**#Fisher’s exact test & FDR**

#**take ‘COG’ for instance**

#‘cog in F1\_COG\_Dietzia\_2634others.xlsx’

cog<-read.csv("cog.csv",header = T,row.names = 1)

c<-t(cog)

for (j in 1:25) {

num=c[,j]

num<-matrix(num,2,2,byrow=T)

a[j]=fisher.test(num)$p.value

}

write.csv(a,"p\_cog.csv")

#after order p\_cog

data<-c(1.16E-36,3.97E-22,1.48E-16,2.37E-09,3.26E-08,7.08E-07,2.43E-06,1.08E-05,0.00128236,0.004527819,0.017489591,0.047165504,0.054272112,0.083282978,0.097530364,0.18302643,0.199319982,0.211029957,0.333967752,0.34115743,0.739670904,0.938181509,1,1,1)

p.adjust (data,method = "BH")

#then, **take ‘core family’ for instance**

#‘F6A\_cpoy\_4gene\_set’

d<-matrix(c(64,728,705,8830),2,2,byrow=T)

fisher.test(d)$p.value

#after fisher.test for these four family set, order the p.value

data<-c(2.84E-51,7.52E-18,1.21E-14,0.4810058)

p.adjust (data,method = "fdr")

**# Wilcoxon rank-sum test**

wilcox.test(x, y, exact=FALSE, correct=FALSE)

**#cor.test**

cor.test(data$var1, data$var2, method = "pearson")