

Gene expression heat maps

Benedikt Rauscher

9/22/2017

Dependencies

Loading the data

We first load the expression data from Excel files.

```
## Table S1
ts1 <- read.xlsx('Table S1.xlsx', rowNames = T, startRow = 4)
## canonical main
canonical <- read.xlsx('canonical main.xlsx', rowNames=T)
## canonical N2
canonical_n2 <- read.xlsx('canonical N2.xlsx', rowNames=T)
## canonical N3
canonical_n3 <- read.xlsx('canonical N3.xlsx', rowNames=T)
```

Draw heat maps

Data normalization

We normalize each dataset by standardizing the per-gene expression values. This highlights differences in gene expression across different samples but loses information about the base expression level of each gene.

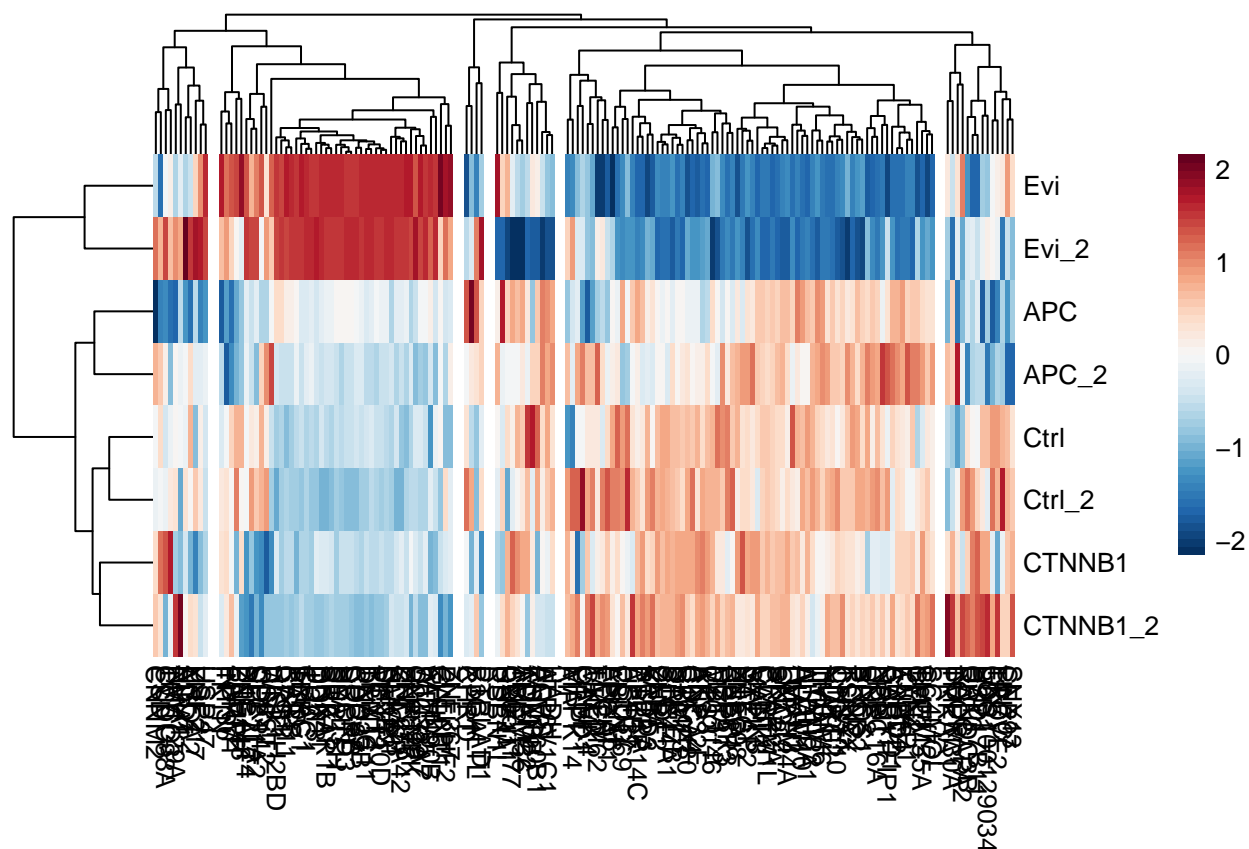
```
## normalize each data set
data_norm <- lapply(list(ts1, canonical, canonical_n2, canonical_n3), function(d){
  ## save names
  cn <- colnames(d)
  ## z-score normalization
  norm <- t(apply(scale(log(d)), 1, function(x) scale(x)))
  colnames(norm) <- cn
  return(t(norm))
})
```

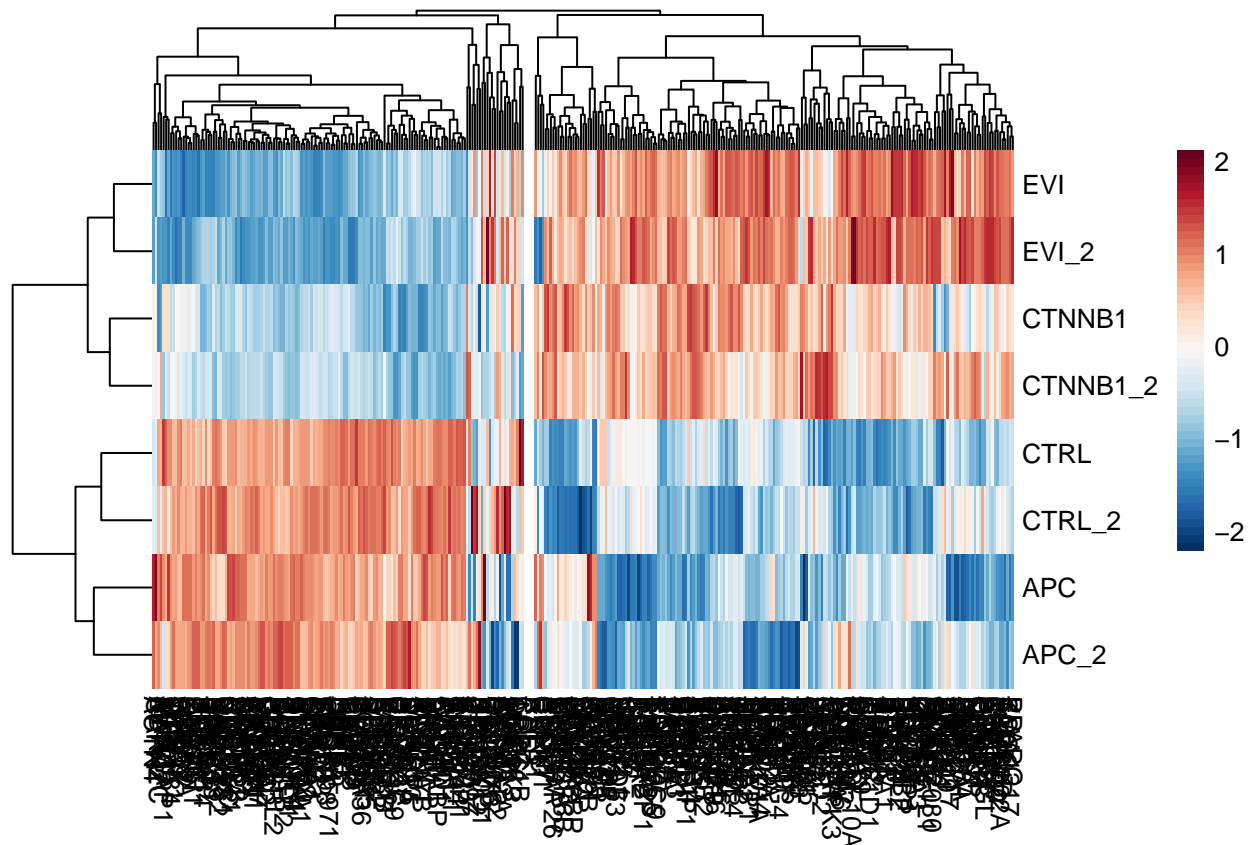
Visualization

We can now visualize the normalized expression values as heatmaps using the `pheatmap` package.

