main

July 10, 2021

1 Generate circlized plot for gender only analysis DEG results

```
[1]: library(biomaRt)
     library(circlize)
     library(tidyverse)
     library(ComplexHeatmap)
```

```
========================================
circlize version 0.4.13
CRAN page: https://cran.r-project.org/package=circlize
Github page: https://github.com/jokergoo/circlize
Documentation: https://jokergoo.github.io/circlize_book/book/

If you use it in published research, please cite:
Gu, Z. circlize implements and enhances circular visualization
  in R. Bioinformatics 2014.

This message can be suppressed by:
  suppressPackageStartupMessages(library(circlize))
========================================
```

```
  Attaching packages                                tidyverse
1.3.1

  ggplot2 3.3.5      purrr   0.3.4
  tibble  3.1.2      dplyr   1.0.7
  tidyr   1.1.3      stringr 1.4.0
  readr   1.4.0      forcats 0.5.1

  Conflicts
tidyverse_conflicts()
  dplyr::filter() masks stats::filter()
  dplyr::lag()    masks stats::lag()
  dplyr::select() masks
biomaRt::select()
```

```
Loading required package: grid
```

```
========================================
ComplexHeatmap version 2.6.2
Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
Github page: https://github.com/jokergoo/ComplexHeatmap
Documentation: http://jokergoo.github.io/ComplexHeatmap-reference

If you use it in published research, please cite:
Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
  genomic data. Bioinformatics 2016.

This message can be suppressed by:
  suppressPackageStartupMessages(library(ComplexHeatmap))
========================================
```

1.1 Prepare data

1.1.1 Get gene annotation

```
[2]: ensembl = useEnsembl(biomart="ensembl", dataset="hsapiens_gene_ensembl")
     biomart = getBM(attributes=c('ensembl_gene_id', 'chromosome_name',
                              'start_position', 'end_position'),
              mart=ensembl)
     biomart %>% head(2)
```

		ensembl_gene_id $<$chr$>$	chromosome_name $<$chr$>$	start_position $<$int$>$	end_position $<$int$>$
A data.frame: 2×4	1	ENSG00000210049	MT	577	647
	2	ENSG00000211459	MT	648	1601

1.1.2 Get logFC for differential expression analysis

```
[3]: extract_bed <- function(fn, biomart){
         bed = data.table::fread(fn) %>%
             select(gencodeID, ensemblID, Symbol, logFC, "adj.P.Val") %>%
             inner_join(biomart, by=c("ensemblID"="ensembl_gene_id")) %>%
             select(chromosome_name, start_position, end_position, logFC, "adj.P.
      →Val") %>%
             mutate(chromosome_name=paste0('chr', chromosome_name))
         bed_EA = bed %>% filter(logFC > 0, adj.P.Val < 0.05)
         bed_AA = bed %>% filter(logFC < 0, adj.P.Val < 0.05)
         bed_nonsig = bed %>% filter(adj.P.Val > 0.05)
         return(list("EA"=bed_EA, "AA"=bed_AA))
     }
```

```
[4]: caudate = extract_bed("../../../caudate/_m/genes/diffExpr_EAvsAA_full.txt",␣
     ↪biomart)
     dlpfc = extract_bed("../../../dlpfc/_m/genes/diffExpr_EAvsAA_full.txt", biomart)
     hippo = extract_bed("../../../hippocampus/_m/genes/diffExpr_EAvsAA_full.txt",␣
     ↪biomart)
     gyrus = extract_bed("../../../dentateGyrus/_m/genes/diffExpr_EAvsAA_full.txt",␣
     ↪biomart)
```

1.2 Circos Plot

```
[5]: plot_circos <- function(caudate, dlpfc, hippo){
         lgd_points = Legend(at=c("Upregulation in AA", "Upregulation in EA"),␣
     ↪type="points",
                             legend_gp=gpar(col = c("red", "blue")),
                             title_position="topleft", title="Sex Bias",
                             background="#FFFFFF")
         circos.clear() # clear plot if there is any
         circos.par("start.degree" = 0) # rotate 90 degrees
         # initialize with ideogram
         # use hg38, default is hg19
         circos.initializeWithIdeogram(species="hg38")
         circos.genomicTrack(caudate, bg.border="#000080",
                             bg.col=add_transparency("#000080", transparency=0.8),
                             panel.fun = function(region, value, ...) {
                                 i = getI(...)
                                 circos.genomicPoints(region, value, pch = 16,
                                                      cex = 0.6, col = c("blue",␣
     ↪"red")[i], ...)
         })
         circos.genomicTrack(dlpfc, bg.border="#8B0000",
                             bg.col=add_transparency("#8B0000", transparency=0.8),
                             panel.fun = function(region, value, ...) {
                                 i = getI(...)
                                 circos.genomicPoints(region, value, pch = 16,
                                                      cex = 0.6, col = c("blue",␣
     ↪"red")[i], ...)
         })
         circos.genomicTrack(hippo, bg.border="#006400",
                             bg.col=add_transparency("#006400", transparency=0.8),
                             panel.fun = function(region, value, ...) {
                                 i = getI(...)
                                 circos.genomicPoints(region, value, pch = 16,
                                                      cex = 0.6, col = c("blue",␣
     ↪"red")[i], ...)
         })
         draw(lgd_points, x=unit(5, "mm"), y=unit(5, "mm"), just=c("left", "bottom"))
     }
```

```
[6]: png(filename = paste0("significant_circos_plot.png"))
     plot_circos(caudate, dlpfc, hippo)
     dev.off()

     pdf(file = paste0("significant_circos_plot.pdf"))
     plot_circos(caudate, dlpfc, hippo)
     dev.off()

     svg(filename = paste0("significant_circos_plot.svg"))
     plot_circos(caudate, dlpfc, hippo)
     dev.off()
```

png: 2

png: 2

png: 2

1.2.1 Plot 4 brain regions

```
[7]: plot_circos_4tissue <- function(caudate, dlpfc, hippo, gyrus){
         lgd_points = Legend(at=c("Upregulation in AA", "Upregulation in EA"),␣
      →type="points",
                             legend_gp=gpar(col = c("red", "blue")),
                             title_position="topleft", title="Sex Bias",
                             background="#FFFFFF")
         circos.clear() # clear plot if there is any
         circos.par("start.degree" = 0,
                    "cell.padding" = c(0, 0, 0, 0),
                    "track.height" = 0.15) # rotate 90 degrees
         # initialize with ideogram
         # use hg38, default is hg19
         circos.initializeWithIdeogram(species="hg38")
         circos.genomicTrack(caudate, bg.border="#E64B35FF",
                             bg.col=add_transparency("#E64B35FF", transparency=0.7),
                             panel.fun = function(region, value, ...) {
                                 i = getI(...)
                                 circos.genomicPoints(region, value, pch = 16,
                                                      cex = 0.6, col = c("blue",␣
      →"red")[i], ...)
         })
         circos.genomicTrack(gyrus, bg.border="#4DBBD5FF",
                             bg.col=add_transparency("#4DBBD5FF", transparency=0.7),
                             panel.fun = function(region, value, ...) {
                                 i = getI(...)
                                 circos.genomicPoints(region, value, pch = 16,
                                                      cex = 0.6, col = c("blue",␣
      →"red")[i], ...)
```

```
    })
    circos.genomicTrack(dlpfc, bg.border="#00A087FF",
                        bg.col=add_transparency("#00A087FF", transparency=0.7),
                        panel.fun = function(region, value, ...) {
                            i = getI(...)
                            circos.genomicPoints(region, value, pch = 16,
                                                 cex = 0.6, col = c("blue",␣
↪"red")[i], ...)
    })
    circos.genomicTrack(hippo, bg.border="#3C5488FF",
                        bg.col=add_transparency("#3C5488FF", transparency=0.7),
                        panel.fun = function(region, value, ...) {
                            i = getI(...)
                            circos.genomicPoints(region, value, pch = 16,
                                                 cex = 0.6, col = c("blue",␣
↪"red")[i], ...)
    })
    draw(lgd_points, x=unit(5, "mm"), y=unit(5, "mm"), just=c("left", "bottom"))
}
```

```
[8]: library(repr)
     options(repr.plot.width=10, repr.plot.height=10)
     plot_circos_4tissue(caudate, dlpfc, hippo, gyrus)
```
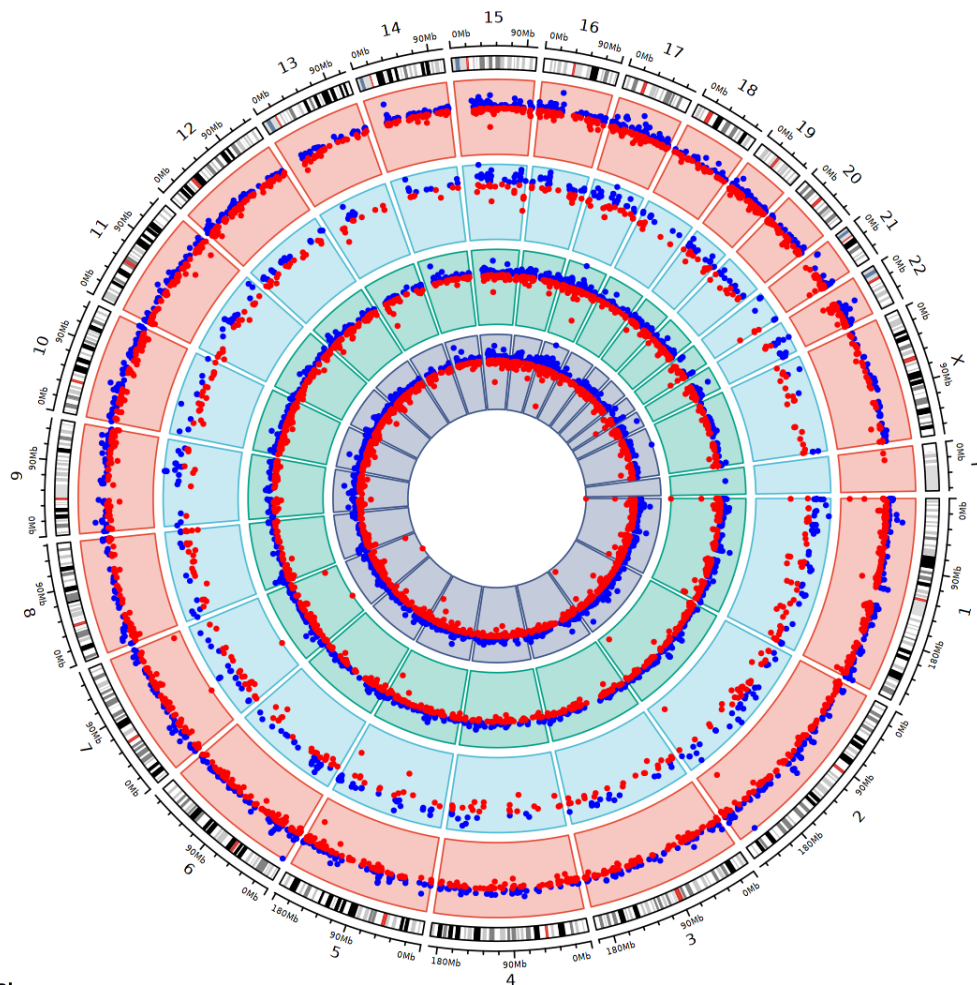
Sex Bias
- Upregulation in AA
- Upregulation in EA

[9]:
```
pdf(file = paste0("significant_circos_plot_4regions.pdf"), width = 10, height =␣
↪10)
plot_circos_4tissue(caudate, dlpfc, hippo, gyrus)
dev.off()
```

png: 2

[10]:
```
svg(filename = paste0("significant_circos_plot_4regions.svg"), width = 10,␣
↪height = 10)
plot_circos_4tissue(caudate, dlpfc, hippo, gyrus)
dev.off()
```

png: 2

1.3 Reproducibility Information

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

```
[1] "2021-07-10 12:41:00 EDT"

   user  system elapsed
 50.143   1.499  58.875

 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     2021-07-10

 Packages
 package       * version   date        lib source
 AnnotationDbi   1.52.0    2020-10-27  [1] Bioconductor
 askpass         1.1       2019-01-13  [1] CRAN (R 4.0.2)
 assertthat      0.2.1     2019-03-21  [1] CRAN (R 4.0.2)
 backports       1.2.1     2020-12-09  [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
 BiocFileCache   1.14.0    2020-10-27  [1] Bioconductor
 BiocGenerics    0.36.1    2021-04-16  [1] Bioconductor
 biomaRt       * 2.46.3    2021-02-09  [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)
 blob            1.2.1     2020-01-20  [1] CRAN (R 4.0.2)
 broom           0.7.8     2021-06-24  [1] CRAN (R 4.0.3)
 cachem          1.0.5     2021-05-15  [1] CRAN (R 4.0.3)
 Cairo           1.5-12.2  2020-07-07  [1] CRAN (R 4.0.2)
 cellranger      1.1.0     2016-07-27  [1] CRAN (R 4.0.2)
 circlize      * 0.4.13    2021-06-09  [1] CRAN (R 4.0.3)
 cli             3.0.0     2021-06-30  [1] CRAN (R 4.0.3)
 clue            0.3-59    2021-04-16  [1] CRAN (R 4.0.3)
 cluster         2.1.0     2019-06-19  [2] CRAN (R 4.0.3)
 colorspace      2.0-2     2021-06-24  [1] CRAN (R 4.0.3)
 ComplexHeatmap* 2.6.2     2020-11-12  [1] Bioconductor
 crayon          1.4.1     2021-02-08  [1] CRAN (R 4.0.3)
```

```
curl            4.3.2     2021-06-23 [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)
dbplyr          2.1.1     2021-04-06 [1] CRAN (R 4.0.3)
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)
forcats       * 0.5.1     2021-01-27 [1] CRAN (R 4.0.2)
fs              1.5.0     2020-07-31 [1] CRAN (R 4.0.2)
generics        0.1.0     2020-10-31 [1] CRAN (R 4.0.2)
GetoptLong      1.0.5     2020-12-15 [1] CRAN (R 4.0.2)
ggplot2       * 3.3.5     2021-06-25 [1] CRAN (R 4.0.3)
GlobalOptions   0.1.2     2020-06-10 [1] CRAN (R 4.0.2)
glue            1.4.2     2020-08-27 [1] CRAN (R 4.0.2)
gtable          0.3.0     2019-03-25 [1] CRAN (R 4.0.2)
haven           2.4.1     2021-04-23 [1] CRAN (R 4.0.3)
hms             1.1.0     2021-05-17 [1] CRAN (R 4.0.3)
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)
lifecycle       1.0.0     2021-02-15 [1] CRAN (R 4.0.3)
lubridate       1.7.10    2021-02-26 [1] CRAN (R 4.0.3)
magrittr        2.0.1     2020-11-17 [1] CRAN (R 4.0.2)
matrixStats     0.59.0    2021-06-01 [1] CRAN (R 4.0.3)
memoise         2.0.0     2021-01-26 [1] CRAN (R 4.0.2)
modelr          0.1.8     2020-05-19 [1] CRAN (R 4.0.2)
munsell         0.5.0     2018-06-12 [1] CRAN (R 4.0.2)
openssl         1.4.4     2021-04-30 [1] CRAN (R 4.0.3)
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)
prettyunits     1.1.1     2020-01-24 [1] CRAN (R 4.0.2)
progress        1.2.2     2019-05-16 [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)
rappdirs        0.3.3     2021-01-31 [1] CRAN (R 4.0.2)
RColorBrewer    1.1-2     2014-12-07 [1] CRAN (R 4.0.2)
Rcpp            1.0.7     2021-07-07 [1] CRAN (R 4.0.3)
readr         * 1.4.0     2020-10-05 [1] CRAN (R 4.0.2)
readxl          1.3.1     2019-03-13 [1] CRAN (R 4.0.2)
repr          * 1.1.3     2021-01-21 [1] CRAN (R 4.0.2)
```

```
reprex          2.0.0    2021-04-02 [1] CRAN (R 4.0.3)
rjson           0.2.20   2018-06-08 [1] CRAN (R 4.0.2)
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)
rstudioapi      0.13     2020-11-12 [1] CRAN (R 4.0.2)
rvest           1.0.0    2021-03-09 [1] CRAN (R 4.0.3)
S4Vectors       0.28.1   2020-12-09 [1] Bioconductor
scales          1.1.1    2020-05-11 [1] CRAN (R 4.0.2)
sessioninfo     1.1.1    2018-11-05 [1] CRAN (R 4.0.2)
shape           1.4.6    2021-05-19 [1] CRAN (R 4.0.3)
stringi         1.6.2    2021-05-17 [1] CRAN (R 4.0.3)
stringr       * 1.4.0    2019-02-10 [1] CRAN (R 4.0.2)
tibble        * 3.1.2    2021-05-16 [1] CRAN (R 4.0.3)
tidyr         * 1.1.3    2021-03-03 [1] CRAN (R 4.0.3)
tidyselect      1.1.1    2021-04-30 [1] CRAN (R 4.0.3)
tidyverse     * 1.3.1    2021-04-15 [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)
xml2            1.3.2    2020-04-23 [1] CRAN (R 4.0.2)

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