

SCEPTRE vs Seurat STAT3

2023-03-14

```
# Load packages.
```

```
library(Seurat)
```

```
## Attaching SeuratObject
```

```
library(SeuratData)
```

```
## -- Installed datasets ----- SeuratData v0.2.2 --
```

```
## v thp1.eccite 3.1.5
```

```
## ----- Key -----
```

```
## v Dataset loaded successfully
```

```
## > Dataset built with a newer version of Seurat than installed
```

```
## (?) Unknown version of Seurat installed
```

```
library(ggplot2)
```

```
library(patchwork)
```

```
library(scales)
```

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## intersect, setdiff, setequal, union
```

```
library(reshape2)
```

```
library(mixtools)
```

```
## mixtools package, version 2.0.0, Released 2022-12-04
```

```
## This package is based upon work supported by the National Science Foundation under Grant No. SES-051
```

```
library(stringr)
library(enrichR)
```

```
## Welcome to enrichR
## Checking connection ...
```

```
## Enrichr ... Connection is Live!
## FlyEnrichr ... Connection is available!
## WormEnrichr ... Connection is available!
## YeastEnrichr ... Connection is available!
## FishEnrichr ... Connection is available!
## OxEEnrichr ... Connection is available!
```

```
library(kableExtra)
```

```
##
## Attaching package: 'kableExtra'
##
## The following object is masked from 'package:dplyr':
##
##     group_rows
```

```
library(varhandle)
```

```
#using absolute paths to download results since files exist on github
code_dir = .get_config_path("LOCAL_CODE_DIR")
data_dir = paste0(code_dir, "/sceptre2-manuscript/writeups/papalexi_analysis/")
sceptre_path = paste0(data_dir,
                       'sceptre_full_mrna_results_with_effect_size.rds')
seurat_stat3_path = paste0(data_dir,
                            'seurat_STAT3_results.rds')
seurat_nfkbia_path = paste0(data_dir,
                             'seurat_NFKBIA_results.rds')
seurat_etv7_path = paste0(data_dir,
                           'seurat_ETV7_results.rds')

sceptre = readRDS(sceptre_path)
seurat_stat3 = readRDS(seurat_stat3_path)
seurat_nfkbia = readRDS(seurat_nfkbia_path)
seurat_etv7 = readRDS(seurat_etv7_path)
```

```
#get significant genes
seurat_etv7_sig = rownames(subset(seurat_etv7, p_val_adj < 0.1))
seurat_stat3_sig = rownames(subset(seurat_stat3, p_val_adj < 0.1))
seurat_nfkbia_sig = rownames(subset(seurat_nfkbia, p_val_adj < 0.1))
```

We see that Seurat-DE finds almost no significant genes after a bonferroni adjustment. \

```
#get number of response genes analyzed per perturbation
grna = unfactor(unique(sceptre$grna_group))
```

Table 1: SCEPTRE: Number of Significant Genes vs Perturbation (FDR = 0.1)

grna	num_significant
CUL3	635
CMTM6	1
ATF2	0
BRD4	748
CAV1	0
CD86	0
ETV7	1
IFNGR1	5472
IFNGR2	5584
IRF1	2579
IRF7	1
JAK2	5574
MARCH8	0
MYC	171
NFKBIA	2
PDCD1LG2	0
POU2F2	2
SMAD4	4389
SPI1	26
STAT1	4790
STAT2	346
STAT3	2
STAT5A	0
TNFRSF14	1
UBE2L6	1

```

n = c()
for(val in grna){
  sceptre_stat3 = subset(sceptre,grna_group == val)
  sceptre_stat3$p_value_adj = p.adjust(sceptre_stat3$p_value,method = "BH")
  sceptre_stat3 = subset(sceptre_stat3,p_value_adj < 0.1)
  n = c(n,nrow(sceptre_stat3))
}

summary_sceptre = data.frame(grna = grna, num_significant = n)
results = kable(summary_sceptre,booktabs = TRUE, linesep = "",
caption = "SCEPTRE: Number of Significant Genes vs Perturbation (FDR = 0.1)")
kable_styling(results,position = "center")

```