main

July 14, 2021

1 Visualize KEGG 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')
    df = df[(df['source'].isin(['KEGG', 'REAC']))].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]:
```
(25, 17)
```

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

1.1 Plot

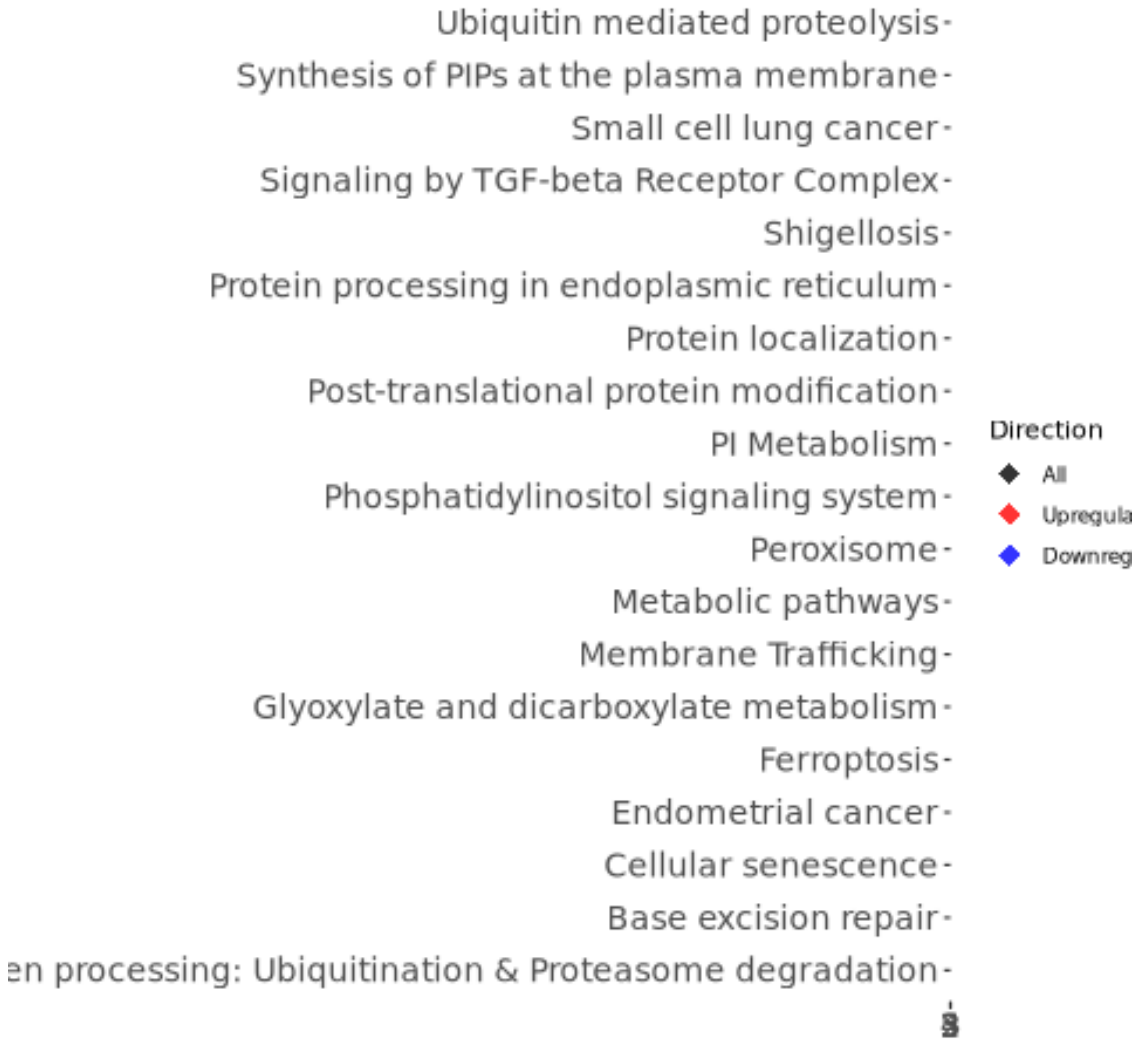
[5]:
```
%load_ext rpy2.ipython
```

[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, "caudate_KEGG_top10_stacked", 10, 6)
```


Ubiquitin mediated proteolysis
Synthesis of PIPs at the plasma membrane
Small cell lung cancer
Signaling by TGF-beta Receptor Complex
Shigellosis
Protein processing in endoplasmic reticulum
Protein localization
Post-translational protein modification
PI Metabolism
Phosphatidylinositol signaling system
Peroxisome
Metabolic pathways
Membrane Trafficking
Glyoxylate and dicarboxylate metabolism
Ferroptosis
Endometrial cancer
Cellular senescence
Base excision repair
en processing: Ubiquitination & Proteasome degradation
-Log10 (p adjust
Direction
All
Upregula
Downreg

[ ]: