

Uk3

Here we plot the correlation matrix and the first 3 eigenvectors of Uk3. Uk3 is the covariance matrix corresponding to the output of the ExtremeDeconvolution algorithm that was initialized with the rank3 SVD approximation of $X'X$. It is the pattern of sharing with the most loading. We demonstrate which patterns have the most loading the pi barplot.

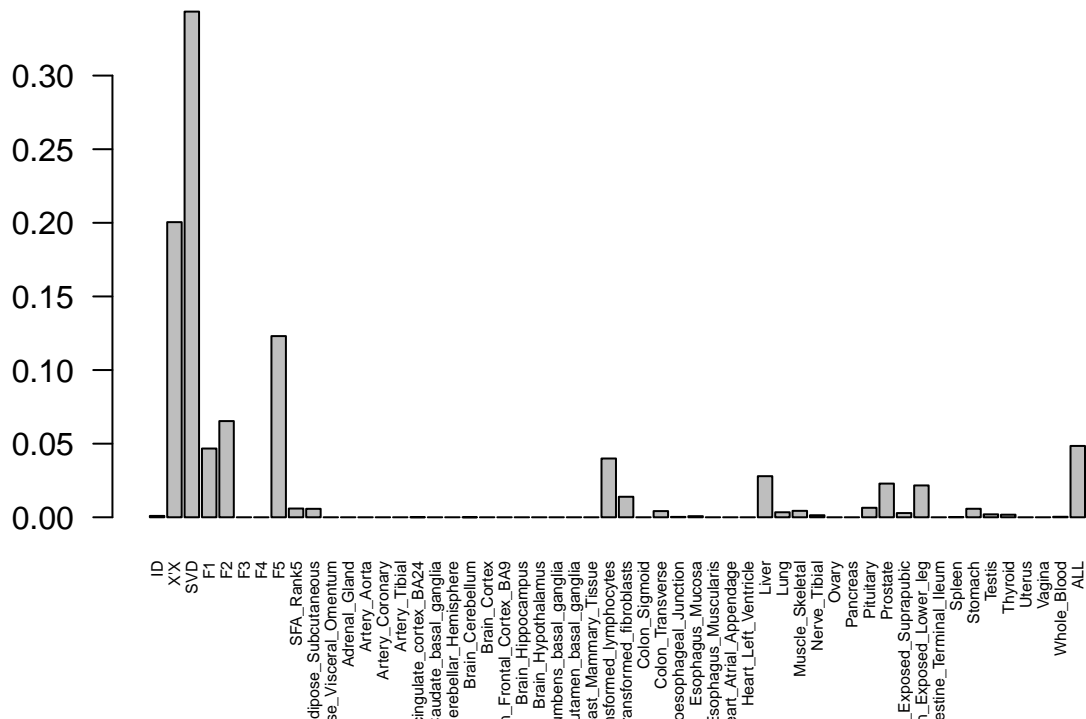
```
library('knitr')
#knitr::opts_chunk$set(cache = TRUE, collapse = TRUE, comment = "#",
#                        fig.path = "figures/Figure3.Rmd", fig.align = "center",
#                        fig.width = 8, fig.height = 6)
#opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/NGRevision/Figureswithres/")
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)

names=colnames(z.stat)
colnames(pi.mat)=c("ID", "X'X", "SVD", "F1", "F2", "F3", "F4", "F5", "SFA_Rank5", c(names, "ALL"))

barplot(colSums(pi.mat),main='WithVmat',las=2,cex.names=0.5)
```

WithVmat



Here, we install necessary packages and load the indices and tissue names:

```
library(ggplot2)
library('colorRamps')
```

