# R语言：多个基因的相关性分析与展示

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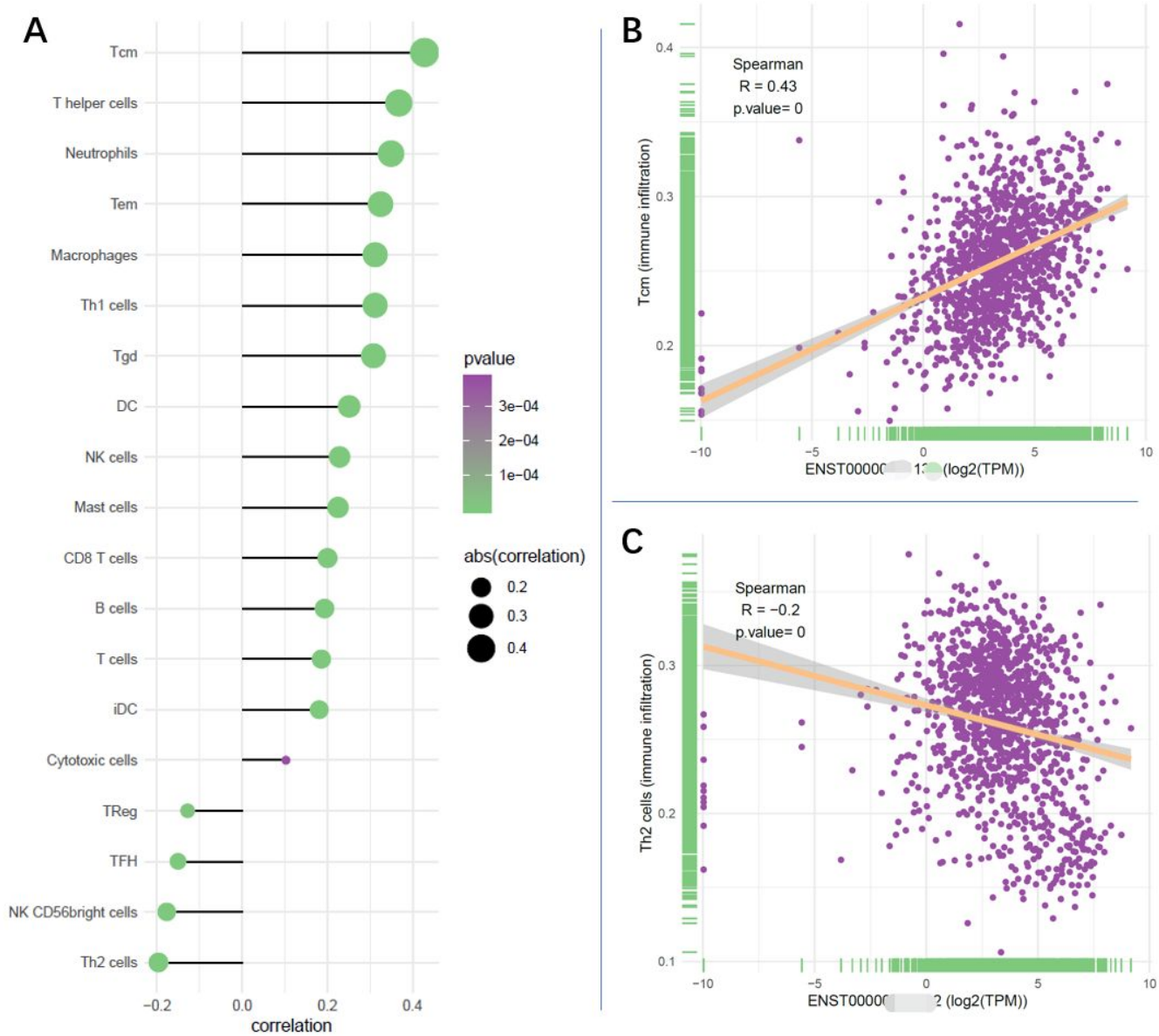
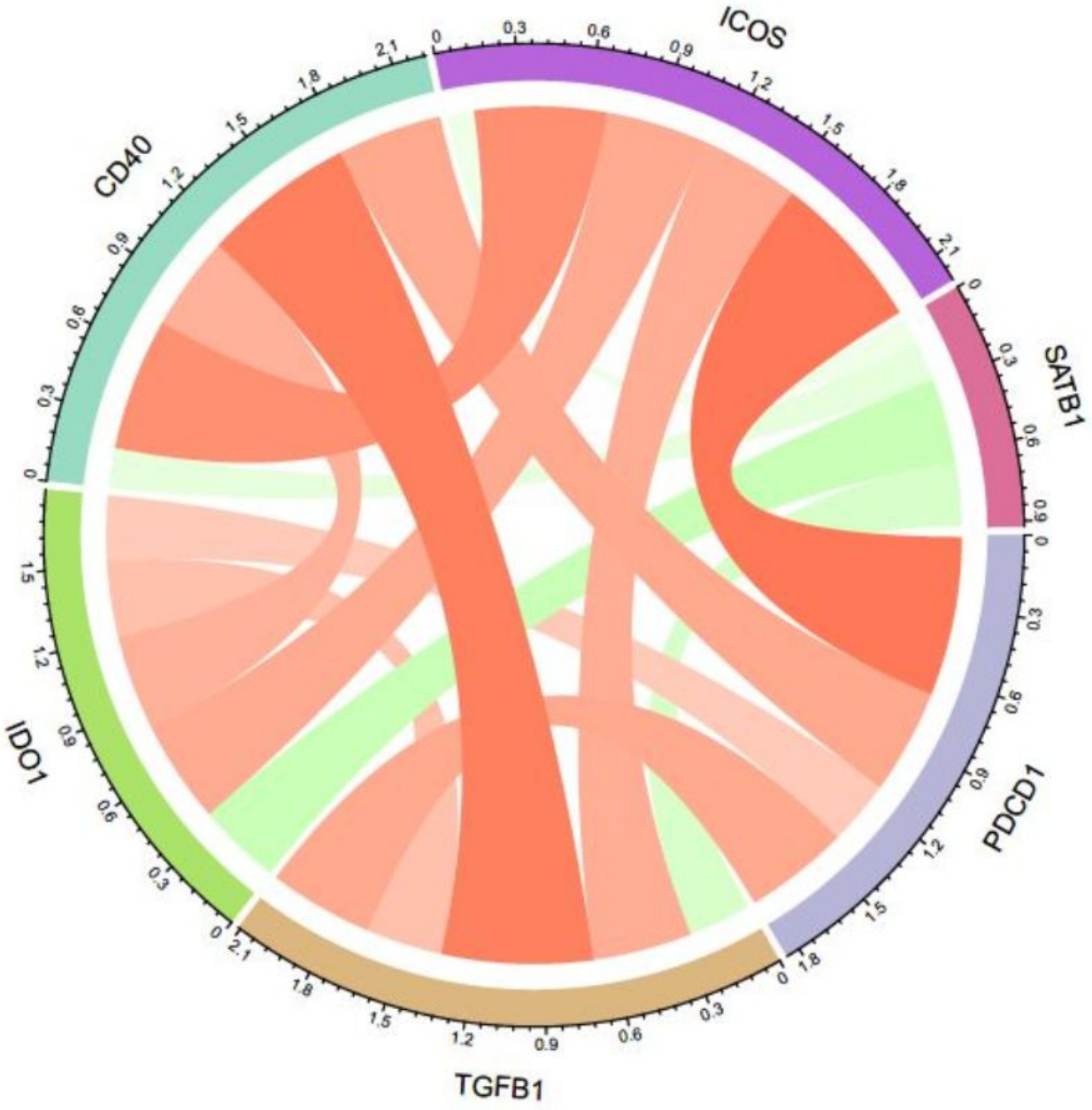
R语言：多个基因的相关性分析与展示。关于批量相关性分析，我们发过两个帖子。单基因批量相关性分析的妙用，又是神器!基于单基因批量相关性分析的GSEA。两两分析的肯定也是没有问题：

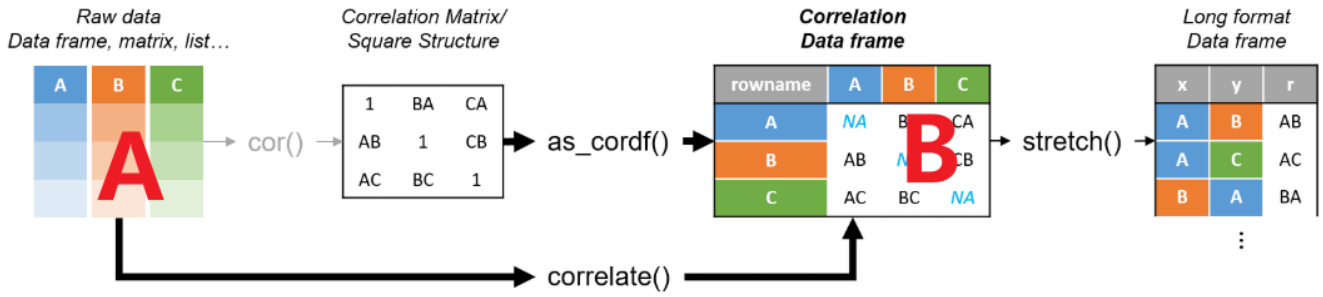


现在的问题是，如果是多个基因分相关性分析，如何快速，方便地分析，然后高效地呈现呢?

我用圈图实现过这个操作：




不过比较麻烦，今天介绍一个R包 corrr，可以方便地做这个事情，而且我认为做的更好。




他有一个主函数correlate可以迅速地分析，实现从A到B的转换。

更重要的是他还配了两个可视化的函数，一个是rplot画热图，一个是network_plot画网络图。

出了主函数外，总共有7个函数

Internal changes ( `cor_df` out):

- `shave()` the upper or lower triangle (set to NA).
- `rearrange()` the columns and rows based on correlation strengths.

a

Reshape structure ( `tbl` or `cor_df` out):

- `focus()` on select columns and rows.
- `stretch()` into a long format.

b

Output/visualizations (console/plot out):

- `fashion()` the correlations for pretty printing.
- `rplot()` the correlations with shapes in place of the values.
- `network_plot()` the correlations in a network.

c

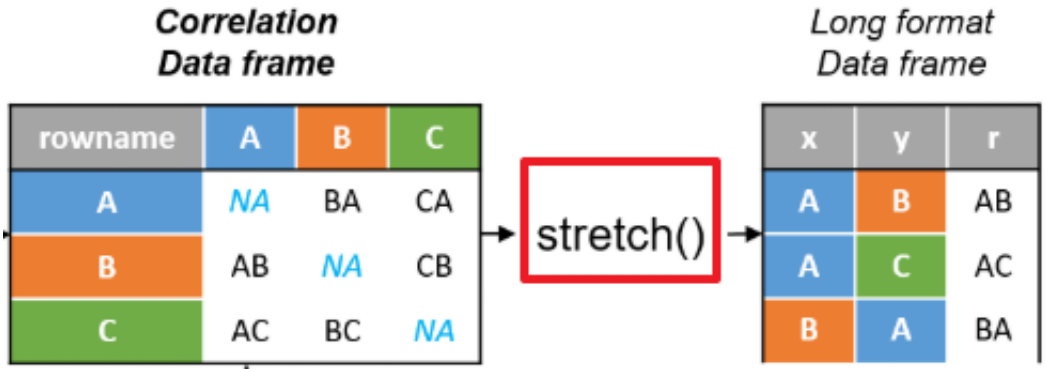
最后一个框里有两个函数已经介绍，还有一个fashion可以简洁化展示数据，去掉NA。

第一个框内的shave函数是把剃刀，可以去掉相关性结果上三角或者下三角并设置为NA

rearrange函数可以按照相关性系数聚类排序。

第二个框内的focus函数，类似于select函数，可以用来筛选想要查看的某行某列数据。

stretch函数可以实现数据从宽边长，如图所示。




下面我们就来实战一下：

首先设置镜像以及按照R包

```
options("repos"=c(CRAN="https://mirrors.tuna.tsinghua.edu.cn/CRAN/"))
install.packages("corrr")
```

运行主函数看看结果

```
library(corrr)
library(dplyr)
x <- datasets::mtcars %>%
  correlate()
```

| | rowname | mpg | cyl | disp | hp | drat | wt | qsec | vs | am | gear | carb |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | mpg | NA | -0.8521620 | -0.8475514 | -0.7761684 | 0.68117191 | -0.8676594 | 0.41868403 | 0.6640389 | 0.59983243 | 0.4802848 | -0.55092507 |
| 2 | cyl | -0.8521620 | NA | 0.9020329 | 0.8324475 | -0.69993811 | 0.7824958 | -0.59124207 | -0.8108118 | -0.52260705 | -0.4926866 | 0.52698829 |
| 3 | disp | -0.8475514 | 0.9020329 | NA | 0.7909486 | -0.71021393 | 0.8879799 | -0.43369788 | -0.7104159 | -0.59122704 | -0.5555692 | 0.39497686 |
| 4 | hp | -0.7761684 | 0.8324475 | 0.7909486 | NA | -0.44875912 | 0.6587479 | -0.70822339 | -0.7230967 | -0.24320426 | -0.1257043 | 0.74981247 |
| 5 | drat | 0.6811719 | -0.6999381 | -0.7102139 | -0.4487591 | NA | -0.7124406 | 0.09120476 | 0.4402785 | 0.71271113 | 0.6996101 | -0.09078980 |
| 6 | wt | -0.8676594 | 0.7824958 | 0.8879799 | 0.6587479 | -0.71244065 | NA | -0.17471588 | -0.5549157 | -0.69249526 | -0.5832870 | 0.42760594 |
| 7 | qsec | 0.4186840 | -0.5912421 | -0.4336979 | -0.7082234 | 0.09120476 | -0.1747159 | NA | 0.7445354 | -0.22986086 | -0.2126822 | -0.65624923 |
| 8 | vs | 0.6640389 | -0.8108118 | -0.7104159 | -0.7230967 | 0.44027846 | -0.5549157 | 0.74453544 | NA | 0.16834512 | 0.2060233 | -0.56960714 |
| 9 | am | 0.5998324 | -0.5226070 | -0.5912270 | -0.2432043 | 0.71271113 | -0.6924953 | -0.22986086 | 0.1683451 | NA | 0.7940588 | 0.05753435 |
| 10 | gear | 0.4802848 | -0.4926866 | -0.5555692 | -0.1257043 | 0.69961013 | -0.5832870 | -0.21268223 | 0.2060233 | 0.79405876 | NA | 0.27407284 |
| 11 | carb | -0.5509251 | 0.5269883 | 0.3949769 | 0.7498125 | -0.09078980 | 0.4276059 | -0.65624923 | -0.5696071 | 0.05753435 | 0.2740728 | NA |

接着往下处理，focus选择要观察的数据，rearrange按照相关性系数排序，shave设置上三角的数据为NA

```
x <- datasets::mtcars %>%
  correlate() %>%
  focus(-cyl, -vs, mirror = TRUE) %>%
  rearrange() %>%
  shave()
```

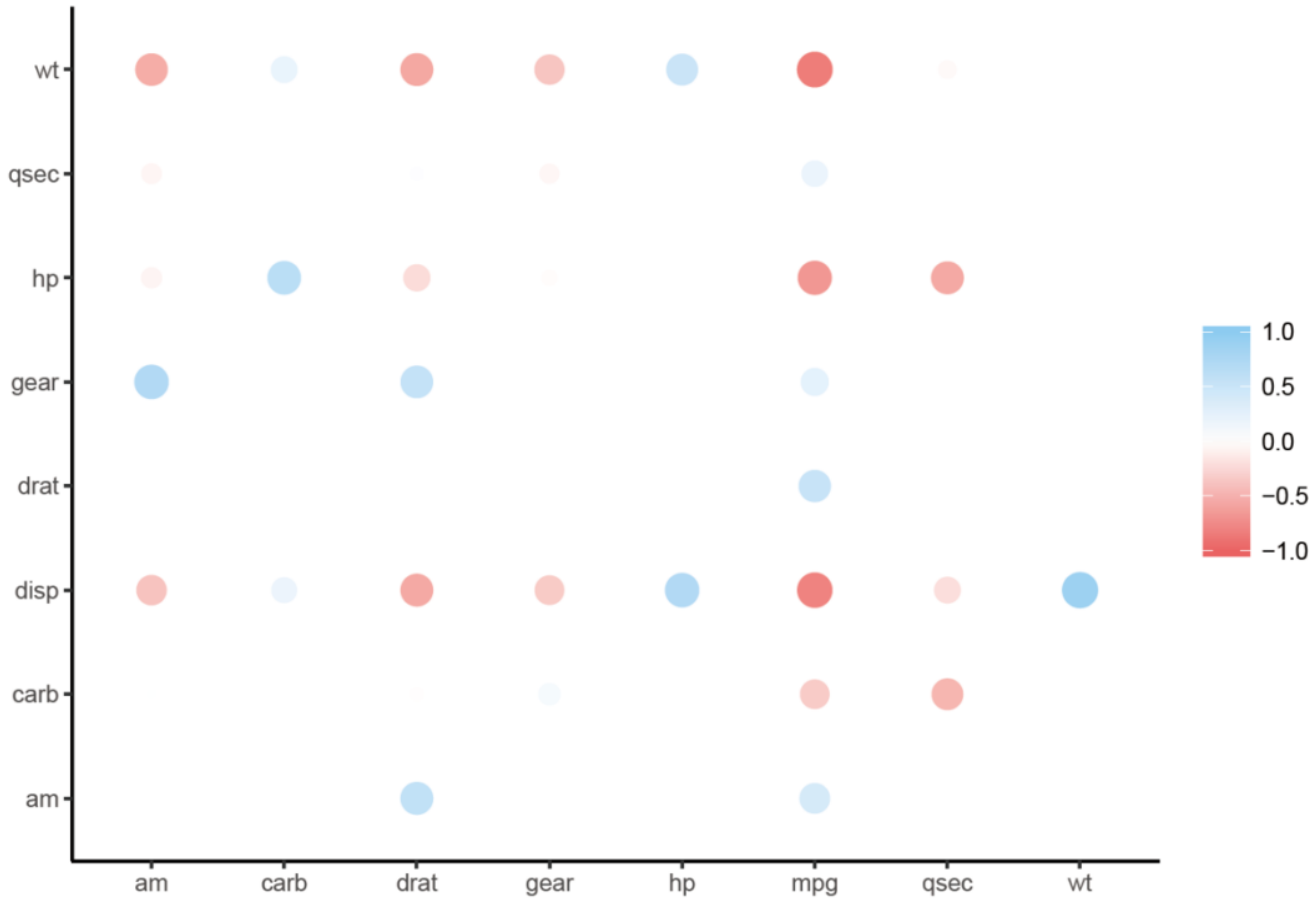
| | rowname | mpg | drat | am | gear | qsec | carb | hp | wt | disp |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | mpg | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| 2 | drat | 0.6811719 | NA | NA | NA | NA | NA | NA | NA | NA |
| 3 | am | 0.5998324 | 0.71271113 | NA | NA | NA | NA | NA | NA | NA |
| 4 | gear | 0.4802848 | 0.69961013 | 0.79405876 | NA | NA | NA | NA | NA | NA |
| 5 | qsec | 0.4186840 | 0.09120476 | -0.22986086 | -0.2126822 | NA | NA | NA | NA | NA |
| 6 | carb | -0.5509251 | -0.09078980 | 0.05753435 | 0.2740728 | -0.6562492 | NA | NA | NA | NA |
| 7 | hp | -0.7761684 | -0.44875912 | -0.24320426 | -0.1257043 | -0.7082234 | 0.7498125 | NA | NA | NA |
| 8 | wt | -0.8676594 | -0.71244065 | -0.69249526 | -0.5832870 | -0.1747159 | 0.4276059 | 0.6587479 | NA | NA |
| 9 | disp | -0.8475514 | -0.71021393 | -0.59122704 | -0.5555692 | -0.4336979 | 0.3949769 | 0.7909486 | 0.8879799 | NA |

可以用fashion简化数据

| | rowname | mpg | drat | am | gear | qsec | carb | hp | wt | disp |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | mpg | | | | | | | | | |
| 2 | drat | .68 | | | | | | | | |
| 3 | am | .60 | .71 | | | | | | | |
| 4 | gear | .48 | .70 | .79 | | | | | | |
| 5 | qsec | .42 | .09 | -.23 | -.21 | | | | | |
| 6 | carb | -.55 | -.09 | .06 | .27 | -.66 | | | | |
| 7 | hp | -.78 | -.45 | -.24 | -.13 | -.71 | .75 | | | |
| 8 | wt | -.87 | -.71 | -.69 | -.58 | -.17 | .43 | .66 | | |
| 9 | disp | -.85 | -.71 | -.59 | -.56 | -.43 | .39 | .79 | .89 | |

fashion(x)

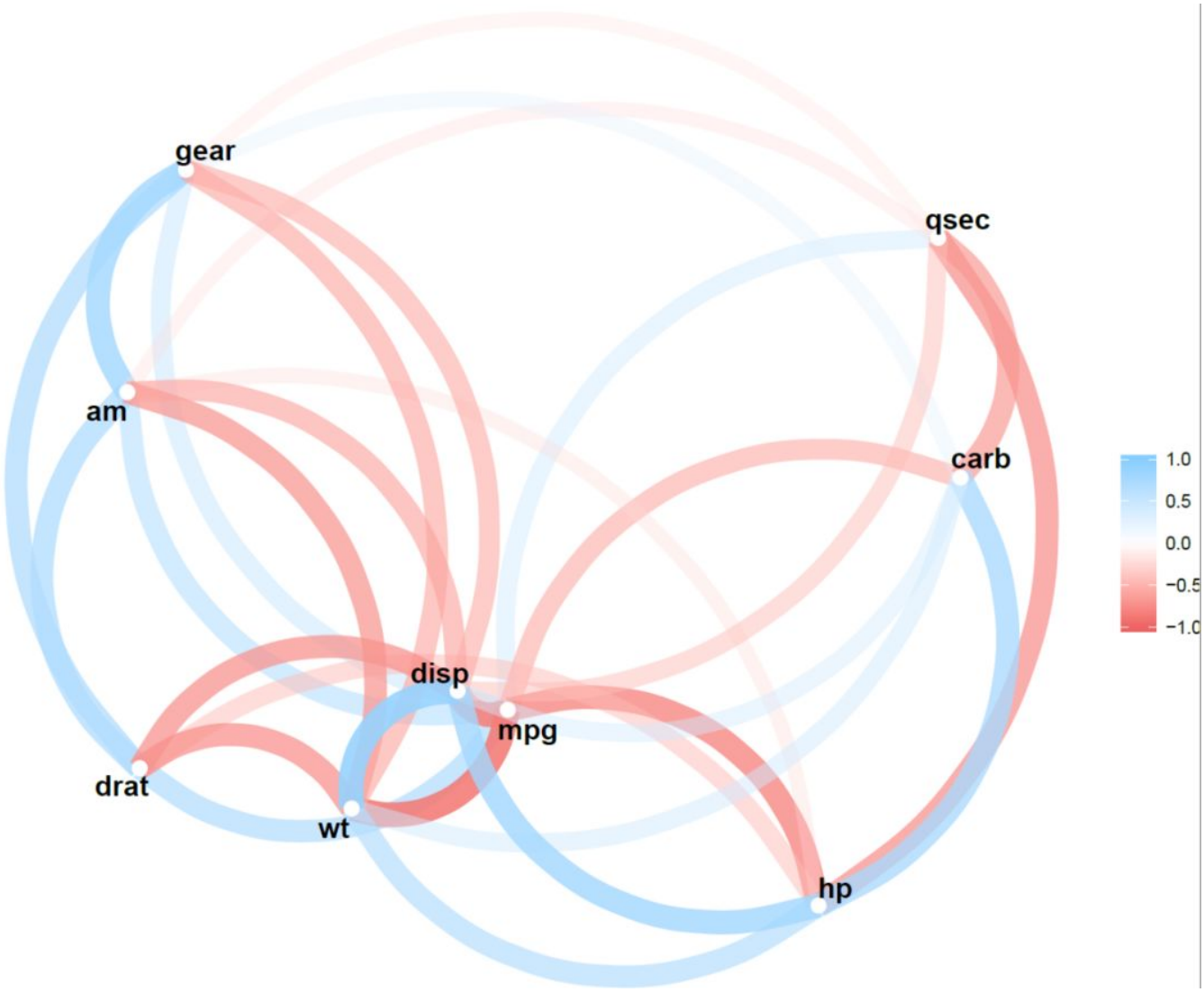
可以用rplot来画图展示数据




也可以用网络图来展示

```
datasets::mtcars %>%
  correlate() %>%
```

```
  focus(-cyl, -vs, mirror = TRUE) %>%
  rearrange() %>%
  network_plot(min_cor = .2)
```




stretch可以实现数据变换

```
x <- datasets::mtcars %>%
  correlate() %>%    # Create correlation data frame (cor_df)
  focus(-cyl, -vs, mirror = TRUE) %>%  # Focus on cor_df without 'cyl'
 and 'vs'
  rearrange() %>%
  stretch()
```

| | x | y | r |
|---|---|---|---|
| 1 | mpg | mpg | NA |
| 2 | mpg | drat | 0.68117191 |
| 3 | mpg | am | 0.59983243 |
| 4 | mpg | gear | 0.48028476 |
| 5 | mpg | qsec | 0.41868403 |
| 6 | mpg | carb | -0.55092507 |
| 7 | mpg | hp | -0.77616837 |
| 8 | mpg | wt | -0.86765938 |
| 9 | mpg | disp | -0.84755138 |
| 10 | drat | mpg | 0.68117191 |
| 11 | drat | drat | NA |
| 12 | drat | am | 0.71271113 |
| 13 | drat | gear | 0.69961013 |

学习一个R包是第一步，第二步就应该想着如何用来展示自己的数据。先来看看我们拥有的数据

```
load(file = "TCGA_steal_data.Rdata")
```

| | subgroup | sample | ESR1 | GATA3 | ERBB2 | FOXA1 | NAT1 | BRCA1 | BRCA2 | BAG1 | BIRC5 | MKI67 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TCGA-AC-A3OD-01B-06R-A22O-07 | LumA | Tumor | 17.114199 | 14.643833 | 13.51263 | 14.193508 | 13.156971 | 11.001648 | 10.675147 | 12.011507 | 9.323800 | 14.036013 |
| TCGA-AR-A251-01A-12R-A169-07 | Basal | Tumor | 10.269148 | 11.465225 | 12.88438 | 8.055327 | 7.814799 | 11.617031 | 10.194470 | 10.988246 | 12.661417 | 14.382202 |
| TCGA-BH-A0B5-11A-23R-A12P-07 | Normal | Normal | 11.145986 | 10.013736 | 10.72469 | 6.556766 | 8.707859 | 9.177904 | 7.104063 | 12.332490 | 6.602116 | 7.676837 |
