

Sample single cell analysis shared with canvasXpressR

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```
library(canvasXpressR)

## Load rt-qpcr data from Guo et al.
data(mat)

## Principal components analysis with K means clustering
set.seed(0)
basePca <- prcomp(mat)
data <- basePca$x[,1:2]
sg <- kmeans(data, centers=3)$cluster
sg[sg==1] <- 'TE'; sg[sg==2] <- 'PE'; sg[sg==3] <- 'EPI';
names(sg) <- rownames(data)
varAnnot <- data.frame(sg)
colnames(varAnnot) <- 'Cell Type'
cx <- canvasXpress(data, varAnnot=varAnnot, graphType='Scatter2D', colorBy='Cell Type')
write(canvasXpressHTML(cx), "pca.html")

## Loading required package: jsonlite

## Warning: package 'jsonlite' was built under R version 3.2.2

## Expression heatmap
cmat <- t(mat)
cx <- canvasXpress(cmat, smpAnnot=varAnnot, graphType='Heatmap',
  smpOverlays=list('Cell Type'),
  colorSpectrum=list("blue", "white", "red"),
  heatmapIndicatorHeight=50,
  heatmapIndicatorHistogram=TRUE,
  heatmapIndicatorPosition='topLeft',
  heatmapIndicatorWidth=60,
  samplesClustered=TRUE,
  variablesClustered=TRUE,
  showSampleNames=FALSE)
write(canvasXpressHTML(cx), "heatmap.html")

## Boxplots
cx <- canvasXpress(t(mat), smpAnnot=varAnnot,
  graphType='Boxplot',
  groupingFactors=list('Cell Type'),
  graphOrientation="vertical")
write(canvasXpressHTML(cx, width=1200), "boxplot.html")

## Trajectories / Trees
library(igraph)
```

```
##  
## Attaching package: 'igraph'
```

```
## The following objects are masked from 'package:stats':  
##  
##      decompose, spectrum
```

```
## The following object is masked from 'package:base':  
##  
##      union
```

```
dis <- dist(mat[1:50,]) ## small tree  
g <- graph.adjacency(as.matrix(dis), weighted=TRUE)  
gmst <- mst(g) ## igraph object  
nodeData <- lapply(names(V(gmst)), function(x) list(name=x, id=x, group=sg[x]))  
edgeData <- apply(get.edgelist(gmst), 1, function(x) list(id1=x[1], id2=x[2]))  
cx <- canvasXpress(nodeData=nodeData,  
                  edgeData=edgeData,  
                  graphType="Network",  
                  colorNodeBy="group",  
                  nodeSize=30,  
                  showAnimation=TRUE)  
write(canvasXpressHTML(cx), "graph.html")
```