Principal Component Analysis

Pre-processing data

We'll be using the gene expression dataset for 17580 genes from 73 samples. There are two phenotypes, 0:no-diesase and 1:Parkinson's. We have an additional dataset containing 3 sample covariates.

```
library(rafalib)

e <- read.delim("data/counts.txt", row.names=1)

tab <- read.delim("data/phen.txt")

c <- read.delim("data/cov.txt", row.names=1)</pre>
```

We take the log-transform of gene expression data and calculate the Z-score.

```
e_prime <- t(e) # Re-order data
L <- log2(1 + e_prime) # Log-transform data
head(L)[,1:2]</pre>
```

```
##
         ENSG0000000003.10 ENSG0000000005.5
## C 0002
                   8.253656
                                     0.7933007
## C_0003
                   8.207424
                                    1.7152768
## C_0004
                   7.940356
                                    2.9929645
## C_0005
                   7.760373
                                    1.7993866
## C_0006
                   7.775682
                                     2.2382442
## C_0008
                                     3.1276069
                   8.086903
```

```
Z <- scale(L) # Z-score
head(Z)[,1:2]</pre>
```

```
ENSG0000000003.10 ENSG0000000005.5
## C_0002
                -0.0964491
                                 -1.27240600
## C_0003
                 -0.1742805
                                 -0.40655202
## C_0004
                 -0.6238893
                                  0.79336080
## C_0005
                 -0.9268921
                                 -0.32756206
## C_0006
                 -0.9011194
                                  0.08458153
## C_0008
                 -0.3771784
                                  0.91980736
```

Computing principal components and percent variance

We use the prcomp function in the stats package to compute PCs of the scaled data.

```
pca <- prcomp(L)
pca$sdev[1:10]</pre>
```

```
## [1] 51.09799 33.10467 27.13555 26.05815 21.33622 18.10651 16.95858
## [8] 14.69798 14.36086 13.52880
```

pca\$rotation[1:5,1:2]

```
## PC2 PC2
## ENSG0000000003.10 0.004307860 -0.005476928
## ENSG0000000005.5 -0.011743743 -0.002597112
## ENSG00000000419.8 -0.003197778 0.003272388
## ENSG00000000457.8 -0.001744380 0.006200323
## ENSG00000000460.12 0.002952869 0.006566861
```

We now extract the variances of the components.

```
pca.var <- pca$sdev^2
pca.var[1:10]

## [1] 2611.0045 1095.9189 736.3379 679.0271 455.2345 327.8456 287.5936
## [8] 216.0307 206.2343 183.0283</pre>
```

Plots of first two PC loadings

```
par(mfrow = c(1, 2))
plot(pca$rotation[1:20, 1], ylim = c(-0.7, 0.7))
plot(pca$rotation[1:20, 2], ylim = c(-0.7, 0.7))
```

