

Pheatmap简介

[^https://blog.csdn.net/sinat_38163598/article/details/72770404]

pheatmap用于绘制聚类热图

- 创建测试数据

```
test <- matrix(rnorm(200), 20, 10)
```

```
test[1:10, seq(1,10,2)] <- test[1:10, seq(1,10,2)] + 3
```

```
test[11:20, seq(2,10,2)] <- test[11:20, seq(2,10,2)] + 3
```

```
test[15:20, seq(2,10,2)] <- test[15:20, seq(2,10,2)] + 3
```

- 绘图

```
pheatmap(test)
```

默认对于行和列均进行聚类：cluster_row=F, cluster_col=F分别取消行和列的聚类，还可以通过设置treeheight_row=0, treeheight_col=0不显示dendrogram

默认矩阵未进行标准化：标准化参数scale，可选"none", "row", "column"

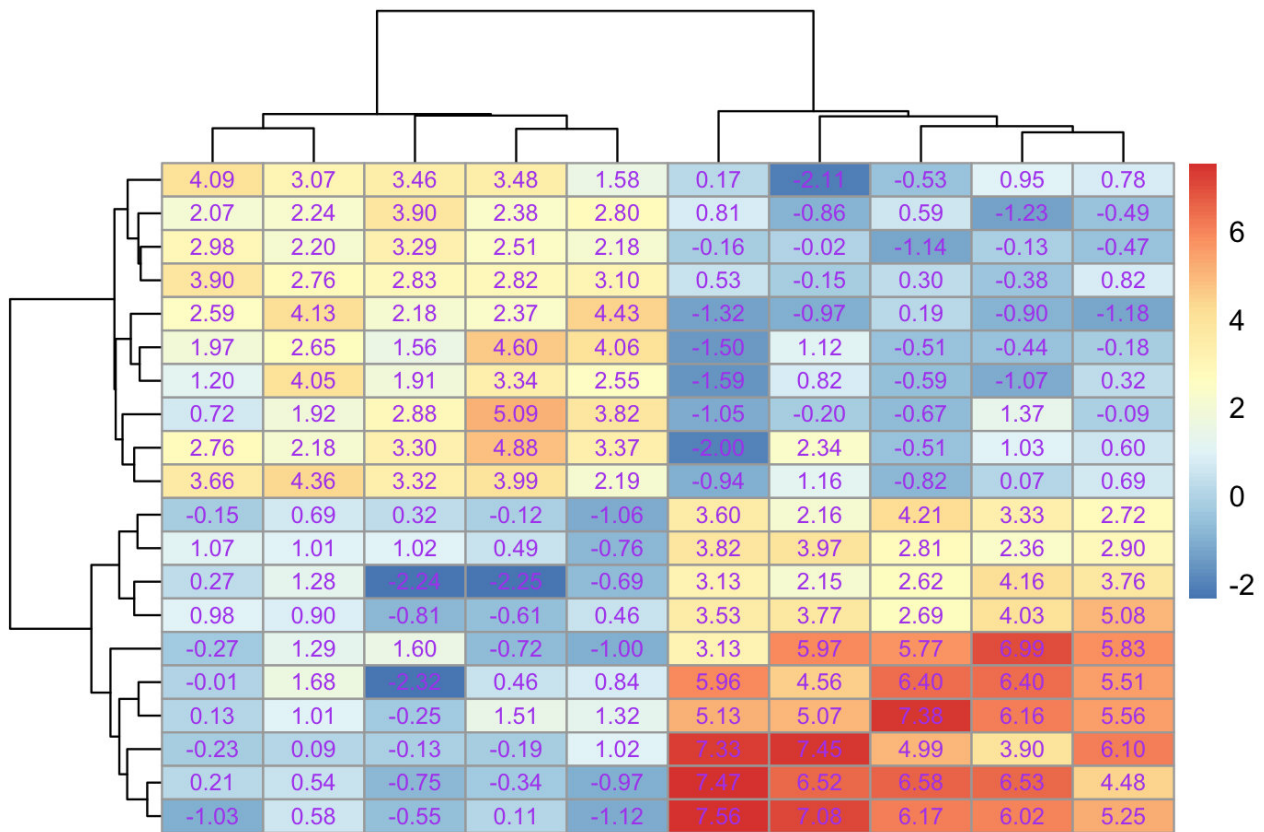
默认热图每个小块之间以灰色隔开：不想要border可以设置为NA，或通过border_color设置为其他颜色

默认legend位于右上方：通过设置legeng=F取消显示legend

热图颜色可通过color调整

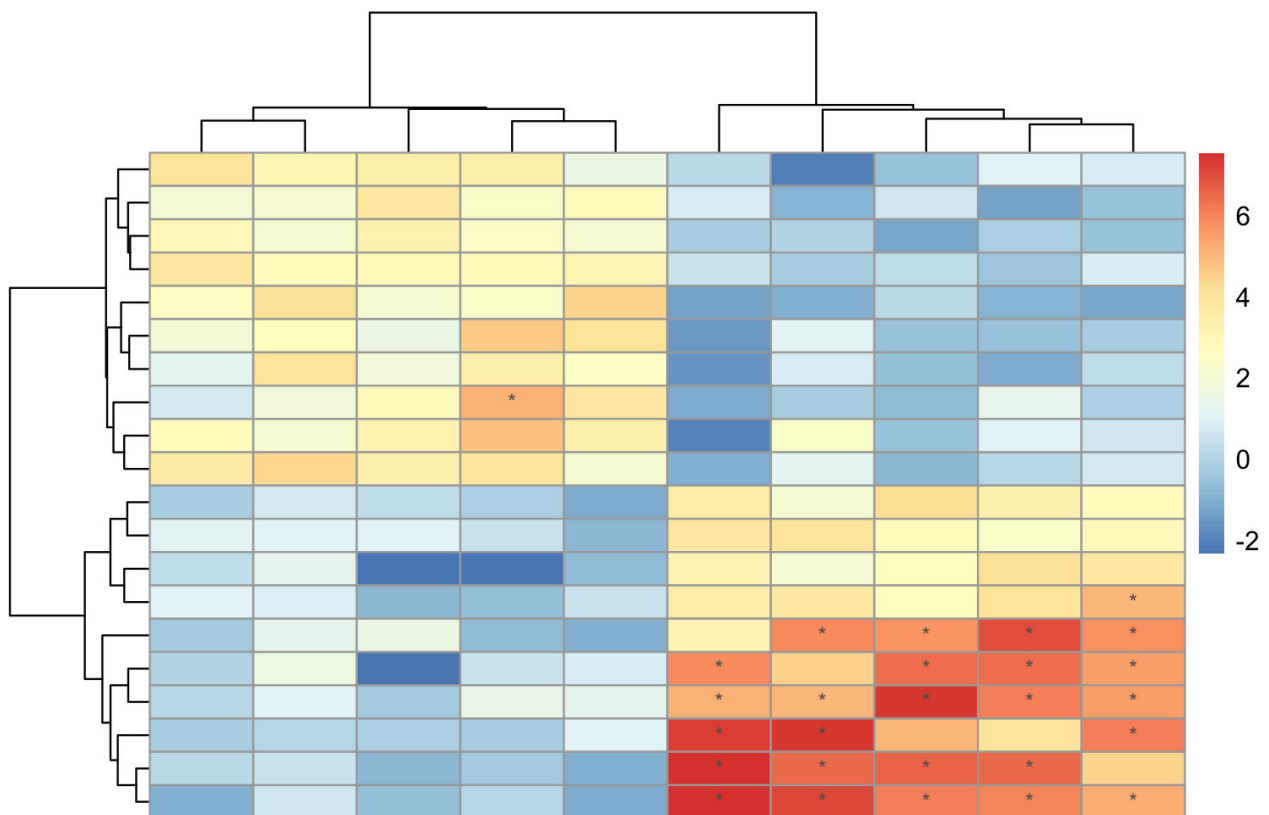
可设置参数display_numbers=T将数值显示在热图格子中，同时使用number_format设置树脂格式，例如 "%.2f" 保留两位小数， "%.1e" 科学计数法显示保留小数点后一位， number_color 设置显示内容颜色

```
pheatmap(test, display_number=T, number_format="%.2f", number_color="purple")
```



```
pheatmap(test, display_number=matrix(ifelse(test > 5, "*", ""),nrow(test)))
```

根据判断选择显示内容



参数设置改变每个格子的大小

mian设置热图的标题；fontsize设置字体大小；filename可直接将热图存出，支持格式png, pdf, tiff, bmp, jpeg，并通过width和height设置图片大小

```
pheatmap(test, cellwidth=15, cellheight=12, main="Example heatmap", fontsize=8,
filename="test.pdf")
```

通过设置注释信息，对行或者列分组，行和列名称对应test的行列名称

```
annotation_col <- data.frame(CellType=factor(rep(c("CT1","CT2",5)), Time=1:5))
```

```
rownames(annotation_col) = paste("Test",1:10,sep="")
```

```
annotation_row <-
```

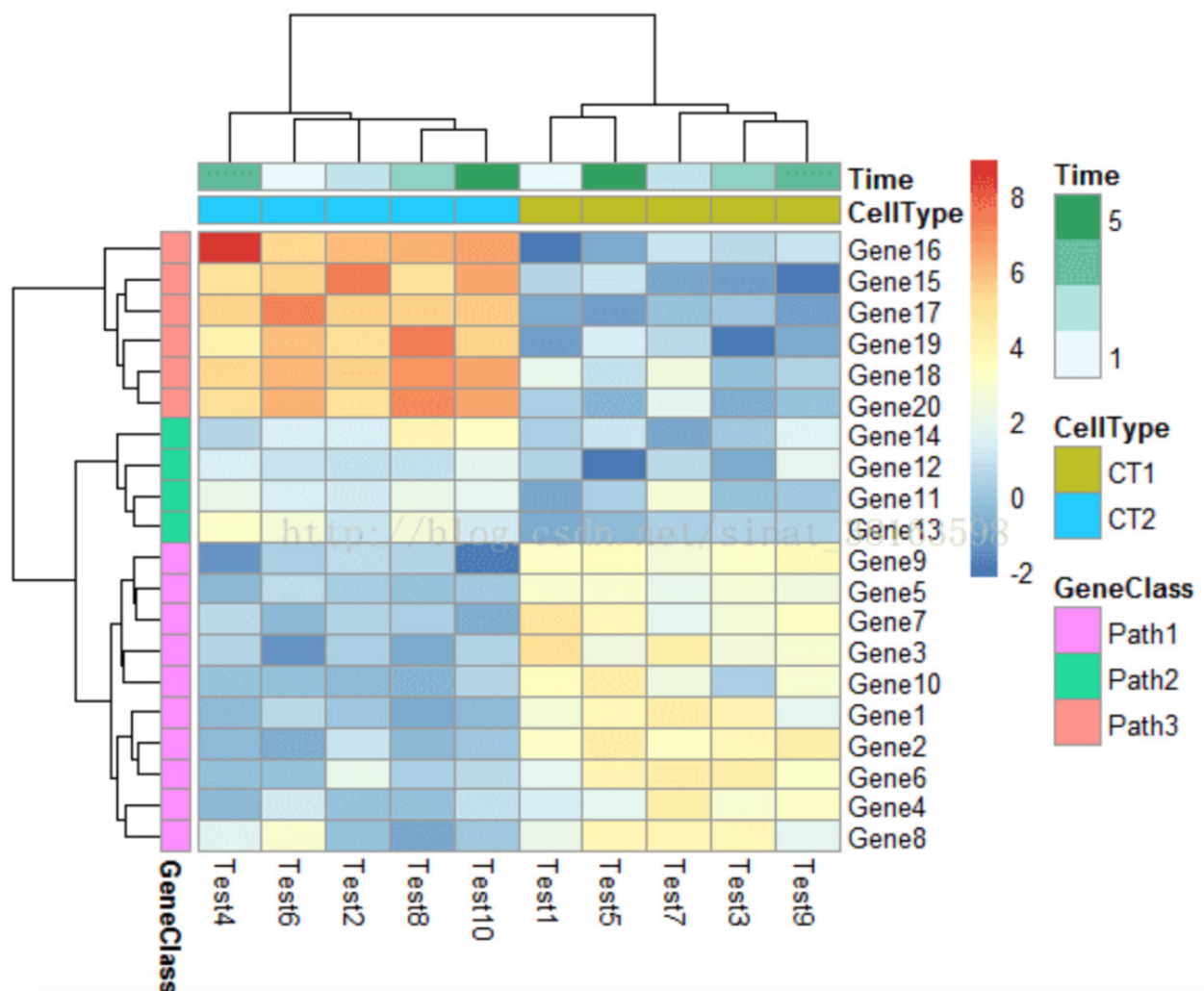
```
data.frame(GeneClass=factor(rep(c("Path1","Path2","Path3"),c(10,4,6))))
```

```
rownames(annotation_row) <- paste("Gene",1:20,sep="")
```

```
pheatmap(test, annotation_col=annotation_col, annotation_row=annotation_row)
```

```
> annotation_row["GeneClass"]
[1] Path1 Path1 Path1 Path1 Path1 Path1 Path1 Path1 Path1 Path1 Path2 Path2
[13] Path2 Path2 Path3 Path3 Path3 Path3 Path3 Path3 Path3
Levels: Path1 Path2 Path3
> annotation_col[,1]
[1] CT1 CT2 CT1 CT2 CT1 CT2 CT1 CT2 CT1 CT2
Levels: CT1 CT2
```

mac未显示出来，不知为何



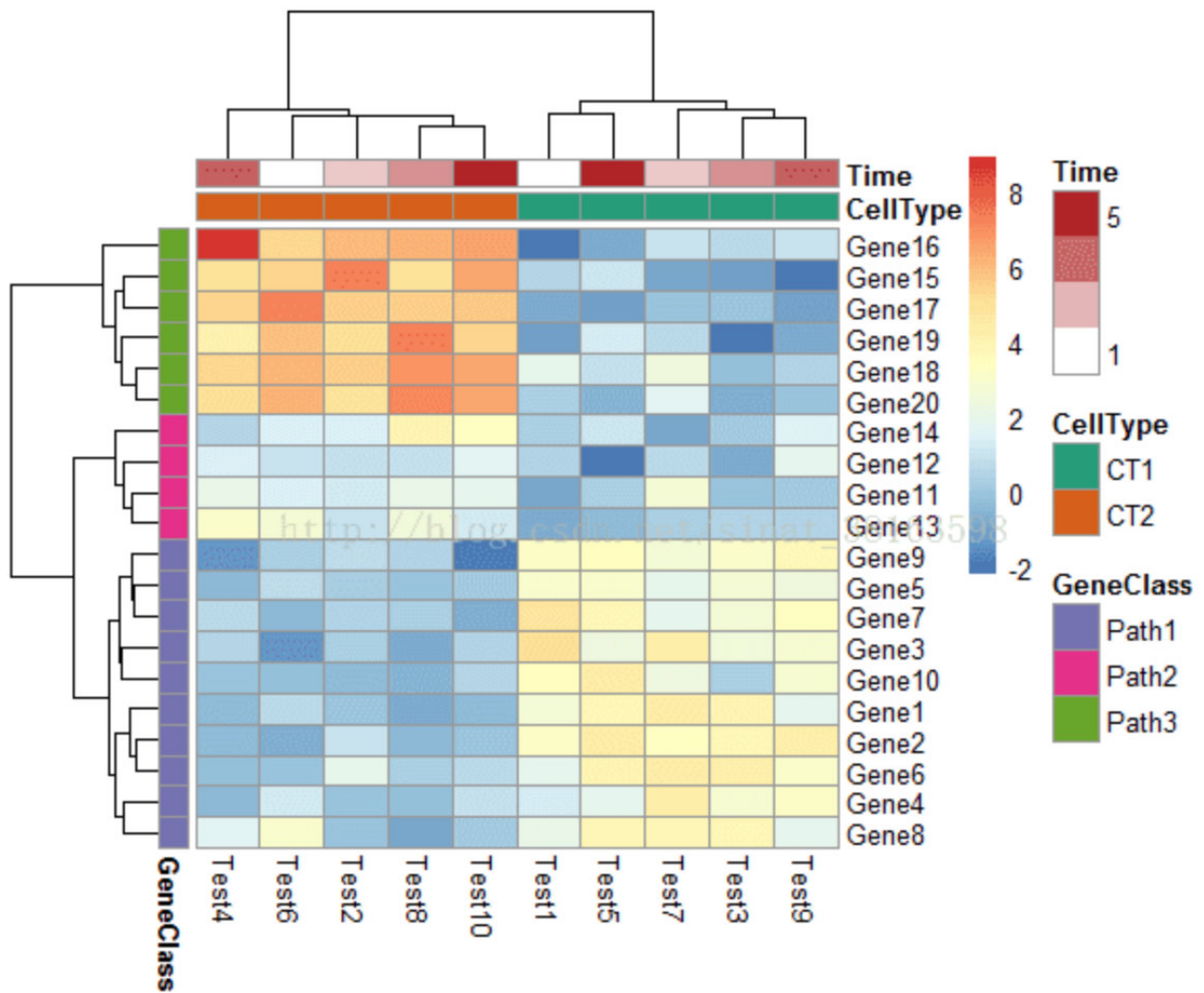
设置各个分组的颜色

```
ann_colors = list(Time = c("white", "firebrick"), CellType = c(CT1 = "#1B9E77",  
CT2 = "#D95F02"), GeneClass = c(Path1 = "#7570B3", Path2 = "#E7298A", Path3 =  
"#66A61E"))
```

list表格对应了行和列的分组信息

```
> ann_colors  
$Time  
[1] "white"      "firebrick"  
  
$CellType  
      CT1      CT2  
"#1B9E77" "#D95F02"  
  
$GeneClass  
      Path1      Path2      Path3  
"#7570B3" "#E7298A" "#66A61E"
```

```
pheatmap(test, annotation_col = annotation_col, annotation_colors = ann_colors,  
main = "Title")
```



根据特定条件将热图分隔开

cutree_rows, cutree_cols: 将行和列的聚类根据等级关系分隔开

```
pheatmap(test, cutree_rows=3, cutree_cols=2)
```

