

# Canonical Population Analysis

*Miquel Salicrú, Sergi Civit, Ferran Reverter*

## Packages

```
library(car)
library(heplots)
```

## Data

Reaven and Miller (1979) examined the relationship among blood chemistry measures of glucose tolerance and insulin in 145 nonobese adults.

```
data(Diabetes)
str(Diabetes)

## 'data.frame':    145 obs. of  6 variables:
## $ relwt  : num  0.81 0.95 0.94 1.04 1 0.76 0.91 1.1 0.99 0.78 ...
## $ glufast: int   80 97 105 90 90 86 100 85 97 97 ...
## $ glutest: int  356 289 319 356 323 381 350 301 379 296 ...
## $ instest: int  124 117 143 199 240 157 221 186 142 131 ...
## $ sspg   : int   55 76 105 108 143 165 119 105 98 94 ...
## $ group  : Factor w/ 3 levels "Normal","Chemical_Diabetic",...: 1 1 1 1 1 1 1 1 1 1 ...
```

## Canonical Population Analysis

within variability

```
sel1<-which(Diabetes$group=="Normal")
sel2<-which(Diabetes$group=="Chemical_Diabetic")
sel3<-which(Diabetes$group=="Overt_Diabetic")

S1<-cov(Diabetes[sel1,-6])
S2<-cov(Diabetes[sel2,-6])
S3<-cov(Diabetes[sel3,-6])

n1<-length(sel1)
n2<-length(sel2)
n3<-length(sel3)
n<-n1+n2+n3
g<-3

S1<-(n1-1)*S1/n1
S2<-(n2-1)*S2/n2
S3<-(n3-1)*S3/n3

W<-(n1*S1+n2*S2+n3*S3) # within
Sp<-W/(n-g) # pooled
```

between variability

```
m<-apply(Diabetes[,-6],2,mean)
m

##          relwt      glufast      glutest      instest      sspg
##  0.9773103 121.9862069 543.6137931 186.1172414 184.2068966

m1<-apply(Diabetes[sel1,-6],2,mean)
m2<-apply(Diabetes[sel2,-6],2,mean)
m3<-apply(Diabetes[sel3,-6],2,mean)

m1

##          relwt      glufast      glutest      instest      sspg
##  0.9372368  91.1842105 349.9736842 172.6447368 114.0000000

m2

##          relwt      glufast      glutest      instest      sspg
##  1.055833  99.305556 493.944444 288.000000 208.972222

m3

##          relwt      glufast      glutest      instest      sspg
##  0.9839394 217.6666667 1043.7575758 106.0000000 318.8787879

v1<-as.matrix(m1-m)
v2<-as.matrix(m2-m)
v3<-as.matrix(m3-m)

B<-n1*v1%*%t(v1)+n2*v2%*%t(v2)+n3*v3%*%t(v3)
B

##          relwt      glufast      glutest      instest      sspg
## relwt      0.3454684      50.62677      558.7517      311.5103      313.2891
## glufast    50.6267698    392731.57914    2073038.9147    -304615.7392    569350.4416
## glutest    558.7517238    2073038.91472    11193292.4756    -1306220.7240    3211652.6115
## instest    311.5103294    -304615.73920    -1306220.7240      599297.5990    -193335.5172
## sspg       313.2890987    569350.44157    3211652.6115     -193335.5172    995189.3057
```

solving

```
A<-solve(Sp)%*%B
vecs<-eigen(A)$vectors

Y<-as.matrix(Diabetes[,-6])%*%vecs

ym1<-t(as.matrix(m1))%*%vecs
ym2<-t(as.matrix(m2))%*%vecs
ym3<-t(as.matrix(m3))%*%vecs

ym1

##          [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] -2.25705 -0.9578447 -1.390952 -0.9486748 0.9076623
```

```
ym2
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]  
## [1,] -3.790624 -1.427346 -1.390952 -0.9486748 0.9076623
```

```
ym3
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]  
## [1,] -6.22582 -0.9102302 -1.390952 -0.9486748 0.9076623
```

```
ym<-rbind(ym1,ym2,ym3)
```

## Outputs

```
Diabetes$g<-0  
Diabetes[sel1,"g"]<-1  
Diabetes[sel2,"g"]<-2  
Diabetes[sel3,"g"]<-3  
  
plot(Y[,1],Y[,2],type="n",xlab="1st canonical dim",ylab="2nd canonical dim")  
points(Y[,1],Y[,2],col=Diabetes$g)  
points(ym[,1],ym[,2],col="blue",pch=19)
```

