Uk3

Here we plot the correlation matrix and the first 3 eigenvectors of Uk3.

```
library('knitr')
```

```
## Warning: package 'knitr' was built under R version 3.2.5
```

```
knitr::opts_chunk$set(cache=TRUE)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/ForNatureTechnicalReports/Figures/
covmat=readRDS("../..//Results_Data/covmatwithzero.rds")

z.stat=read.table("../../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../../Results_Data/piswithzero.rds")$pihat
pi.mat=matrix(pis,ncol=54,nrow=22,byrow = T)
```

```
## Warning in matrix(pis, ncol = 54, nrow = 22, byrow = T): data length [1189]
## is not a sub-multiple or multiple of the number of rows [22]
```

```
library(gplots)
```

```
##
## Attaching package: 'gplots'
```

```
## The following object is masked from 'package:stats':
##
##     lowess
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.2.5
```

```
library('colorRamps')
#install.packages("fields")
library(fields)
```

```
## Warning: package 'fields' was built under R version 3.2.5
```

```
## Loading required package: spam
```

```
## Warning: package 'spam' was built under R version 3.2.5
```

```
## Loading required package: grid
```

```
## Spam version 1.4-0 (2016-08-29) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.
```

```
##
## Attaching package: 'spam'

## The following objects are masked from 'package:base':
##
##     backsolve, forwardsolve

## Loading required package: maps

## Warning: package 'maps' was built under R version 3.2.5
```

```r
k=3
hclust.2=function (d, method = "average", members = NULL) {hclust(d, method, members)}
  x=cov2cor(covmat[[k]])
x[x<0]=0
  colnames(x)=names
  rownames(x)=names


h=read.table("../../Analysis/uk3rowindices.txt")[,1]
```

Now we orduce the heatmap. Note that this is flipped in the paper:

```r
smat=(x[(h),(h)])
smat[lower.tri(smat)] <- NA

library(lattice)
```

```
## Warning: package 'lattice' was built under R version 3.2.5
```

```r
#print(levelplot(smat,col.regions = jet.colors,xlab = "",ylab = "",colorkey = TRUE))



#clrs <- colorRampPalette(rev(c("purple","#FC8D59","#FEE090","#FFFFBF","#E0F3F8","#91BFDB","#4575B4")))

clrs <- colorRampPalette(rev(c("#D73027","#FC8D59","#FEE090","#FFFFBF",
                    "#E0F3F8","#91BFDB","#4575B4")))(64)
#clrs[63:64] <- "darkviolet"
lat=x[rev(h),rev(h)]
lat[lower.tri(lat)] <- NA
print(levelplot(lat,col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))
```
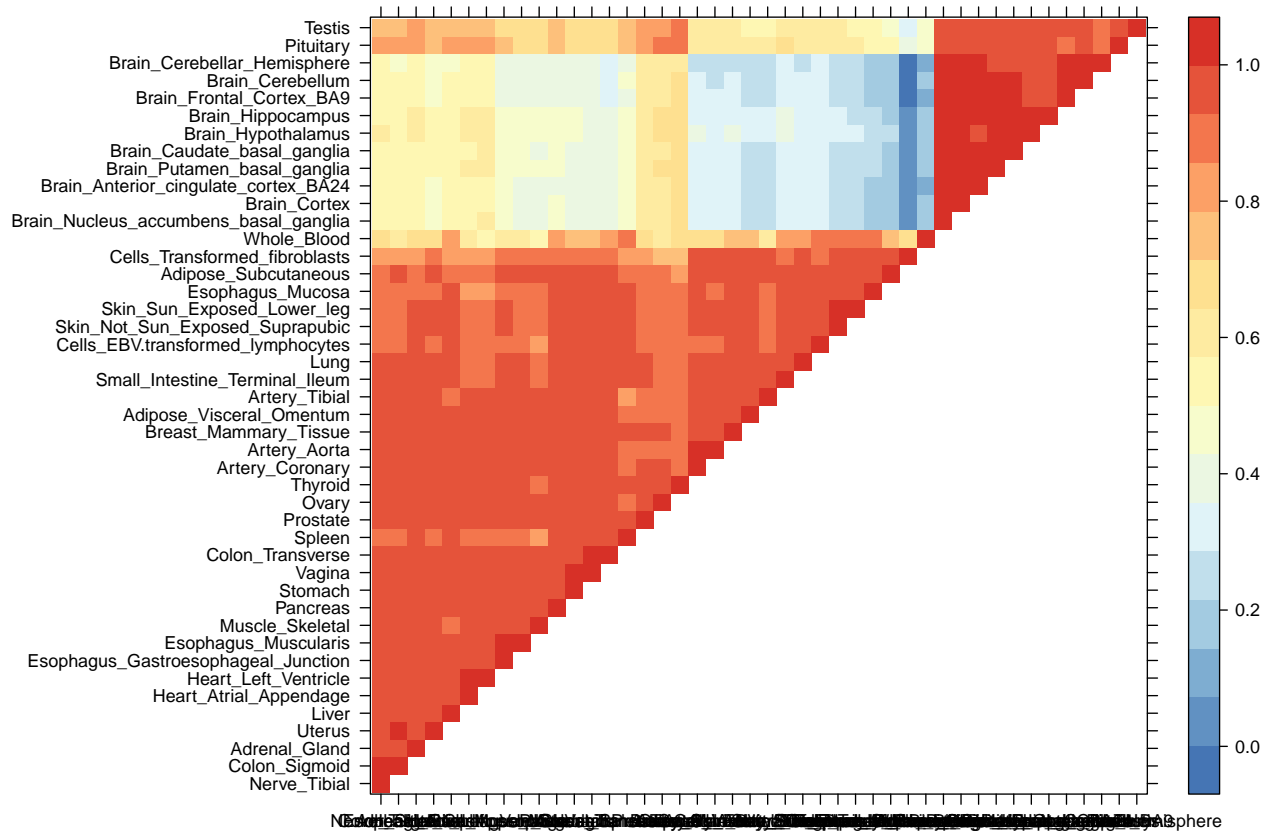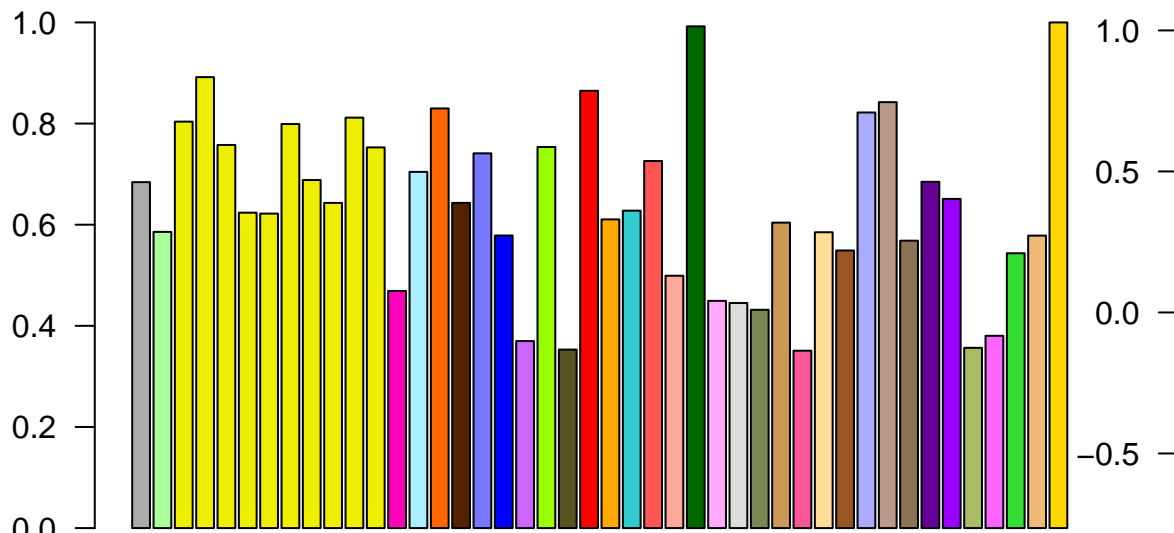
Now let's do the eigenplots:

```r
missing.tissues=c(7,8,19,20,24,25,31,34,37)
color.gtex=read.table("../../Data/GTExColors.txt",sep = '\t', comment.char = '')[-missing.tissues,]

k=3
vold=svd(covmat[[k]])$v;u=svd(covmat[[k]])$u

v=vold[h,]##shuffle so correct order
names=names[h]
color.gtex=color.gtex[h,]
for(j in 1:3){
barplot(v[,j]/v[,j][which.max(abs(v[,j]))],names="",cex.names=0.5,las=2,main=paste0("EigenVector",j,"Uk
```

EigenVector1Uk3

EigenVector3Uk3

4