

```
#####
mu <- 10
sigma <- 2
c <- 10
n <- 20
x <- rnorm(n,mu,sigma)
z <- (mean(x)-c)/sqrt(sigma^2/n)
z

qnorm(0.025)
qnorm(0.975)
pvalue <- pnorm(-abs(z))+1-pnorm(abs(z))
pvalue

nx <- 10
ny <- 15
x <- rnorm(nx,10,1)
y <- rnorm(ny,10,1)
sx <- var(x)
sy <- var(y)
sp <- ((nx-1)*sx+(ny-1)*sy)/(nx+ny-2)
t <- (mean(x)-mean(y))/sqrt(sp*(1/nx+1/ny))

x <- c(43.2,44.3,22.3,31.4,56.6)
nx <- length(x)
y <- c(34.7,43.5,65.3,11.3,29.4,19.0,39.6)
ny <- length(y)

#####

n1 <- 2000
n2 <- 2500
n <- n1+n2
sequence1 <- sample(c(1:4),n1,prob=c(0.25,0.25,0.25,0.25),rep=T)
sequence2 <- sample(c(1:4),n2,prob=c(0.25,0.25,0.25,0.25),rep=T)

table(sequence1)
sequence1
table(sequence2)
sequence2

obs.table <- matrix(0,nrow=2,ncol=4)
fit.table <- matrix(0,nrow=2,ncol=4)
obs.table[1,]_table(sequence1)
obs.table[2,]_table(sequence2)
chi.stat <- 0
lr.stat <- 0
for(i in 1:2){
  for(j in 1:4){
    fit.table[i,j] <- sum(obs.table[i,])*sum(obs.table[,j])/n
    chi.stat <- chi.stat + ((obs.table[i,j]-fit.table[i,j])^2)
    /fit.table[i,j]
    lr.stat <- lr.stat + 2*obs.table[i,j]*log(obs.table[i,j]
    /fit.table[i,j])
  }
}
chi.stat
lr.stat

#####
```

```
n <- 5000
pmatch <- 0.25
sequence1 <- sample(c(1:4),n,prob=c(0.25,0.25,0.25,0.25),rep=T)
sequence2 <- sample(c(1:4),n,prob=c(0.25,0.25,0.25,0.25),rep=T)
b <- length(sequence1[sequence1 == sequence2])
pvalue <- pbinom(b,n,pmatch)

n <- 5000
k <- 3
p <- 0.25
nits <- 1000
xmax_rep(0,nits)
for(i in 1:nits){
  x <- rbinom(n,k,p)
  xmax[i] <- max(x)+k
}
hist(xmax)

nits <- 10
n <- 1000
match.count_rep(0,nits)
for(i in 1:nits){
  pmatch <- 0.25
  sequence1 <- sample(c(1:4),n,prob=c(0.25,0.25,0.25,0.25),rep=T)
  sequence2 <- sample(c(1:4),n,prob=c(0.25,0.25,0.25,0.25),rep=T)
  match <- length(sequence1[sequence1 == sequence2])
  match.count[i] <- sum(match)
}
match.count
```