

HeatmapR

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```
setwd('/Users/davidkaplan/Desktop/Ewing/Ahood')

library(dplyr)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(tidyr)
library(tibble)
library(ggplot2)
library(RColorBrewer)
library(reshape)

##
## Attaching package: 'reshape'
## The following objects are masked from 'package:tidyr':
##
##   expand, smiths
## The following object is masked from 'package:dplyr':
##
##   rename

library(plotly)

##
## Attaching package: 'plotly'
## The following object is masked from 'package:reshape':
##
##   rename
## The following object is masked from 'package:ggplot2':
##
##   last_plot
## The following object is masked from 'package:stats':
##
```

```

##      filter
## The following object is masked from 'package:graphics':
##
##      layout
library(cluster)
library(NbClust)
library(factoextra)

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
library(dendextend)

##
## -----
## Welcome to dendextend version 1.15.1
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## Or contact: <tal.galili@gmail.com>
##
## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## -----
##
## Attaching package: 'dendextend'
##
## The following object is masked from 'package:stats':
##
##      cutree
library(gsubfn)

## Loading required package: proto
## Warning in doTryCatch(return(expr), name, parentenv, handler): unable to load shared object '/Library
##   dlopen(/Library/Frameworks/R.framework/Resources/modules//R_X11.so, 6): Library not loaded: /opt/X
##   Referenced from: /Library/Frameworks/R.framework/Versions/4.0/Resources/modules/R_X11.so
##   Reason: image not found
##
## Could not load tcltk. Will use slower R code instead.
Loading datasets
CRISPR_gene_effect <- read.csv('CRISPR_gene_effect.csv')
AJUBA <- read.csv('Ajuba_to_colorectal.csv')

Filter top 50 gene names (Gets rid of values)
AJUBA_top <- AJUBA[1:50,-2]
AJUBA_top <- as.data.frame(AJUBA_top)

Filter only for colorectal cancer cell lines
sample_info <- read.csv('sample_info.csv')
target_disease <- filter(
  .data=sample_info,

```

```

    primary_disease == 'Colon/Colorectal Cancer'
)

DepMapID <- CRISPR_gene_effect %>%
  filter(DepMap_ID %in% target_disease$DepMap_ID)

```

Filter for only the top 50 genes associated with AJUBA

```
Genes <- DepMapID[,which((names(DepMapID) %in% AJUBA_top$AJUBA_top)==TRUE)]
```

Add Cell lines as index

```
rownames(Genes) <- DepMapID$DepMap_ID
```

Transpose data

```
gene_t <- t(Genes)
gene_t[,0]
```

```

##
## AKR1D1..6718.
## AMER3..205147.
## CCM2..83605.
## CMTM5..116173.
## CTDNEP1..23399.
## CYTH1..9267.
## DDIT3..1649.
## DHRS1..115817.
## EIF4G3..8672.
## ETNPPL..64850.
## HAX1..10456.
## HS6ST1..9394.
## INKA1..389119.
## KRTAP20.2..337976.
## LEXM..163747.
## LOR..4014.
## LYZ..4069.
## MDGA2..161357.
## METTL17..64745.
## NBL1..4681.
## NMI..9111.
## NOL8..55035.
## NR2C2AP..126382.
## NUP58..9818.
## OPN4..94233.
## P2RY13..53829.
## R3HDM2..22864.
## RAB3IP..117177.
## REM2..161253.
## RPF2..84154.
## RPP38..10557.
## RPS16..6217.
## RRS1..23212.
## RTF2..51507.
## SAMD13..148418.
## SELE..6401.

```

```
## SH2D5..400745.
## SLC30A6..55676.
## SNRNP70..6625.
## SPINK9..643394.
## SSB..6741.
## TCERG1..10915.
## TCHH..7062.
## TNP2..7142.
## TNRC18..84629.
## TPI1..7167.
## TXNRD1..7296.
## UBXN10..127733.
## UTP25..27042.
## WDR75..84128.
```

```
data_melt <- melt(gene_t)
```

Plot heatmap

```
my_matrix <- as.matrix(gene_t)
# coul <- colorRampPalette(brewer.pal(8, "PiYG"))(25)
heatmap(my_matrix)
```