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

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

```
k=3

x=cov2cor(covmat[[k]])
x[x<0]=0
colnames(x)=names
rownames(x)=names

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

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

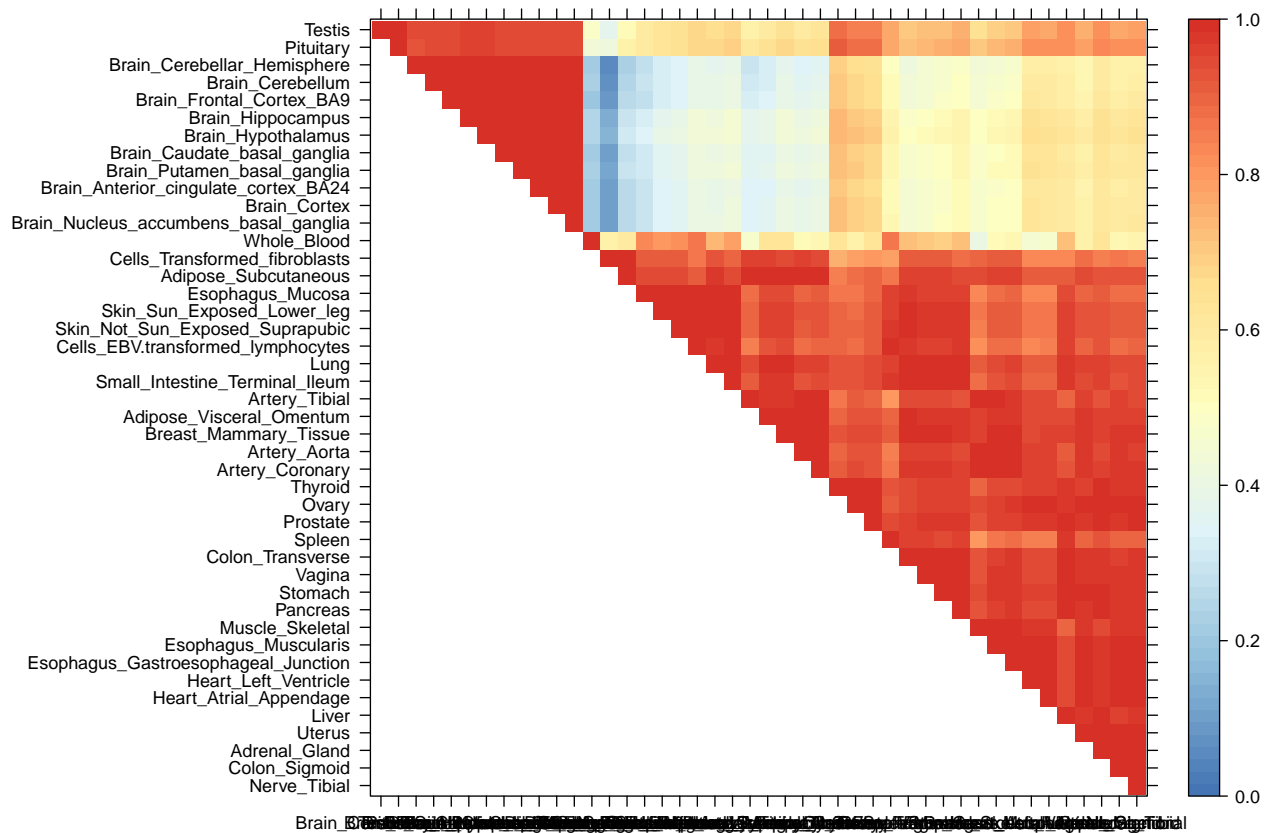
```
smat=(x[(h),(h)])
smat[lower.tri(smat)] <- NA

library(lattice)

clrs <- colorRampPalette(rev(c("#D73027", "#FC8D59", "#FEE090", "#FFFFBF",
                              "#E0F3F8", "#91BFDB", "#4575B4")))(64)

lat=x[rev(h),rev(h)]

lat[lower.tri(lat)] <- NA
n=nrow(lat)
print(levelplot(lat[n:1,], col.regions = clrs, xlab = "", ylab = "", colorkey = TRUE, at=seq(0,1,length.out=
```



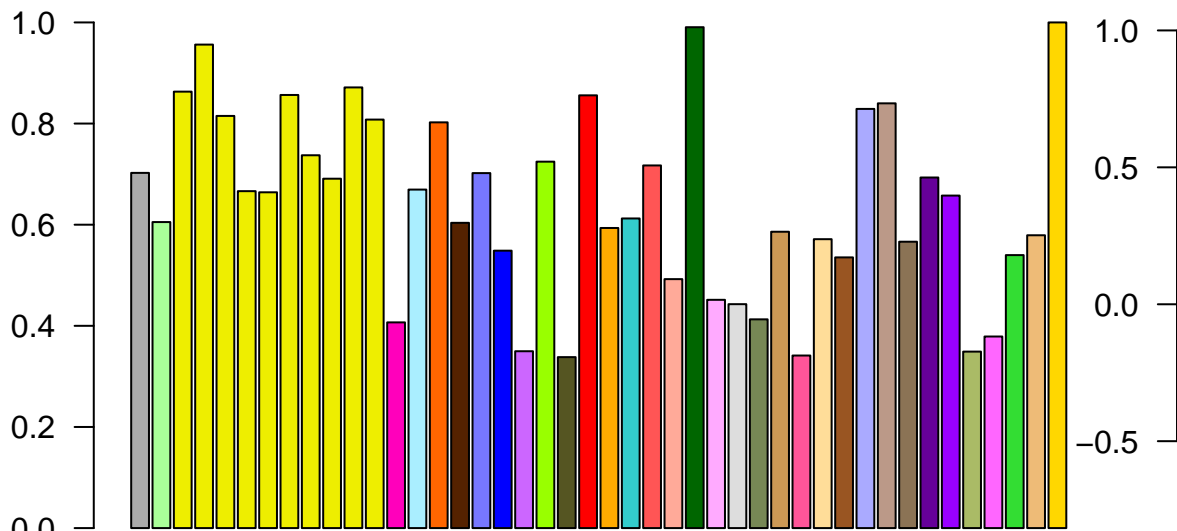
Now let's do the eigenplots:

```
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,]

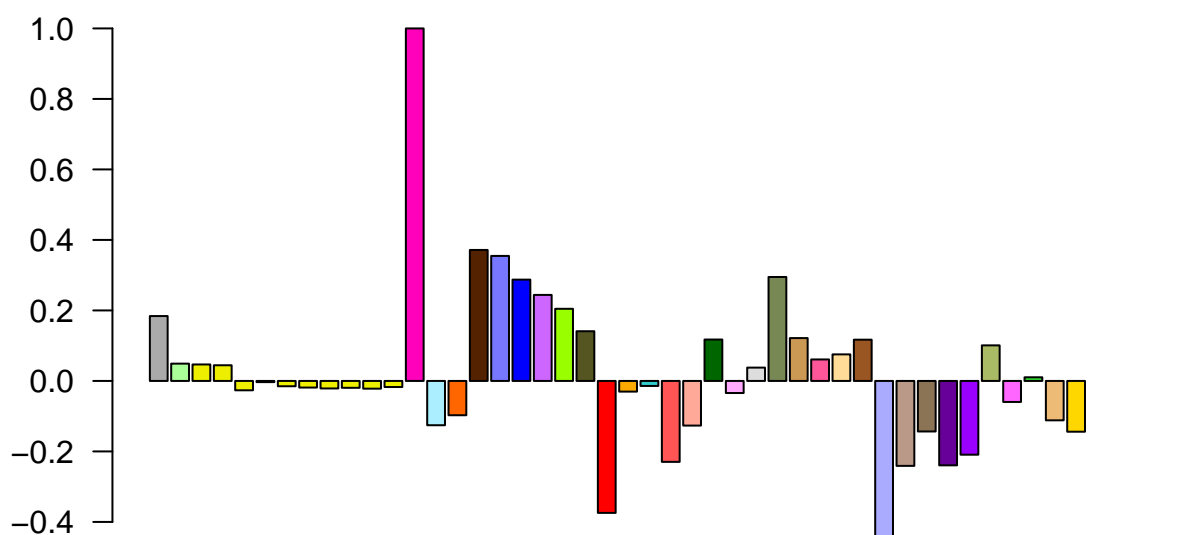
k=3
vold=svd(covmat[[k]])$v;u=svd(covmat[[k]])$u;d=svd(covmat[[k]])$d

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"))
}
```

EigenVector1 Uk3



EigenVector3Uk3


$$(d^2 / \text{sum}(d^2)) [1:3]$$

```
## [1] 0.885241028 0.113500988 0.001257984
```