

TF SCEPTRE vs Seurat in monocytes, with same QC

2023-04-04

Introduction

This is a followup analysis of Gene's IRF1-analysis-v2 writeup, with two main differences: **The ChIP-seq data is from CD14+ monocytes rather than K562 and the Seurat QC is matched to that of SCEPTRE.** Here, we consider two ways of determining transcription factor target genes: those that are in the hTFtarget database and those that have at least one ChIP-seq peak within 5kb of their TSS. These two align reasonably well; see the table below.

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	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;">Database \ SCEPTRE</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;">Database \ Seurat</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;">Ground truth \ Method</div>	SCEPTRE	Seurat
database	1.257	1.227
pvalue	0.000	0.001