| TCGA-E2-A1IK-01A-11R-A144-07 | LumA | Tumor | 16.578416 | 15.887390 | 12.31860 | 15.445781 | 10.071785 | 9.625762 | 8.348021 | 12.448767 | 10.424083 | 10.896239 |
| TCGA-E2-A15C-01A-31R-A12D-07 | LumA | Tumor | 15.862655 | 15.311567 | 15.00679 | 14.561364 | 13.758525 | 9.898625 | 9.482084 | 12.523272 | 9.049277 | 11.058604 |
| TCGA-B6-A2IU-01A-32R-A18M-07 | LumA | Tumor | 14.918471 | 16.558116 | 15.35859 | 14.572697 | 14.939840 | 10.477670 | 9.173315 | 12.878968 | 10.969791 | 11.890226 |
| TCGA-AR-A1AS-01A-11R-A12P-07 | LumB | Tumor | 15.282775 | 15.303211 | 14.34886 | 14.609227 | 11.613343 | 10.896709 | 9.577009 | 11.894230 | 10.791917 | 12.003516 |
| TCGA-BH-A0BD-01A-11R-A034-07 | Basal | Tumor | 13.886896 | 15.479474 | 13.75643 | 13.537705 | 11.542180 | 11.008007 | 10.501126 | 12.094719 | 11.519836 | 13.704851 |
| TCGA-BH-A209-11A-42R-A157-07 | Normal | Normal | 12.821612 | 13.364987 | 13.13093 | 12.205101 | 9.186887 | 9.498667 | 8.968440 | 11.647156 | 8.105495 | 9.721665 |
| TCGA-AQ-A04J-01A-02R-A034-07 | Basal | Tumor | 9.487192 | 11.350316 | 13.24661 | 9.569889 | 8.718935 | 8.829380 | 10.809382 | 11.608352 | 12.146518 | 13.822314 |
| TCGA-A7-A13D-01A-13R-A12P-07 | Basal | Tumor | 8.332443 | 11.923866 | 15.02004 | 9.375892 | 8.357641 | 10.208300 | 9.866419 | 11.001496 | 12.563890 | 14.004373 |
| TCGA-E2-A158-11A-22R-A12D-07 | Normal | Normal | 12.033338 | 11.024592 | 12.80200 | 9.960504 | 8.512144 | 8.933581 | 8.260284 | 12.105891 | 8.132622 | 9.364193 |
| TCGA-E9-A22D-01A-11R-A157-07 | LumB | Tumor | 14.027911 | 15.607285 | 16.74466 | 14.671518 | 11.211293 | 10.569418 | 9.624489 | 12.572274 | 12.051591 | 12.958580 |
| TCGA-C8-A138-01A-11R-A115-07 | Her2 | Tumor | 11.634667 | 14.919210 | 15.13878 | 14.275422 | 12.174608 | 9.303917 | 10.302666 | 12.471778 | 10.658132 | 11.591685 |
| TCGA-AO-A12H-01A-11R-A115-07 | LumA | Tumor | 17.179502 | 16.468731 | 13.72460 | 16.195024 | 11.490957 | 9.100716 | 8.842238 | 14.412712 | 10.195152 | 11.046726 |
| TCGA-BH-A0E0-01A-11R-A056-07 | Basal | Tumor | 10.441638 | 14.232268 | 13.72584 | 9.705740 | 7.768527 | 10.256238 | 8.668756 | 12.270381 | 11.420427 | 14.191153 |

