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

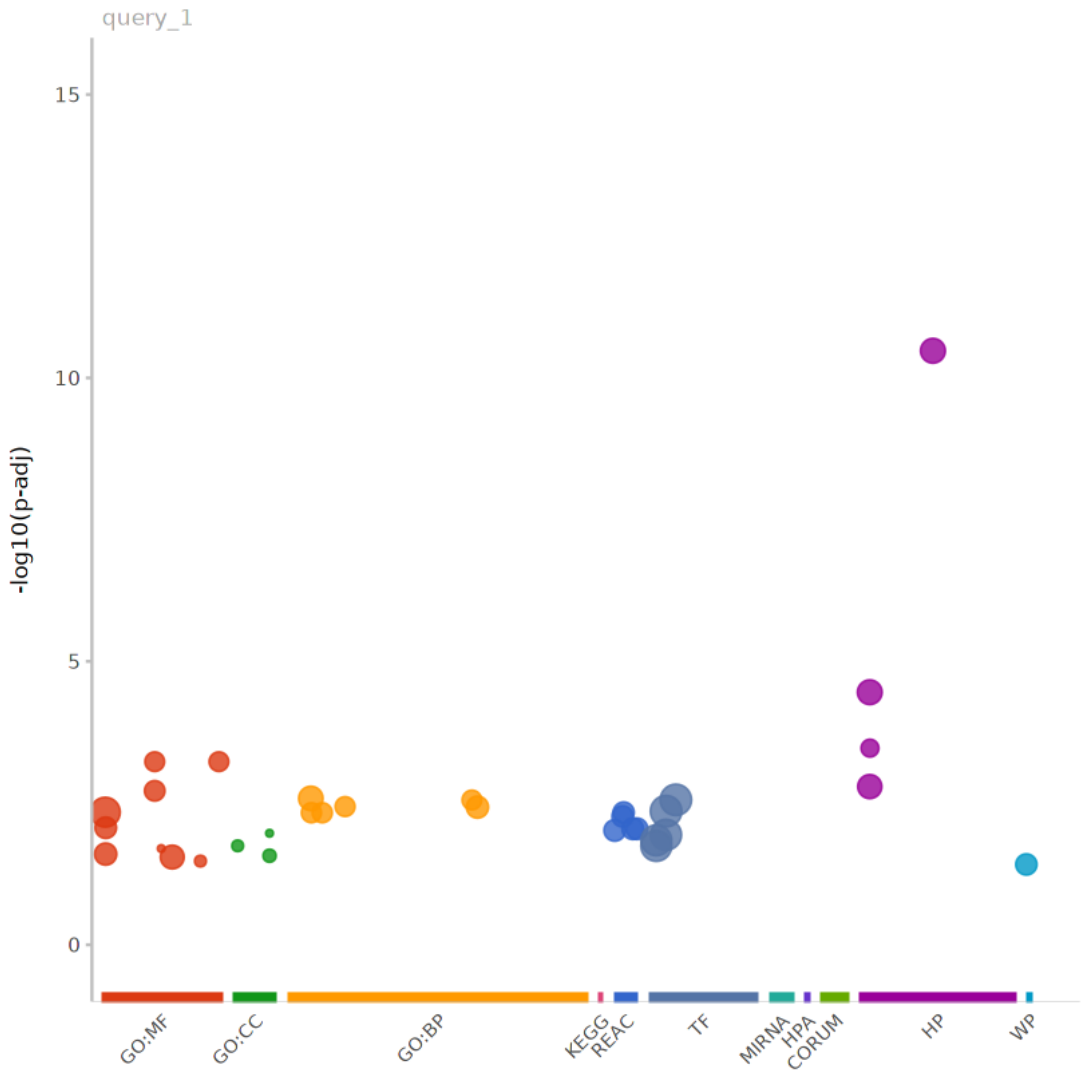
gencodeID <chr>	ensemblID <chr>	Symbol <chr>	logFC <dbl>	adj.P.Val <dbl>
ENSG00000229236.1	ENSG00000229236	TTTY10	6.919904	5.186692e-243
ENSG00000154620.5	ENSG00000154620	TMSB4Y	7.017845	4.942051e-238

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)
    }
}
```

[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)
```



