

```

1. library(multtest), library(Biobase)
2.
data(golub)
golub.frame <- data.frame(golub)
row.names(golub.frame) <- paste("g",1:nrow(golub.frame), sep = "")
3.
ann.dat2= data.frame(golub.cl)
data=list(x=golub.frame,y=data.frame(golub.cl))
4.
wilcox.test.all.genes <- function(x,s1,s2) {
x1 <- x[s1]
x2 <- x[s2]
x1 <- as.numeric(x1)
x2 <- as.numeric(x2)
t.out <- wilcox.test(x1,x2, alternative="two.sided",exact=F, correct=T)
out <- as.numeric(t.out$statistic)
return(out)
}

original.wmw.run <- apply(golub.frame,1,wilcox.test.all.genes,s1=ann.dat2==0,s2=ann.dat2==1)

5.
wlist = replicate(500, apply(golub.frame[,sample(ncol(golub.frame))], 1, wilcox.test.all.genes, s1=ann.dat2==0,
s2=ann.dat2==1))
ps.max= apply(wlist, 1, max)

6. t.test(ps.max)
      One Sample t-test

data:  ps.max
t = 1309, df = 3050, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 237.9143 238.6281
sample estimates:
mean of x
 238.2712

subsetV<-original.wmw.run[original.wmw.run>238.2712,,drop=FALSE]

```

	original.vmw.run
g23	249
g55	251
g66	258
g81	244
g96	274
g126	262
g127	256
g135	244
g158	246
g172	253
g174	262
g182	261
g184	244
g192	241
g202	255
g204	263
g207	246
g220	240
g226	244
g232	250
g239	247
g246	254
g248	244
g253	266
g259	266
g282	242
g283	271
g286	260
g297	257
g304	243
g307	252
g309	245
g313	248
g314	246
g320	241
g323	262
g329	275
g330	245
g335	254
g344	259
g345	274
g357	247
g376	244
g391	245
g394	290
g395	250
g399	247
g407	240
g422	270
g453	242
g462	259
g479	248
g489	250
g490	248
g494	251
g515	264
g522	257
g523	283
g546	274
g560	262
g561	281
g563	255
g590	245
g620	239
g621	269
g634	243
g648	271
g688	256
g695	251
g698	241
g701	240
g703	285
g704	273
g713	266
g715	240
g717	283
g725	252
g738	271
g746	277
g763	248
g764	241
g785	256
g801	263
g807	248
g811	249
g835	272
g838	283
g839	272
g846	242
g849	272
g862	259
g866	269
g922	272
g963	250
g971	242
g984	283
g1006	275
g1011	243
g1014	259
g1019	254
g1025	244
g1030	244
g1037	281
g1042	284
g1045	270
g1060	264
g1070	260
g1081	249
g1086	278
g1094	244
g1101	258

g1109	239
g1110	242
g1145	262
g1161	245
g1162	261
g1174	240
g1175	239
g1202	256
g1225	254
g1245	245
g1253	255
g1271	268
g1293	255
g1316	255
g1327	267
g1334	266
g1337	244
g1348	241
g1359	244
g1368	279
g1381	248
g1445	263
g1453	254
g1455	266
g1456	261
g1459	250
g1468	245
g1470	243
g1474	250
g1480	242
g1489	242
g1491	242
g1513	241
g1524	282
g1542	266
g1547	243
g1559	260
g1564	246
g1579	245
g1585	267
g1598	275
g1610	249
g1616	258
g1629	245
g1638	262
g1640	265
g1642	265
g1649	246
g1653	259
g1671	254
g1691	266
g1696	250
g1723	256
g1732	264
g1766	252
g1773	247

g1787	245
g1805	249
g1807	241
g1811	284
g1817	272
g1834	290
g1856	263
g1869	272
g1882	260
g1883	281
g1903	253
g1909	275
g1916	273
g1920	274
g1926	248
g1939	268
g1943	239
g1944	249
g1947	254
g1948	252
g1955	240
g1959	272
g1963	250
g1978	271
g1993	246
g1995	287
g2002	283
g2020	265
g2032	239
g2052	240
g2061	241
g2079	244
g2087	247
g2105	252
g2110	249
g2122	270
g2179	267
g2180	259
g2208	248
g2213	252
g2216	249
g2235	252
g2236	242
g2244	246
g2262	247
g2265	259
g2266	272
g2276	245
g2285	244
g2289	274
g2297	257
g2302	254
g2307	260
g2313	265
g2318	239
g2330	241
g2330	241
g2343	239
g2347	250
g2356	263
g2365	243
g2374	242
g2386	288
g2402	262
g2410	256
g2418	279
g2430	259
g2438	262
g2459	244
g2466	259
g2489	288
g2506	240
g2538	240
g2576	242
g2593	258
g2616	270
g2627	253
g2642	240
g2645	272
g2673	250
g2686	253
g2693	244
g2702	279
g2736	261
g2753	260
g2786	246
g2801	274
g2803	247
g2829	273
g2851	281
g2860	272
g2879	272
g2903	242
g2939	291
g2950	258
g2955	267
g2985	252
g3046	276