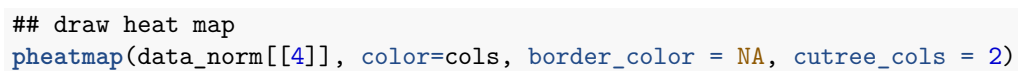
```
## heatmap colours
cols <- rev(colorRampPalette(c('#67001f', '#b2182b', '#d6604d',
                              '#f4a582', '#fddbc7', '#f7f7f7',
                              '#d1e5f0', '#92c5de', '#4393c3',
                              '#2166ac', '#053061'))(50))

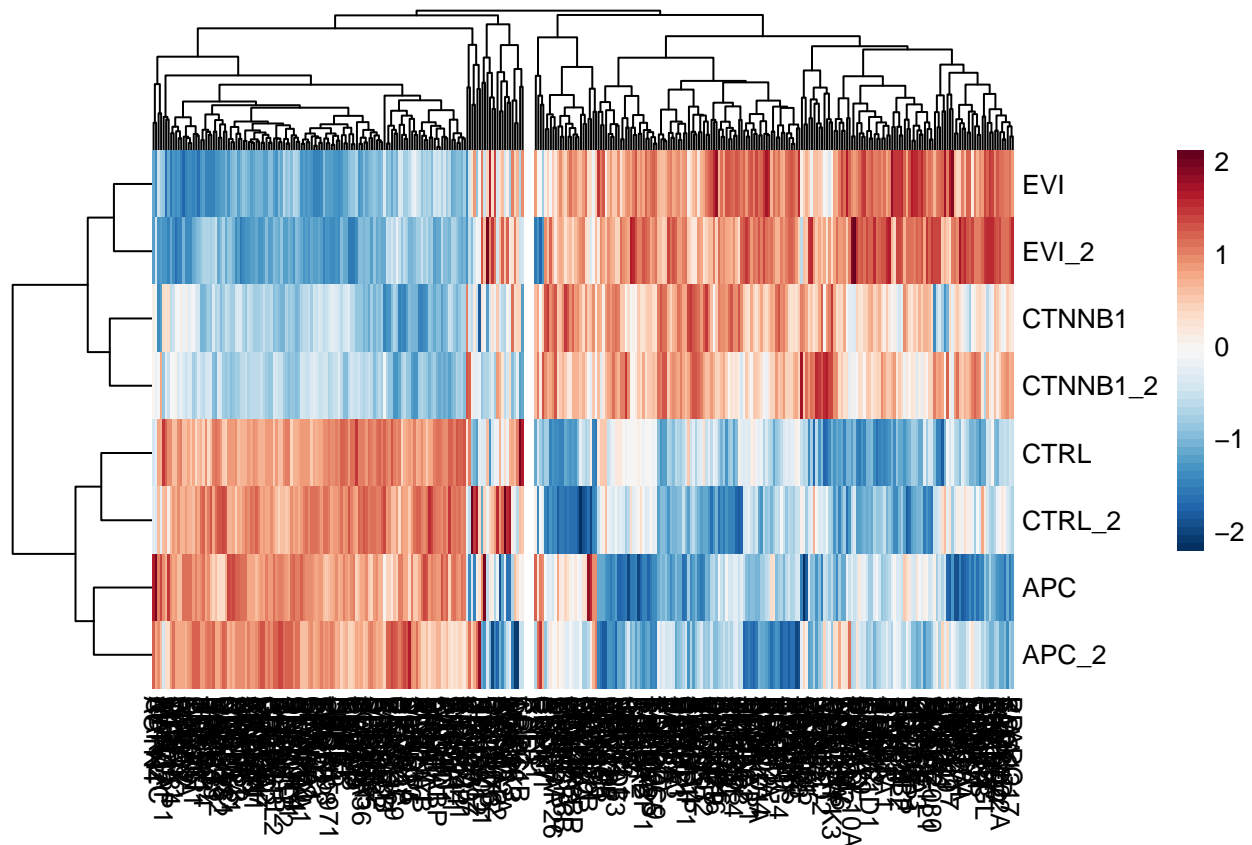
## draw heat map
pheatmap(data_norm[[1]], color=cols, border_color = NA, cutree_cols = 6)
```





```
## draw heat map
pheatmap(data_norm[[3]], color=cols, border_color = NA, cutree_cols = 2)
```





Session info

```
sessionInfo()
```

```
## R version 3.4.1 (2017-06-30)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Sierra 10.12.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] forcats_0.2.0    stringr_1.2.0    dplyr_0.7.4
## [4] purrr_0.2.4      readr_1.1.1      tidyr_0.7.2
## [7] tibble_1.4.2     ggplot2_2.2.1.9000 tidyverse_1.2.1
## [10] pheatmap_1.0.8   openxlsx_4.0.17
##
## loaded via a namespace (and not attached):
```

```

## [1] reshape2_1.4.3      haven_1.1.1          lattice_0.20-35
## [4] colorspace_1.3-2     htmltools_0.3.6      yaml_2.1.16
## [7] rlang_0.1.6.9003     pillar_1.1.0         foreign_0.8-69
## [10] glue_1.2.0           RColorBrewer_1.1-2   modelr_0.1.1
## [13] readxl_1.0.0         bindrcpp_0.2         bindr_0.1
## [16] plyr_1.8.4           munsell_0.4.3        gtable_0.2.0
## [19] cellranger_1.1.0     rvest_0.3.2          psych_1.7.8
## [22] evaluate_0.10.1      knitr_1.18           parallel_3.4.1
## [25] broom_0.4.3          Rcpp_0.12.15         scales_0.5.0.9000
## [28] backports_1.1.2      jsonlite_1.5         mnormt_1.5-5
## [31] hms_0.4.1            digest_0.6.14        stringi_1.1.6
## [34] grid_3.4.1           rprojroot_1.3-2      cli_1.0.0
## [37] tools_3.4.1          magrittr_1.5         lazyeval_0.2.1
## [40] crayon_1.3.4         pkgconfig_2.0.1      xml2_1.2.0
## [43] lubridate_1.7.1      rstudioapi_0.7       assertthat_0.2.0
## [46] rmarkdown_1.8        httr_1.3.1           R6_2.2.2
## [49] nlme_3.1-131         compiler_3.4.1

```