

Distribution_of_MV_Test_Statistics

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```
library(ggplot2)
library(mvtnorm)
library(MASS)

#when sigma is known

mu <- c(0,0) # true population mean (mu_0)
V <- matrix(c(16,7,7,4), nrow = 2, ncol = 2, byrow = TRUE) # true cov matrix

## simulating the distribution

# Sample size
n <- 30

# number of samples
sample.reps <- 1000

#test statistics array
ts.arr <- c()

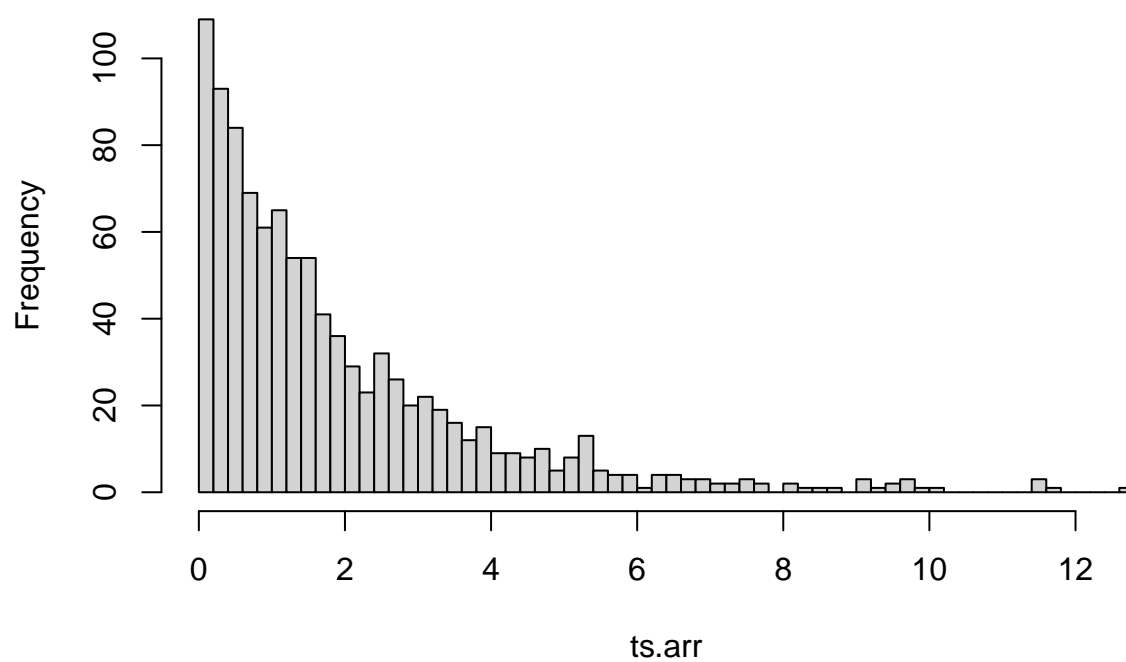
for(i in 1:sample.reps){
  # generate a sample size n
  sample.data <- as.data.frame(rmvnorm(n, mean=mu, sigma = V))
  #calculate the sample mean
  sample.x.bar <- colMeans(sample.data)

  #calculate the MD
  test.stat <- n*t(sample.x.bar-mu)%*%solve(V)%*%(sample.x.bar-mu)

  ts.arr <- c(ts.arr, test.stat)
}

hist(ts.arr, breaks = 50) #histogram of the test statistics
```

Histogram of ts.arr



```
x.arr <- seq(0,20,length=1000)
y.fit.arr <- dchisq(x.arr, 2)

{hist(ts.arr, breaks=50, probability = T)
  lines(x.arr, y.fit.arr, col="blue",lwd=2)}
```

Histogram of ts.arr

