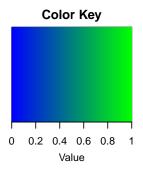
uk3

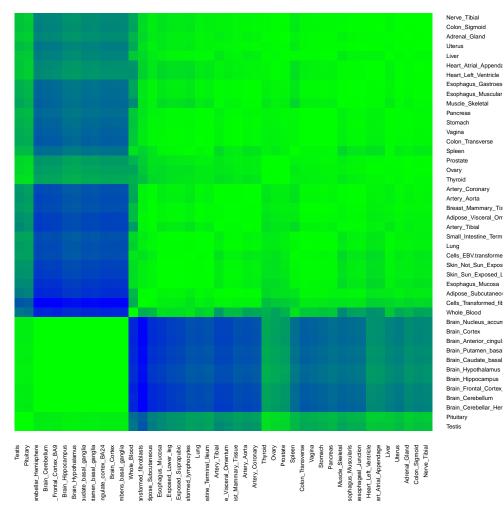
Here we plot the correlation matrix and the first 3 eigenvectors of Uk3.

library('knitr')

```
knitr::opts_chunk$set(cache=TRUE)
opts_chunk$set(fig.path = "/Users/sarahurbut/Dropbox/PaperEdits/Paper/Figures/")
covmat=readRDS("../Data/covmatAug13withED.rds")
z.stat=read.table("../Data/maxz.txt")
names=colnames(z.stat)
pis=readRDS("../Data/pisAug13withED.rds")$pihat
pi.mat=matrix(pis,ncol=54,nrow=22,byrow = T)
library(gplots)
library(ggplot2)
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
\# h=heatmap.2((x),symm=TRUE,dendrogram="none",density="none",trace="none",col=blue2green(256),main=past
\# heatmap.2((x[h\$rowInd, h\$rowInd]), Colv=FALSE, Rowv=FALSE, symm=TRUE, dendrogram="none", density="none", training for the strength of th
h=heatmap.2((x), #symm=TRUE,
                                       dendrogram="none", density="none", trace="none", col=blue2green(256), main=paste0("Cov2CorU", k,
```



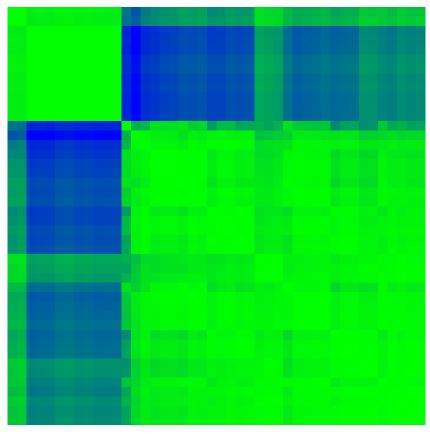
Cov2CorU3pihat=0.67



heatmap.2((x[h\$rowInd,h\$rowInd]),Colv=FALSE,Rowv=FALSE,symm=TRUE,dendrogram="none",density="none",trace

Color Key 0 0.2 0.4 0.6 0.8 1 Value

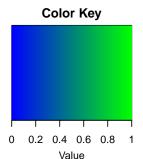
Cov2CorU3pihat=0.67



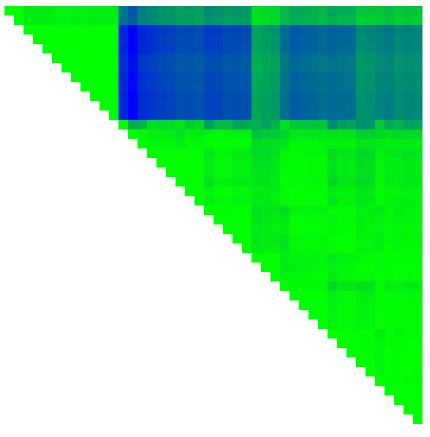
Pituitary Brain_Cerebellar_Her Brain_Cerebellum Brain Frontal Cortex Brain_Hippocampus Brain_Hypothalamus Brain Caudate basal Brain_Putamen_basa Brain_Anterior_cingul Brain Cortex Brain Nucleus accur Whole_Blood Cells_Transformed_fit Adipose Subcutaneo Esophagus_Mucosa Skin_Sun_Exposed_L Skin Not Sun Expos Cells_EBV.transforme Small Intestine Term Artery_Tibial Adipose_Visceral_Orr Breast_Mammary_Tis Artery Aorta Artery_Coronary Thyroid Ovary Prostate Spleen Colon Transverse Vagina Pancreas Muscle_Skeletal Esophagus_Muscular Esophagus_Gastroes Heart Left Ventricle Heart_Atrial_Appenda Uterus Adrenal_Gland Nerve_Tibial

Teets
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Profiles — Penturary
Brain _ Cerebellum
Brain _ Cerebellum
Brain _ Hippocarmus
Brain _ Cortex
March _ Desal_ganglia
Whole Blood
ansformed_Ibriodhasis
Signes_Subcutareous
Exposed_Lower_leg
Exposed_Lower_leg
Exposed_Lower_leg
Exposed_Lower_leg
Stronged _ Murch _ Stronger _ Lung
stine_Terminal_lieum
Artery_Aorta
Artery_Tibail
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Artery_Townsun
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Arterial_Appendage
Arterial_Appendage
Arterial_Appendage
Colon_Sigmoid
Colon_Sigmoid
Colon_Sigmoid

```
main=paste0("Cov2CortUk3"),
cexRow=0.5,cexCol=0.5,cex.main=0.5)
```



Cov2CortUk3



Pituitary Brain_Cerebellar_Her Brain_Cerebellum Brain Frontal Cortex Brain_Hippocampus Brain_Hypothalamus Brain_Caudate_basal Brain_Putamen_basa Brain_Anterior_cingul Brain_Cortex Brain Nucleus accur Whole_Blood Cells_Transformed_fit Adipose Subcutaneo Esophagus_Mucosa Skin_Sun_Exposed_L Skin_Not_Sun_Expos Cells_EBV.transforme Lung Small_Intestine_Term Artery_Tibial Adipose_Visceral_Orr Breast_Mammary_Tis Artery_Aorta Artery_Coronary Ovary Prostate Spleen Colon Transverse Vagina Stomach Pancreas Muscle Skeletal Esophagus_Muscular Esophagus_Gastroes Heart_Left_Ventricle Heart_Atrial_Appenda Uterus Adrenal_Gland Colon_Sigmoid Nerve_Tibial

Pitulary

Pitulary

Pitulary

Piconal Cortex, BA9

Brain, Lipportalemus

Brain, Cortex

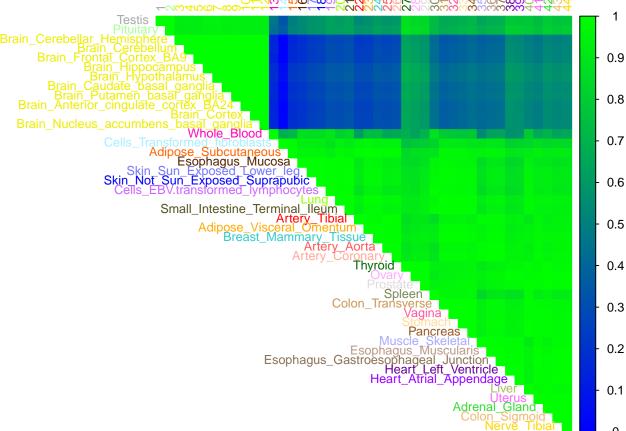
Artery, Aorra

Artery, Aorr

```
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])
library('corrplot')
```

```
colnames(x)=NULL
corrplot((x[h$rowInd,h$rowInd]),type="upper",cl.lim=c(0,1),tl.col=col[h$rowInd],tl.cex=0.8,method="color
## Warning in ind1:ind2: numerical expression has 2 elements: only the first
```

Warning in ind1:ind2: numerical expression has 2 elements: only the first ## used



Let's try with different ordering:

```
all.tissue.order=read.table("../../Dropbox/alltissueorder.txt")[,1]
  x=cov2cor(covmat[[k]])
x[x<0]=0
  colnames(x)=names
  rownames(x)=names
smat=x[(all.tissue.order),(all.tissue.order)]
smat[lower.tri(smat)] <- NA</pre>
heatmap.2(smat, #symm=TRUE,
          Rowv=FALSE, Colv=FALSE,
```

```
dendrogram="none",density="none",trace="none",#col=redblue,
col=blue2green(256),
main=paste0("Cov2CortUk3"),
cexRow=0.5,cexCol=0.5,cex.main=0.5)
```

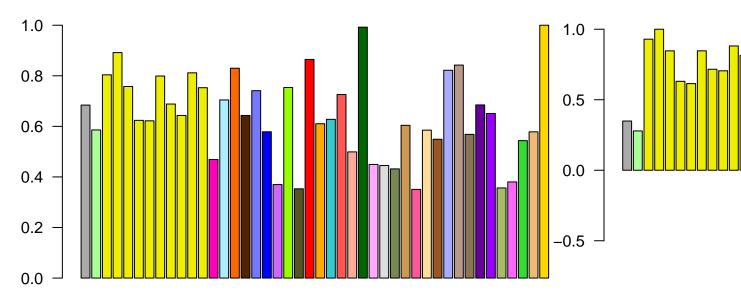
Eigenplots:

```
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,]

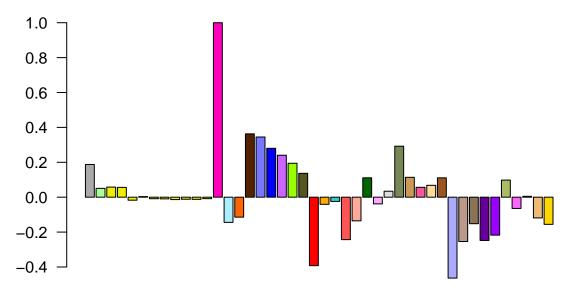
names=colnames(z.stat)
vold=svd(covmat[[k]])$v;u=svd(covmat[[k]])$u

v=vold[h$rowInd,]##shuffle so correct order
names=names[h$rowInd]
color.gtex=color.gtex[h$rowInd,]
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



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.