

main

November 24, 2021

1 Boxplots for permutations analysis (male downsampling to female level)

```
[1]: library(tidyverse)
      library(ggpubr)
```

```
Attaching packages
1.3.1

      tidyverse
ggplot2 3.3.5    purrr   0.3.4
tibble  3.1.6    dplyr   1.0.7
tidyr   1.1.4    stringr 1.4.0
readr   2.1.0    forcats 0.5.1
```

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

1.1 Function and configuration

```
[2]: save_ggplots <- function(p, fn, w=6, h=6){
      for(ext in c('.svg', '.png', '.pdf')){
        ggsave(p, filename=paste0(fn, ext), width=w, height=h)
      }
    }
```

```
[3]: config = list(
      "Caudate" = "../.../caudate/subsampling_male/deg_summary/_m/permutations.
      ↪ csv",
      "DLPFC" = "../.../dlpfc/subsampling_male/deg_summary/_m/permutations.csv",
      "Hippocampus" = "../.../hippocampus/subsampling_male/deg_summary/_m/
      ↪ permutations.csv"
    )
```

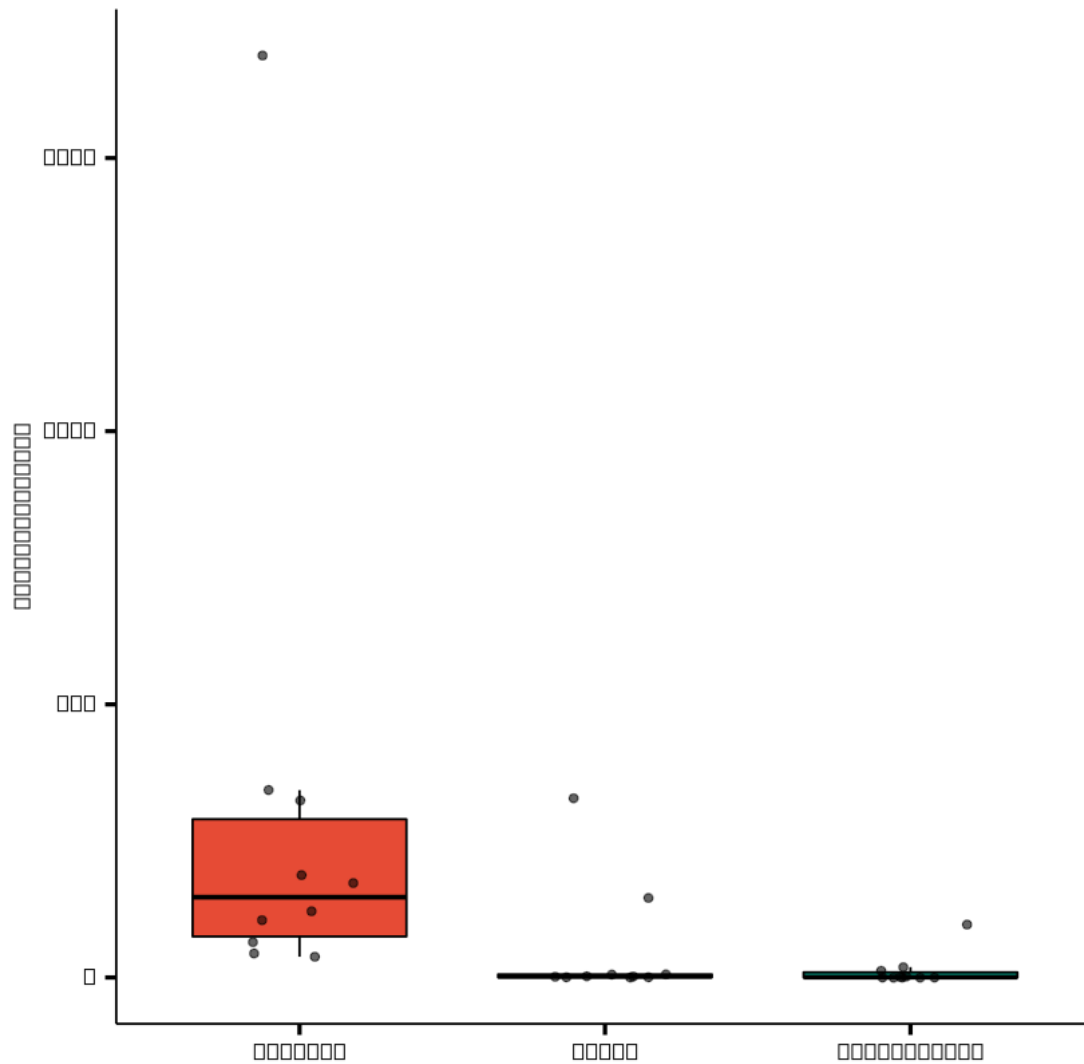
1.2 Merge dataframes

```
[4]: datalist = list()
for(tissue in c("Caudate", "DLPFC", "Hippocampus")){
  df = data.table::fread(config[[tissue]])
  df$tissue <- tissue # maybe you want to keep track of which iteration
  # produced it?
  datalist[[tissue]] <- df
}
big_df <- bind_rows(datalist) %>%
  select(Symbol, gencodeID, logFC, t, adj.P.Val, Permutation, tissue)
big_df %>% head()
```

