

Heatmap4 Vignette

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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 data.RData file from the package to access the data
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[1:9,1:6])
```

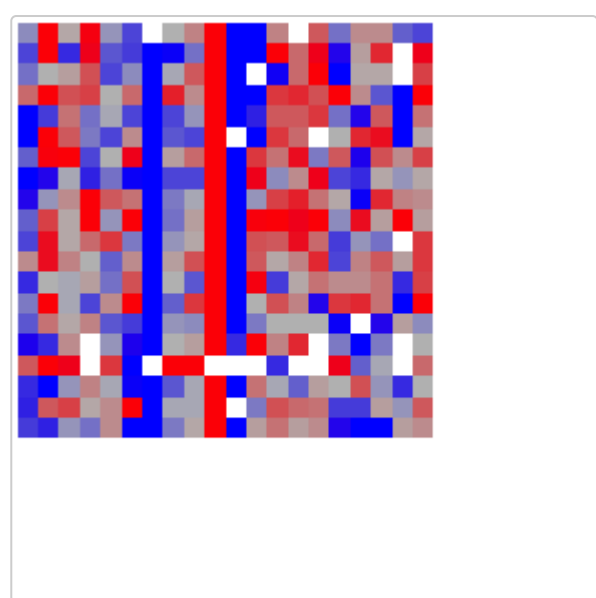
```
##      id      sex age_year smoking smoking_packYear alcohol
## 18 X1      male       60      yes                20      yes
## 30 X2      female     53      yes                35      yes
## 19 X3      male       52      yes                34      yes
## 5  X4      female     56      yes                80      yes
## 20 X5      male       65      yes                47      yes
## 21 X6      female     76      no                 0      no
## 4  X7      male       49      yes                23      yes
## 22 X8      female     65      yes                 8      no
## 23 X9      male       57      yes                40      yes
```

```
# Sample portion of anno (heatmap examples will use [1:22])
print(anno[1:2,1:2])
```

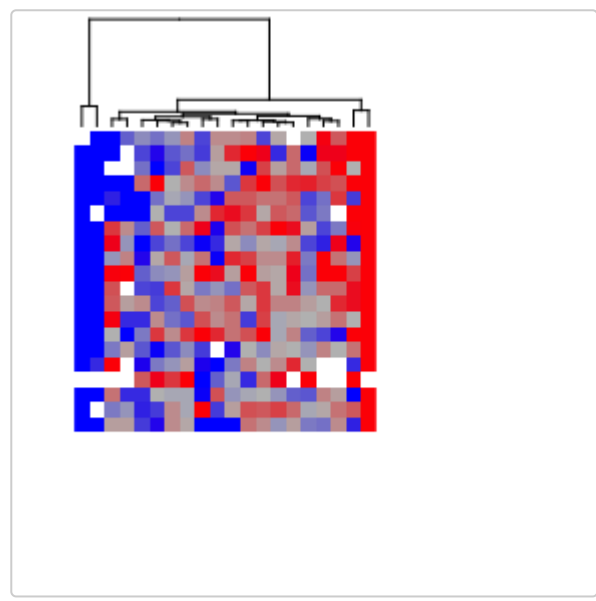
```
##      Chrom      kb
## 1         1 1082
## 3         1 3318
```

4. Generate Heatmap

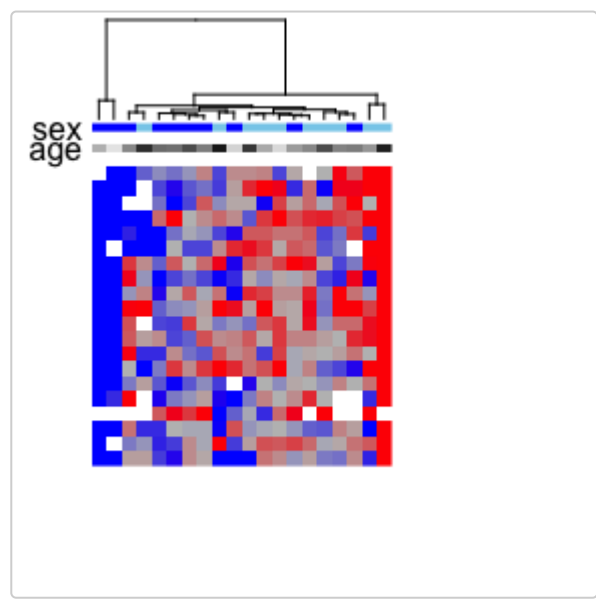
```
# Default heatmap
generate_heatmap(genomDat, input_legend = FALSE)
```



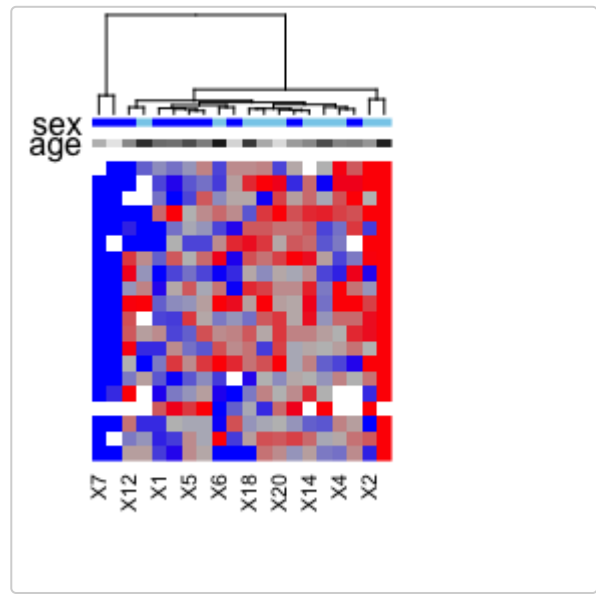
```
# Heatmap with column dendrogram
generate_heatmap(genomDat, col_info = column_df, col_dend = TRUE, input_legend = FALSE)
```



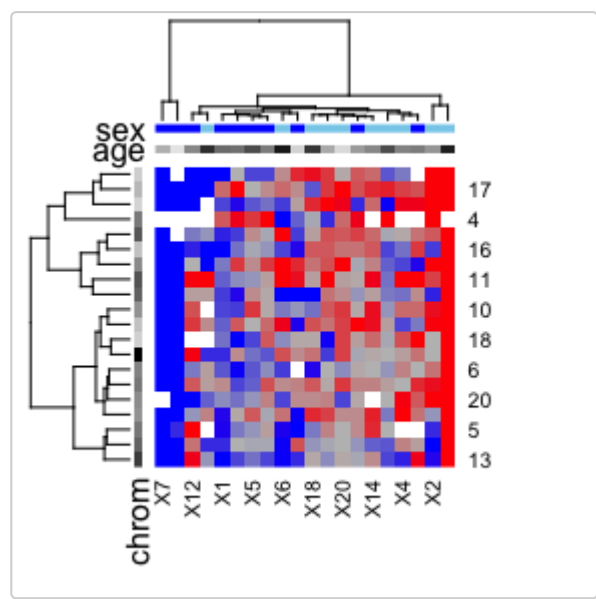
```
# Heatmap with column dendrogram, column annotations
generate_heatmap(genomDat, col_info = column_df, col_dend = TRUE, col_anno = TRUE,
input_legend = FALSE )
```



```
# Heatmap with column dendrogram, column annotations, column label
generate_heatmap(genomDat, col_lab = TRUE, col_info = column_df,
col_anno = TRUE, col_dend = TRUE, input_legend = FALSE)
```

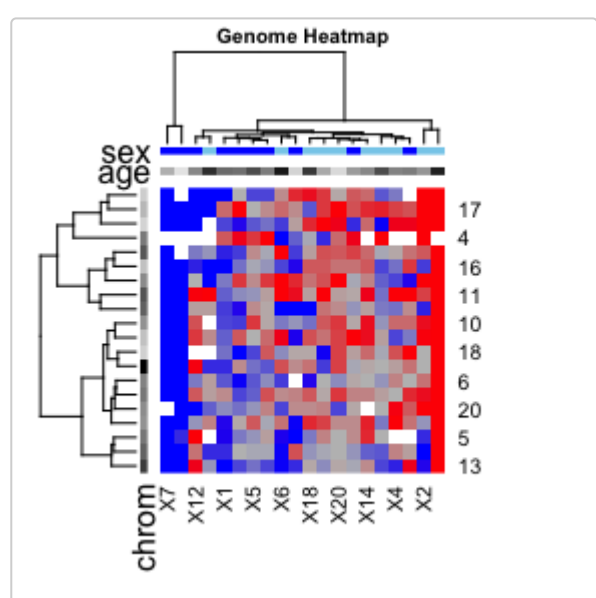


```
# Heatmap with all annotations
generate_heatmap(genomDat, col_lab = TRUE, row_lab = TRUE, col_anno = TRUE,
row_anno = TRUE, col_info = column_df, row_info = row_df, col_dend = TRUE,
row_dend = TRUE, input_legend = FALSE)
```



5. More

```
# Add a title
generate_heatmap(genomDat, col_lab = TRUE, row_lab = TRUE, col_anno = TRUE,
row_anno = TRUE, col_info = column_df, row_info = row_df, col_dend = TRUE,
row_dend = TRUE, input_legend = FALSE, h_title = "Genome Heatmap")
```



```
# Change 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 = column_df, row_info = row_df, col_dend = TRUE, input_legend =
FALSE, col_anno_var = c("age", "sex"), row_anno_var = c("chrom"), h_title = "Genome Heatmap",
plot_info = main_plot, col_var_info = cate_color, row_var_info = cate_color)
```

