main

July 9, 2021

1 Functional enrichment analysis with g:Profiler

```
[1]: library(tidyverse)
     library(gprofiler2)
```

```
  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()
```

1.1 Load DEG results

```
[2]: deg <- data.table::fread("../../_m/genes/diffExpr_maleVfemale_FDR05.txt") %>%
         select(gencodeID, ensemblID, Symbol, logFC, "adj.P.Val")
     deg %>% head(2)
```

A data.table: 2 × 5

| gencodeID | ensemblID | Symbol | logFC | adj.P.Val |
<chr>	<chr>	<chr>	<dbl>	<dbl>
ENSG00000229807.10	ENSG00000229807	XIST	-9.296137	1.953623e-272
ENSG00000114374.12	ENSG00000114374	USP9Y	8.683679	1.953623e-272

1.2 Calculated enrichment and visual plot

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

1

```
[4]: gostres <- gost(query=deg$ensemblID, organism="hsapiens")
     gostres$result %>%
         data.table::fwrite(file = "allDEGs_functional_enrichment.txt", sep="\t")

     p <- gostplot(gostres, capped = FALSE, interactive = FALSE)
     print(p)
     save_ggplots("allDEGs_manhattan", p, 9, 5)
```



```
[5]: gostres$result
```

A data.frame: 9 × 14
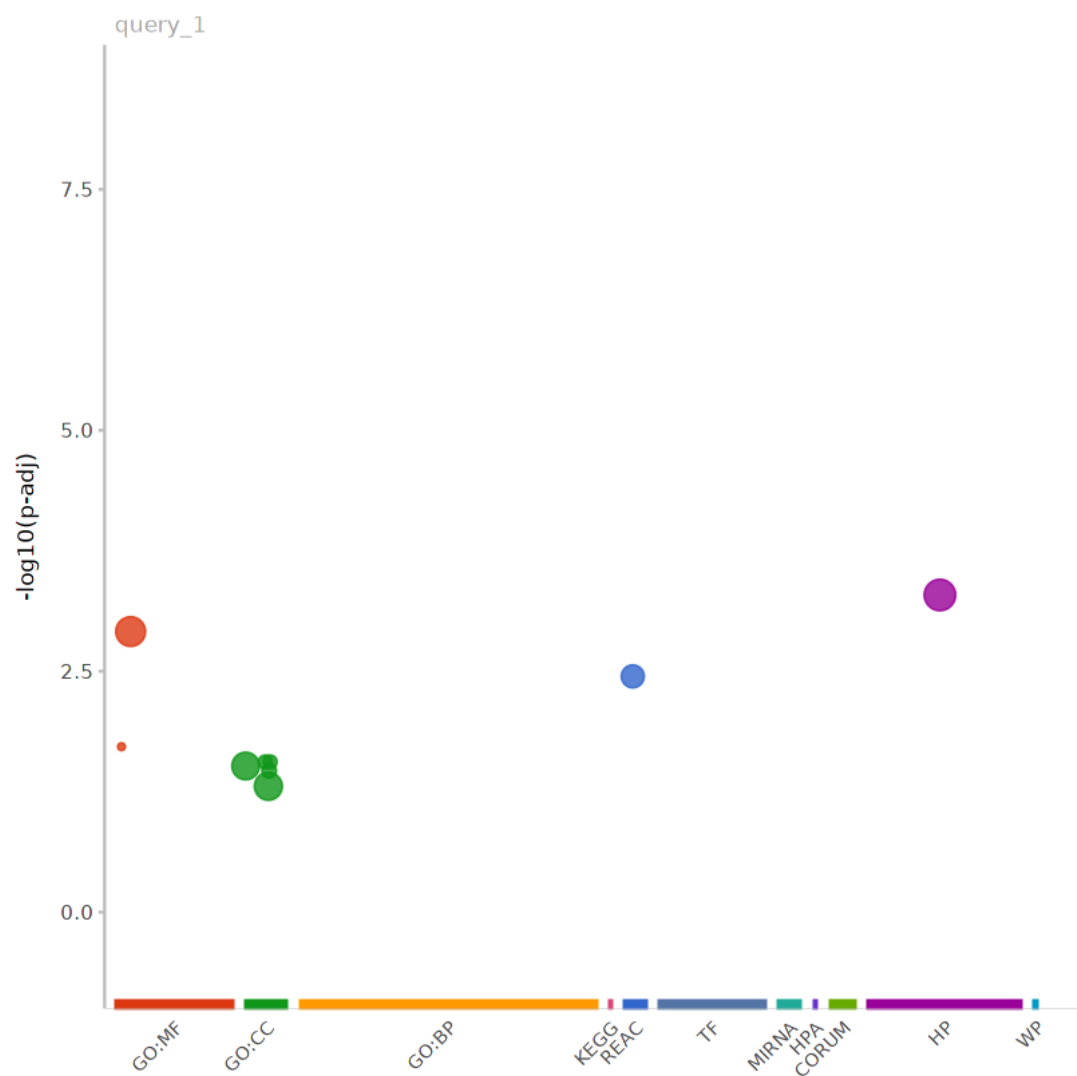
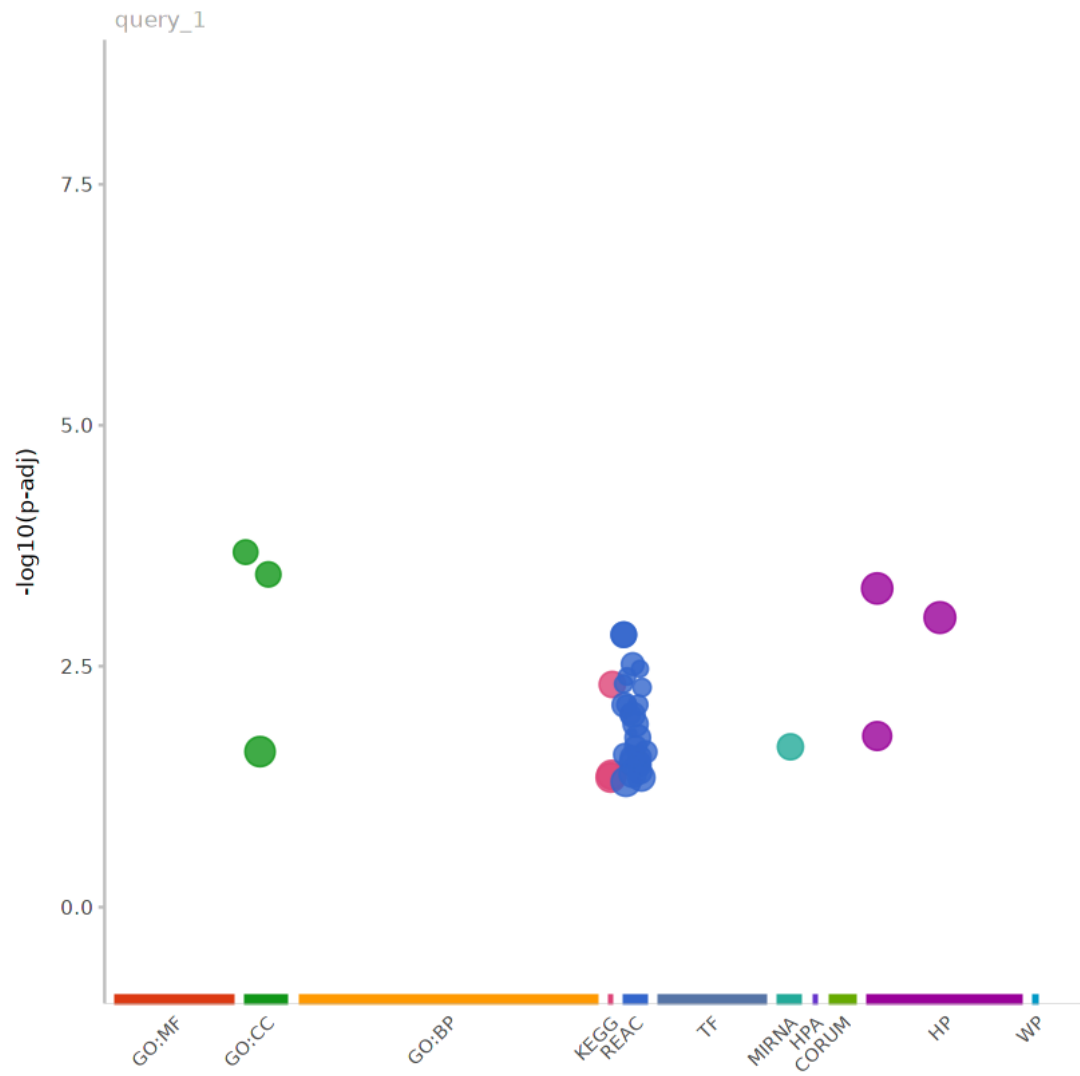| query | significant | p_value | term_size | query_size | intersection_size | precisi |
<chr>	<lgl>	<dbl>	<int>	<int>	<int>	<dbl>
query_1	TRUE	0.0276133974	19	247	4	0.0161
query_1	TRUE	0.0276133974	19	247	4	0.0161
query_1	TRUE	0.0304527360	111	247	8	0.0323
query_1	TRUE	0.0341649388	20	247	4	0.0161
query_1	TRUE	0.0494796315	119	247	8	0.0323
query_1	TRUE	0.0012262224	173	243	12	0.0493
query_1	TRUE	0.0192182533	16	243	4	0.0164
query_1	TRUE	0.0005117774	257	73	17	0.2328
