

TF SCEPTRE vs Seurat in monocytes, with same QC

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Introduction

Here we analyze the performance of SCEPTRE and Seurat on the broad condition gene sets from the hTFtarget database. You can input the TF you want to analyze in the code chunk below.

```
#get the TF name  
#TF_names = c("STAT1", "STAT2", "BRD4", "MYC", "SMAD4", "IRF1")  
TF_name = "SMAD4"
```

Compare SCEPTRE and Seurat results with ChIP-seq scores

Let's first look at how the SCEPTRE and Seurat discoveries align with each other.

Table 1: Comparing SCEPTRE versus Seurat discoveries.

SCEPTRE \ Seurat	FALSE	TRUE
FALSE	7538	1154
TRUE	864	3700

This table suggests that SCEPTRE and Seurat results have decent, but imperfect, agreement. Also note that the total numbers of discoveries made by the two methods are nearly the same. Next, let's look at how the SCEPTRE and Seurat discoveries align with the ChIP-seq target genes (as identified by either the hTFtarget database or directly from the ChIP-seq data).

Table 2: Comparing SCEPTRE to database.

<div style="text-align: right;">SCEPTRE</div> <div style="text-align: left;">Database</div>	FALSE	TRUE	Prop
FALSE	7865	4031	0.339
TRUE	827	533	0.392
Prop	0.095	0.117	

Table 3: Comparing Seurat to database.

<div style="text-align: right;">Seurat</div> <div style="text-align: left;">Database</div>	FALSE	TRUE	Prop
FALSE	7599	4297	0.361
TRUE	803	557	0.41
Prop	0.096	0.115	

The proportions are the proportion of **TRUE** values in each row or column. For example, 0.576 of the genes found by SCEPTRE are marked as TF targets in the database (i.e. SCEPTRE has specificity 0.576). From these tables, we see that **SCEPTRE has slightly lower sensitivity and specificity than Seurat**. We can summarize each 2-by-2 table via its odds ratio (the p-values are all extremely small). The resulting odds ratios are shown below.

Table 4: Enrichment odds ratios, comparing to database and our ChIP-seq target assignments.

<div style="text-align: right;">Method</div> <div style="text-align: left;">Ground truth</div>	SCEPTRE	Seurat
database	1.257	1.227
pvalue	0.000	0.001