7.

```
fit <- lmFit(golub.frame)
emp<- eBayes(fit)
emp$p.value
```

8.

```
sortpval <- apply(emp$p.value, 2, sort)
subsetP<-sortpval[sortpval<0.05,,drop=FALSE]
subsetPg<-sortpval[sortpval>0.05,,drop=FALSE]
```

```
intersect(rownames(subsetP), rownames(subsetV))
```

```
[1] "g1014" "g1145" "g0466" "g1807" "g2753" "g1102" "g253" "g560" "g2438" "g1723" "g2365" "g158" "g1025" "g1489" "g1869" "g2330" "g849" "g866" "g2642" "g1787" "g391" "g785" "g479" "g1834" "g2105" "g1944" "g394" "g1368" "g2386"
[30] "g2174" "g2903" "g1943" "g815" "g746" "g2165" "g113" "g1773" "g152" "g282" "g494" "g84" "g283" "g390" "g2402" "g1101" "g210" "g1042" "g821" "g213" "g1993" "g1459" "g2955" "g66" "g1883" "g238" "g1474" "g2803" "g2116"
[59] "g1070" "g1110" "g2538" "g1579" "g1445" "g1955" "g176" "g2985" "g1856" "g329" "g239" "g395" "g1271" "g2244" "g490" "g2686" "g1642" "g246" "g2593" "g2213" "g1564" "g2489" "g422" "g2356" "g207" "g1559" "g1006" "g126" "g1811"
[88] "g2313" "g1926" "g1903" "g846" "g2343" "g323" "g2418" "g807" "g327" "g2307" "g23" "g1653" "g2122" "g1045" "g611" "g1640" "g1817" "g1060" "g2079" "g1470" "g715" "g1816" "g648" "g1916" "g2645" "g922" "g1316" "g1094" "g1480"
[117] "g555" "g1455" "g1468" "g1766" "g462" "g1225" "g703" "g2673" "g704" "g172" "g135" "g2347" "g1359" "g469" "g999" "g174" "g2180" "g1086" "g522" "g54" "g2878" "g1805" "g2427" "g725" "g833" "g107" "g1599" "g1453" "g2430"
[146] "g1582" "g2893" "g2297" "g862" "g1598" "g182" "g2302" "g1610" "g453" "g297" "g2410" "g1081" "g1245" "g2179" "g1524" "g2801" "g304" "g971" "g1046" "g2829" "g2002" "g1109" "g184" "g2880" "g226" "g695" "g738" "g515" "g2939"
[175] "g81" "g96" "g1691" "g1162" "g2318" "g2285" "g1314" "g1947" "g220" "g2266" "g202" "g2851" "g1293" "g1381" "g1995" "g2276" "g1671" "g2130" "g1348" "g2061" "g698" "g2235" "g1161" "g713" "g764" "g1963" "g2052" "g2236" "g1649"
[204] "g2032" "g509" "g2786" "g2289" "g1337" "g1491" "g763" "g1959" "g1585" "g1175" "g1011" "g344" "g286" "g1978" "g2616" "g2950" "g114" "g717" "g145"
```

```
intersect(rownames(subsetPg), rownames(subsetV))
```

```
[1] "g88" "g701" "g2702" "g834" "g1696" "g2020" "g1513" "g807" "g801" "g1948" "g1327" "g335" "g1456" "g1732" "g232" "g2506" "g1438" "g1920" "g204" "g1253" "g259" "g688" "g1174" "g1030" "g1909" "g2576" "g561" "g127" "g1037"
[30] "g1882" "g2262" "g2459" "g1547" "g2736" "g1219" "g2087" "g248" "g2208" "g330" "g863" "g523" "g1629"
```

9.

```
t.test.all.genes <- function(x,s1,s2) {
x1 <- x[s1]
x2 <- x[s2]
x1 <- as.numeric(x1)
x2 <- as.numeric(x2)
t.out <- t.test(x1,x2, alternative="two.sided",var.equal=T)
out <- as.numeric(t.out$p.value)
return(out)
}
pv <- apply(golub.frame,1,t.test.all.genes,s1=ann.dat2==0,s2=ann.dat2==1)

pv <- data.frame(pv)
```

```
subsetS<-pv[pv<0.01,,drop=FALSE]
intersect(rownames(subsetS), rownames(empV))
subsetemp<-empV[same,,drop=FALSE]
comb<- cbind(subsetS, subsetemp)
colnames(comb) <- c("Student t-test", "Empirical bayes")
```

```
plot(comb[,1],comb[,2], xlab="Student t-test", ylab="Empirical bayes", main="Student t-test vs Empirical Bayes test")
```

Student t-test vs Empirical Bayes test