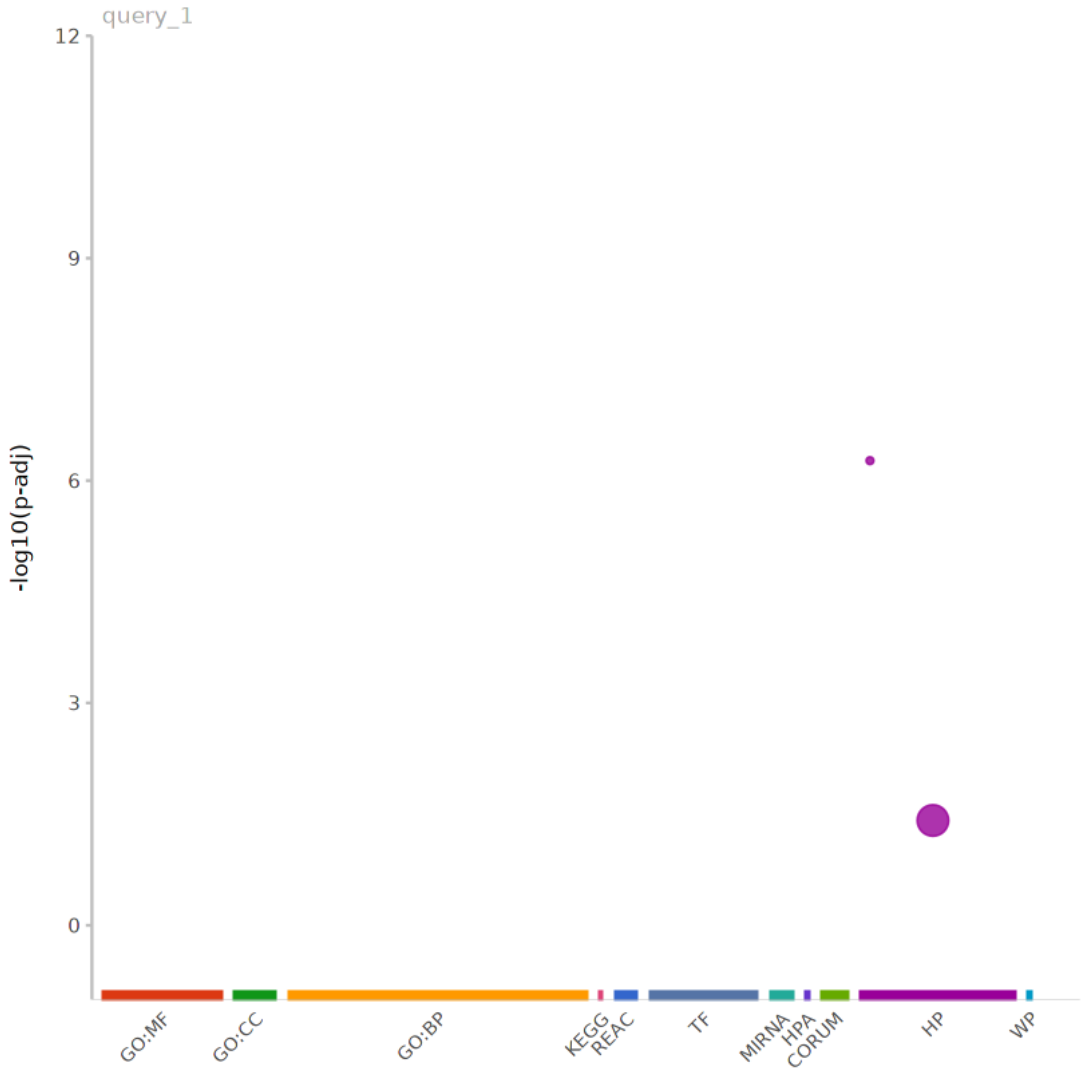
[5]:
```
gostres$result
```

A data.frame: 33 × 14

query <chr>	significant <lgl>	p_value <dbl>	term_size <int>	query_size <int>	intersection_size <int>	precis <dbl>
query_1	TRUE	2.614418e-03	203	49	7	0.1428
query_1	TRUE	2.788989e-03	30	49	4	0.0816
query_1	TRUE	3.645112e-03	32	49	4	0.0816
query_1	TRUE	3.728391e-03	74	49	5	0.1020
query_1	TRUE	4.682296e-03	34	49	4	0.0816
query_1	TRUE	4.682296e-03	34	49	4	0.0816
query_1	TRUE	1.077759e-02	4	50	2	0.0400
query_1	TRUE	1.793235e-02	5	50	2	0.0400
query_1	TRUE	2.685315e-02	6	50	2	0.0400
query_1	TRUE	5.879357e-04	30	51	4	0.0784
query_1	TRUE	5.879357e-04	30	51	4	0.0784
query_1	TRUE	1.921572e-03	40	51	4	0.0784
query_1	TRUE	4.577848e-03	4252	51	26	0.5098
query_1	TRUE	8.603469e-03	58	51	4	0.0784
query_1	TRUE	2.004613e-02	4	51	2	0.0392
query_1	TRUE	2.509197e-02	76	51	4	0.0784
query_1	TRUE	2.832690e-02	154	51	5	0.0980
query_1	TRUE	3.335180e-02	5	51	2	0.0392
query_1	TRUE	3.316055e-11	257	16	13	0.8125
query_1	TRUE	3.502438e-05	241	16	9	0.5625
query_1	TRUE	3.396003e-04	17	16	4	0.2500
query_1	TRUE	1.617914e-03	179	16	7	0.4375
query_1	TRUE	4.632805e-03	50	32	4	0.1250
query_1	TRUE	5.423068e-03	52	32	4	0.1250
query_1	TRUE	8.983216e-03	59	32	4	0.1250
query_1	TRUE	8.983216e-03	59	32	4	0.1250
query_1	TRUE	9.604582e-03	60	32	4	0.1250
query_1	TRUE	2.770219e-03	11217	54	47	0.8703
query_1	TRUE	4.396942e-03	11838	54	48	0.8888
query_1	TRUE	1.147271e-02	8290	54	39	0.7222
query_1	TRUE	1.433755e-02	7621	54	37	0.6851
query_1	TRUE	1.804064e-02	7686	54	37	0.6851
query_1	TRUE	3.825083e-02	53	21	3	0.1428

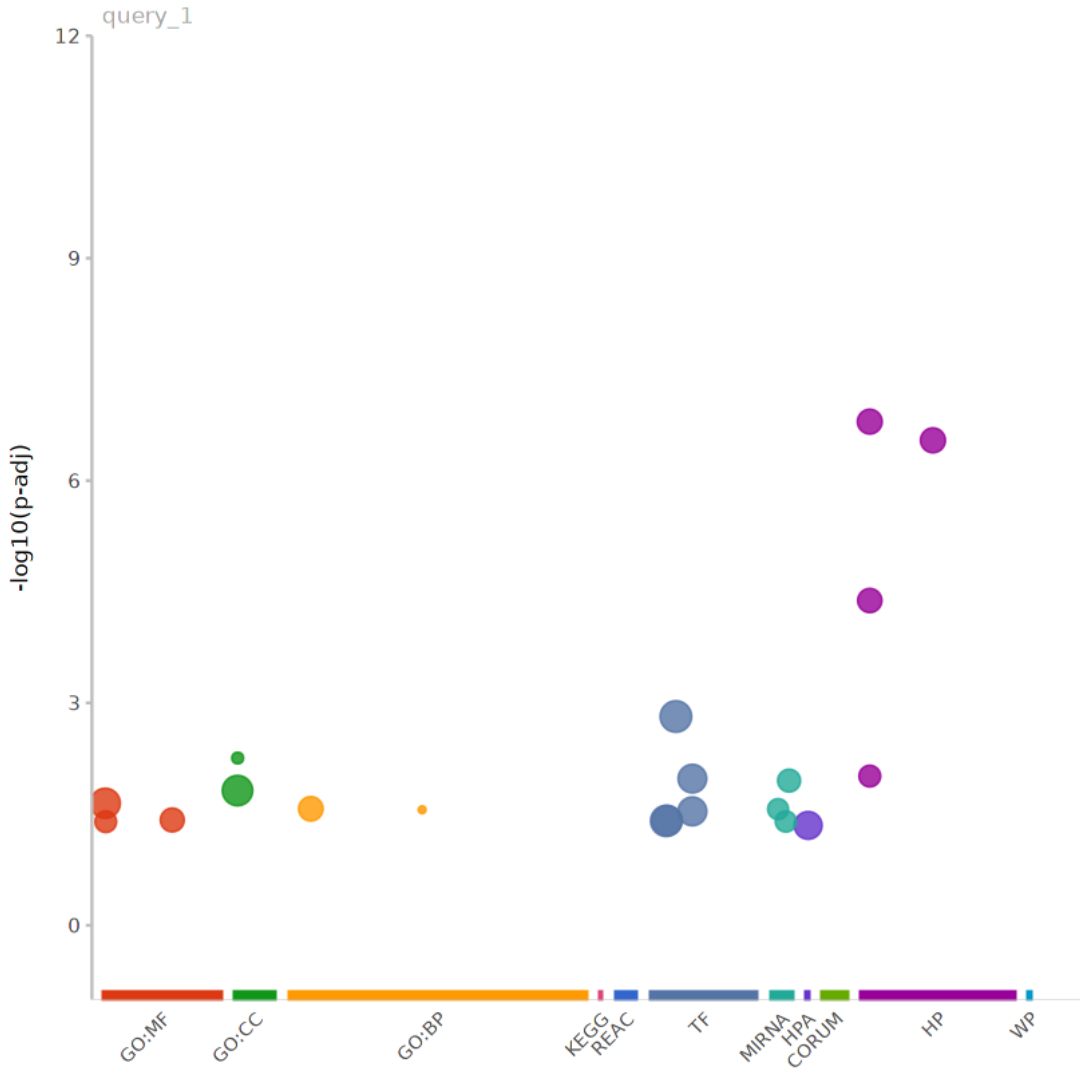
[6]:
```
deg_male = deg %>% filter(logFC > 0)
gostres <- gost(query=deg_male$ensemblID, organism="hsapiens")
gostres$result %>%
    data.table::fwrite(file = "male_bias_DEGs_functional_enrichment.txt",␣
 ↪sep="\t")

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
12
9
6
3
0
-log10(p-adj)
GO:MF
GO:CC
GO:BP
KEGG
REAC
TF
MIRNA
HPA
CORUM
HP
WP

[ ]: