

How can I use pheatmap() in R to create heatmaps?

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Pheatmap() is a powerful function in R that allows users to easily create heatmaps. Heatmaps are graphical representations of data where values are represented by colors on a grid. Pheatmap() takes in a matrix or data frame as input and generates a visually appealing heatmap that allows for quick and intuitive interpretation of the data. The function offers a variety of customization options such as color schemes, clustering, and annotation, making it a versatile tool for data analysis and visualization. By utilizing pheatmap() in R, users can efficiently explore their data and identify patterns, trends, and relationships in a visually appealing manner.

Use pheatmap() in R to Create Heatmaps

You can use the pheatmap() function from the pheatmap package in R to create highly customized heatmaps.

The following examples show how to use this function in practice with the following fake dataset:

```
#make this example reproducible  
set.seed(1)
```

```
#create matrix with fake data values
```

```
data = matrix(rnorm(100), 20, 5)
```

```
data = data + 3
```

```
data = data + 2
```

```
data = data + 4
```

```
#add column names and row names
```

```
colnames(data) = paste("T", 1:5, sep = "")
```

```
rownames(data) = paste("Gene", 1:20, sep = "")
```

```
#view matrix
```

```
data
```

```
T1 T2 T3 T4 T5
```

```
Gene1  2.37354619  3.918977  2.8354764  5.401618
2.431331
Gene2  3.18364332  3.782136  2.7466383  2.960760
2.864821
Gene3  2.16437139  3.074565  3.6969634  3.689739
4.178087
Gene4  4.59528080  1.010648  3.5566632  3.028002
1.476433
Gene5  3.32950777  3.619826  2.3112443  2.256727
3.593946
Gene6  2.17953162  2.943871  2.2925048  3.188792
3.332950
Gene7  3.48742905  2.844204  3.3645820  1.195041
4.063100
Gene8  3.73832471  1.529248  3.7685329  4.465555
2.695816
Gene9  3.57578135  2.521850  2.8876538  3.153253
3.370019
```

Gene10 2.69461161 3.417942 3.8811077 5.172612
3.267099

Gene11 1.51178117 3.358680 2.3981059 2.475510
1.457480

Gene12 0.38984324 1.897212 1.3879736 1.290054
3.207868

Gene13 -0.62124058 2.387672 2.3411197 2.610726
3.160403

Gene14 -2.21469989 1.946195 0.8706369 1.065902
2.700214

Gene15 1.12493092 4.622940 7.4330237 4.746367
7.586833

Gene16 -0.04493361 5.585005 7.9803999 6.291446
6.558486

Gene17 -0.01619026 5.605710 5.6327785 5.556708
4.723408

Gene18 0.94383621 5.940687 4.9558654 6.001105
5.426735

Gene19 0.82122120 7.100025 6.5697196 6.074341
4.775387

Gene20 0.59390132 6.763176 5.8649454 5.410479
5.526599

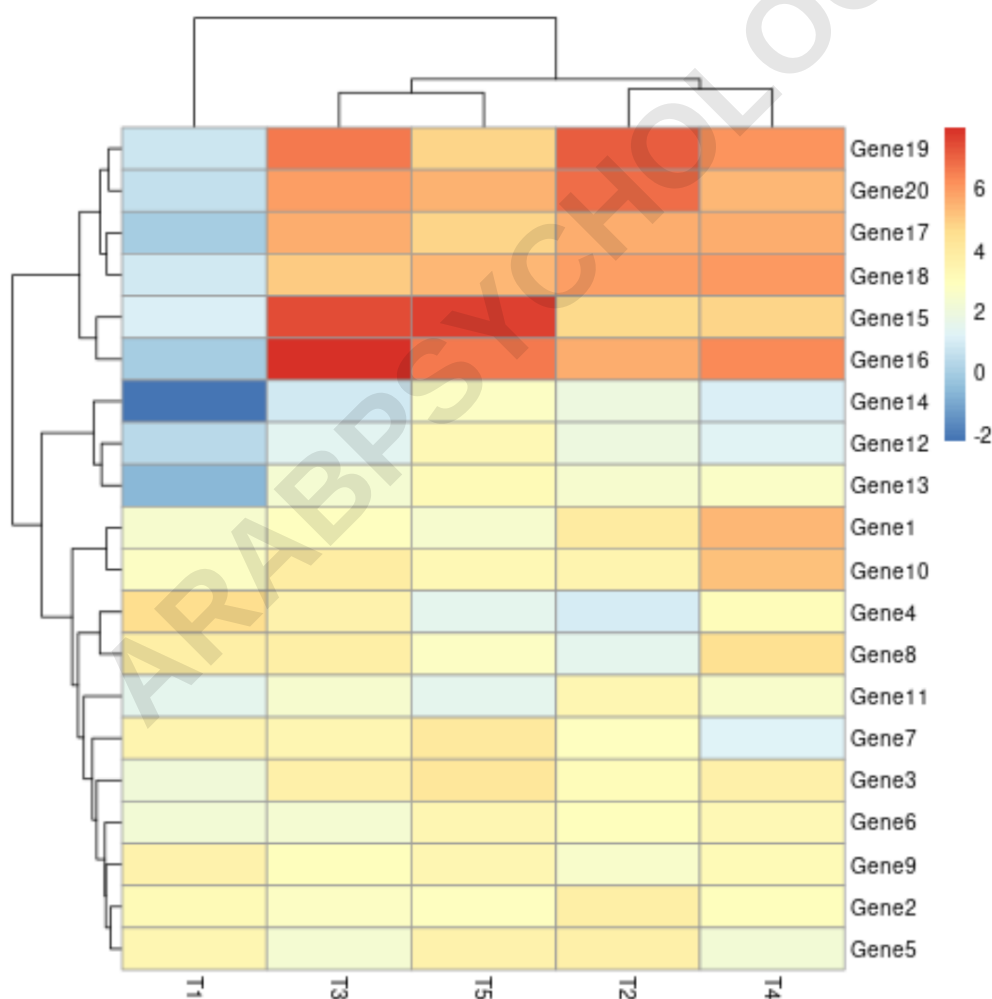
Example 1: Create Basic Heatmap

We can create a heatmap with the default settings in pheatmap to visualize all of the values in the matrix:

```
library(pheatmap)
```

```
#create basic heatmap
```

```
pheatmap(data)
```



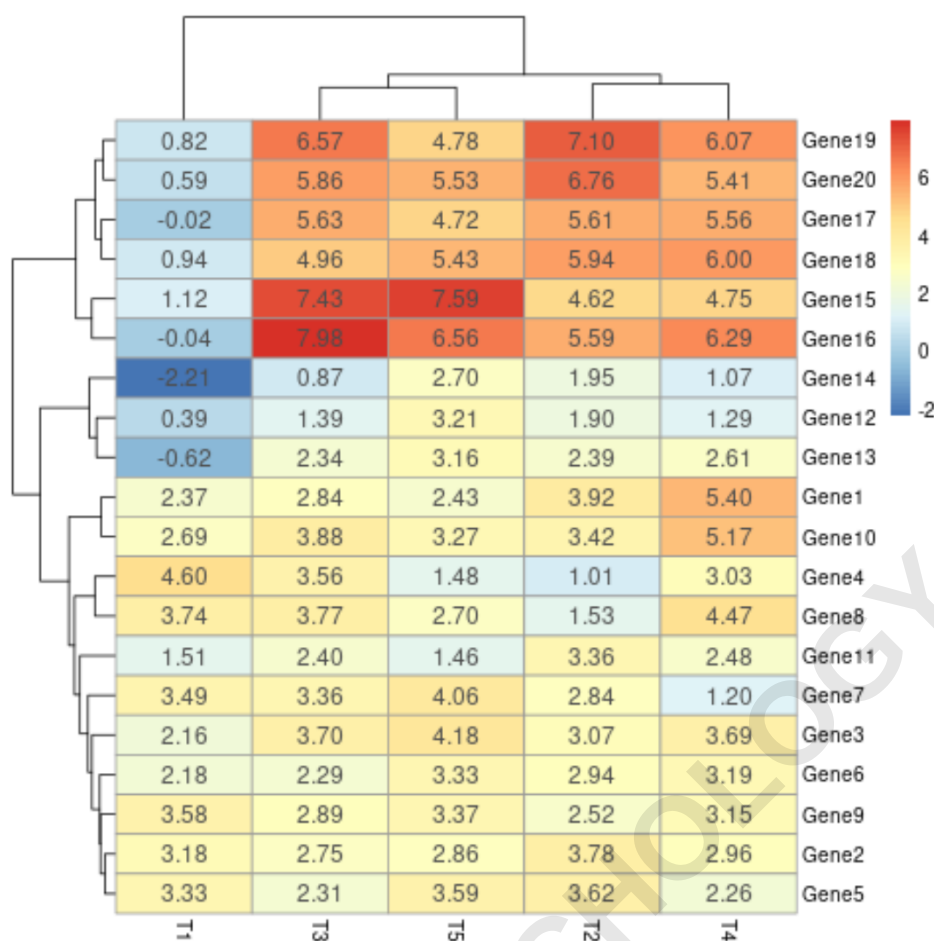
Example 2: Create Heatmap with Cell Labels

We can create use the arguments `display_numbers` and `fontsize_number` to display the numerical values in each cell of the heatmap with a specific font size:

```
library(pheatmap)
```

```
#create heatmap with numerical labels in cells
```

```
pheatmap(data,          display_numbers=TRUE,  
          fontsize_number=12)
```



Note: The default value for fontsize_number is 8.

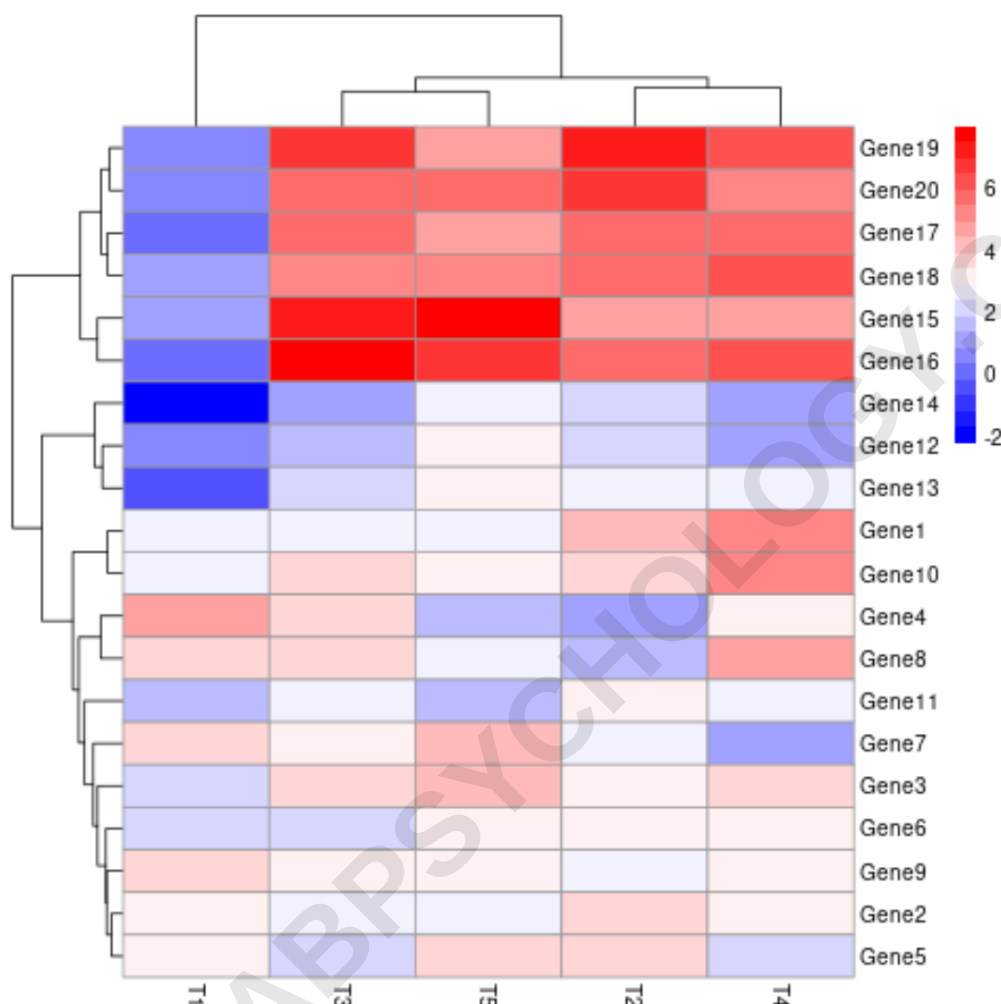
Example 3: Create Heatmap with Custom Colors

We can create use the `colorRampPalette` argument to specify the colors to use for the low, medium and high values in the heatmap as well:

```
library(pheatmap)
```

```
#create heatmap with custom colors
```

```
pheatmap(data, color=colorRampPalette(c("blue",
"white", "red"))(20))
```



The low values are now shown in blue, the middle values are shown in white, and the high values are shown in red.