# Using meshes for MeSH term enrichment and semantic analyses

Guangchuang Yu

data(GSE12418\_eset, package="curatedOvarianData")
eset = Biobase::exprs(GSE12418\_eset)
d = data.frame(gene=rownames(eset), expr=apply(eset, 1, median, na.rm=T))
id=clusterProfiler::bitr(d$gene, "SYMBOL", 'ENTREZID', 'org.Hs.eg.db')

## 'select()' returned 1:many mapping between keys and columns

## Warning in clusterProfiler::bitr(d$gene, "SYMBOL", "ENTREZID",
## "org.Hs.eg.db"): 3% of input gene IDs are fail to map...

d <- merge(d, id, by.x='gene', by.y='SYMBOL')

geneList = d$expr
names(geneList) = d$ENTREZID
geneList = sort(geneList, decreasing=T)
de = names(geneList)[abs(geneList) >1]

library(meshes)
data(hsamd)

x <- enrichMeSH(de, MeSHDb = "MeSH.Hsa.eg.db", database='gendoo', category = 'C')
x <- DOSE::setReadable(x, 'org.Hs.eg.db', 'ENTREZID')
y <- gseMeSH(geneList, MeSHDb = "MeSH.Hsa.eg.db", database='gendoo', category = 'C', nPerm=10000)

p1 <- dotplot(x, showCategory=15)
p2 <- cnetplot(x, foldChange=geneList)
p3 <- emapplot(x)
p4 <- ridgeplot(y, fill='pvalue', showCategor=15)

require(cowplot)
plot\_grid(p1, p4, ncol=1, labels=c("C", "D")) %>%
 plot\_grid(p3, ., ncol=2, labels = c("B", "")) %>%
 plot\_grid(p2, ., ncol=1, labels = c("A", ""), rel\_heights=c(.8, 1))

## Picking joint bandwidth of 0.224



## Session Info

sessionInfo()

## R version 3.4.3 (2017-11-30)
## Platform: x86\_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.3
##
## 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] parallel stats4 stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
## [1] cowplot\_0.9.2 ggplot2\_2.2.1 meshes\_1.5.2
## [4] org.Hs.eg.db\_3.5.0 AnnotationDbi\_1.40.0 IRanges\_2.12.0
## [7] S4Vectors\_0.16.0 Biobase\_2.38.0 BiocGenerics\_0.24.0
## [10] DOSE\_3.5.2 rvcheck\_0.0.9 rmarkdown\_1.9
## [13] roxygen2\_6.0.1 magrittr\_1.5 BiocInstaller\_1.28.0
##
## loaded via a namespace (and not attached):
## [1] viridis\_0.5.1 tidyr\_0.8.0 bit64\_0.9-7
## [4] viridisLite\_0.3.0 splines\_3.4.3 ggraph\_1.0.1
## [7] assertthat\_0.2.0 DO.db\_2.9 blob\_1.1.1
## [10] ggrepel\_0.7.0 pillar\_1.2.1 RSQLite\_2.1.0
## [13] backports\_1.1.2 glue\_1.2.0 digest\_0.6.15
## [16] qvalue\_2.10.0 colorspace\_1.3-2 htmltools\_0.3.6
## [19] plyr\_1.8.4 pkgconfig\_2.0.1 clusterProfiler\_3.7.1
## [22] purrr\_0.2.4 GO.db\_3.5.0 scales\_0.5.0
## [25] tweenr\_0.1.5 enrichplot\_0.99.14 BiocParallel\_1.12.0
## [28] ggforce\_0.1.1 tibble\_1.4.2 UpSetR\_1.3.3
## [31] lazyeval\_0.2.1 memoise\_1.1.0 evaluate\_0.10.1
## [34] MASS\_7.3-49 xml2\_1.2.0 tools\_3.4.3
## [37] data.table\_1.10.4-3 stringr\_1.3.0 MeSH.db\_1.9.0
## [40] munsell\_0.4.3 bindrcpp\_0.2.2 compiler\_3.4.3
## [43] rlang\_0.2.0 units\_0.5-1 grid\_3.4.3
## [46] ggridges\_0.5.0 igraph\_1.2.1 labeling\_0.3
## [49] gtable\_0.2.0 DBI\_0.8 reshape2\_1.4.3
## [52] R6\_2.2.2 gridExtra\_2.3 knitr\_1.20
## [55] dplyr\_0.7.4 MeSHDbi\_1.14.0 bit\_1.1-12
## [58] udunits2\_0.13 bindr\_0.1.1 fastmatch\_1.1-0
## [61] commonmark\_1.4 fgsea\_1.4.1 rprojroot\_1.3-2
## [64] GOSemSim\_2.5.1 stringi\_1.1.7 Rcpp\_0.12.16