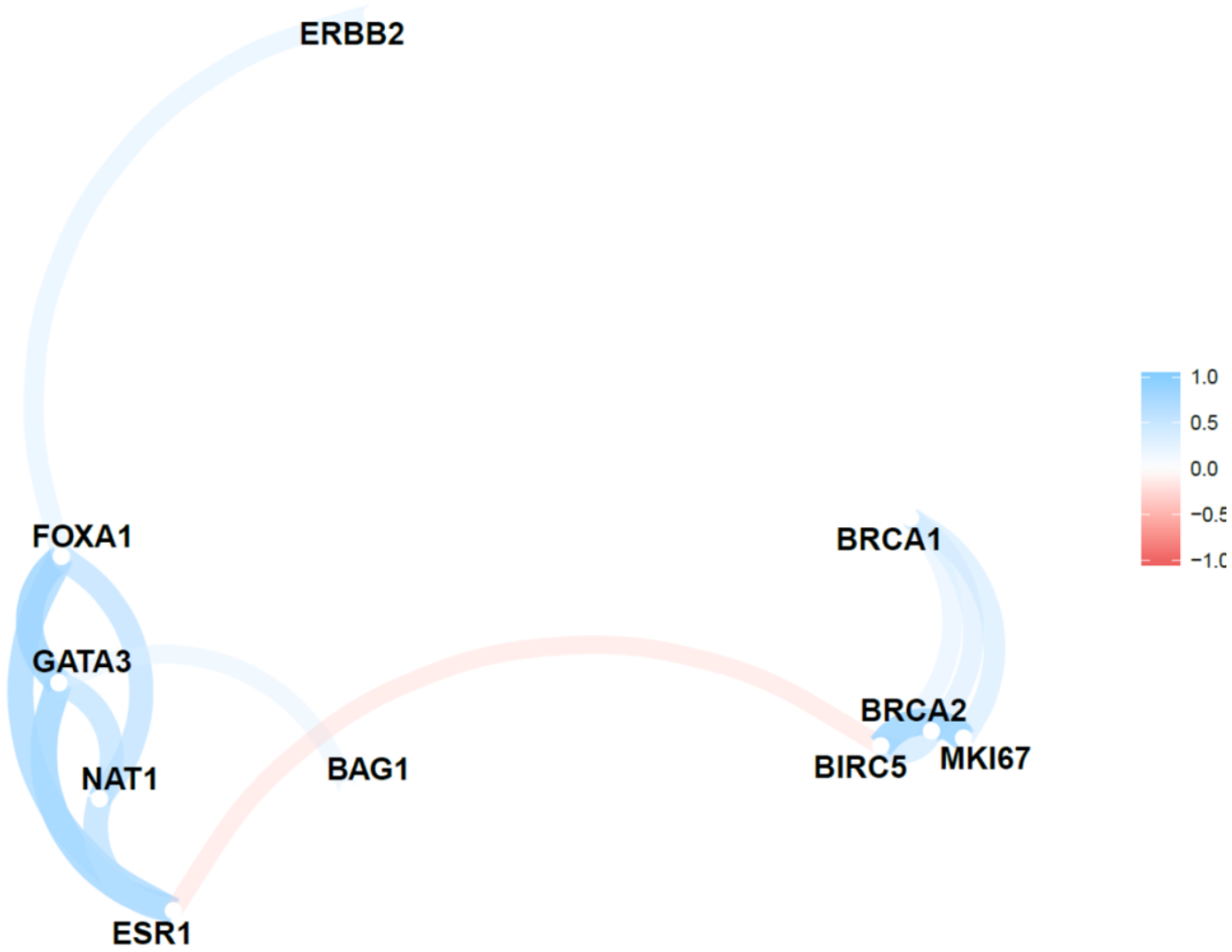
这个数据我们已经很熟悉了，前面两列可以不要

```
data <- TCGA_steal_data[,-c(1:2)]
```

这样我们就跟这个R包对接上了。

直接画图试试

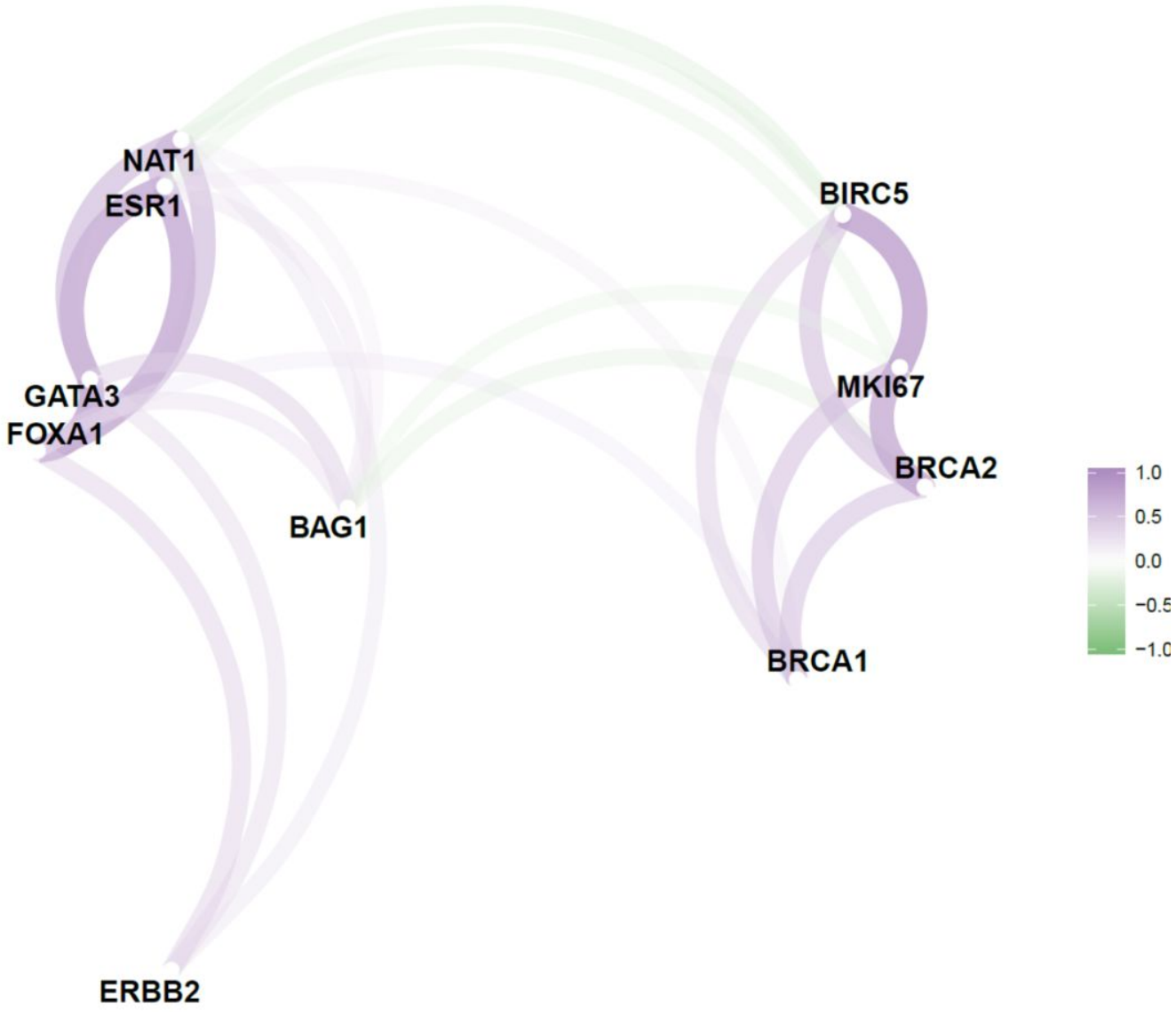
```
data %>%
  correlate() %>%
  rearrange() %>%
  network_plot()
```



这个图很有意思，我们看到总体分为两群，其中一群是FOXA1，GATA3，ESR1，这是乳腺癌的数据，这三个能聚在一起是符合背景的，因为这三个分子可以决定luminal A型。不过我不知道的是NAT1这个基因跟他们关系这么密切。

另外一群是BRCA1，BRCA2，MKI67，他们之间是正相关，这个可以查一下文献，看看是否是这个样子。

correlate有参数可以限定相关性分析的方法，network_plot也有参数可以设置最终的颜色，以下我给大家展示一下我的洋葱配色




说实话，我挺喜欢这个图的。

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