This dataset is the age-adjusted death rates and life expectancy at birth with race and sex in the US, and that can allow people understanding what changing of life and death in the ago and now, males and females, races.

2015.data<-subset(Death\_rates\_and\_life,Death\_rates\_and\_life=='2015’)

2005.data<-subset(Death\_rates\_and\_life,Death\_rates\_and\_life==‘2005’)

y2015.life<-y2015.data$`Age-adjusted Death Rate`

y2005.life<-y2005.data$`Age-adjusted Death Rate`

sd.y2015<-sd(y2015.life)

> sd.y2005<-sd(y2005.life)

mean.y2015<-mean(y2015.life)

> mean.y2005<-mean(y2005.life)

> len\_y2015<-length(y2015.life)

> len\_y2005<-length(y2005.life)

> sd.y15.y05<-sqrt(sd.y2015^2/len\_y2015+sd.y2005^2/len\_y2005)

> zeta<-(mean.y2015-mean.y2005)/sd.y15.y05

> plot(x=seq(from=-5, to=5, by=0.1), y=dnorm(seq(from=-5, to=5, by=0.1),mean = 0),type = 'l',xlab='difference',ylab = 'possibility’)

abline(v=zeta,col='red’)

p=1-pnorm(zeta)

[1] 0.5

y1995.data<-subset(Death\_rates\_and\_life,Death\_rates\_and\_life=='1995’)

y1995.life<-y1995.data$`Age-adjusted Death Rate`

sd.y2015<-sd(y2015.life)

sd.y1995<-sd(y1995.life)

> mean.y2015<-mean(y2015.life)

> mean.y1995<-mean(y1995.life)

> len\_y2015<-length(y2015.life)

> len\_y1995<-length(y1995.life)

> sd.y15.y95<-sqrt(sd.y2015^2/len\_y2015+sd.y1995^2/len\_y1995)

> zeta<-(mean.y2015-mean.y1995)/sd.y15.y95

> plot(x=seq(from=-5, to=5, by=0.1), y=dnorm(seq(from=-5, to=5, by=0.1),mean = 0),type = 'l',xlab='difference',ylab = 'possibility’)

> abline(v=zeta,col='red’)

> p=1-pnorm(zeta)

> p

[1] 0.992645

y2015.life<-y2015.data$`Average Life Expectancy (Years)`

> y1995.life<-y1995.data$`Average Life Expectancy (Years)`

> sd.y2015<-sd(y2015.life)> sd.y1995<-sd(y1995.life)

> mean.y2015<-mean(y2015.life)

> mean.y1995<-mean(y1995.life)

> len\_y2015<-length(y2015.life)

> len\_y1995<-length(y1995.life)

> sd.y15.y95<-sqrt(sd.y2015^2/len\_y2015+sd.y1995^2/len\_y1995)>

> zeta<-(mean.y2015-mean.y1995)/sd.y15.y95

plot(x=seq(from=-5,to=5,by=0.1),y=dnorm(seq(from=-5,to=5,by=0.1),mean=0),type = 'l',xlab='difference',ylab='possible’)

> abline(v=zeta,col='red’)

> p=1-pnorm(zeta)

> p

[1] 0.01207821

ma.fe<-subset(Death\_rates\_and\_life,Death\_rates\_and\_life$Sex=='Male'|Death\_rates\_and\_life$Sex=='Female’)

PermutationTestSecond::Permutation(Death\_rates\_and\_life,"Sex","Average Life Expectancy (Years)",1000,"Male","Female")[1] 0

> p=1-pnorm(zeat)> p

[1] 1.892619e-09

> PermutationTestSecond::Permutation(Death\_rates\_and\_life,"Sex","Age-adjusted Death Rate",1000,"Male","Female")

[1] 0