main

November 24, 2021

1 Gene term enrichment analysis

```
[1]: suppressMessages({
         library(clusterProfiler)
         library(org.Hs.eg.db)
         library(enrichplot)
         library(pathview)})
```

```
[2]: extract_geneList <- function(dft, keytype='EntrezID'){
         dft = na.exclude(dft)
         gg = as.vector(dft[, 'logFC'])
         names(gg) = as.vector(dft[, keytype])
         gg = sort(gg, decreasing=TRUE)
         return(gg)
     }


     extract_geneSet <- function(dft, keytype='EntrezID'){
         dft = na.exclude(dft)
         gg = subset(dft, adj.P.Val <= 0.05)
         gene = as.vector(gg[, keytype])
         return(gene)
     }
```

```
[3]: run_pathview <- function(geneList, pathwayID){
         pathview(gene.data = geneList, pathway.id = pathwayID,
                  species = 'hsa', limit = list(gene=0.75, cpd=0.75))
     }
```

1.1 Genes

```
[4]: inputfile = "../../_m/genes/diffExpr_szVctl_full.txt"

     zz = read.delim(inputfile)
     geneList1 = extract_geneList(zz)
```

```
[5]: aa_uniprot <- merge(bitr(names(geneList1), fromType="ENTREZID",
                              toType=c("UNIPROT", "ENSEMBL"), OrgDb="org.Hs.eg.db"),
                          zz, by.x='ENSEMBL', by.y='ensemblID')
     aa_kegg <- merge(bitr_kegg(aa_uniprot[['UNIPROT']], fromType='uniprot',
                              toType='kegg', organism='hsa'),
                      aa_uniprot, by.x='uniprot', by.y='UNIPROT')
```

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

Warning message in bitr(names(geneList1), fromType = "ENTREZID", toType =
c("UNIPROT", :
"10.19% of input gene IDs are fail to map…"
Reading KEGG annotation online:

Warning message in bitr_kegg(aa_uniprot[["UNIPROT"]], fromType = "uniprot",
toType = "kegg", :
"24.36% of input gene IDs are fail to map…"

```
[6]: geneList2 = extract_geneList(aa_kegg, 'kegg')
     gene2 = extract_geneSet(aa_kegg, 'kegg')
```

1.1.1 Pathview plotting

```
[7]: run_pathview(geneList2, "hsa04020")
```

Info: Downloading xml files for hsa04020, 1/1 pathways..

Info: Downloading png files for hsa04020, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/sex_differences_
sz/interaction_sex_sz/by_sex_sz/caudate/male_analysis/dopamine_system/_m

Info: Writing image file hsa04020.pathview.png

```
[8]: run_pathview(geneList2, "hsa04728")
```

Info: Downloading xml files for hsa04728, 1/1 pathways..

Info: Downloading png files for hsa04728, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/sex_differences_
sz/interaction_sex_sz/by_sex_sz/caudate/male_analysis/dopamine_system/_m

```
Info: Writing image file hsa04728.pathview.png
```

[9]: `run_pathview(geneList2, "hsa04713")`

```
Info: Downloading xml files for hsa04713, 1/1 pathways..

Info: Downloading png files for hsa04713, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/sex_differences_
sz/interaction_sex_sz/by_sex_sz/caudate/male_analysis/dopamine_system/_m

Info: Writing image file hsa04713.pathview.png
```

1.2 Session Info

[10]:
```
Sys.time()
proc.time()
options(width=120)
sessioninfo::session_info()
```

```
[1] "2021-11-24 12:16:02 EST"

   user  system elapsed
  9.999   0.373  77.472
```

$platform $version 'R version 4.1.2 (2021-11-01)'

$os 'Arch Linux'

$system 'x86_64, linux-gnu'

$ui 'X11'

$language '(EN)'

$collate 'en_US.UTF-8'

$ctype 'en_US.UTF-8'

$tz 'America/New_York'

$date '2021-11-24'

$pandoc '2.14.1 @ /usr/bin/pandoc'

$packages A packages_info: 113 × 11

	package	ondiskversion	loadedversion	path
	<chr>	<chr>	<chr>	<chr>
AnnotationDbi	AnnotationDbi	1.54.1	1.54.1	/hom
ape	ape	5.5	5.5	/hom
aplot	aplot	0.1.1	0.1.1	/hom
assertthat	assertthat	0.2.1	0.2.1	/hom
base64enc	base64enc	0.1.3	0.1-3	/hom
Biobase	Biobase	2.52.0	2.52.0	/hom
BiocGenerics	BiocGenerics	0.38.0	0.38.0	/hom
BiocParallel	BiocParallel	1.26.2	1.26.2	/hom
Biostrings	Biostrings	2.60.2	2.60.2	/hom
bit	bit	4.0.4	4.0.4	/hom
bit64	bit64	4.0.5	4.0.5	/hom
bitops	bitops	1.0.7	1.0-7	/hom
blob	blob	1.2.2	1.2.2	/hom
cachem	cachem	1.0.6	1.0.6	/hom
cli	cli	3.1.0	3.1.0	/hom
clusterProfiler	clusterProfiler	4.0.5	4.0.5	/hom
colorspace	colorspace	2.0.2	2.0-2	/hom
cowplot	cowplot	1.1.1	1.1.1	/hom
crayon	crayon	1.4.2	1.4.2	/hom
data.table	data.table	1.14.2	1.14.2	/hom
DBI	DBI	1.1.1	1.1.1	/hom
digest	digest	0.6.28	0.6.28	/hom
DO.db	DO.db	2.9	2.9	/hom
DOSE	DOSE	3.18.3	3.18.3	/hom
downloader	downloader	0.4	0.4	/hom
dplyr	dplyr	1.0.7	1.0.7	/hom
ellipsis	ellipsis	0.3.2	0.3.2	/hom
enrichplot	enrichplot	1.12.3	1.12.3	/hom
evaluate	evaluate	0.14	0.14	/hom
fansi	fansi	0.5.0	0.5.0	/hom
Rcpp	Rcpp	1.0.7	1.0.7	/hom
RCurl	RCurl	1.98.1.5	1.98-1.5	/hom
repr	repr	1.1.3	1.1.3	/hom
reshape2	reshape2	1.4.4	1.4.4	/hom
Rgraphviz	Rgraphviz	2.36.0	2.36.0	/hom
rlang	rlang	0.4.12	0.4.12	/hom
RSQLite	RSQLite	2.2.8	2.2.8	/hom
S4Vectors	S4Vectors	0.30.2	0.30.2	/hom
scales	scales	1.1.1	1.1.1	/hom
scatterpie	scatterpie	0.1.7	0.1.7	/hom
sessioninfo	sessioninfo	1.2.1	1.2.1	/hom
shadowtext	shadowtext	0.0.9	0.0.9	/hom
stringi	stringi	1.7.5	1.7.5	/hom
stringr	stringr	1.4.0	1.4.0	/hom
tibble	tibble	3.1.6	3.1.6	/hom
tidygraph	tidygraph	1.2.0	1.2.0	/hom
tidyr	tidyr	1.1.4	1.1.4	/hom
tidyselect	tidyselect	1.1.1	1.1.1	/hom
tidytree	tidytree	0.3.6	0.3.6	/hom
treeio	treeio	1.16.2	1.16.2	/hom

4

$hash $emoji 1. ' ' 2. ' ' 3. ' '

    $emo_text 1. 'black small square' 2. 'rolling on the floor laughing' 3. 'gem stone'