	Symbol <chr>	gencodeID <chr>	logFC <dbl>	t <dbl>	adj.P.Val <dbl>	Permutation <int>
A data.table: 6 × 7	GDNF-AS1	ENSG00000248587.7	1.0159219	8.553727	1.566672e-09	2
	GDNF	ENSG00000168621.14	0.8188297	6.045744	1.541499e-04	2
	NSUN5P2	ENSG00000106133.17	-0.3648580	-6.031454	1.541499e-04	2
	KCNH5	ENSG00000140015.19	0.5558007	5.980020	1.541499e-04	2
	PAPPA	ENSG00000182752.9	0.7535862	5.862024	2.130430e-04	2
	RMDN2	ENSG00000115841.19	-0.3193313	-5.796196	2.403024e-04	2

```
[5]: bxp = big_df %>% group_by(Permutation, tissue) %>% summarize(Size = n()) %>%
  as.data.frame %>% pivot_wider(names_from = tissue, values_from = Size) %>%
  replace_na(list(DLPFC = 0, Hippocampus = 0)) %>%
  pivot_longer(-Permutation, names_to="Tissue", values_to="DEGs") %>%
  mutate_if(is.character, as.factor) %>%
  ggboxplot(x="Tissue", y="DEGs", fill="Tissue", add="jitter",
    xlab='', palette="npg", ylab="Number of DEGs",
    add.params=list(alpha=0.6), outlier.shape=NA,
    panel.labs.font=list(face='bold'), legend="",
    ggtheme=theme_pubr(base_size=20))+
    font("xy.title", face="bold")
save_ggplots(bxp, "permutation_boxplots_3regions", 6, 5)
bxp
```

