# STAT 812: Computational Statistics

Simulation for Studying Point Estimation and Hypothesis Testing Procedures

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## Contents

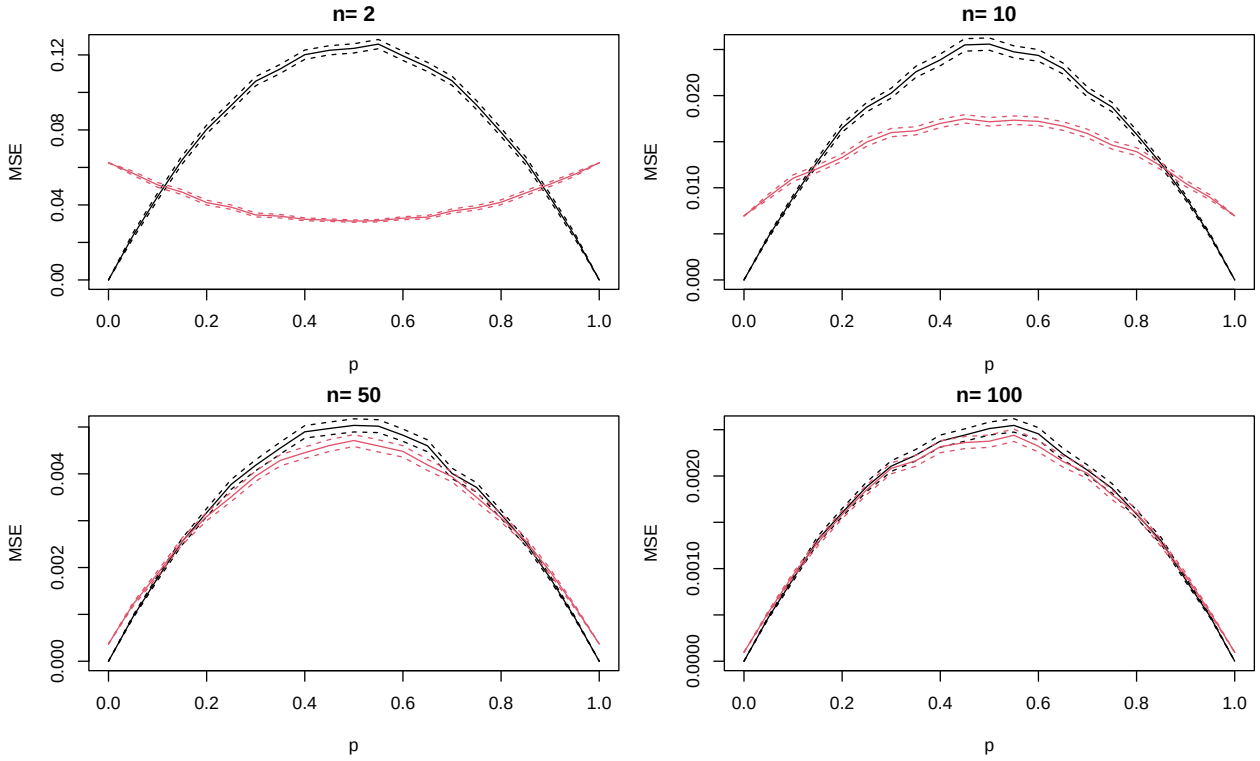


## 1 Using simulation to study two estimators of proportions

```
## Estimating Functios
p_est1 <- function(x) mean(x)

p_est2 <- function(x) {
    n <- length (x)
    (sum(x) + 1) / (n+2)
}

## Functions for estimating MSE
mse_est_mc <- function(n,p,no_sim,p_est)
{
    sq_error <- rep(0, no_sim)
    for(i_sim in 1:no_sim)
    {  sq_error[i_sim] <- (p_est( rbinom(n,1,p) ) - p)^2
    }
    list(mse=mean(sq_error), sd = sqrt(var(sq_error)/no_sim) )
}


mse_p1 <- function(n,p,no_sim)
{
```

```
    sq_error <- rep(0, no_sim)
    for(i_sim in 1:no_sim)
    {  sq_error[i_sim] <- (p1_est( rbinom(n,1,p) ) - p)^2
    }
    list(mse=mean(sq_error), sd = sqrt(var(sq_error)/no_sim) )
}

mse_p2 <- function(n,p,no_sim)
{
    sq_error <- rep(0, no_sim)
    for(i_sim in 1:no_sim)
    {  sq_error[i_sim] <- (p2_est( rbinom(n,1,p) ) - p)^2
    }
    list(mse=mean(sq_error), sd = sqrt(var(sq_error)/no_sim) )
}

## Simulation
par( mfrow=c(2,2), mar=c(4,4,2,1) )

no_sim <- 10000

p_set <- seq(0,1,by = 0.05)

risk_est1 <- risk_est2 <- rep(0, length(p_set))
sd_risk_est1 <- sd_risk_est2 <- rep(0, length(p_set))


n_set <- c(2,10,50,100)

for( n in n_set )
{

    for(i in 1:length(p_set) )
    {
        output_est <- mse_est_mc(n=n,p=p_set[i],no_sim=no_sim,p_est1)
        risk_est1[i] <- output_est$mse
        sd_risk_est1[i] <- output_est$sd

        output_est <- mse_est_mc(n=n,p=p_set[i],no_sim=no_sim,p_est2)
        risk_est2[i] <- output_est$mse
        sd_risk_est2[i] <- output_est$sd

    }

    plot(p_set, risk_est1,type="l",
         xlab="p",ylab="MSE",main=paste("n=",n))
    points(p_set, risk_est1 + 1.96*sd_risk_est1,type="l",lty=2)
    points(p_set, risk_est1 - 1.96*sd_risk_est1,type="l",lty=2)

    points(p_set, risk_est2,type="l",col=2)
    points(p_set, risk_est2 + 1.96*sd_risk_est2,type="l",lty=2,col=2)
    points(p_set, risk_est2 - 1.96*sd_risk_est2,type="l",lty=2,col=2)
```

```
}
```




