

IRF1 SCEPTRE vs Seurat in monocytes, Changing 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.

```
## \begin{table}[!htbp]
## \caption{Enrichment odds ratios, comparing to database and our ChIP-seq target assignments.\label{ro}
## \begin{center}
## \begin{tabular}{lrrrr}
## \toprule
## \multicolumn{1}{l}{\diagbox{Ground truth}{Method}}&\multicolumn{1}{c}{SCEPTRE}&\multicolumn{1}{c}{Se
## \midrule
## 0.1&5.027&&4.784&&0&&0\&\tabularnewline
## 0.25&3.710&&3.750&&0&&0\&\tabularnewline
## 0.5&2.959&&2.957&&0&&0\&\tabularnewline
## 0.75&2.376&&2.430&&0&&0\&\tabularnewline
## \bottomrule
## \end{tabular}\end{center}
## \end{table}
```