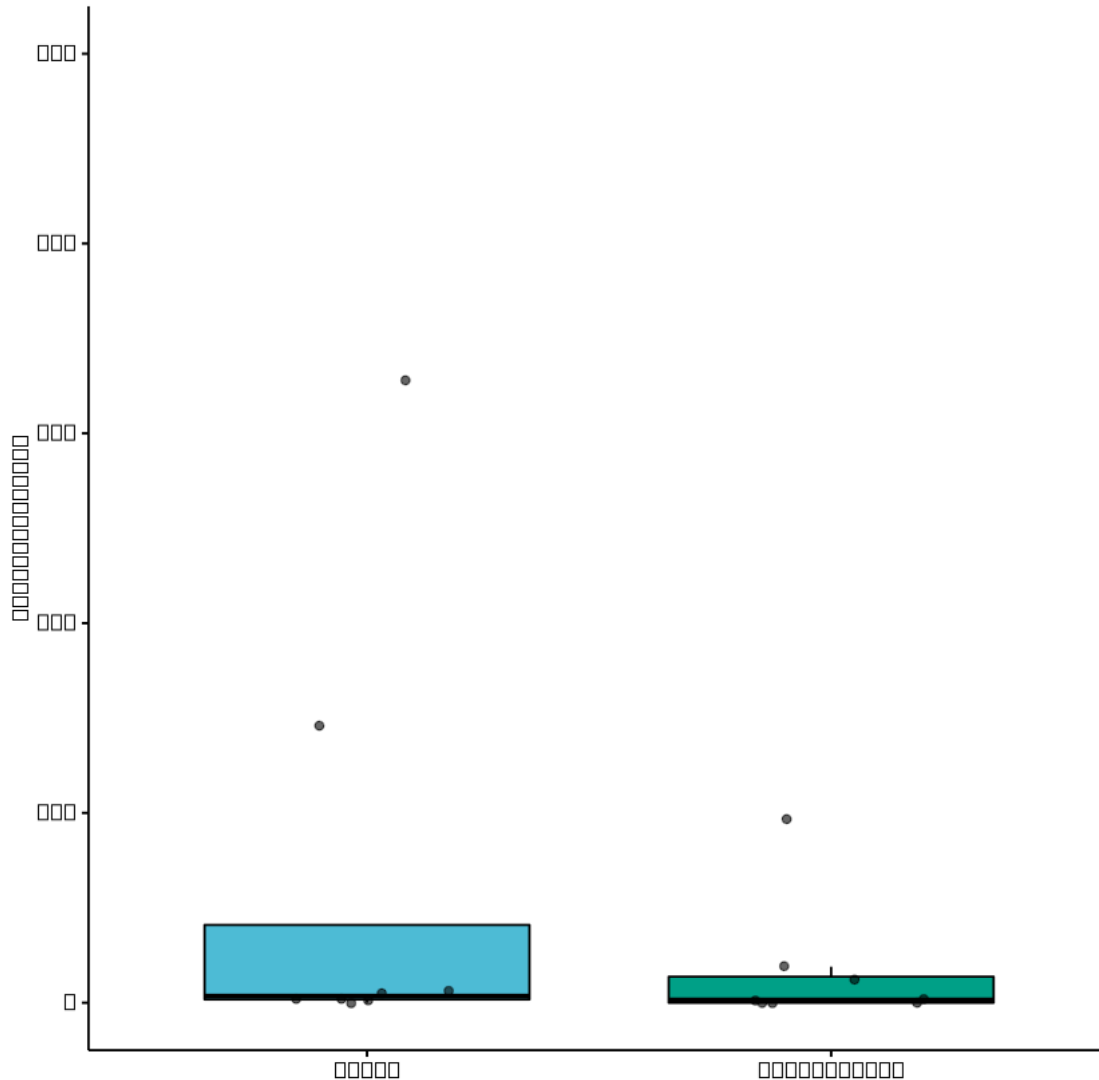
`summarise()` has grouped output by 'Permutation'. You can override using the
`.groups` argument.



```
[6]: bxp = big_df %>% filter(tissue != "Caudate") %>%
  group_by(Permutation, tissue) %>% summarize(Size = n()) %>%
  as.data.frame %>% pivot_wider(names_from = tissue, values_from = Size) %>%
  replace_na(list(DLPFC = 0, Hippocampus = 0)) %>%
  pivot_longer(-Permutation, names_to="Tissue", values_to="DEGs") %>%
  mutate_if(is.character, as.factor) %>%
  ggboxplot(x="Tissue", y="DEGs", fill="Tissue", add="jitter",
            xlab='', palette=get_palette("npg", 3)[2:3], ylab="Number of DEGs",
            add.params=list(alpha=0.6), outlier.shape=NA,
            panel.labs.font=list(face='bold', size = 18),
            legend="", ylim=c(0, 500))+
  font("xy.title", size=18, face="bold") +
```

```
font("xy.text", size=16)
save_ggplots(bxp, "permutation_boxplots_2regions", 6, 5)
bxp
```

`summarise()` has grouped output by 'Permutation'. You can override using the `.groups` argument.



```
[7]: big_df %>% group_by(Permutation, tissue) %>% summarize(Size = n()) %>%
  as.data.frame %>% pivot_wider(names_from = tissue, values_from = Size) %>%
  replace_na(list(DLPFC = 0, Hippocampus = 0)) %>%
  pivot_longer(-Permutation, names_to="Tissue", values_to="DEGs") %>%
  mutate_if(is.character, as.factor) %>%
```

```
group_by(Tissue) %>% summarize(Mean = mean(DEGs), Median = median(DEGs),  
  Std = sd(DEGs))
```

`summarise()` has grouped output by 'Permutation'. You can override using the `.groups` argument.

