

Papalexi Analysis Sceptre

2023-02-16

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.1      v purrr  1.0.1
## v tibble  3.1.8      v dplyr  1.1.0
## v tidyr   1.3.0      v stringr 1.5.0
## v readr   2.1.4      v forcats 1.0.0
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(httr)
library(rlist)
library(jsonlite)
```

```
##
## Attaching package: 'jsonlite'
##
## The following object is masked from 'package:purrr':
##
##     flatten
```

```
library(varhandle)
library(stringi)
```

```
#using absolute paths to download results since files exist on github
data.dir = '/Users/kmason/sceptre2-manuscript/writeups/papalexi_analysis/'
gene_path = paste0(data.dir, 'gene_result.rds')
protein_path = paste0(data.dir, 'protein_result.rds')
gene_result = readRDS(gene_path)
protein_result = readRDS(protein_path)
```

```
#See which gene perturbations are associated with PDL1 protein expression
```

```
#get pvalues from sceptre
P_adj = protein_result[,1]
#unlist pvalues
P_adj = unlist(P_adj)
#some pvalues are negative so take absolute value
P_adj = abs(P_adj)
#make numeric
P_adj = as.numeric(P_adj)
```

```
#perform BH procedure
P_adj = p.adjust(P_adj,method = 'BH')

#replace results matrix pvalues with adjusted pvalues
protein_adjusted= cbind(P_adj,protein_result[,c(2,3)])
```

The authors state that they found 8 perturbations to be significantly associated with PDL1 protein expression. These 8 perturbations are BRD4,MYC,CUL3,IRF1,STAT1,IFNGR1,IFNGR2,and JAK2.

```
#filter to just look at PDL1 pvalues
protein_PDL1 = protein_adjusted[which(protein_adjusted[,3] == 'PDL1')]
#get significant perturbations
sig_genes = subset(protein_PDL1,P_adj < 0.05)$grna_group
#unfactor
sig_genes = unfactor(sig_genes)
cat(paste0('Significant perturbations for the expression of PDL1 protein are:\n ',paste(sig_genes,collapse = '\n ')))
```

```
## Significant perturbations for the expression of PDL1 protein are:
## IRF1,BRD4,CUL3,CMTM6,CD86,IFNGR1,IFNGR2,JAK2,MYC,PDCD1LG2,STAT1,STAT3
```

The authors state that “Importantly, perturbation of these eight genes did not result in appreciable shifts in CD86 or PD-L2 protein expression,suggesting that these regulatory effects are specific to PD-L1’. I will now check to see if this is true when using SCEPTRE.

```
#filter to just look at PDL2 pvalues
protein_PDL2 = protein_adjusted[which(protein_adjusted[,3] == 'PDL2')]
#get significant perturbations
sig_genes = subset(protein_PDL2,P_adj < 0.05)$grna_group
#unfactor
sig_genes = unfactor(sig_genes)
cat(paste0('Significant perturbations for the expression of PDL2 protein are:\n ',paste(sig_genes,collapse = '\n ')))
```

```
## Significant perturbations for the expression of PDL2 protein are:
## IRF1,BRD4,CUL3,CMTM6,CD86,MYC,NFKBIA,PDCD1LG2
```

```
#filter to just look at CD86 pvalues
protein_CD86 = protein_adjusted[which(protein_adjusted[,3] == 'CD86')]
#get significant perturbations
sig_genes = subset(protein_CD86,P_adj < 0.05)$grna_group
#unfactor
sig_genes = unfactor(sig_genes)
cat(paste0('Significant perturbations for the expression of CD86 protein are:\n ',paste(sig_genes,collapse = '\n ')))
```

```
## Significant perturbations for the expression of CD86 protein are:
## IRF1,BRD4,CMTM6,CD86,IFNGR1,IFNGR2,JAK2,MYC,POU2F2,STAT1
```