

Laboratorio43-MD

Leislle R. Manjarrez O.

2023-03-07

Hecho con gusto por Leislle R. Manjarrez O.

Laboratorio 43- Mapa de calor termico con pheatmap DATOS GENETICOS TOMADOS DE Sahir Bhatnagar. PRACTICA DE CODERS

Objetivo: Realizar un heatmap con datos geneticos En este ejercicio vamos a: 1. Cargar nuestra matriz hipotetica de datos y dataframes adicionales 2. Realizar varios heatmaps

Un mapa de calor es una representacion grafica de datos que utiliza un sistema de codificacion de colores para representar diferentes valores

Primero instalar la paqueteria install.packages("pheatmap")

Llamar a la libreria

```
library(pheatmap)
```

Importar datos para realizar el laboratorio. Para este caso son 3 archivos a utilizar

```
file.choose()
```

```
## [1] "C:\\\\Users\\\\leisl\\\\OneDrive\\\\Doctorado\\\\Semestre-3\\\\Temas-Selectos-1-Complejidad-Económica\\\\Modulo3\\\\Semana7-Labs-Salas-Cápsulas\\\\Lab43\\\\heatmap_data.csv"
```

Creamos un objeto con estructura matricial con el primer archivo

```
genes <- as.matrix(read.csv("heatmap_data.csv",
                             sep = ",",
                             header = T,
                             row.names = 1))
```

Realizamos lo mismo con el segundo archivo, solo que no se crea como matriz el objeto

```
annotation_col <- read.csv ("annotation_col.csv",
                            header = T,
                            row.names = 1)
```

Realizamos lo mismo con el segundo archivo, solo que no se crea como matriz el objeto

```
annotation_row <- read.csv ("annotation_row.csv",
                            header = T,
                            row.names = 1)
```

Visualimos los objetos creados

```
head(annotation_col)
```

```
##      Exposure Type
## Patient1     X=0 T-cell
## Patient2     X=0 T-cell
## Patient3     X=0 B-cell
## Patient4     X=0 B-cell
## Patient5     X=0 B-cell
## Patient6     X=0 T-cell
```

```
head(annotation_row)
```

```
##      Pathway
## Gene1      1
## Gene2      1
## Gene3      1
## Gene4      1
## Gene5      1
## Gene6      1
```

```
head(genes)
```

```
##      Patient1 Patient2 Patient3 Patient4 Patient5 Patient6
## Gene1 -0.1914190 -1.23415247 -0.04346178 0.14572108 -0.4017205 -0.47780933
```

```

## Gene2 -0.8978632 0.39549549 0.56691534 -0.59602679 -0.5403446 0.30994709
## Gene3 1.0639177 2.79564490 -0.49031509 -0.64460585 0.8419138 -0.03060928
## Gene4 0.3524772 0.07475244 0.15824275 0.06590853 1.0301932 -0.75700251
## Gene5 -0.5016748 0.21616881 -0.86702910 2.05925069 -0.2852306 0.38657171
## Gene6 0.8912122 0.19006278 0.45290320 0.22524625 -1.3451477 0.19676648
## Patient7 Patient8 Patient9 Patient10 Patient11 Patient12
## Gene1 0.72489958 -0.8400540 -0.26876091 0.8554139 -0.38300228 2.1056414
## Gene2 -2.56387048 -0.8002420 -0.93974510 -1.4978654 1.05754874 -0.1412128
## Gene3 1.21073382 0.2117729 -1.80738611 -0.1644144 -0.93277688 -0.7008772
## Gene4 -0.06960328 -0.6135344 -0.97209294 -1.9856584 0.33354084 -0.3210905
## Gene5 -0.61616107 0.3948389 0.01428765 0.1381662 -1.24444669 1.0542546
## Gene6 0.87490575 1.8090748 0.56535820 -1.3780365 0.02064252 0.7432685
## Patient13 Patient14 Patient15 Patient16 Patient17 Patient18
## Gene1 -2.0796547 0.3926738 -0.3275861 0.06475283 -0.9468868 2.2042625
## Gene2 0.1824537 0.7270752 0.7598014 -0.79105318 1.1075292 -1.2417662
## Gene3 0.7580885 -0.4085302 -0.5938818 -2.21024093 0.3202009 -0.3225851
## Gene4 -1.7248673 -0.8580878 -0.8287558 0.10434044 -0.4613396 -1.5759535
## Gene5 -0.8787687 0.4198948 0.6714675 -1.50933762 0.5416448 -0.5347452
## Gene6 -0.3934806 -0.2330466 1.9699721 0.67023026 0.0777672 -0.3915463
## Patient19 Patient20 Patient21 Patient22 Patient23 Patient24
## Gene1 0.1305819 -0.9590820 0.01324484 0.13116034 -0.39338267 -0.86842820
## Gene2 1.4334107 0.6888356 0.19155636 0.04112143 -0.05389741 -2.28008430
## Gene3 -0.5807339 -0.5930431 0.91492888 0.48364813 0.45701613 -0.53466053
## Gene4 -2.3485178 -0.1821325 1.15552779 -0.71283716 0.51263785 0.91432865
## Gene5 -1.0311090 -0.4013906 0.63063044 -0.17180124 -0.39731650 -0.02896519
## Gene6 -0.7518261 1.1974742 -2.38884049 -1.00750636 -0.76215238 -0.46993625
## Patient25 Patient26 Patient27 Patient28 Patient29 Patient30
## Gene1 0.8049046 1.13419598 2.2361832 1.98108224 -1.5605465 -0.3719644
## Gene2 -0.7984835 0.52352075 -0.6941869 0.44401674 -1.2257144 -0.3365469
## Gene3 -0.9064944 -0.05174234 -0.9536200 -0.52797919 2.1410835 0.1145885
## Gene4 1.8500087 1.08404478 -0.2339720 1.04833856 0.2042004 1.1052790
## Gene5 -0.1089267 -0.68282587 -1.3068335 1.41365938 0.5630042 0.4840631
## Gene6 0.2788190 -1.14006748 0.4499973 -0.02990369 0.1661135 0.2607776
## Patient31 Patient32 Patient33 Patient34 Patient35 Patient36
## Gene1 -0.3840099 -1.1273078 0.1871252 0.1475202 0.03237855 -0.42900425
## Gene2 -0.8503873 1.4977985 0.2566567 -3.1752249 -0.94983592 -0.72350860
## Gene3 0.5241392 -0.9540873 -1.4425236 -0.6800585 -0.14691688 -0.50635095
## Gene4 -0.5244872 -1.4009811 1.3371564 0.5631570 1.29972910 -0.45795799
## Gene5 0.4878866 1.7555319 -0.86191515 -0.1644978 -0.42539226 -0.49172730
## Gene6 0.1562598 -0.9946169 1.1628469 -1.2573368 -0.07837179 0.08223501
## Patient37 Patient38 Patient39 Patient40 Patient41 Patient42
## Gene1 0.33529162 0.1818661 0.42800297 0.9446814 0.2644923 1.335756834
## Gene2 -0.27857460 1.9543720 -0.05495977 -0.4114871 0.7401658 0.008715203
## Gene3 0.39580323 -0.6526755 -1.05907168 -1.4637260 -0.6186848 0.047562829
## Gene4 -1.19048778 -1.7474434 1.40744720 0.6549129 0.1531150 -0.682953375
## Gene5 -0.73701170 1.3052400 -1.14329891 0.3246862 -1.3306489 1.873875472
## Gene6 -0.08521123 -0.3090280 0.10158118 0.7143744 -0.5985401 -1.280031908
## Patient43 Patient44 Patient45 Patient46 Patient47 Patient48
## Gene1 -0.9201471 -0.15988566 0.41094328 1.15669990 -1.1382433 0.3888261
## Gene2 0.7434033 0.87522888 -0.08200795 0.32232558 1.7590597 0.4829078
## Gene3 -0.5369265 0.03713017 -1.78242480 0.05321785 0.2805443 -0.2527920
## Gene4 0.2010020 0.61501856 0.17777356 -2.18242865 1.3059855 -0.2200998
## Gene5 -0.0708853 0.01088582 -0.45800801 0.23781198 0.4467863 1.0348718
## Gene6 1.5674514 0.59221040 1.22617486 0.20014207 -0.2175501 1.9100552
## Patient49 Patient50 Patient51 Patient52 Patient53 Patient54
## Gene1 -0.9417235 -0.3634009 0.6500217 1.217186800 0.3382127 0.05192587
## Gene2 0.5951544 0.1217592 0.9036597 0.989590157 0.8029135 0.10421014
## Gene3 1.6551133 1.6842638 0.7237972 0.728516467 1.0743686 0.61618344
## Gene4 0.8827351 0.5503069 0.8777356 0.791009360 1.3761190 0.69776784
## Gene5 -1.0850389 -1.6732696 0.4600214 0.261368623 1.2212942 0.94268985
## Gene6 -0.1725657 -0.2007031 0.4967394 0.008966304 1.4341420 1.15412737
## Patient55 Patient56 Patient57 Patient58 Patient59 Patient60
## Gene1 0.3257424 -0.06434959 0.6196039 -0.23269083 -0.40850155 0.18857006
## Gene2 0.3009573 -0.18753766 0.5516071 -0.05198074 -0.01472637 0.37699822
## Gene3 0.3362600 0.25931124 0.5836730 -0.18053283 -0.32484082 0.01956794
## Gene4 0.6443327 -0.31033843 0.4916839 -0.30400951 -0.04765219 0.16127680
## Gene5 0.1134553 -0.37706377 0.3935072 -0.34949890 -0.07029771 0.31386420
## Gene6 0.6282095 0.04270884 0.4424634 -0.38263680 -0.61840297 -0.19083501
## Patient61 Patient62 Patient63 Patient64 Patient65 Patient66
## Gene1 1.527898 -0.2090918 0.210887355 0.3198519 -0.4167878 -0.3503641
## Gene2 1.827180 -0.3097833 -0.451597237 0.6847742 -0.8642619 -0.5080373
## Gene3 1.886491 -0.2350833 -0.761962665 0.6436591 -0.5830015 -0.3095560
## Gene4 1.762873 -0.8218814 0.006762145 0.5448299 -0.5761444 -0.3965535
## Gene5 1.580930 -0.7711957 0.239483867 0.6340696 -0.5849178 -0.2704581
## Gene6 1.749115 -0.7216649 0.048957642 0.7149472 -0.7862657 -0.0779615
## Patient67 Patient68 Patient69 Patient70 Patient71 Patient72
## Gene1 -0.5489264 0.5726243 -0.5313927 0.27078821 0.14571614 -0.66589871
## Gene2 -1.0206620 0.1632526 -0.4544773 0.09900432 0.15944750 -0.57791407
## Gene3 -0.2447520 0.3191393 -0.5235272 -0.34297912 0.08474145 -0.13633796

```

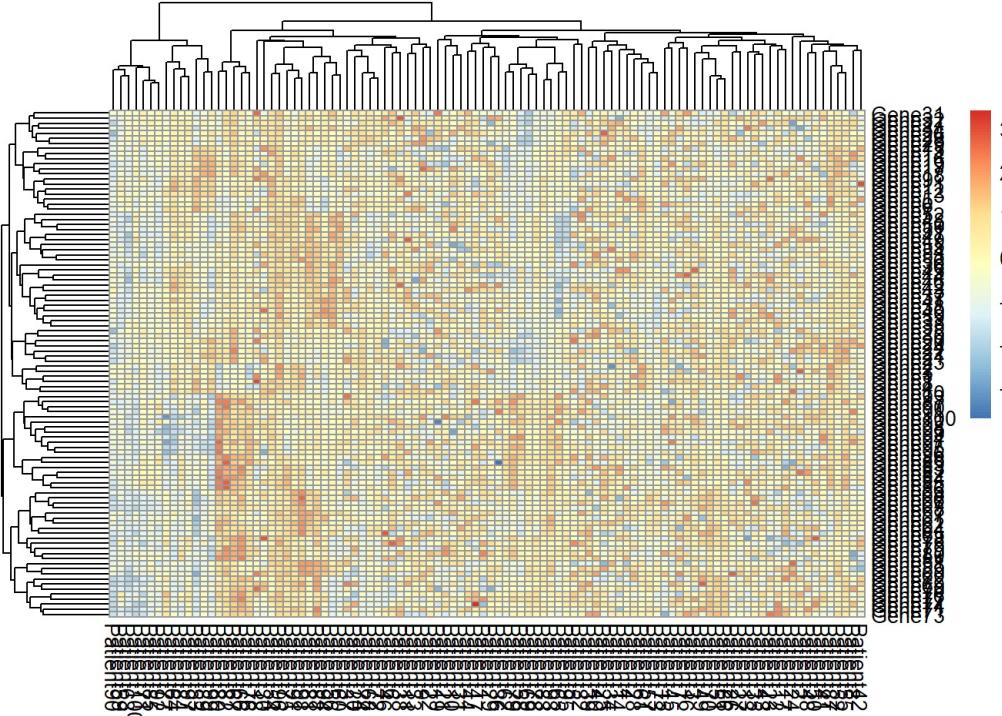
```

## Gene4 -0.1044274 -0.2725753 -1.0068622 -0.37290580 -0.44833985  0.05406805
## Gene5 -0.7091737  0.2009113 -1.2193432 -0.31872201 -0.34516308 -0.17606101
## Gene6 -0.6217682  0.1547980 -1.4346890 -0.49663421 -0.55641251  0.18217433
##      Patient73 Patient74 Patient75 Patient76 Patient77 Patient78
## Gene1  0.1000597 1.2940671 0.1141746 -1.726205 -1.34953165 -1.1208061
## Gene2 -0.3807574 0.8803995 0.4649511 -1.839578 -0.72696309 -1.1746608
## Gene3 -0.6972972 1.0442151 0.4661972 -1.865234 -0.58109976 -1.0831933
## Gene4 -0.9049703 0.8882609 0.4530711 -1.542892 -0.63700691 -1.0119427
## Gene5 -0.5125383 0.7691193 0.3960111 -1.099504  0.02174752 -0.8357138
## Gene6 -0.5380627 0.6771250 0.7040822 -1.206419  0.14627739 -0.4231169
##      Patient79 Patient80 Patient81 Patient82 Patient83 Patient84
## Gene1 -1.3284299 -1.578165 -1.1013507 -0.2693101 -0.7350758  0.21795396
## Gene2 -1.2572564 -1.990208 -0.7885746 -0.2458110 -0.5132985  0.14704968
## Gene3 -1.1175975 -1.418960 -0.6578907 -0.2739664 -0.1786217 -0.30483948
## Gene4 -1.2580033 -1.437544 -0.6305132 -0.8585567  0.1245479 -0.20382935
## Gene5 -0.8669833 -1.247814 -1.0187291 -1.1244006  0.4473386 -0.34042064
## Gene6 -1.1108248 -1.113213 -1.2332920 -1.0126220  0.7037447 -0.02028928
##      Patient85 Patient86 Patient87 Patient88 Patient89 Patient90
## Gene1 -0.8943702 0.80170050 1.906741  0.92490244 -0.43834903 -0.26494105
## Gene2 -0.6596127 0.51289302 2.054226  0.39142586 -0.31073065 -0.45460600
## Gene3 -0.4612304 0.16639722 1.688485  0.40493721 -0.09089255  0.02166592
## Gene4 -0.1481704 0.06073162 2.119237 -0.04475271 -0.21506705 -0.71066021
## Gene5 -0.1161524 -0.44684525 2.027723 -0.33787611  0.15452827 -0.67558326
## Gene6 -0.4371058 -0.75481756 1.997926 -0.38433254  0.48732131 -0.80311326
##      Patient91 Patient92 Patient93 Patient94 Patient95 Patient96
## Gene1 1.0082713 -1.1387438 -0.3013357 -1.5809698 -1.4174691 1.8197438
## Gene2 1.2946590 -1.3506249 -0.7065800 -0.9575529 -0.9023188 2.1331045
## Gene3 0.9955628 -1.3143317 -0.2995042 -0.4976484 -0.7629150 1.8045605
## Gene4 0.9588467 -1.1112996 -0.4288897 -1.1036385 -0.4148775 1.3249769
## Gene5 1.1997252 -0.7535715 -0.3499271 -1.6749291 -0.7465204 0.9305900
## Gene6 1.4514865 -1.1020250 -0.4133264 -1.7403712 -0.9174716 0.3268849
##      Patient97 Patient98 Patient99 Patient100
## Gene1 0.17188029 1.823032 0.4342243 -0.6986283
## Gene2 -0.52896430 1.116291 0.5419882 -1.0395483
## Gene3 -0.48371973 1.391186 0.6750507 -1.4937080
## Gene4 -0.08633347 1.222353 0.8210392 -1.3347219
## Gene5 -0.19508380 1.391158 0.6028290 -1.0537915
## Gene6 -0.11497634 1.037765 0.3437560 -1.1895746