## 2 Using simulation to study t-test on non-normal observations

```
# SIMULATE T TESTS ON DATA FROM A T DISTRIBUTION.  Simulates k data
# sets, each consisting of n data points that are drawn independently
# from the t distribution with df degrees of freedom.  For each data
# set, the p-value for a two-sided t test of the null hypothesis that
# the mean is mu (default 0) is computed.  The value returned by this
# function is the vector of these k p-values.

t.test.sim <- function (N, n, df, mu.true =0, mu=0)
{
    pvalues <- numeric(N)

    for (i in 1:N)
    { x <- rt (n, df) + mu.true
    pvalues[i] <- t.test.pvalue(x,mu)
    }

    pvalues
}


# FIND THE P-VALUE FOR A TWO-SIDED T TEST.  The data is given by the first
# argument, x, which must be a numeric vector.  The mean under the null
# hypothesis is given by the second argument, mu, which defaults to zero.
#
```

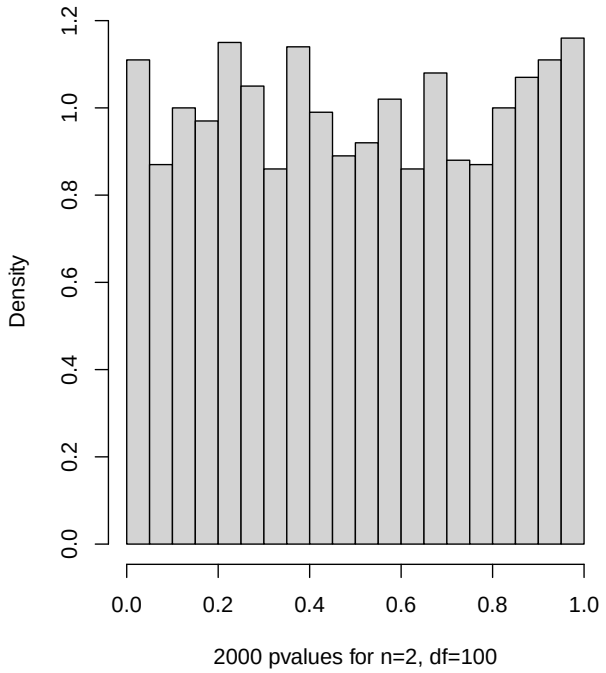
```r
# Note:  This function is just for illustrative purposes.  The p-value
# can be obtained using the built-in t.test function with the expression:
#
#     t.test(x,mu=mu)$p.value

t.test.pvalue <- function (x, mu=0)
{
    if (!is.numeric(x) || !is.numeric(mu) || length(mu)!=1)
    { stop("Invalid argument")
    }

    n <- length(x)

    if (n<2)
    { stop("Can't do a t test with less than two data points")
    }

    t <- (mean(x)-mu) / sqrt(var(x)/n)

    2 * pt (-abs(t), n-1)
}
```

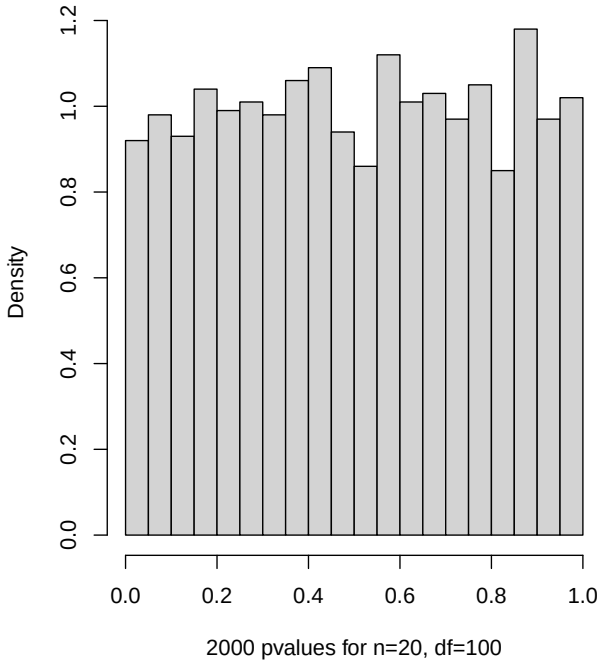
## 2.1 Distribution of p-value of t.test under $H_0$

```r
N <- 2000

bins <- 20
```

