

Uk5

Here we plot the correlation matrix and the first 3 eigenvectors of Uk2.

```
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/NGRevision/Figureswithres/")
covmat=readRDS("../Results_Data/covmatwithzero.rds")

covmat=readRDS("../Data_vhat/covmatwithvhat.rds")

z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../Data_vhat/piswithvhat.rds")$pihat
pi.mat=matrix(pis[-length(pis)],ncol=54,nrow=22,byrow = T)
```

```
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
```

```
k=5
colSums(pi.mat)[k]
```

```
## [1] 0.06533516
```

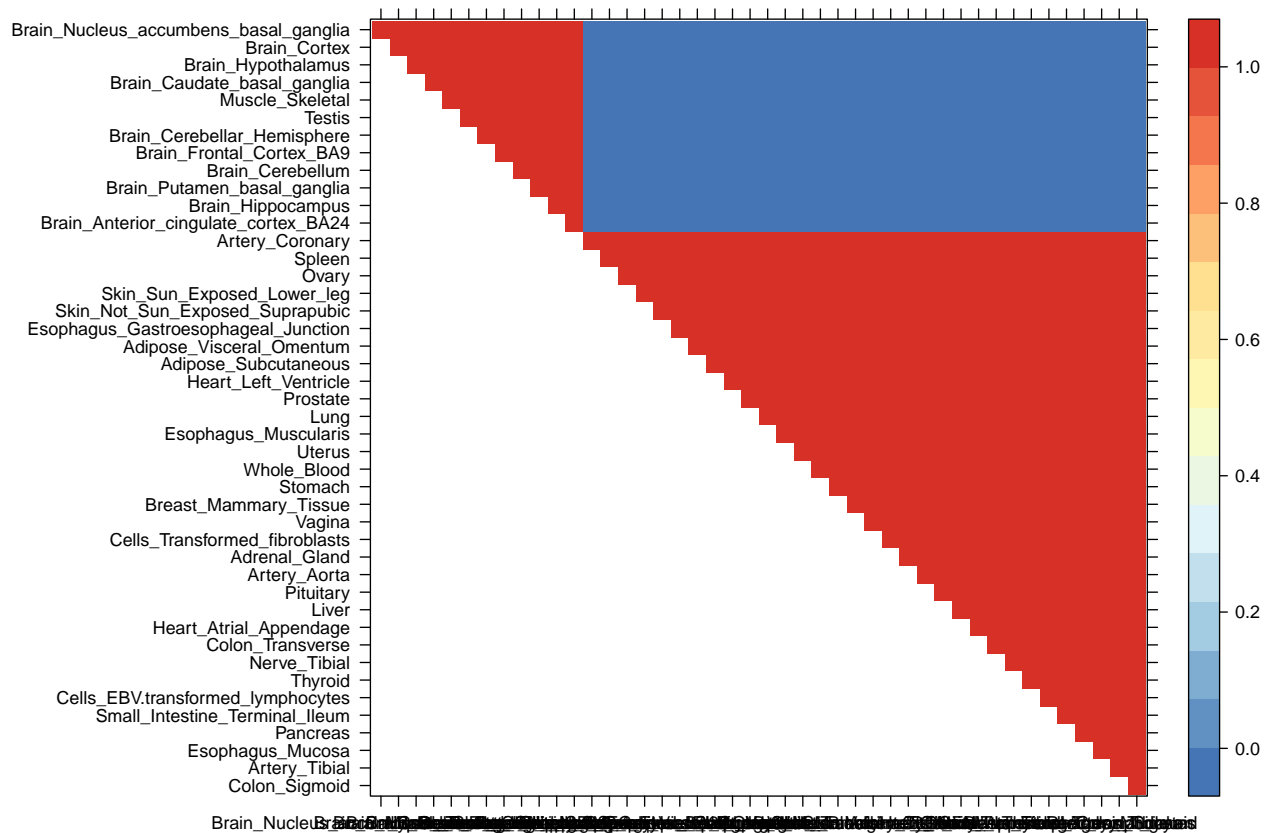
```
hclust.2=function (d, method = "average", members = NULL) {hclust(d, method, members)}
  x=cov2cor(covmat[[k]])
x[x<0]=0
  colnames(x)=names
  rownames(x)=names

h=read.table(paste0("../Data/uk",k,"rowIndices.txt"))[,1]
```

Lattice

```
library(lattice)

clrs <- colorRampPalette(rev(c("#D73027", "#FC8D59", "#FEE090", "#FFFFBF",
  "#E0F3F8", "#91BFDB", "#4575B4")))(64)
#clrs[63:64] <- "darkviolet"
lat=x[rev(h),rev(h)]
#lat=x[h,h]
lat[lower.tri(lat)] <- NA
n=nrow(lat)
print(levelplot(lat[n:1,],col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))
```



And the SVD Plots:

```
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,]
col = as.character(color.gtex[,2])

k=5
h=read.table(paste0("../Data/uk",k,"rowIndices.txt"))[,1]

g=1
v=svd(covmat[[k]])$v[h,]
rownames(v)=colnames(v)=names[h]
par(mar=c(8,4.1,4.1,2.1))
barplot(v[,g]/v[which.max(abs(v[,g])),g],las=2,main=paste("Eigenvector",g,"of Uk",k),cex.names = 0.5,co
```

Eigenvector 1 of Uk 2

