main

July 11, 2021

1 Generate circlized plot for 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)
```

A data.frame: 2 × 4

	ensembl_gene_id <chr>	chromosome_name <chr>	start_position <int>	end_position <int>
1	ENSG00000210049	MT	577	647
2	ENSG00000211459	MT	648	1601

1.1.2 Get logFC for differential expression analysis

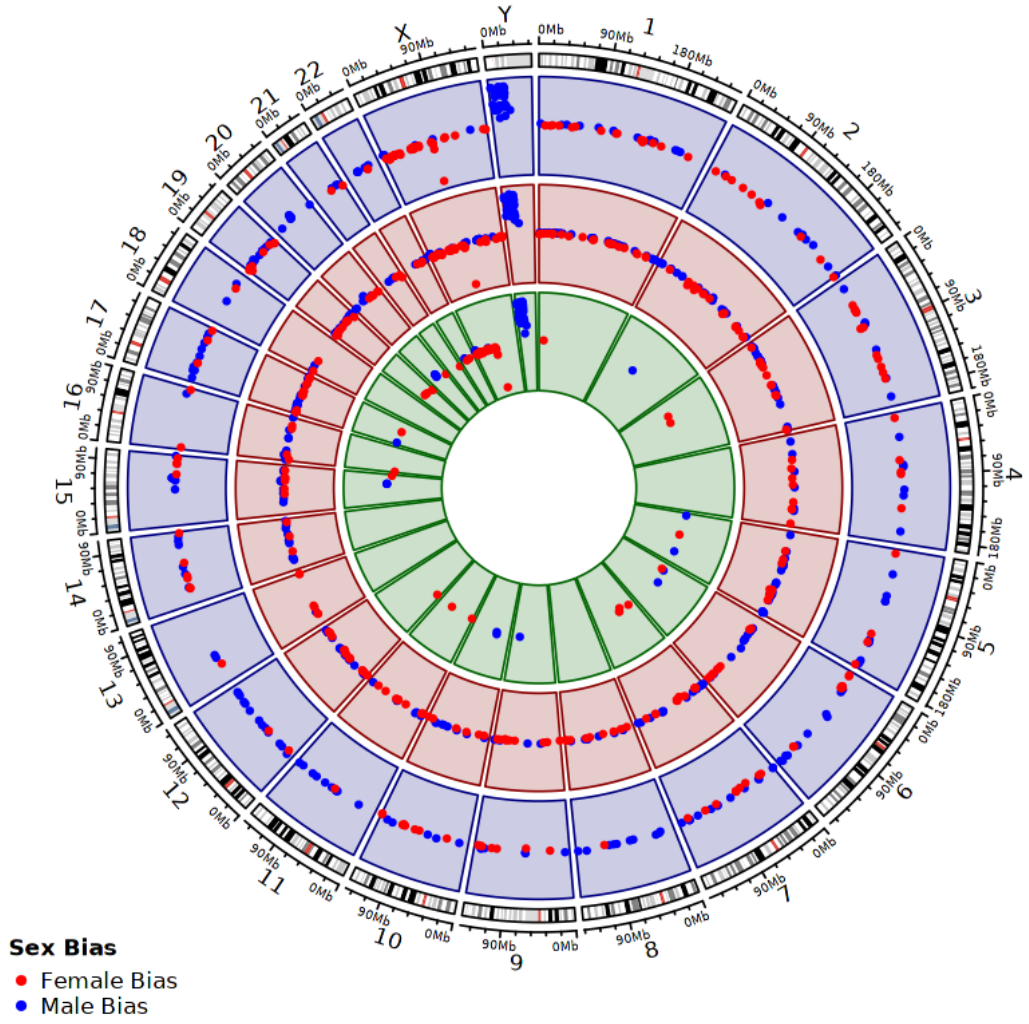
[3]:
```
extract_bed <- function(fn, biomart){
    bed = data.table::fread(fn) %>%
        select(gencodeID, ensemblID, Symbol, logFC, "adj.P.Val") %>%
        inner_join(biomart, by=c("ensemblID"="ensembl_gene_id")) %>%
        select(chromosome_name, start_position, end_position, logFC, "adj.P.
↪Val")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

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

1.2 Circos Plot

[5]:
```
plot_circos <- function(caudate, dlpfc, hippo){
    lgd_points = Legend(at=c("Female Bias", "Male Bias"), 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" = 90) # 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]:
```
plot_circos(caudate, dlpfc, hippo)
```



[7]:
```
R.devices::devEval(c("pdf", "png", "svg"),
                   name="significant_circos_plot",
                   {plot_circos(caudate, dlpfc, hippo)})
```

$pdf 'figures/significant_circos_plot.pdf'

$png 'figures/significant_circos_plot.png'

$svg 'figures/significant_circos_plot.svg'