query_1	TRUE	0.0035767152	50	159	7	0.0440

```
[6]: deg_male = deg %>% filter(logFC > 0)
     gostres <- gost(query=deg_male$ensemblID, organism="hsapiens")
     gostres$result %>%
         data.table::fwrite(file = "male_bias_DEGs_functional_enrichment.txt",␣
      ↪sep="\t")

     p <- gostplot(gostres, capped = FALSE, interactive = FALSE)
     print(p)
     save_ggplots("male_bias_DEGs_manhattan", p, 9, 5)
```
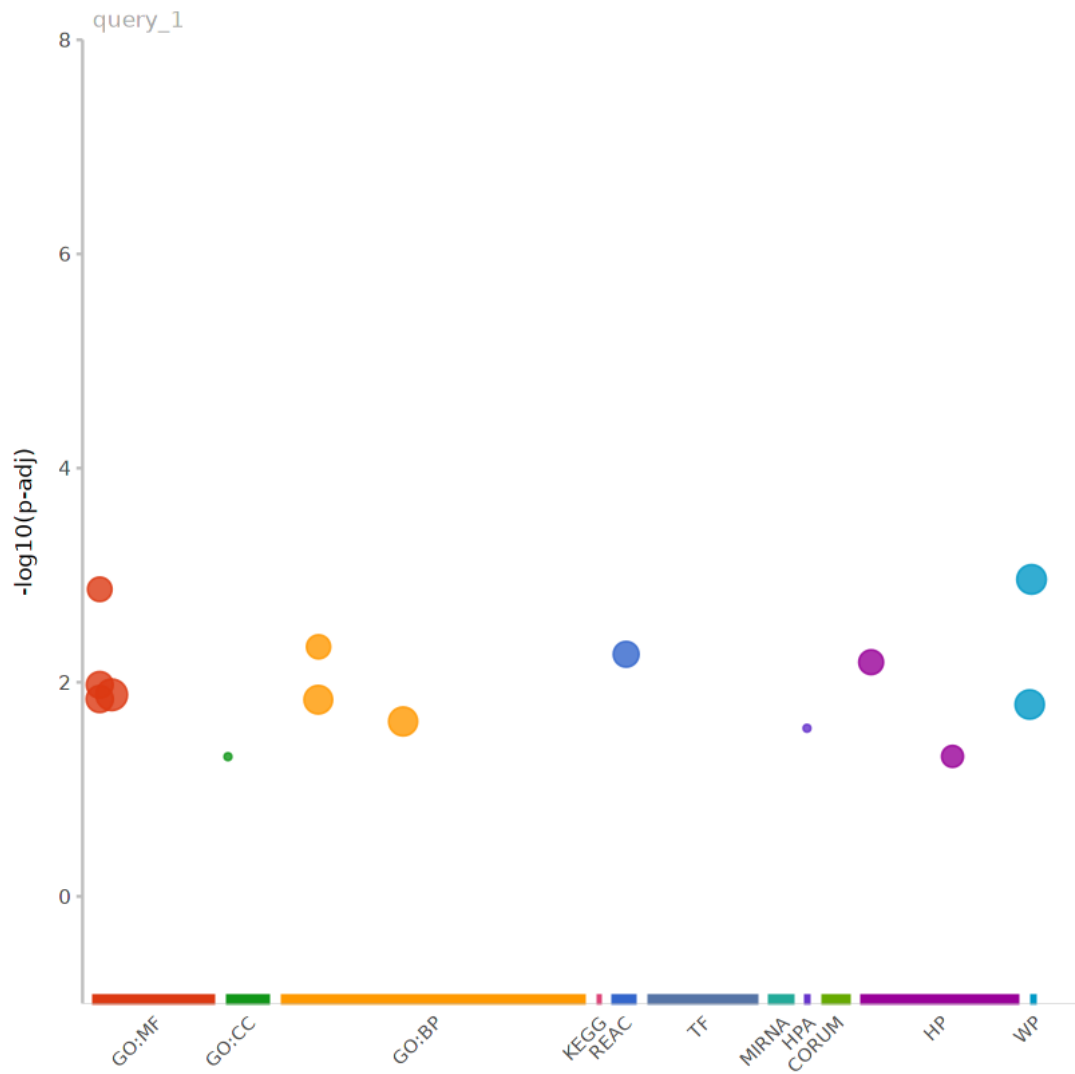
```
[7]: deg_female = deg %>% filter(logFC < 0)
     gostres <- gost(query=deg_female$ensemblID, organism="hsapiens")
     gostres$result %>%
         data.table::fwrite(file = "female_bias_DEGs_functional_enrichment.txt",⊔
      ↪sep="\t")

     p <- gostplot(gostres, capped = FALSE, interactive = FALSE)
     print(p)
     save_ggplots("female_bias_DEGs_manhattan", p, 9, 5)
```

query_1