

# Heatmap4 Vignette

Anishka Dhar

5/3/2022

## 1. Introduction

This package takes the original heatmap function and reduces the argument complexity.

A heatmap is a false color image (image(t(x))) with a dendrogram added to the top and left side. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out.

## 2. Loading Libraries

```
library(heatmap4)
```

## 3. Example Data

We will use the data sets genomDat, phen, and anno to map and generate column and row annotations.

The data set genomDat is 2x2 matrix with gene expression data (subjects, genes). The phen (phenotype) data set displays the clinical information of the subject. The anno data set consists of gene mapping information.

```
# Load the rda file from the package to access the data sets
setwd("~/Downloads/heatmap4")
load(file = 'data_gen.RData')
```

```
# Sample portion of genomDat (heatmap examples will use [1:20,1:20])
print(genomDat[1:9,1:6])
```

```
##      X1      X2      X3      X4      X5      X6
## 1 -0.27 -0.33 -0.06 -0.15  0.09 -0.57
## 2 -0.33  0.21  0.27  0.03  0.09  0.66
## 3 -0.30 -0.66 -0.06  0.12 -0.03 -0.45
## 4  0.21  1.89  0.42   NA  0.30 -0.48
## 5 -0.39 -0.30  0.09   NA -0.06 -0.39
## 6 -0.21  0.15  0.03  0.12 -0.21 -0.27
## 7 -0.12  0.78 -0.03 -0.24  0.09  0.72
## 8 -0.30  0.00 -0.03  0.06 -0.15  0.24
## 9  0.09  0.39  0.12  0.00 -0.18  0.09
```

```
# Sample portion of phen (heatmap examples will use [1:39])
print(phen[1:2,1:2])
```

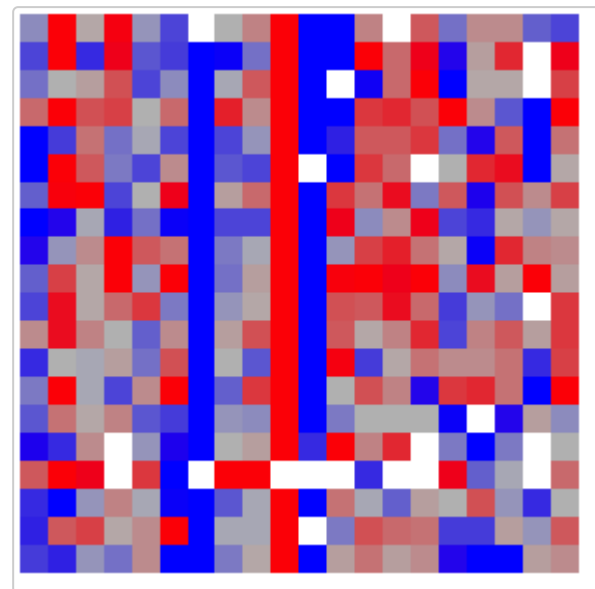
```
##      age      sex
## 18    60    male
## 30    53  female
```

```
# Sample portion of anno (heatmap examples will use [1:22])
print(anno[1:1,1:1])
```

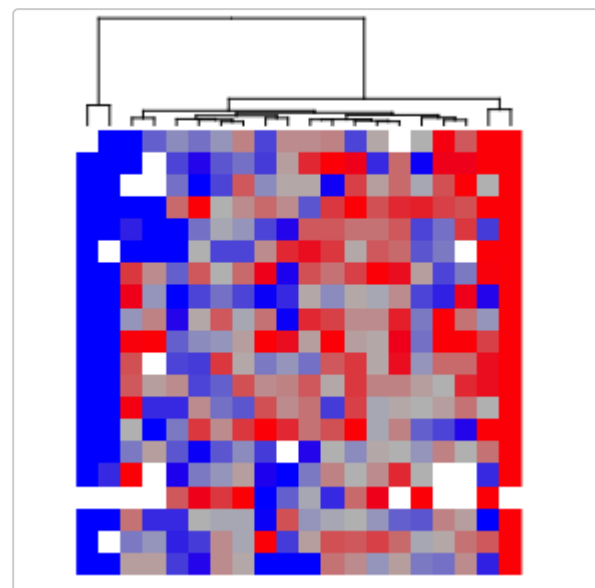
```
## [1] 215
```

## 4. Generate Heatmap

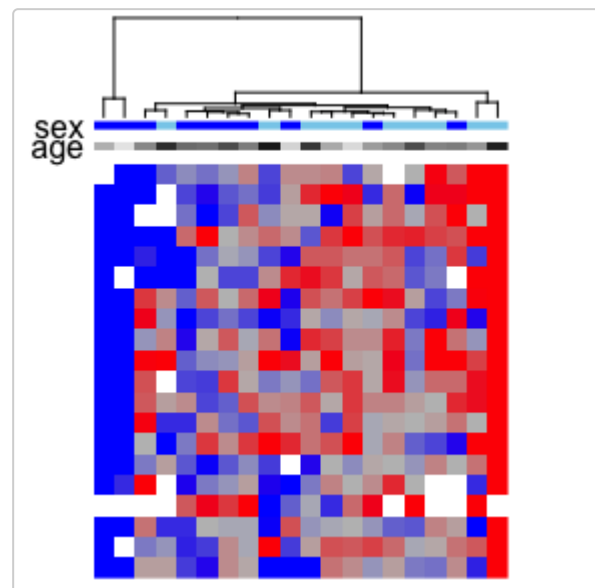
```
# Default heatmap
generate_heatmap(genomDat)
```



