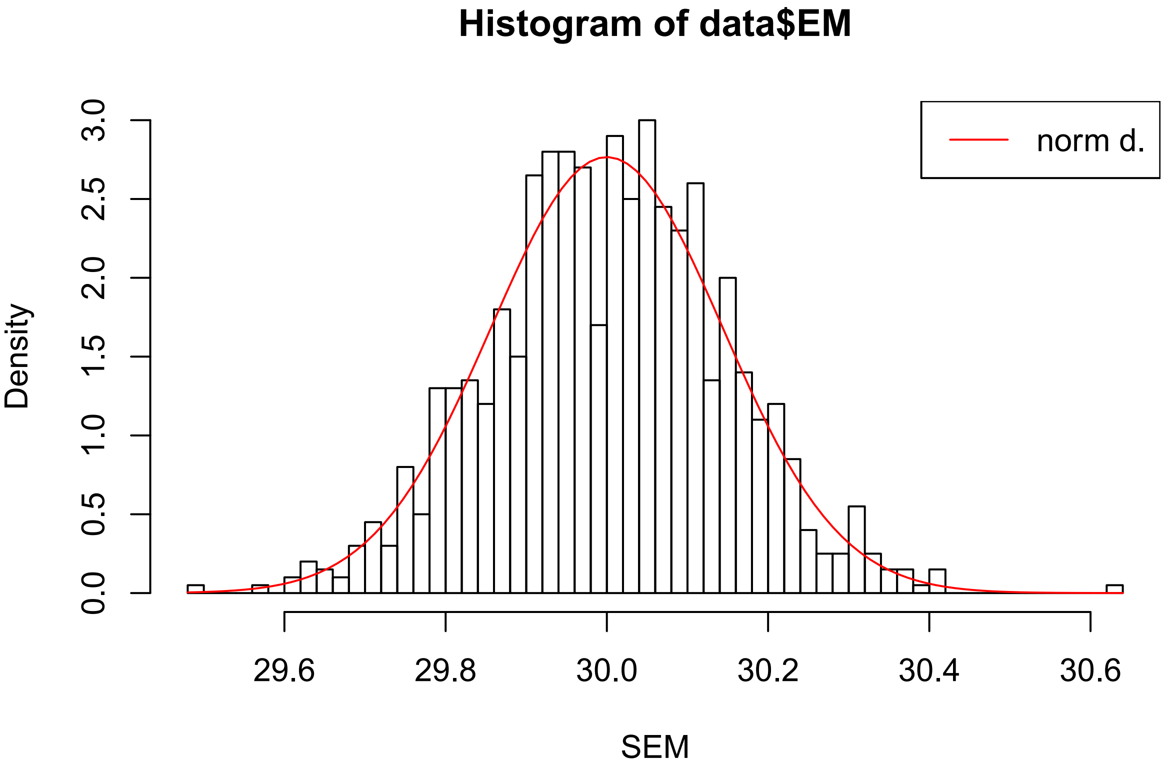
```
data_100$SEM <- SEM_f(100)
cat("rep:", data_100$rep,
    ", var_EM:", data_100$var_EM,
    ", sd_EM:", data_100$sd_EM)
```

```
## rep: 100 , var_EM: 0.2215541 , sd_EM: 0.4706954
```

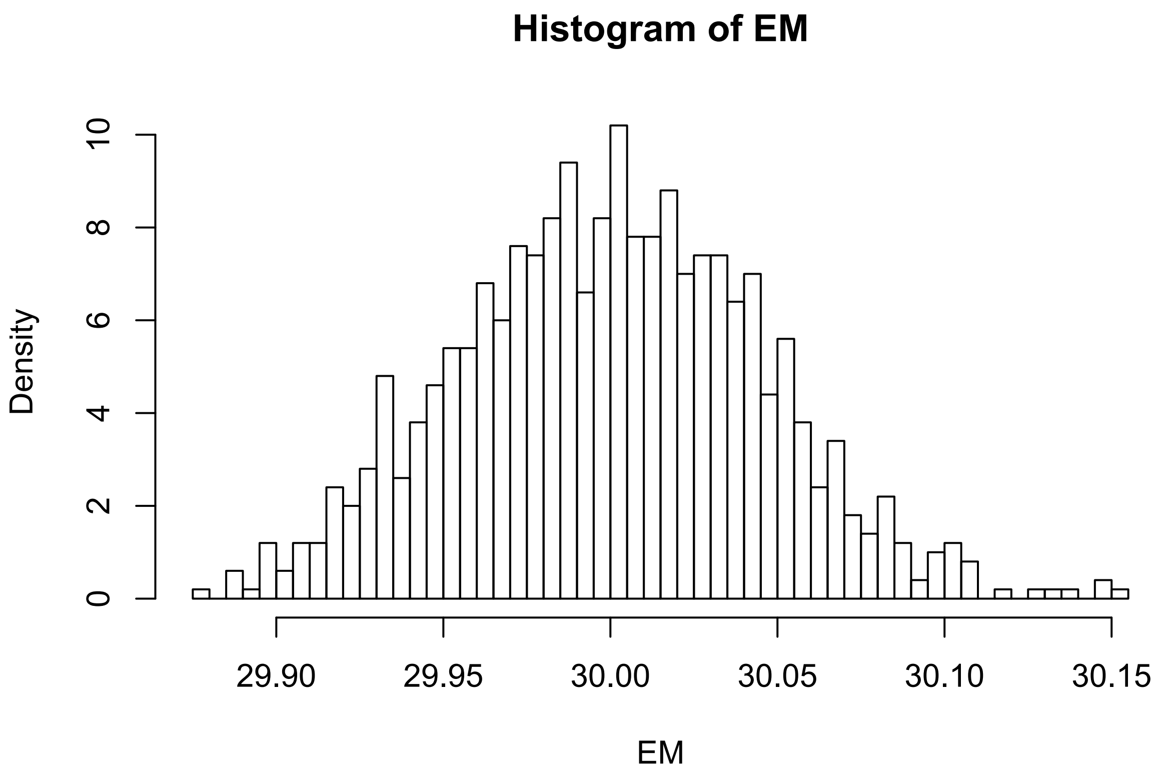
```
cat("sd_EM:", data_100$sd_EM, ", SEM:", data_100$SEM)
```

```
## sd_EM: 0.4706954 , SEM: 0.1442269
```

```
plot_f(100)
```



```
data_10000 <- samp_est_f(10000)
```



```
## rep: 10000 , var_EM: 0.002062334 , sd_EM: 0.04541293
```