```

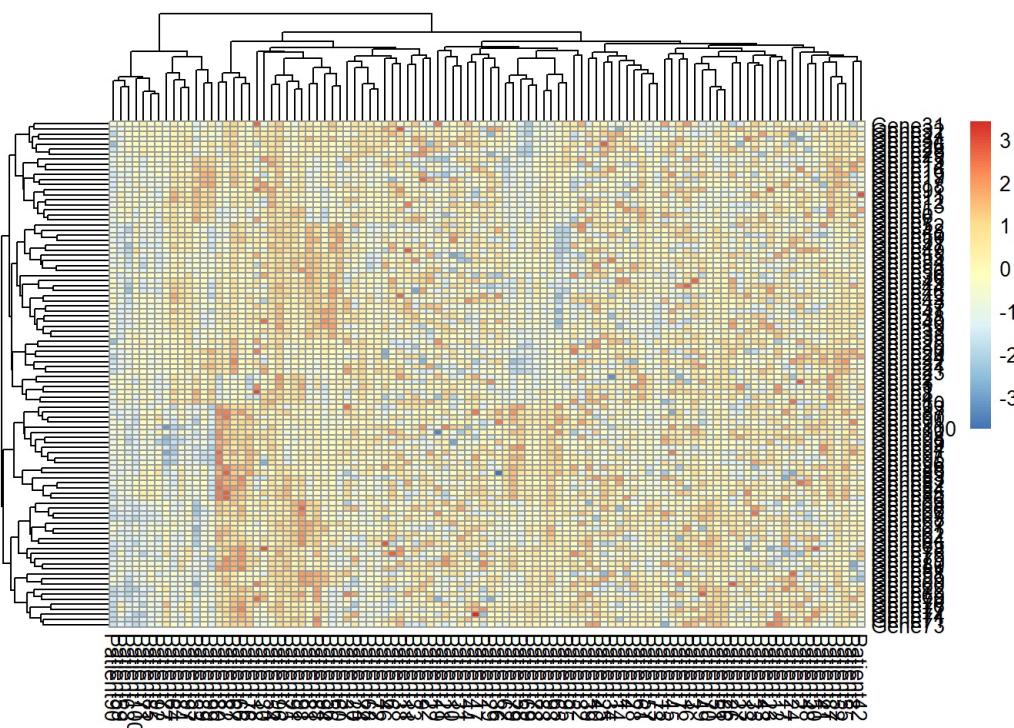
Generar el grafico con pheatmap. Es importante señalar que los clusters (dendrogramas) se generan de forma automática

```
pheatmap(genes)
```



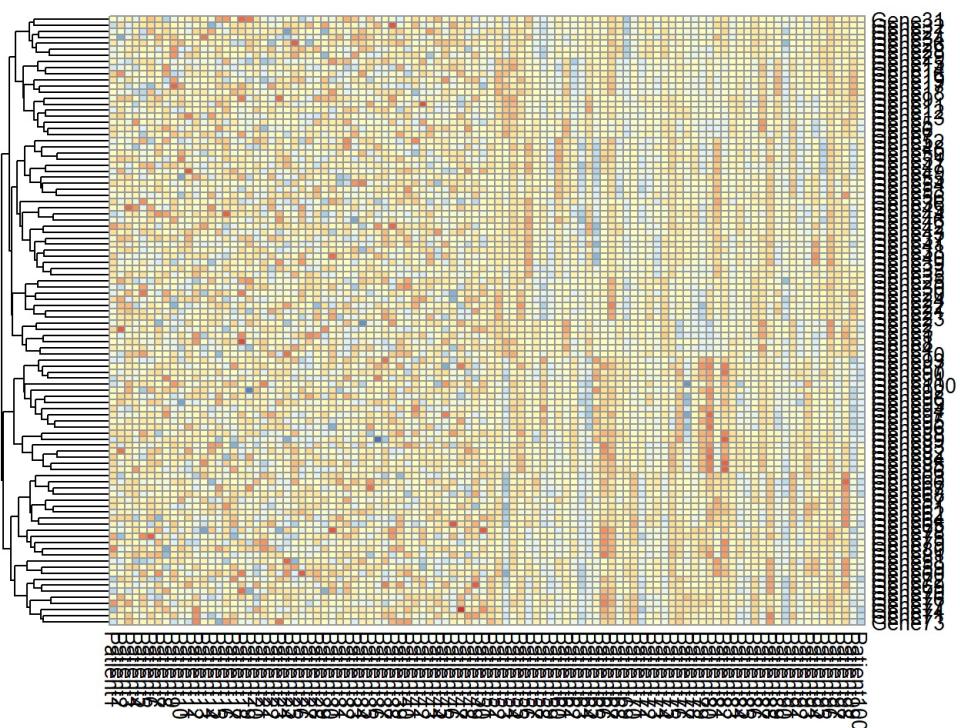
Cambiar el tamaño de la fuente

```
pheatmap(genes, fontsize = 6)
```



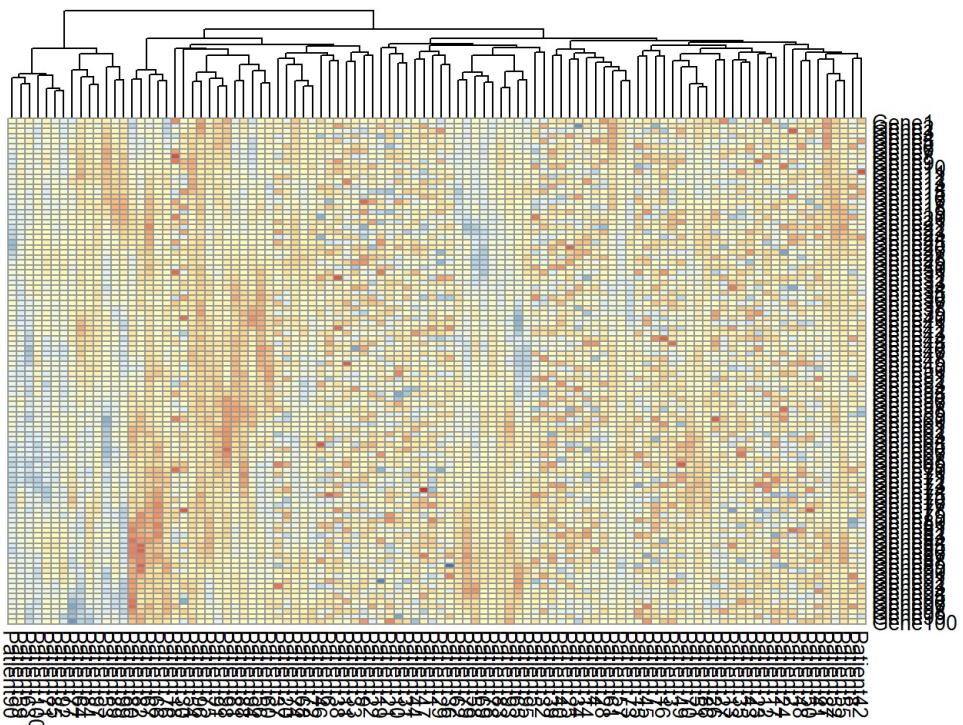
Por default R clustea los renglones, en este caso los genes estan en los reglones y es lo que clustea. Para quitar el dendrograma de los pacientes (eje de la x) utilizamos las siguientes instrucciones

```
pheatmap(genes, fontsize = 6, cluster_rows = T, cluster_cols = F)
```



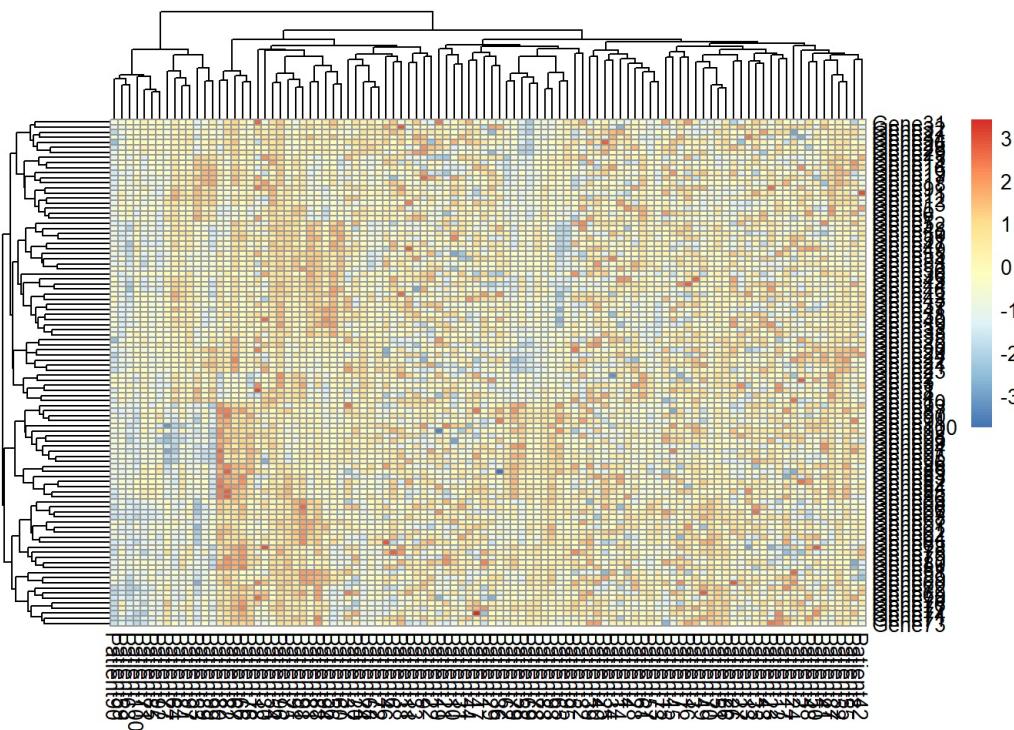
Como práctica ahora hacemos lo contrario, eliminamos los genes (eje de la y) dejando a los pacientes

```
pheatmap(genes, fontsize = 6, cluster_rows = F, cluster_cols = T)
```



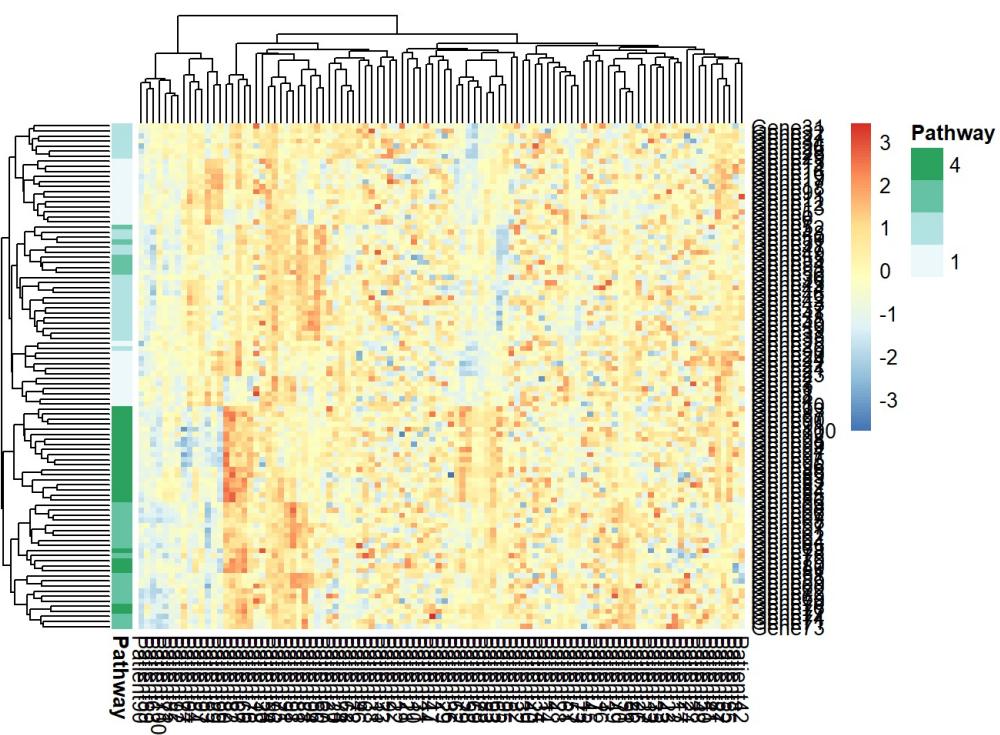
Para regresar al grafico original

```
pheatmap(genes, frontsize = 6, cluster_rows = T, cluster_cols = T)
```



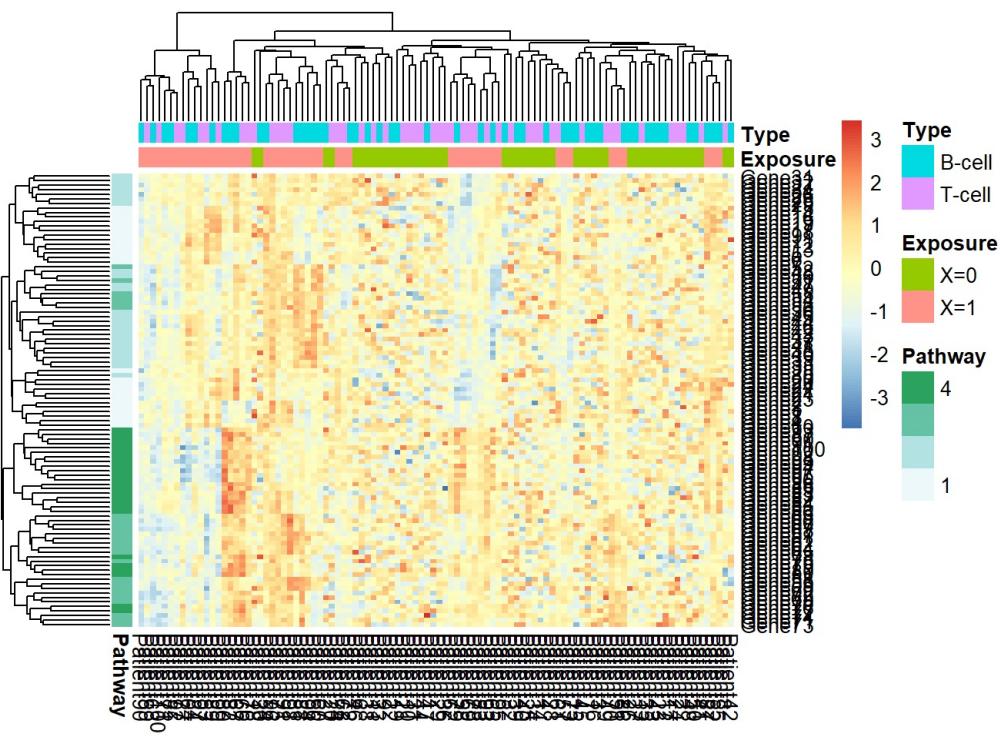
Para ver patrones subyacentes a las anotaciones de los renglones

```
pheatmap(genes, frontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row)
```



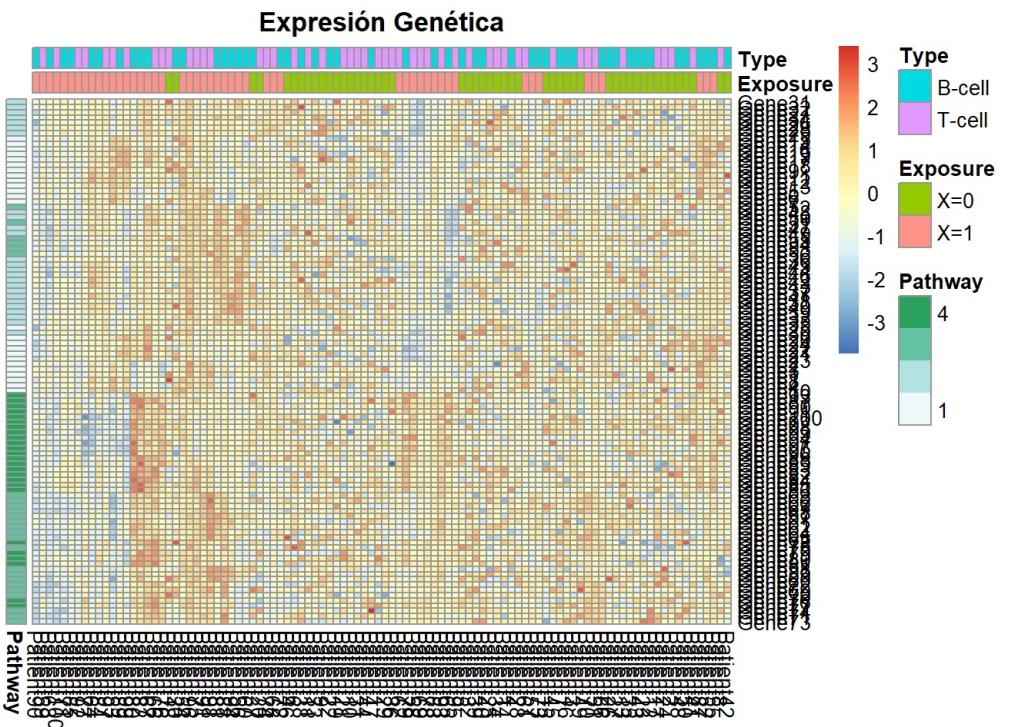
Para ver patrones subyacentes a las anotaciones de los renglones y las columnas

```
pheatmap(genes, fontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row, annotation_col = annotation_col)
```



Para quitar dendrogramas y colocar un título

```
pheatmap(genes, fontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row, annotation_col = annotation_col, treeheight_row = 0, treeheight_col = 0, main = "Expresión Genética")
```

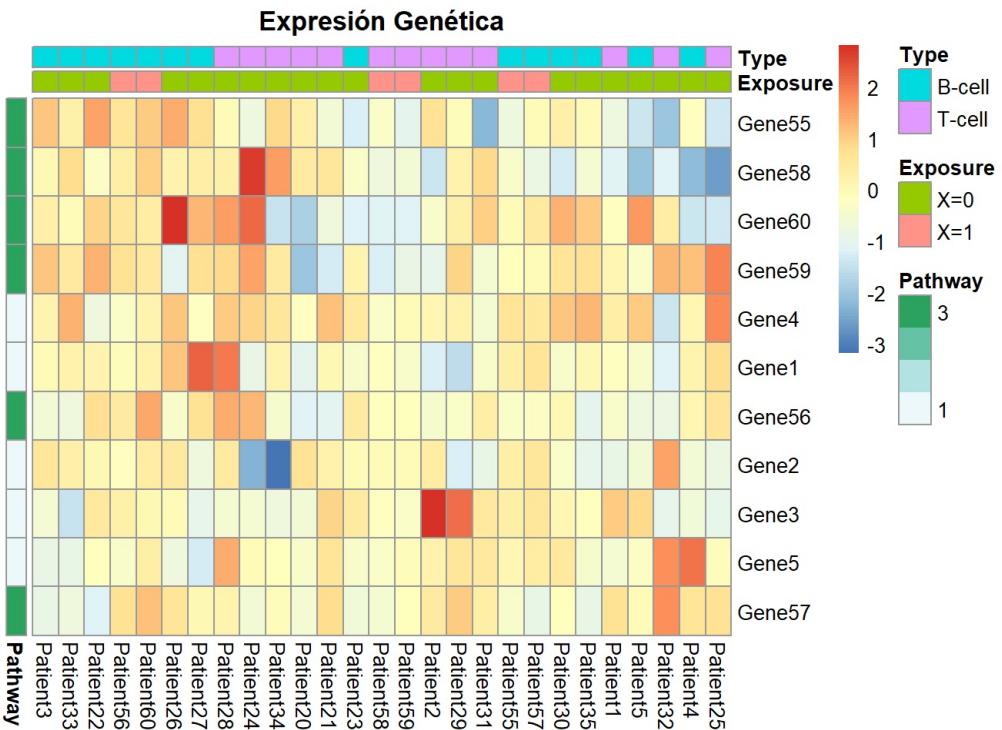


Para extraer datos de forma específico (un subconjunto de la totalidad), se crea objeto con ciertas características

```
sub <- genes [c(1:5, 55:60), c(1:5, 20:35, 55:60)]
```

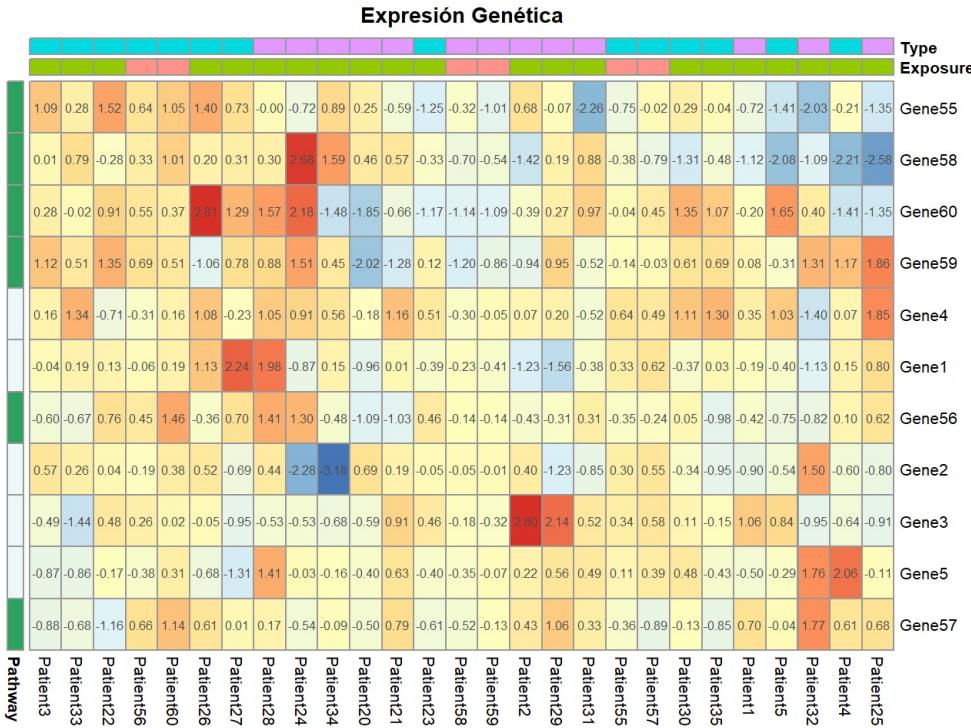
Para graficar el nuevo objeto o subconjunto de datos reciclamos el código y solo cambiamos genes por sub

```
heatmap(sub, fontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row, annotation_col = annotation_col, treeheight_row = 0, treeheight_col = 0, main = "Expresión Genética")
```



Para aumentar el tamaño de las columnas sea mayor, no aparezca la anotación de las leyendas y desplegar los número dando un tamaño

```
heatmap(sub, fontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row, annotation_col = annotation_col, treeheight_row = 0, treeheight_col = 0, main = "Expresión Genética", fontsize = 8, annotation_legend = FALSE, display_numbers = TRUE, fontsize_number = 6)
```



