main

August 5, 2021

1 Gene term enrichment analysis

```
[1]: library(pathview)
     library(dplyr)
```

```
################################################################################
Pathview is an open source software package distributed under GNU General
Public License version 3 (GPLv3). Details of GPLv3 is available at
http://www.gnu.org/licenses/gpl-3.0.html. Particullary, users are required to
formally cite the original Pathview paper (not just mention it) in publications
or products. For details, do citation("pathview") within R.

The pathview downloads and uses KEGG data. Non-academic uses may require a KEGG
license agreement (details at http://www.kegg.jp/kegg/legal.html).
################################################################################


Attaching package: 'dplyr'


The following objects are masked from 'package:stats':

    filter, lag


The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

1.1 Prep data

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

     geneList = data.table::fread(inputfile) %>% na.exclude() %>%
         tibble::rownames_to_column() %>% select(logFC, EntrezID) %>%
         distinct(EntrezID, .keep_all=TRUE) %>%
         tibble::column_to_rownames("EntrezID") %>% as.vector
     genes = data.table::fread(inputfile) %>% na.exclude() %>%
         filter(`adj.P.Val` <= 0.05) %>% tibble::rownames_to_column() %>%
         select(EntrezID) %>% distinct(EntrezID, .keep_all=TRUE) %>%
         as.vector
```

1.2 Pathview plotting

```
[3]: run_pathview <- function(pathwayID, native=TRUE){
         pathview(gene.data=geneList, pathway.id=pathwayID,
             species='hsa', limit=list(gene=0.5, cpd=0.5),
                 kegg.native=native)
     }
```

```
[4]: run_pathview("hsa04020")
     run_pathview("hsa00350")
```

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/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04020.pathview.png

Info: Downloading xml files for hsa00350, 1/1 pathways..

Info: Downloading png files for hsa00350, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa00350.pathview.png

```
[5]: run_pathview("hsa04724")
     run_pathview("hsa04725")
     run_pathview("hsa04726")
     run_pathview("hsa04727")
```

Info: Downloading xml files for hsa04724, 1/1 pathways..

Info: Downloading png files for hsa04724, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04724.pathview.png

Info: Downloading xml files for hsa04725, 1/1 pathways..

Info: Downloading png files for hsa04725, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04725.pathview.png

Info: Downloading xml files for hsa04726, 1/1 pathways..

Info: Downloading png files for hsa04726, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04726.pathview.png

Info: Downloading xml files for hsa04727, 1/1 pathways..

Info: Downloading png files for hsa04727, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB

rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04727.pathview.png

[6]:
```
run_pathview("hsa04728") # dopamine
run_pathview("hsa04728", FALSE)
```

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/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04728.pathview.png

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04728.pathview.pdf

[7]:
```
run_pathview("hsa04024")
run_pathview("hsa04540")
```

Info: Downloading xml files for hsa04024, 1/1 pathways..

Info: Downloading png files for hsa04024, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04024.pathview.png

Info: Downloading xml files for hsa04540, 1/1 pathways..

Info: Downloading png files for hsa04540, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04540.pathview.png
```

```
[8]:  ## Circadian
      run_pathview("hsa04713")
      run_pathview("hsa04710")
```

```
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/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04713.pathview.png

Info: Downloading xml files for hsa04710, 1/1 pathways..

Info: Downloading png files for hsa04710, 1/1 pathways..

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

Info: Working in directory /ceph/users/jbenja13/github_projects/LieberInstituteB
rainSeqPhase3CaudateSchizophrenia/analysis/differential_expression/kegg_pathways
/_m

Info: Writing image file hsa04710.pathview.png
```

1.3 Session Info

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

```
[1] "2021-08-05 11:04:08 EDT"

   user  system elapsed
 33.130   2.285  52.010
```

```
 Session info
setting   value
version   R version 4.0.3 (2020-10-10)
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      2021-08-05

 Packages
package         * version  date        lib source
AnnotationDbi     1.52.0   2020-10-27  [1] Bioconductor
assertthat        0.2.1    2019-03-21  [1] CRAN (R 4.0.2)
base64enc         0.1-3    2015-07-28  [1] CRAN (R 4.0.2)
Biobase           2.50.0   2020-10-27  [1] Bioconductor
BiocGenerics      0.36.1   2021-04-16  [1] Bioconductor
Biostrings        2.58.0   2020-10-27  [1] Bioconductor
bit               4.0.4    2020-08-04  [1] CRAN (R 4.0.2)
bit64             4.0.5    2020-08-30  [1] CRAN (R 4.0.2)
bitops            1.0-7    2021-04-24  [1] CRAN (R 4.0.3)
blob              1.2.1    2020-01-20  [1] CRAN (R 4.0.2)
cachem            1.0.5    2021-05-15  [1] CRAN (R 4.0.3)
cli               3.0.0    2021-06-30  [1] CRAN (R 4.0.3)
crayon            1.4.1    2021-02-08  [1] CRAN (R 4.0.3)
data.table        1.14.0   2021-02-21  [1] CRAN (R 4.0.3)
DBI               1.1.1    2021-01-15  [1] CRAN (R 4.0.2)
digest            0.6.27   2020-10-24  [1] CRAN (R 4.0.2)
dplyr           * 1.0.7    2021-06-18  [1] CRAN (R 4.0.3)
ellipsis          0.3.2    2021-04-29  [1] CRAN (R 4.0.3)
evaluate          0.14     2019-05-28  [1] CRAN (R 4.0.2)
fansi             0.5.0    2021-05-25  [1] CRAN (R 4.0.3)
fastmap           1.1.0    2021-01-25  [1] CRAN (R 4.0.2)
generics          0.1.0    2020-10-31  [1] CRAN (R 4.0.2)
glue              1.4.2    2020-08-27  [1] CRAN (R 4.0.2)
graph             1.68.0   2020-10-27  [1] Bioconductor
htmltools         0.5.1.1  2021-01-22  [1] CRAN (R 4.0.2)
httr              1.4.2    2020-07-20  [1] CRAN (R 4.0.2)
IRanges           2.24.1   2020-12-12  [1] Bioconductor
IRdisplay         1.0      2021-01-20  [1] CRAN (R 4.0.2)
IRkernel          1.2      2021-05-11  [1] CRAN (R 4.0.3)
jsonlite          1.7.2    2020-12-09  [1] CRAN (R 4.0.2)
KEGGgraph         1.50.0   2020-10-27  [1] Bioconductor
KEGGREST          1.30.1   2020-11-23  [1] Bioconductor
lifecycle         1.0.0    2021-02-15  [1] CRAN (R 4.0.3)
magrittr          2.0.1    2020-11-17  [1] CRAN (R 4.0.2)
```

```
memoise        2.0.0     2021-01-26 [1] CRAN (R 4.0.2)
org.Hs.eg.db   3.12.0    2021-02-24 [1] Bioconductor
pathview     * 1.30.1    2020-12-10 [1] Bioconductor
pbdZMQ         0.3-5     2021-02-10 [1] CRAN (R 4.0.3)
pillar         1.6.1     2021-05-16 [1] CRAN (R 4.0.3)
pkgconfig      2.0.3     2019-09-22 [1] CRAN (R 4.0.2)
png            0.1-7     2013-12-03 [1] CRAN (R 4.0.2)
purrr          0.3.4     2020-04-17 [1] CRAN (R 4.0.2)
R6             2.5.0     2020-10-28 [1] CRAN (R 4.0.2)
Rcpp           1.0.7     2021-07-07 [1] CRAN (R 4.0.3)
RCurl          1.98-1.3  2021-03-16 [1] CRAN (R 4.0.3)
repr           1.1.3     2021-01-21 [1] CRAN (R 4.0.2)
Rgraphviz      2.34.0    2020-10-27 [1] Bioconductor
rlang          0.4.11    2021-04-30 [1] CRAN (R 4.0.3)
RSQLite        2.2.7     2021-04-22 [1] CRAN (R 4.0.3)
S4Vectors      0.28.1    2020-12-09 [1] Bioconductor
sessioninfo    1.1.1     2018-11-05 [1] CRAN (R 4.0.2)
tibble         3.1.2     2021-05-16 [1] CRAN (R 4.0.3)
tidyselect     1.1.1     2021-04-30 [1] CRAN (R 4.0.3)
utf8           1.2.1     2021-03-12 [1] CRAN (R 4.0.3)
uuid           0.1-4     2020-02-26 [1] CRAN (R 4.0.2)
vctrs          0.3.8     2021-04-29 [1] CRAN (R 4.0.3)
withr          2.4.2     2021-04-18 [1] CRAN (R 4.0.3)
XML            3.99-0.6  2021-03-16 [1] CRAN (R 4.0.3)
XVector        0.30.0    2020-10-27 [1] Bioconductor
zlibbioc       1.36.0    2020-10-27 [1] Bioconductor

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0
[2] /usr/lib/R/library
```