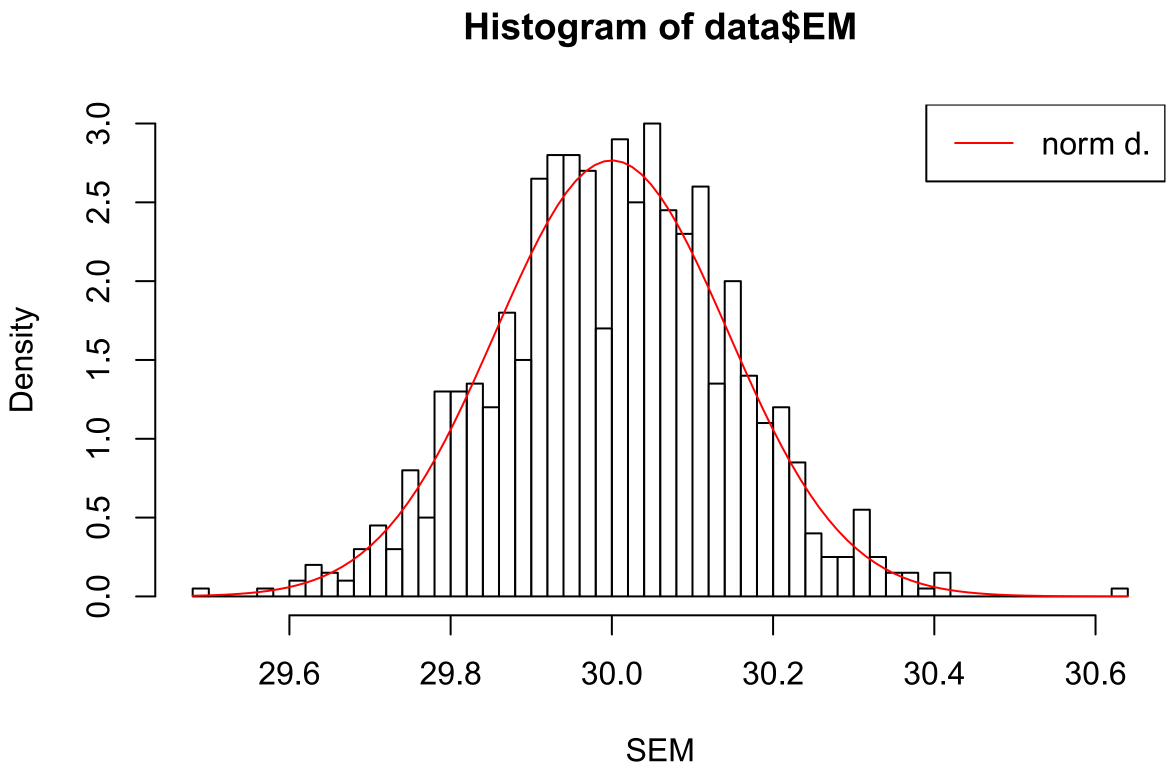
```
data_10000$SEM <- SEM_f(10000)
cat("rep:", data_10000$rep,
    ", var_EM:", data_10000$var_EM,
    ", sd_EM:", data_10000$sd_EM)
```

```
## rep: 10000 , var_EM: 0.002062334 , sd_EM: 0.04541293
```

```
cat("sd_EM:", data_10000$sd_EM, ", SEM:", data_10000$SEM)
```

```
## sd_EM: 0.04541293 , SEM: 0.1442269
```

```
plot_f(10000)
```


Histogram of data$EM
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
29.6
29.8
30.0
30.2
30.4
30.6
SEM
norm d.