

## 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.

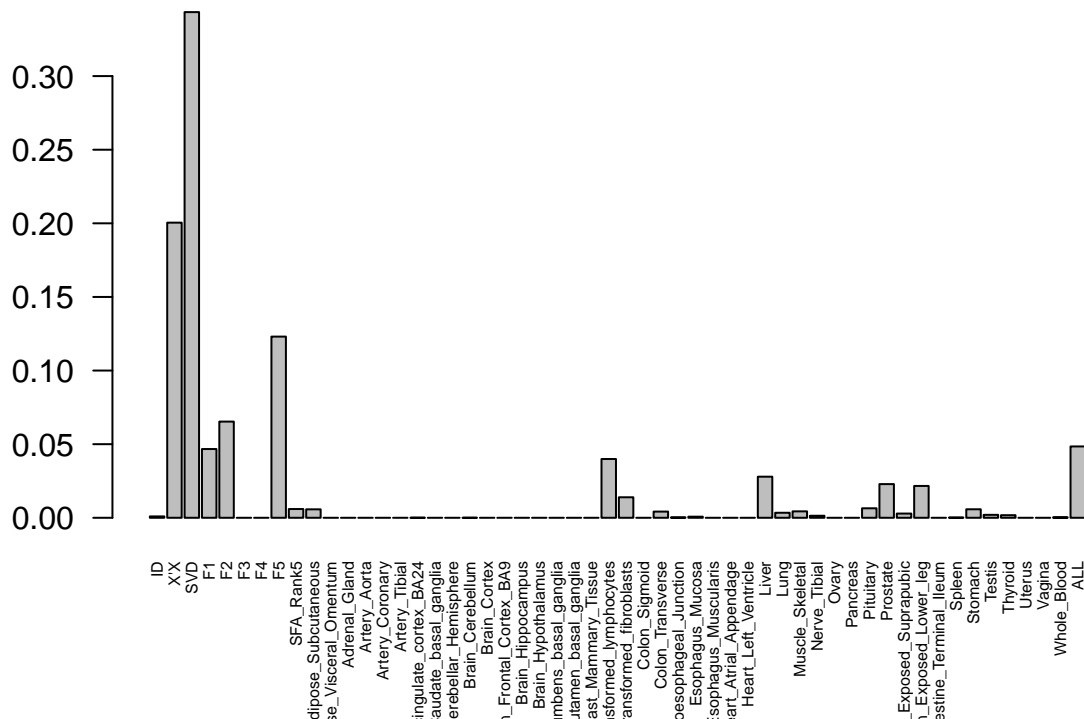
```
library('knitr')
knitr::opts_chunk$set(cache = TRUE, collapse = TRUE, comment = "#",
  fig.path = "figures/Figure3.Rmd", fig.align = "center",
  fig.width = 8, fig.height = 6)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/NGRevision/Figureswithres/")
covmat=readRDS("../Data_vhat/covmatwithvhat.rds")

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(gplots)
library(ggplot2)
library('colorRamps')
#install.packages("fields")
library(fields)
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 orduce the heatmap. Note that this is flipped in the paper:

```

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

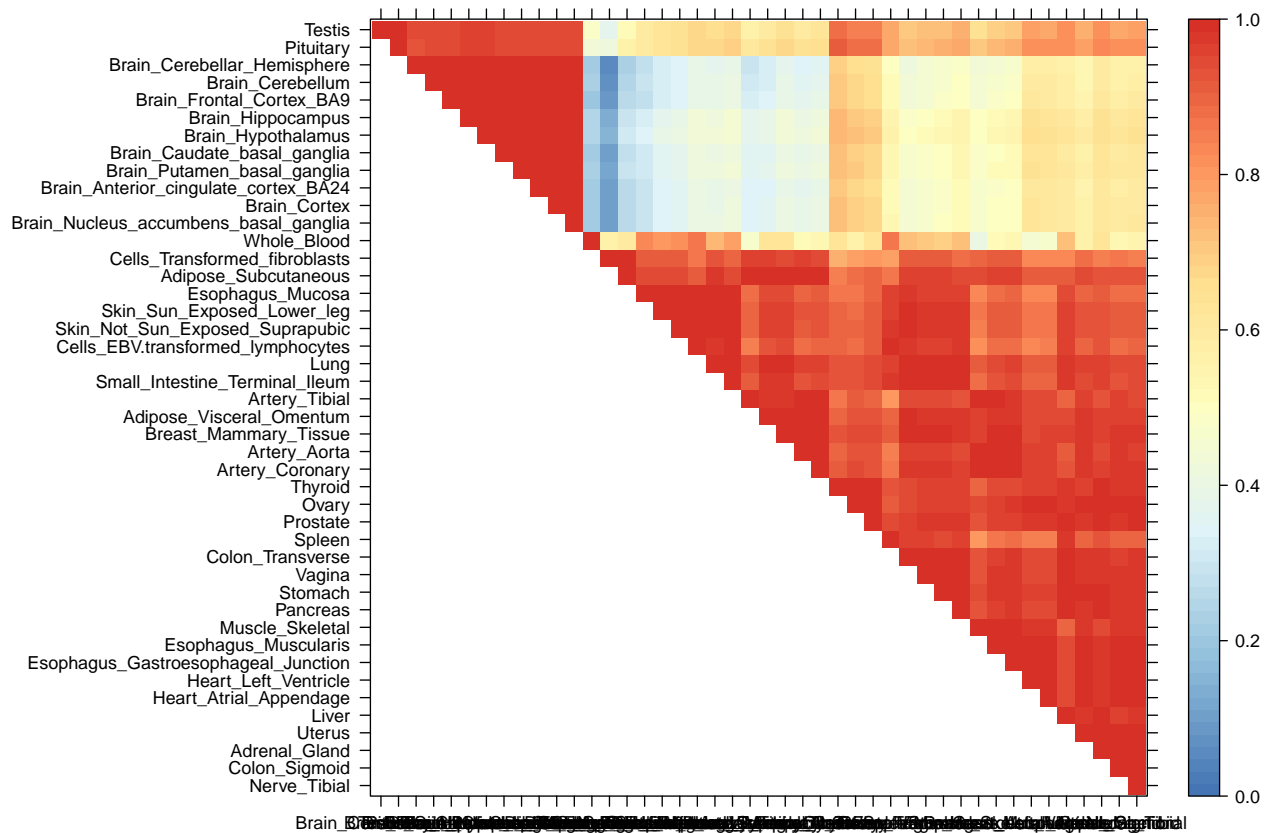
library(lattice)

clrs <- colorRampPalette(rev(c("#D73027", "#FC8D59", "#FEE090", "#FFFFBF",
                             "#EOF3F8", "#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=

```



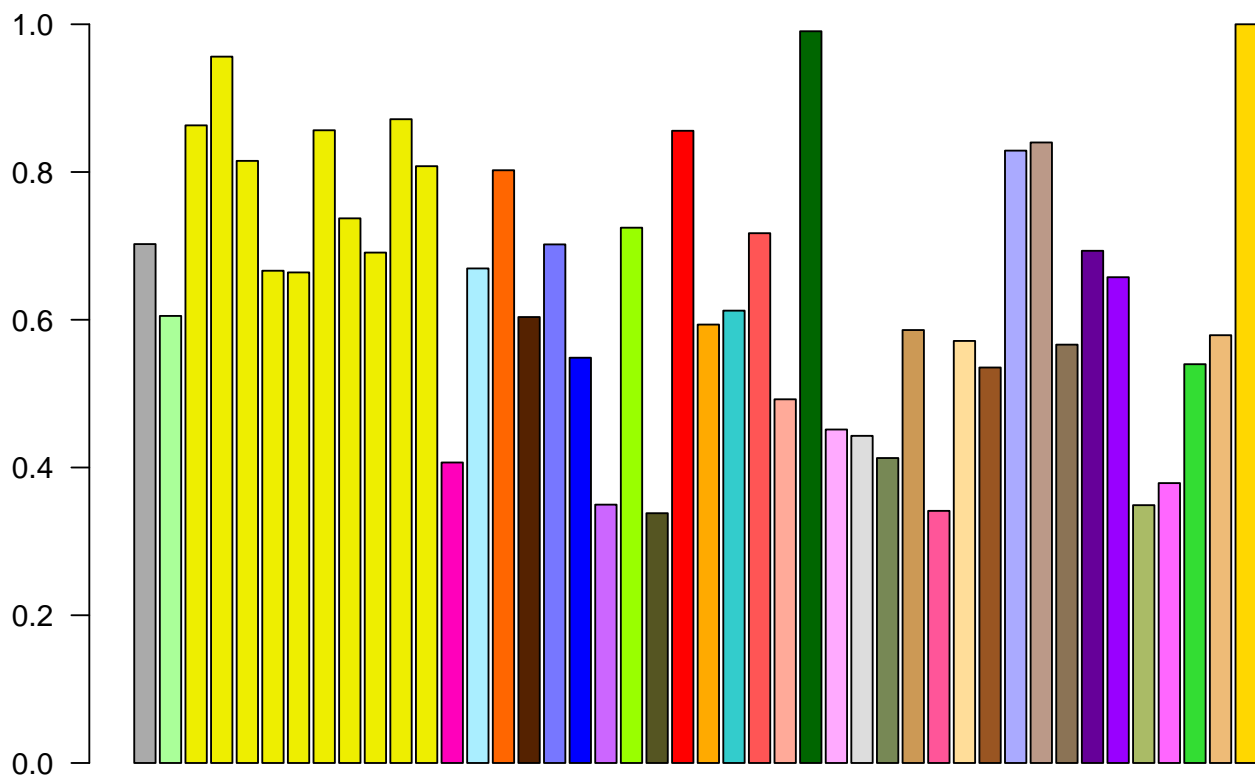
Now let's do the eigenplots:

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

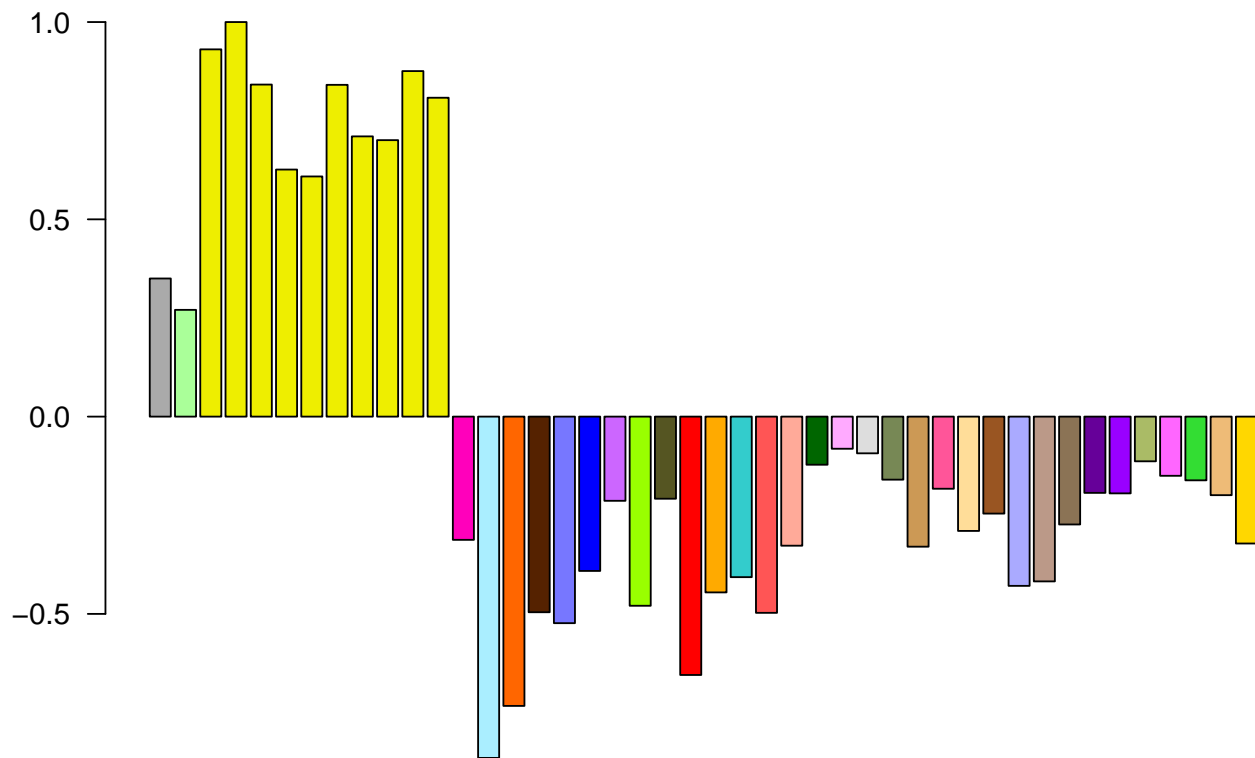
k=3
vold=svd(covmat[[k]])$v;u=svd(covmat[[k]])$u;d=svd(covmat[[k]])$d

v=vold[h,]##shuffle so correct order
names=names[h]
color.gt看ex=color.gt看ex[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"))
}
```

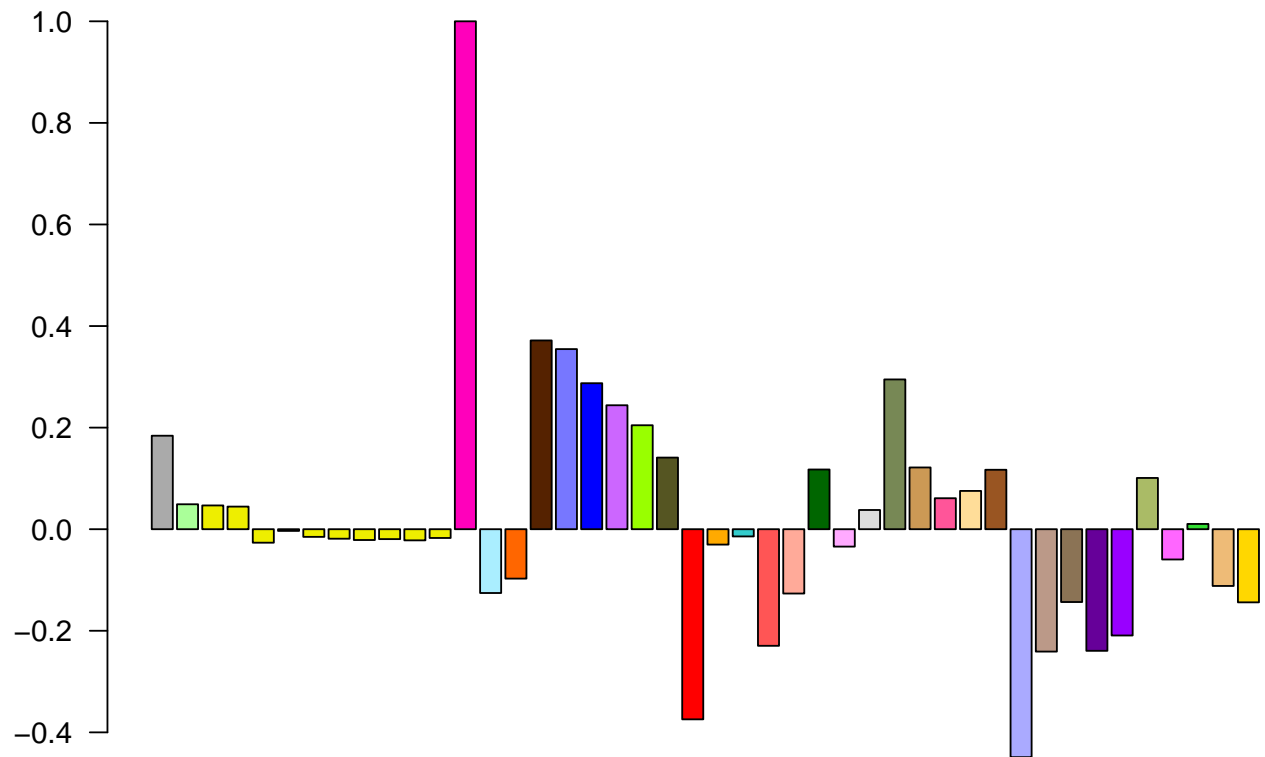
**EigenVector1Uk3**



**EigenVector2Uk3**



### EigenVector3Uk3



```
(d^2/sum(d^2))[1:3]  
# [1] 0.885241028 0.113500988 0.001257984
```