### 2.1.1 Tests with 100 degrees of freedom, with 2 and 20 data points.

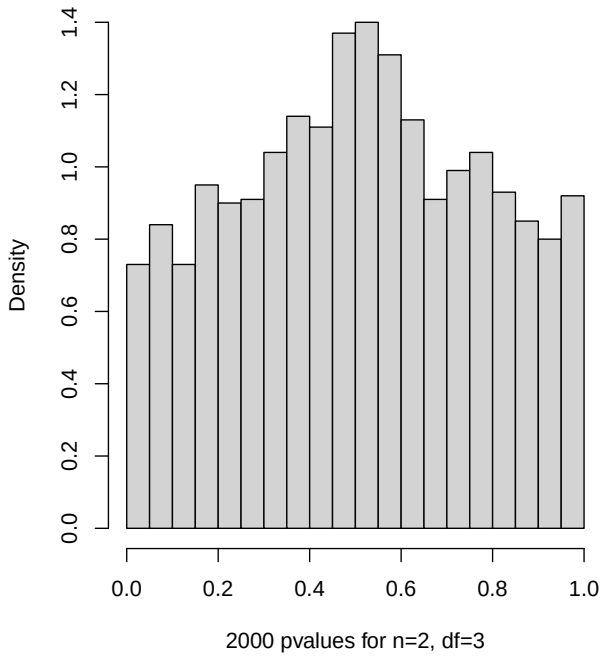
```r
par (mfrow = c(1,2))

hist (t.test.sim(N,2,100), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=2, df=100"))

hist (t.test.sim(N,20,100), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=20, df=100"))
```

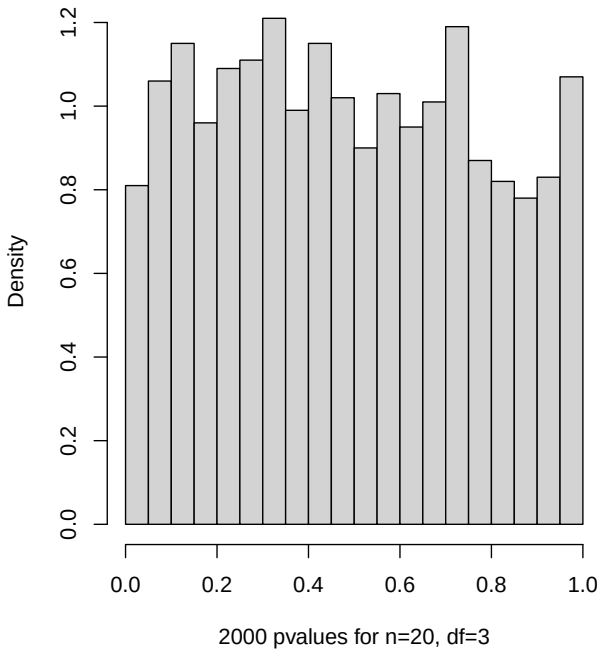



### 2.1.2 Tests with 3 degrees of freedom, with 2 and 20 data points.

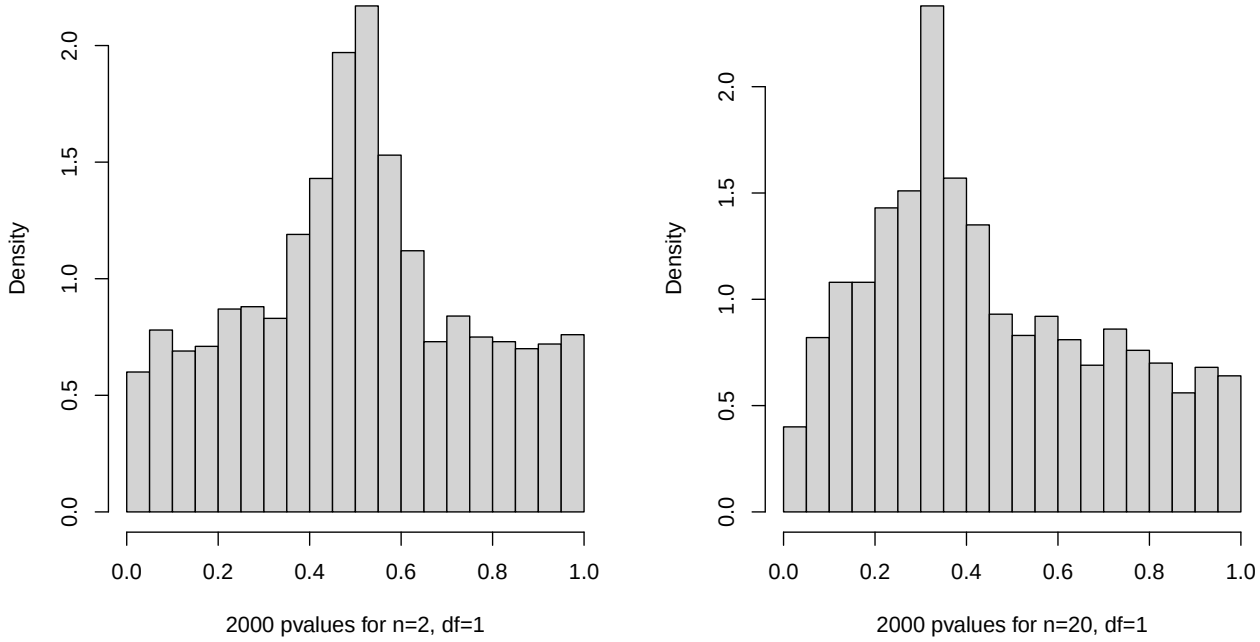
```
par (mfrow = c(1,2))

hist (t.test.sim(N,2,3), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=2, df=3"))

hist (t.test.sim(N,20,3), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=20, df=3"))
```



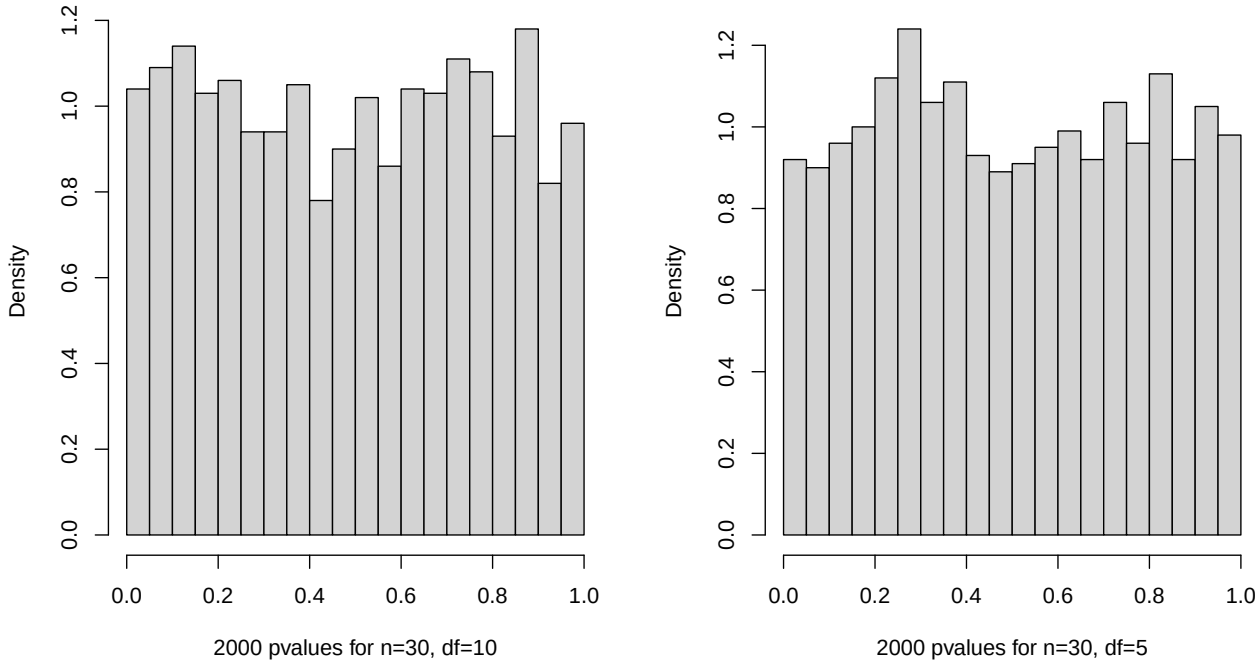
### 2.1.3 Tests with 1 degree of freedom, with 2 and 20 data points.

```
par (mfrow = c(1,2))

hist (t.test.sim(N,2,1), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=2, df=1"))

hist (t.test.sim(N,20,1), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=20, df=1"))
```




### 2.1.4 Tests with 10 and 5 degrees of freedom, with 30 data points.

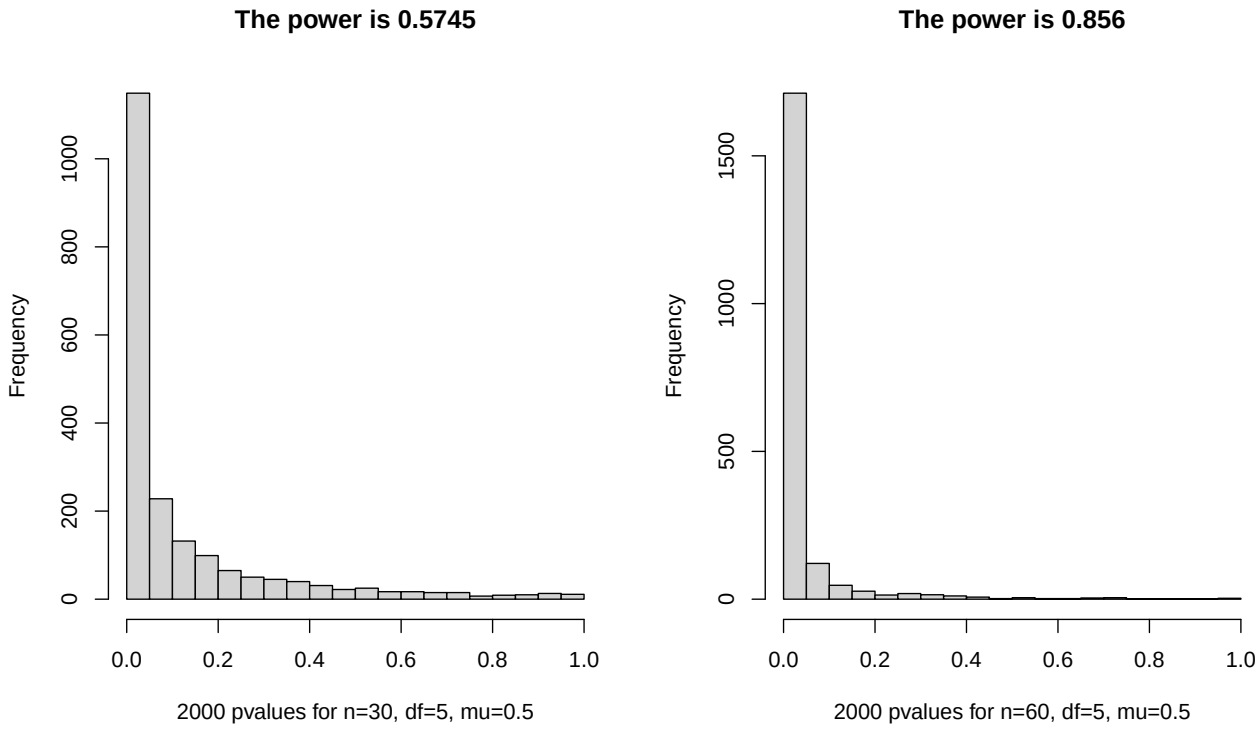
```
par (mfrow = c(1,2))
hist (t.test.sim(N,30,10), nclass=bins, prob=T,
      main="",xlab=paste(N,"pvalues for n=30, df=10"))

hist (t.test.sim(N,30,5), nclass=bins, prob=T,
      main="", xlab=paste(N,"pvalues for n=30, df=5"))
```




## 2.2 Find the power of t.test

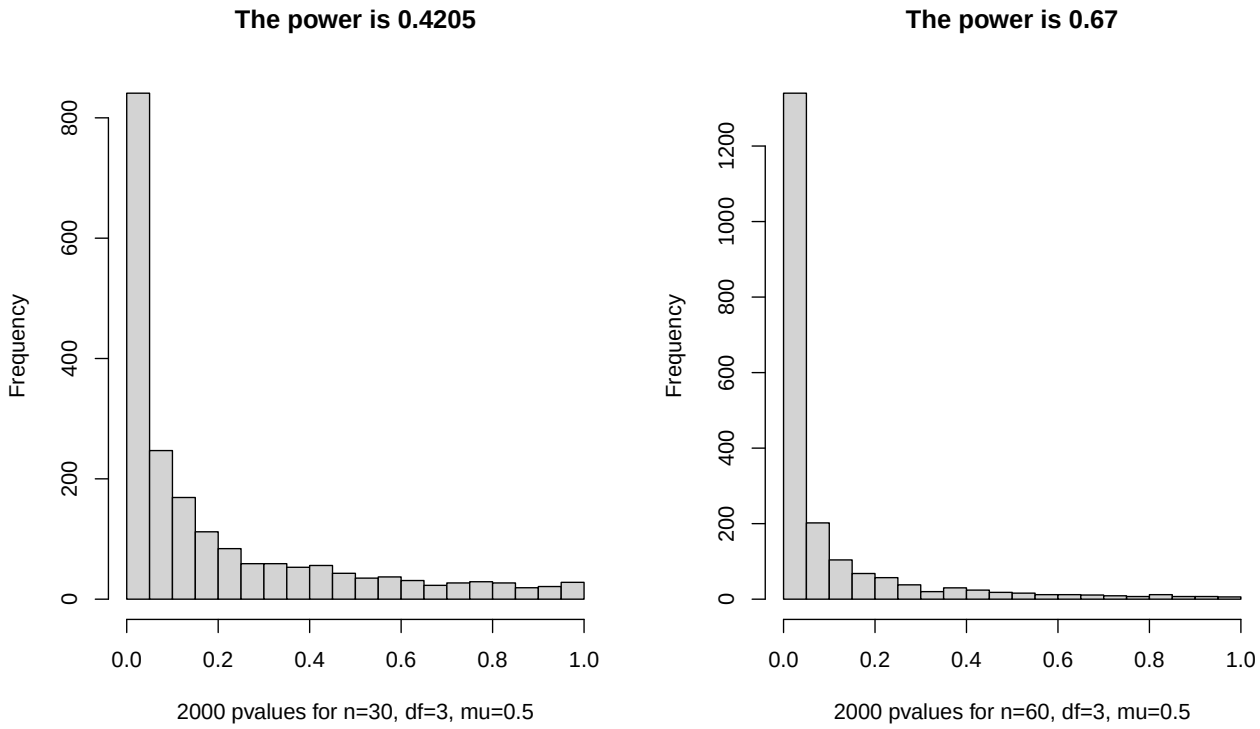
## 2.3 Find the power of t.test for df = 5

```
pvaues_H1_30 <- t.test.sim(N,30,5, mu.true = 0.5, mu = 0 )
pvaues_H1_60 <- t.test.sim(N,60,5, mu.true = 0.5, mu = 0 )

par (mfrow = c(1,2))

hist(pvaues_H1_30, nclass = 20, main = paste ("The power is", mean (pvaues_H1_30 < 0.05)), xlab=paste(N
hist(pvaues_H1_60, nclass = 20, main = paste ("The power is", mean (pvaues_H1_60 < 0.05)), xlab=paste(N
```




## 2.4 Find the power of t.test for df = 3

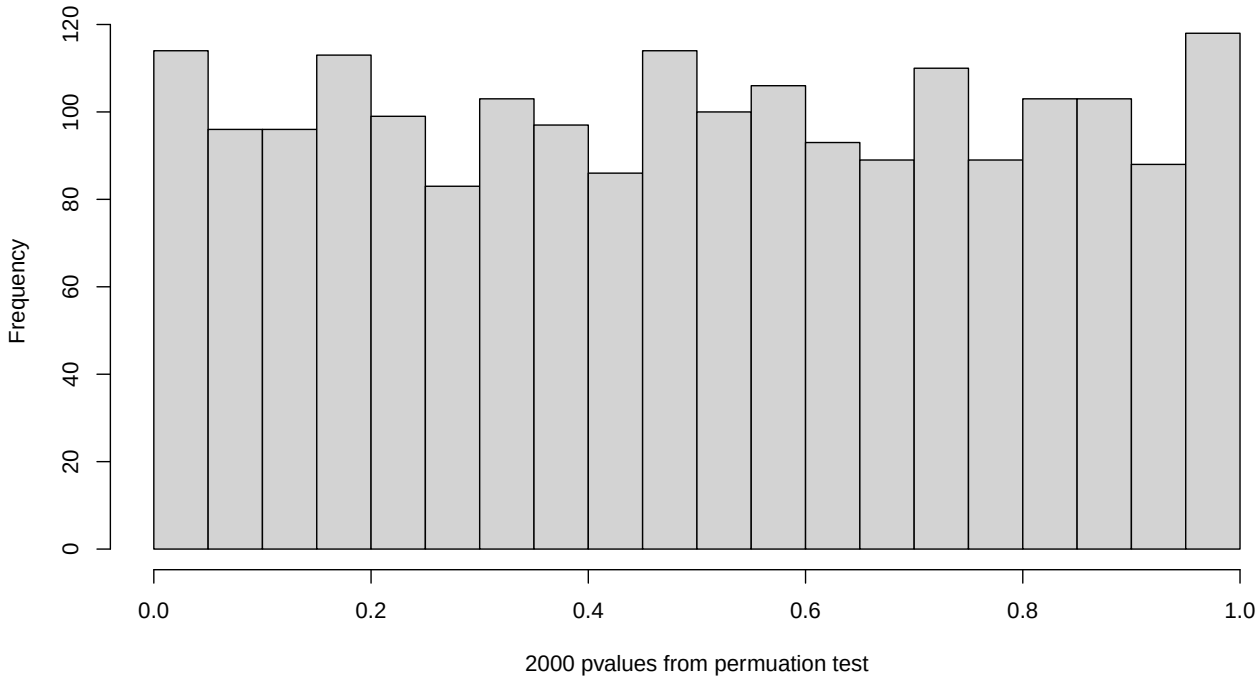
```
pvaues_H1_30 <- t.test.sim(N,30,3, mu.true = 0.5, mu = 0 )
pvaues_H1_60 <- t.test.sim(N,60,3, mu.true = 0.5, mu = 0 )

par (mfrow = c(1,2))

hist(pvaues_H1_30, nclass = 20, main = paste ("The power is", mean (pvaues_H1_30 < 0.05)), xlab=paste(N
hist(pvaues_H1_60, nclass = 20, main = paste ("The power is", mean (pvaues_H1_60 < 0.05)),xlab=paste(N,
```




## 3 Using simulation to study a permuation test

```
# COMPUTE THE P-VALUE FOR A PERMUTATION TEST OF CORRELATION.  Tests the null
# hypothesis that the the vectors x and y are independent, versus the
# alternative that they are correlated (either positively or negatively).
# The vectors x and y are given as the first and second arguments; they
# must be of equal length.
#

perm.cor.test <- function (x, y, no.perm=100)
{
    real.abs.cor <- abs(cor(x,y))
    permuted.abs.cor <- rep (0, no.perm)
    for (i in 1:no.perm)
    {
      permuted.abs.cor[i] <- abs(cor(x,sample(y)))

    }

    mean (permuted.abs.cor > real.abs.cor)
}

# TEST ON NORMALLY-DISTRIBUTED DATA, COMPARED TO TEST BASED ON NORMAL DIST.

test.perm.norm <- function(no.sim,no.perm)
{
    pvalue <- rep(0,no.sim)

    for(i in 1:no.sim)
```

```
    {
        x <- rnorm(20)
        y <- rnorm(20)

        pvalue[i] <- perm.cor.test(x,y,no.perm)
    }

    pvalue
}


pv <- test.perm.norm(2000,100)
par (mfrow = c(1,1))
hist(pv,20, xlab="2000 pvalues from permuation test",main="")
```




# 4 Using simulation to study a power regression test

## 4.1 R Functions for REGRESSION USING BEST POWER TRANSFORMATION

```
# Takes as arguments a
# vector of predictor values and a vector of response values (of equal
# length).  The predictor values must be non-negative.  Finds the
# power transformation for the predictors that produces the highest
# correlation (in absolute value) with the response, chosing the power
# from the powers argument (which defaults to seq(0.1,2.0,by=0.1).
# Returns the pvalue

pvalue.lm.pow <- function (x, y, powers=seq(0.1,4.0,by=0.1))
{
    if (!is.vector(x,"numeric") || !is.vector(y,"numeric")
```

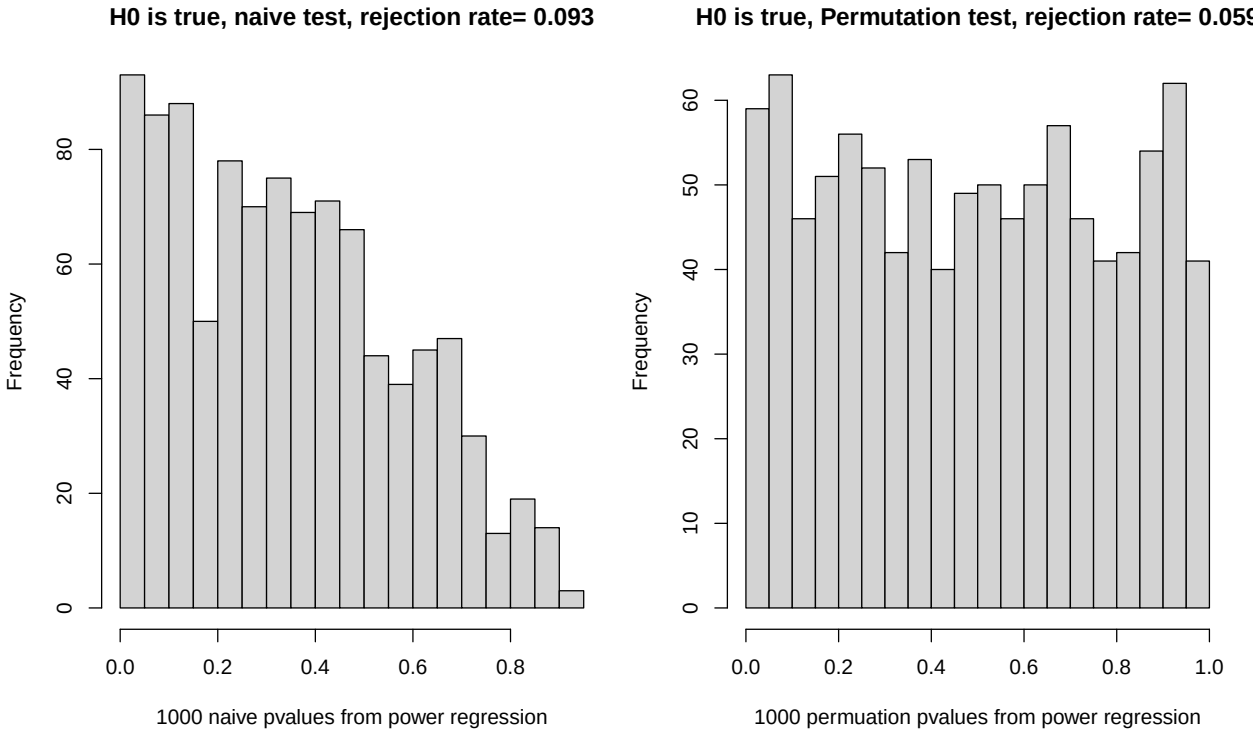
```
        || length(x)!=length(y))
    {
      stop("Arguments should be numeric vectors of equal length")
    }

    if (any(x<0))
    {
      stop("Predictors must be non-negative")
    }

    n <- length(x)

    # Find the power that produces the highest correlation with the response.

    best.r <- 0

    for (p in powers)
    {
      r <- cor(x^p,y)
      if (abs(r)>=abs(best.r))
      {
        power <- p
        best.r <- r
      }
    }

    # Return the best power and the linear model using that power.

    xp <- x^power
    #return naive pvalue
    coef(summary(lm(y~xp)))[2,4]
}

# TEST VALIDITY OF THE NAIVE P-VALUES.  Simulates the results of
# naively interpreting pvalues for the regression on the best
# power of the predictor variable (from pvalue.lm.pow) as a real pvalue.
# The arguments of this function are the vector of predictor variables
# to use (x), the number of datasets to simulate (N), and possible
# further arguments that are passed on to pvalue.lm.pow.  N datasets of n
# cases are generated in which x is as specified and the corresponding
# y values are generated independently from the standard normal
# distribution (without reference to x).  The result is the vector of
# N p-values obtained from the models that pvalue.lm.pow chooses for these
# datasets.  Since the null hypothesis of no relationship is true,
# these p-values should be uniformly distributed between 0 and 1, if
# they are valid.

test.lm.power <- function (x, N, ...)
{
    n <- length(x)

    # Simulate N datasets and record the naive p-value found for each.
```

```
    pvalues <- rep(0,N)

    for (k in 1:N)
    {
        y <- rnorm(n)

        pvalues[k] <- pvalue.lm.pow(x,y,...)
    }

    # Return the vector of N p-values that were obtained.

    pvalues
}

# FIND PERMUTATION PVALUE FOR REGRESSION USING BEST POWER TRANSFORM.
# Takes as arguments the vectors of predictors (x) and responses (y),
# as for pvalue.lm.pow, the number of permutations to use in finding the
# p-value (default is 100), and possible further arguments that are
# passed on to pvalue.lm.pow.  Returns the p-value from the permutation
# test, which is (roughly) the fraction of times that reg.pow applied
# to a randomly shuffled data sets gives a smaller p-value than reg.pow
# gives when applied to the actual dataset.  In detail, the pvalue is
# count/perms, with count being the number of smaller p-values
# obtained from permuted datasets.  If the null hypothesis of no
# relationship is true, these p-values will be uniformly distributed
# over the possible values (ie, roughly uniform between 0 and 1).

pvalue.perm.lm.pow <- function (x, y, no.perm=100, ...)
{
    # Find the naive p-value using pvalue.lm.pow for the actual data.

    actual <- pvalue.lm.pow(x,y,...)

    # Count how many times pvalue.lm.pow applied to a random permutation finds
    # a model with as small a naive p-value as for the actual data.

    permuted_pvalue <- rep(0, no.perm)
    for (k in 1:no.perm)
    {
      permuted_pvalue[k] <- pvalue.lm.pow(x,sample(y),...)
    }

    mean (permuted_pvalue < actual)
}

#TEST VALIDITY OF THE PERMUATION PVALUES. The method is the same as for
#test.lm.power. When power.sim is not 0, it can be used to calculate the power
#of the test

test.perm.power <- function (x, power.sim, N=100, resid.std.dev=1, ...)
{
    n <- length(x)
```

```
    pvalues <- rep(0,N)

    for (k in 1:N)
    {
      y <- x^power.sim + rnorm(n,0,resid.std.dev)
      pvalues[k] <- pvalue.perm.lm.pow(x,y,...)
    }
    pvalues
}
```

## 4.2 Checking the uniformity of p-values under $H_0$

```
par(mfrow=c(1,2),mar=c(4,4,3,1))

x <- exp(rnorm(20))

naive.pv <- test.lm.power(x, 1000)
perm.pv <- test.perm.power(x,0,1000, no.perm=99)

hist(naive.pv,nclass=20,xlab="1000 naive pvalues from power regression",
     main=paste("H0 is true, naive test, rejection rate=", mean (naive.pv< 0.05)))
hist(perm.pv,nclass=20,
     xlab="1000 permuation pvalues from power regression",
     main=paste("H0 is true, Permutation test, rejection rate=", mean (perm.pv< 0.05)))
```




## 4.3 The statistical power of the permuation test

```
perm.pv.alt1 <- test.perm.power(x,1.5,1000,no.perm=99)
```

```r
#p-value when the true power in function is 0.5
perm.pv.alt2 <- test.perm.power(x,0.5,1000,no.perm=99)

par(mfrow=c(1,2),mar=c(4,4,3,1))

hist(perm.pv.alt1,nclass=20,
     xlab="1000 permuation pvalues from power regression",
     main= paste0("H1: y = x^1.5 + e, permutation test, rej. rate=",
          mean (perm.pv.alt1< 0.05))
)

hist(perm.pv.alt2,nclass=20,
     xlab="1000 permuation pvalues from power regression",
     main= paste0("H1: y = x^0.5 + e, permutation test, rej. rate=",
          mean (perm.pv.alt2< 0.05))
)
```