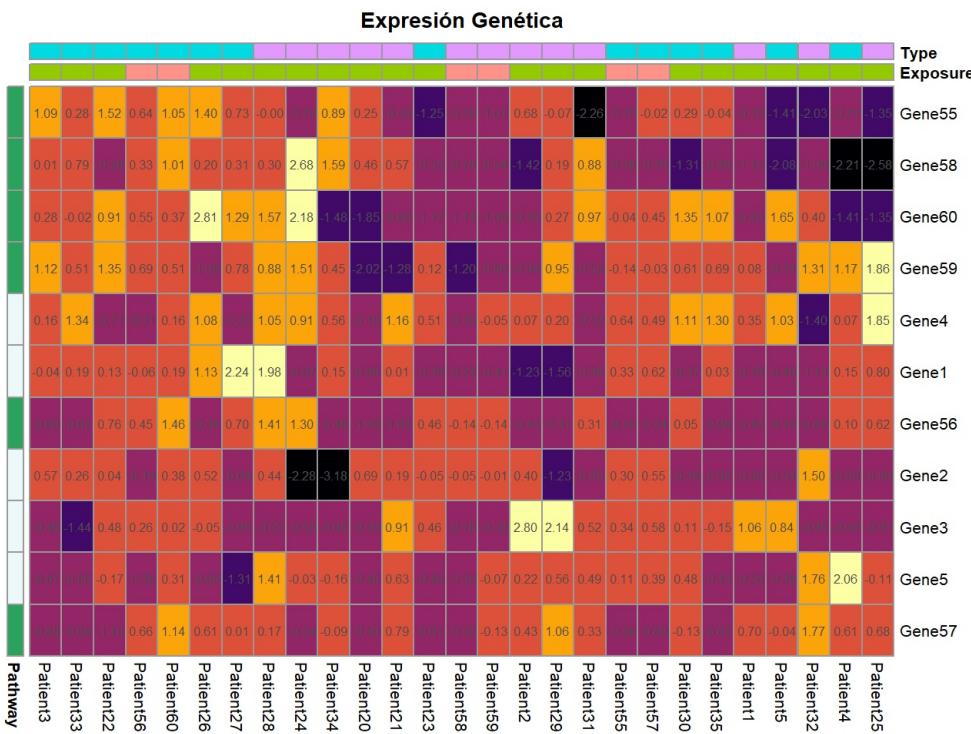
Para cambiar color llamar la paqueteria de viridis

```
library(viridis)
```

```
## Loading required package: viridisLite
```

Reciclamos código anterior y con viridis llamamos a la opción plasma, magma, viridis, inferno

```
heatmap(sub, frontsize = 6, cluster_rows = T, cluster_cols = T, annotation_row = annotation_row, annotation_col = annotation_col, treeheight_row = 0, treeheight_col = 0, main = "Expresión Genética", fontsize = 8, annotation_l legend = FALSE, display_numbers = TRUE, fontsize_number = 6, col = viridis_pal(option = "inferno")) (6))
```



Para visualizar la distancia entre los genes

dist(sub)

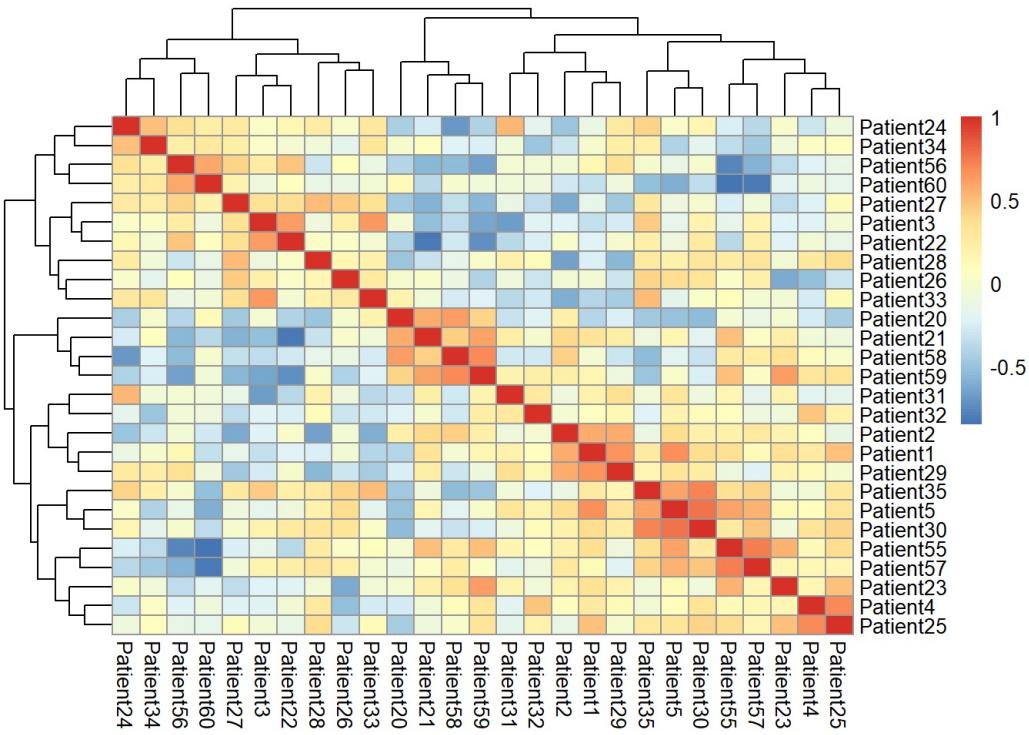
```

##          Gene1    Gene2    Gene3    Gene4    Gene5    Gene55   Gene56   Gene57
## Gene2  6.506125
## Gene3  7.823569 7.021725
## Gene4  5.253565 7.649124 6.516104
## Gene5  6.411847 5.977640 5.967513 6.184570
## Gene55 5.703940 6.969997 7.096321 6.837653 7.534618
## Gene56 4.544832 6.723925 6.542745 5.805165 5.150859 6.028094
## Gene57 6.124657 6.069362 5.550487 6.004035 3.881691 7.122986 5.209746
## Gene58 7.417422 8.796956 8.462521 7.874145 8.030439 6.777444 6.292359 7.669524
## Gene59 6.189649 8.293720 7.977707 6.115718 5.821355 7.317126 4.835770 6.104449
## Gene60 6.623226 8.133474 7.665999 6.837342 7.659167 7.569942 6.373711 7.296198
##           Gene58   Gene59
## Gene2
## Gene3
## Gene4
## Gene5
## Gene55
## Gene56
## Gene57
## Gene58
## Gene59 8.312043
## Gene60 7.813793 6.992657

```

Para identificar el mapa de calor de la correlacion de los datos en este caso de los pacientes

```
pheatmap(cor(sub))
```



Generamos un objeto con la matriz transpuesta y generamos mapa genes y no pacientes

```

trans <- t(sub)
pheatmap(cor(trans))

```

