

# 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", :  
"10.11% of input gene IDs are fail to map..."  
Reading KEGG annotation online:

Warning message in bitr\_kegg(aa\_uniprot[["UNIPROT"]], fromType = "uniprot",  
toType = "kegg", :  
"24.32% 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/female\_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/female\_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/female\_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 12:12:59 EST"
```

```
   user  system elapsed
9.980   0.380  78.498
```

```
$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'
```

	package <chr>	ondiskversion <chr>	loadedversion <chr>	path <chr>
	AnnotationDbi	1.54.1	1.54.1	/hom
	ape	5.5	5.5	/hom
	aplot	0.1.1	0.1.1	/hom
	assertthat	0.2.1	0.2.1	/hom
	base64enc	0.1.3	0.1-3	/hom
	Biobase	2.52.0	2.52.0	/hom
	BiocGenerics	0.38.0	0.38.0	/hom
	BiocParallel	1.26.2	1.26.2	/hom
	Biostrings	2.60.2	2.60.2	/hom
	bit	4.0.4	4.0.4	/hom
	bit64	4.0.5	4.0.5	/hom
	bitops	1.0.7	1.0-7	/hom
	blob	1.2.2	1.2.2	/hom
	cachem	1.0.6	1.0.6	/hom
	cli	3.1.0	3.1.0	/hom
	clusterProfiler	4.0.5	4.0.5	/hom
	colorspace	2.0.2	2.0-2	/hom
	cowplot	1.1.1	1.1.1	/hom
	crayon	1.4.2	1.4.2	/hom
	data.table	1.14.2	1.14.2	/hom
	DBI	1.1.1	1.1.1	/hom
	digest	0.6.28	0.6.28	/hom
	DO.db	2.9	2.9	/hom
	DOSE	3.18.3	3.18.3	/hom
	downloader	0.4	0.4	/hom
	dplyr	1.0.7	1.0.7	/hom
	ellipsis	0.3.2	0.3.2	/hom
	enrichplot	1.12.3	1.12.3	/hom
	evaluate	0.14	0.14	/hom
\$packages A packages_info: 113 × 11	fansi	0.5.0	0.5.0	/hom
	Rcpp	1.0.7	1.0.7	/hom
	RCurl	1.98.1.5	1.98-1.5	/hom
	repr	1.1.3	1.1.3	/hom
	reshape2	1.4.4	1.4.4	/hom
	Rgraphviz	2.36.0	2.36.0	/hom
	rlang	0.4.12	0.4.12	/hom
	RSQLite	2.2.8	2.2.8	/hom
	S4Vectors	0.30.2	0.30.2	/hom
	scales	1.1.1	1.1.1	/hom
	scatterpie	0.1.7	0.1.7	/hom
	sessioninfo	1.2.1	1.2.1	/hom
	shadowtext	0.0.9	0.0.9	/hom
	stringi	1.7.5	1.7.5	/hom
	stringr	1.4.0	1.4.0	/hom
	tibble	3.1.6	3.1.6	/hom
	tidygraph	1.2.0	1.2.0	/hom
	tidyr	1.1.4	1.1.4	/hom
	tidyselect	1.1.1	1.1.1	/hom
	tidytree	0.3.6	0.3.6	/hom
	treeio	1.16.2	1.16.2	/hom

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

**\$emo\_text** 1. 'black small square' 2. 'rolling on the floor laughing' 3. 'gem stone'