Perturb-seq inference: `sceptre`

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1 Overview

In the `sceptreIGVF` package, I have implemented a function called `inference_sceptre()`, which takes as input a `MuData` object and outputs another `MuData` object with the inference results (p-value and log fold change) added. There are currently no additional arguments to this function, and it runs `sceptre` with all default arguments. The capability to specify additional arguments will be added in the future.

Here is a demo:

```
library(sceptreIGVF)
library(MultiAssayExperiment)
library(ggplot2)
```

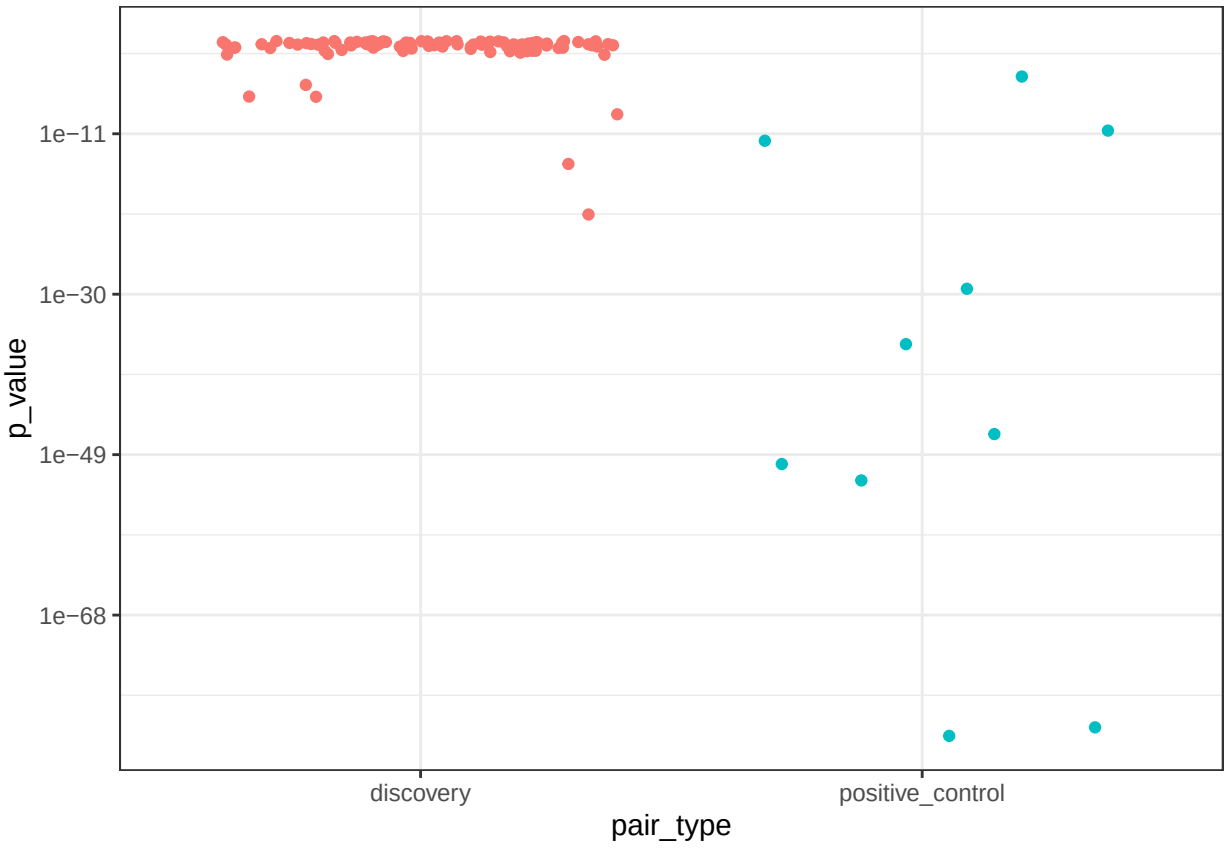
```
data("mudata_inference")
mudata_out <- inference_sceptre(mudata_inference)
```

```
## Welcome to sceptre.
## Submit issues on the sceptre website: github.com/Katsevich-Lab/sceptre
## Read the sceptre manual: timothy-barry.github.io/sceptre-book/
```

```
metadata(mudata_out)$test_results |>
    as.data.frame() |>
    head()
```

```
##           gene_id intended_target_name        pair_type      p_value    log2_fc
## 1 ENSG00000187109      ENSG00000187109 positive_control 4.941655e-83 -0.7542542
## 2 ENSG00000114850      ENSG00000114850 positive_control 5.065197e-82 -1.8660050
## 3 ENSG00000134851      ENSG00000134851 positive_control 8.874414e-53 -0.9552938
## 4 ENSG00000163866      ENSG00000163866 positive_control 7.684199e-51 -1.2229365
## 5 ENSG00000181610      ENSG00000181610 positive_control 2.736911e-47 -1.3298467
## 6 ENSG00000113552      ENSG00000113552 positive_control 1.222514e-36 -1.7534278
```

```
metadata(mudata_out)$test_results |>
    as.data.frame() |>
    na.omit() |>
    ggplot(aes(x = pair_type, color = pair_type, y = p_value)) +
    geom_jitter() +
    scale_y_log10() +
    theme_bw() +
    theme(legend.position = "none")
```


1e−11
1e−30
1e−49
1e−68
p_value
discovery
positive_control
pair_type