main

July 14, 2021

1 Visualize GO analysis

[1]:
```
import numpy as np
import pandas as pd
```

[2]:
```
def get_top_GO(tissue, fn, label):
    df = pd.read_csv(fn, sep='\t').sort_values('p_value').head(10)
    df['Log10'] = -np.log10(df['p_value'])
    df['Tissue'] = tissue
    df['Direction'] = label
    return df
```

[3]:
```
tissue = 'caudate'
config = {
    'All': '../../_m/DEGs_functional_enrichment.tsv',
    'Up': '../../_m/upreg_DEGs_functional_enrichment.tsv',
    'Down': '../../_m/downreg_DEGs_functional_enrichment.tsv',
}

df = pd.DataFrame()
for bias in ['All', 'Up', 'Down']:
    df = pd.concat([df, get_top_GO(tissue, config[bias], bias)], axis=0)

df.shape
```

[3]:
```
(30, 17)
```

[4]:
```
df.to_csv("%s_functional_analysis.tsv" % tissue, sep='\t', index=False)
```

1.1 Plot

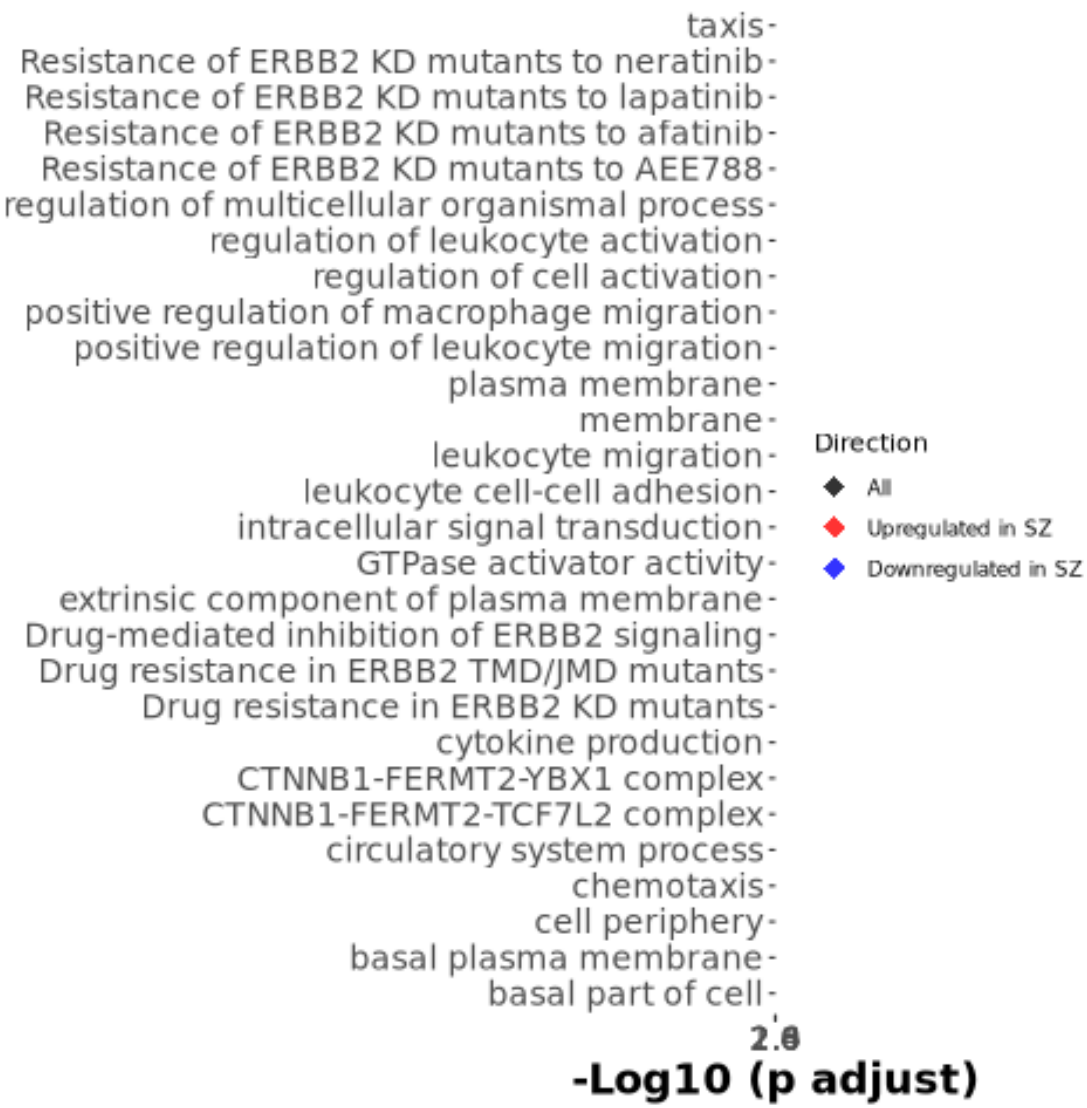
[5]:
```
%load_ext rpy2.ipython
```

[6]:
```
%%R -i df
library(ggplot2)
library(tidyverse)

save_plot <- function(p, fn, w, h){
```

```
    for(ext in c('.svg', '.png', '.pdf')){
        ggsave(file=paste0(fn,ext), plot=p, width=w, height=h)
    }
}

plot_GO <- function(){
    cbPalette <- c("#000000", "Red", "Blue")
    gg1 = df %>%
        ggplot(aes(x=Log10, y=term_name, color=Direction)) +
        geom_point(shape=18, alpha=0.8, size=4) + labs(y='', x='-Log10 (p␣
 ↪adjust)') +
        theme_bw() +
        scale_colour_manual(name="Direction", values=cbPalette,
                            labels=c("All", "Upregulated in SZ", "Downregulated␣
 ↪in SZ")) +
        geom_vline(xintercept = -log10(0.05), linetype = "dotted") +
        theme(axis.text=element_text(size=14),
              axis.title=element_text(size=18, face='bold'),
              strip.text=element_text(size=18, face='bold'))
    return(gg1)
}
```

```
R[write to console]:   Attaching packages
                      tidyverse 1.3.1

R[write to console]:   tibble  3.1.2      dplyr   1.0.7
  tidyr   1.1.3      stringr 1.4.0
  readr   1.4.0      forcats 0.5.1
  purrr   0.3.4

R[write to console]:   Conflicts
tidyverse_conflicts()
  dplyr::filter() masks stats::filter()
  dplyr::lag()    masks stats::lag()
```

[7]:
```
%%R
gg1 = plot_GO()
print(gg1)
save_plot(gg1, "dlpfc_GO_top10_stacked", 10, 6)
```


taxis
Resistance of ERBB2 KD mutants to neratinib
Resistance of ERBB2 KD mutants to lapatinib
Resistance of ERBB2 KD mutants to afatinib
Resistance of ERBB2 KD mutants to AEE788
regulation of multicellular organismal process
regulation of leukocyte activation
regulation of cell activation
positive regulation of macrophage migration
positive regulation of leukocyte migration
plasma membrane
membrane
leukocyte migration
leukocyte cell-cell adhesion
intracellular signal transduction
GTPase activator activity
extrinsic component of plasma membrane
Drug-mediated inhibition of ERBB2 signaling
Drug resistance in ERBB2 TMD/JMD mutants
Drug resistance in ERBB2 KD mutants
cytokine production
CTNNB1-FERMT2-YBX1 complex
CTNNB1-FERMT2-TCF7L2 complex
circulatory system process
chemotaxis
cell periphery
basal plasma membrane
basal part of cell
2.0
-Log10 (p adjust)
Direction
All
Upregulated in SZ
Downregulated in SZ

[ ]: