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/NGRevision/Figureswithres/")

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

z.stat=read.table("../../Data_what/covmatwithvhat.rds")

names=colnames(z.stat)

pis=readRDS("../../Data_vhat/piswithvhat.rds")$pihat

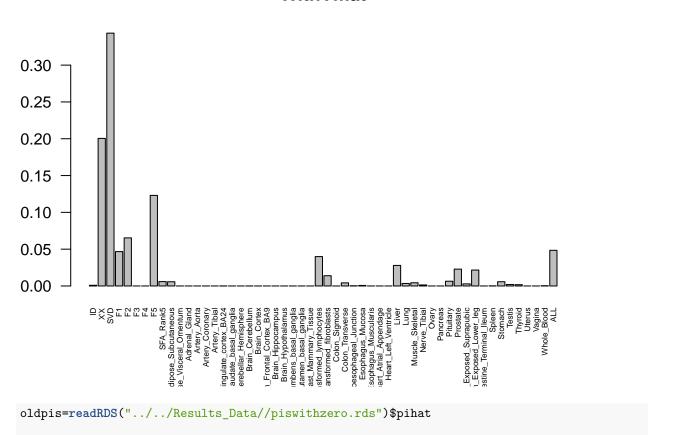
pi.mat=matrix(pis[-length(pis)],ncol=54,nrow=22,byrow = T)

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)
```

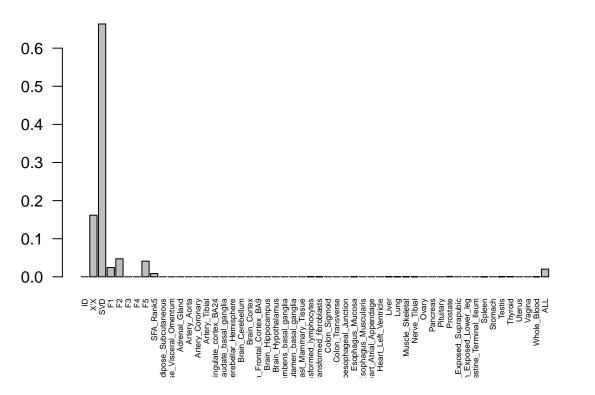
WithVmat



pi.matold=matrix(oldpis[-length(oldpis)],ncol=54,nrow=22,byrow = T)

```
colnames(pi.matold)=c("ID","X'X","SVD","F1","F2","F3","F4","F5","SFA_Rank5",c(names,"ALL"))
barplot(colSums(pi.matold),main='OLD',las=2,cex.names=0.5)
```

OLD



```
library(gplots)
library('colorRamps')
#install.packages("fields")
library(fields)
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</pre>
```

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

```
smat=(x[(h),(h)])
smat[lower.tri(smat)] <- NA
library(lattice)</pre>
```

```
#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",</pre>
                                                      "#E0F3F8", "#91BFDB", "#4575B4")))(64)
lat=x[rev(h),rev(h)]
\#lat=x[h,h]
lat[lower.tri(lat)] <- NA</pre>
n=nrow(lat)
print(levelplot(lat[n:1,],col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE,at=seq(0,1,length.out=
                                                        Testis
                                 Pituitary
            Brain_Cerebellar_Hemisphere
               Brain_Cerebellum
Brain_Frontal_Cortex_BA9
   Brain_Holla_Cottee_BA9

Brain_Hippocampus

Brain_Hypothalamus

Brain_Caudate_basal_ganglia

Brain_Putamen_basal_ganglia

Brain_Anterior_cingulate_cortex_BA24

Brain_Cortex
                                                                                                                                                       0.8
Brain_Nucleus_accumbens_basal_ganglia Whole_Blood
            Cells_Transformed_fibroblasts
Adipose_Subcutaneous
     Skin_Sun_Exposed_Lower_leg
Skin_Not_Sun_Exposed_Suprapubic
Cells_EBV.transformed_lymphocytes
Lung
                                                                                                                                                       0.6
          Small_Intestine_Terminal_Ileum
             Artery_Tibial
Adipose_Visceral_Omentum
Breast_Mammary_Tissue
Artery_Aorta
                         Artery_Coronary
Thyroid
Ovary
Prostate
                                                                                                                                                       0.4
                                   Spleen
                        Colon_Transverse
Vagina
Stomach
                                Pancreas
 Muscle_Skeletal
Muscle_Skeletal
Esophagus_Muscularis
Esophagus_Gastroesophageal_Junction
Heart_Left_Ventricle
Heart_Atrial_Appendage
                                                                                                                                                       0.2
                                     Liver
                                   Uterus
                           Adrenal Gland
                           Colon_Sigmoid
                             Nerve_Tibial
                                   Brain 1807
```

#print(levelplot(lat,col.regions = clrs,xlab = "",ylab = "",colorkey = TRUE))

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
v=vold[h,]##shuffle so correct order
names=names[h]
```

EigenVector1Uk3

