Evaluating several methods on the Schraivogel discovery pairs

Tim

2023-04-10

I apply several methods to a subset of the Schraivogel discovery pairs: Schraivogel method, Seurat DE, and NB regression. I also apply four variants of SCEPTRE to the data: exact vs. approximate, and with vs. without batch included as a covariate. I notate these four variants as follows: SCEPTRE-exact-with-batch, SCEPTRE-exact-no-batch, SCEPTRE-approximate-with-batch, and SCEPTRE-approximate-no-batch.

I load the SCEPTRE results that Gene generated on the Schraivogel discovery pairs.

```
schraivogel_chr8_result_dir <- paste0(LOCAL_SCEPTRE2_DATA_DIR, "results/schraivogel_analysis/")
gk_sceptre_schraivogel_res <- readRDS(paste0(schraivogel_chr8_result_dir, "sceptre_schraivogel_chr_8_res
```

Many of the p-values are small. In fact, about 50% of the p-values are less than 0.001, which seems a bit strange. Let us randomly sample 5,000 of the pairs for which SCEPTRE produces a p-value below 0.001.

```
pairs_to_analyze <- gk_sceptre_schraivogel_res |>
    dplyr::filter(p_value < 0.001) |>
    dplyr::sample_n(5000) |>
    dplyr::select(response_id, grna_group)
```

I subject these pairs to NB regression, Seurat DE, Schraivogel Method, SCEPTRE-exact-with-batch, SCEPTRE-exact-no-batch, SCEPTRE-approximate-with-batch, and SCEPTRE-approximate-no-batch. These methods (especially Seurat DE and Schraivogel Method) take some time to run.