	Tissue <fct>	Mean <dbl>	Median <dbl>	Std <dbl>
A tibble: 3 × 4	Caudate	308.8	147.0	496.27094
	DLPFC	49.0	2.0	107.99177
	Hippocampus	13.1	0.5	30.18995

1.3 Reproducibility Information

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

```
[1] "2021-11-24 10:00:03 EST"
```

```
   user  system elapsed  
11.733   0.630   13.089
```

```
$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>
	abind	1.4.5	1.4-5	/home/jbenja
	assertthat	0.2.1	0.2.1	/home/jbenja
	backports	1.4.0	1.4.0	/home/jbenja
	base64enc	0.1.3	0.1-3	/home/jbenja
	broom	0.7.10	0.7.10	/home/jbenja
	car	3.0.12	3.0-12	/home/jbenja
	carData	3.0.4	3.0-4	/home/jbenja
	cellranger	1.1.0	1.1.0	/home/jbenja
	cli	3.1.0	3.1.0	/home/jbenja
	colorspace	2.0.2	2.0-2	/home/jbenja
	crayon	1.4.2	1.4.2	/home/jbenja
	data.table	1.14.2	1.14.2	/home/jbenja
	DBI	1.1.1	1.1.1	/home/jbenja
	dbplyr	2.1.1	2.1.1	/home/jbenja
	digest	0.6.28	0.6.28	/home/jbenja
	dplyr	1.0.7	1.0.7	/home/jbenja
	ellipsis	0.3.2	0.3.2	/home/jbenja
	evaluate	0.14	0.14	/home/jbenja
	fansi	0.5.0	0.5.0	/home/jbenja
	farver	2.1.0	2.1.0	/home/jbenja
	fastmap	1.1.0	1.1.0	/home/jbenja
	forcats	0.5.1	0.5.1	/home/jbenja
	fs	1.5.0	1.5.0	/home/jbenja
	generics	0.1.1	0.1.1	/home/jbenja
	ggplot2	3.3.5	3.3.5	/home/jbenja
	ggpubr	0.4.0	0.4.0	/home/jbenja
	ggsci	2.9	2.9	/home/jbenja
	ggsignif	0.6.3	0.6.3	/home/jbenja
	glue	1.5.0	1.5.0	/home/jbenja
\$packages A packages_info: 73 × 11	gtable	0.3.0	0.3.0	/home/jbenja
	pbdZMQ	0.3.6	0.3-6	/home/jbenja
	pillar	1.6.4	1.6.4	/home/jbenja
	pkgconfig	2.0.3	2.0.3	/home/jbenja
	purrr	0.3.4	0.3.4	/home/jbenja
	R6	2.5.1	2.5.1	/home/jbenja
	Rcpp	1.0.7	1.0.7	/home/jbenja
	readr	2.1.0	2.1.0	/home/jbenja
	readxl	1.3.1	1.3.1	/home/jbenja
	repr	1.1.3	1.1.3	/home/jbenja
	reprex	2.0.1	2.0.1	/home/jbenja
	rlang	0.4.12	0.4.12	/home/jbenja
	rstatix	0.7.0	0.7.0	/home/jbenja
	rstudioapi	0.13	0.13	/home/jbenja
	rvest	1.0.2	1.0.2	/home/jbenja
	scales	1.1.1	1.1.1	/home/jbenja
	sessioninfo	1.2.1	1.2.1	/home/jbenja
	stringi	1.7.5	1.7.5	/home/jbenja
	stringr	1.4.0	1.4.0	/home/jbenja
	svglite	2.0.0	2.0.0	/home/jbenja
	systemfonts	1.0.3	1.0.3	/home/jbenja

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

\$emo_text 1. 'rose' 2. 'person bowing: medium-light skin tone' 3. 'bat'