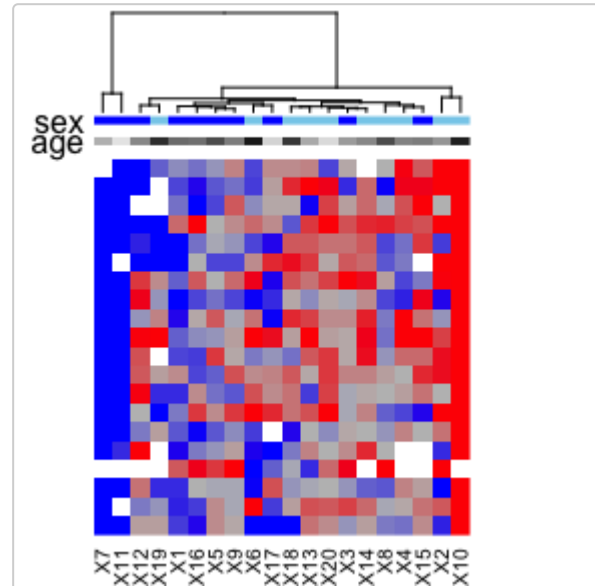
```
# Heatmap with column dendrogram
generate_heatmap(genomDat, col_dend = TRUE)
```



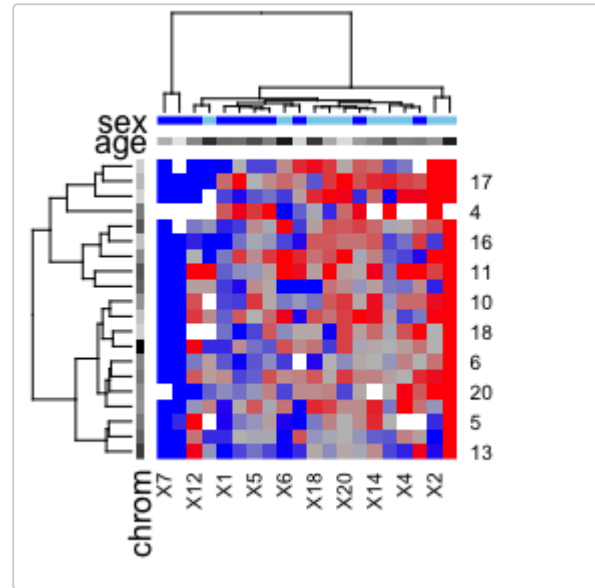
```
# Heatmap with column dendrogram, column annotations
generate_heatmap(genomDat, col_info = phen, col_dend = TRUE, col_anno = TRUE)
```



```
# Heatmap with column dendrogram, column annotations, column label
generate_heatmap(genomDat, col_lab = TRUE, col_info = phen,
col_anno = TRUE, col_dend = TRUE, plot_info = list(margins = c(2,2)))
```

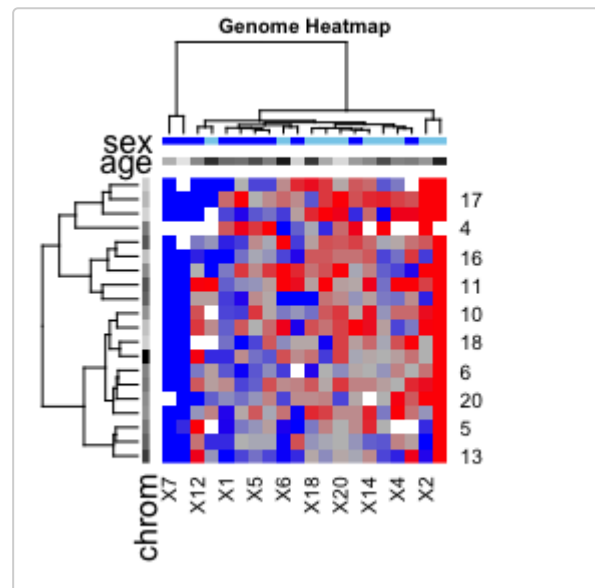


```
# Heatmap with all annotations
generate_heatmap(genomDat, col_lab = TRUE, row_lab = TRUE, col_anno = TRUE,
row_anno = TRUE, col_info = phen, row_info = anno, col_dend = TRUE,
row_dend = TRUE, plot_info = list(margins = c(5,5)))
```



## 5. More

```
# Add a title
generate_heatmap(genomDat, col_lab = TRUE, row_lab = TRUE, col_anno = TRUE,
row_anno = TRUE, col_info = phen, row_info = anno, col_dend = TRUE,
row_dend = TRUE, h_title = "Genome Heatmap", plot_info = list(margins = c(5,5)))
```



```
# Change plot and annotation colors and font size
main_plot = list("cexCol" = 1.25, "cexRow" = 1.5, "cexRowSide" = 1, "cexColSide" = 1 )
cate_color = list(age = list(color = c("light blue", "blue")), chrom = list(color = c("pink",
"purple")))

generate_heatmap(genomDat, col_lab = TRUE, row_lab = TRUE, col_anno = TRUE, row_anno = TRUE,
col_info = phen, row_info = anno, col_dend = TRUE, row_dend = TRUE, h_title = "Genome Heatmap",
plot_info = main_plot, heatmap_color = c("light blue","purple","pink"), col_var_info = cate_color,
row_var_info = cate_color)
```

