

Tradeseq

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```
suppressMessages(library(dplyr))
suppressMessages(library(Seurat))
suppressMessages(library(patchwork))
suppressMessages(library(slingshot))
suppressMessages(library(ggplot2))
suppressMessages(library(tradeseq))
suppressMessages(library(ComplexHeatmap))
suppressMessages(library(SingleCellExperiment))
suppressMessages(library(formatR))
```

Loading tradeseq results

```
sce_slingshot <- readRDS("sce_slingshot.rds")
```

Select the gene with different expression pattern across the 2 lineages

```
patternRes <- patternTest(sce_slingshot)
patternRes <- patternRes[patternRes$waldStat >= 200,]
```

```
gene_list_lo <- rownames(patternRes[order(patternRes$fcMedian, decreasing =
TRUE),,)] [1:200]
```

```
# Remove 6 genes that look like outliers
gene_list_lo <- gene_list_lo[ !gene_list_lo %in%
c("Sftpc", "Igkc", "Ighg3", "Elov11", "Slpi", "Gsn")]
```

```
yhatSmooth <- predictSmooth(sce_slingshot, gene = gene_list_lo, nPoints = 50, tidy =
FALSE)
```

```
Heatmap_diffGenes <- ComplexHeatmap::Heatmap(t(scale(t(yhatSmooth))),
      cluster_columns = FALSE,
      show_row_names = T,
      show_column_names = F)
```

```
#tidyHeatmap::save_pdf(Heatmap_diffGenes, "Heatmap_diffGenes.pdf", width = 20, height =
65, units = "cm")
```

Find gene with similar expression across lineage

```
assoRes <- associationTest(sce_slingshot)
assoRes <- assoRes[order(assoRes$waldStat, decreasing = TRUE),]

gene_list_lo <- rownames(assoRes[order(assoRes$waldStat, decreasing = TRUE),])[1:200]

yhatSmooth <- predictSmooth(sce_slingshot, gene = gene_list_lo, nPoints = 50, tidy = FALSE)

Heatmap_same_Genes<- ComplexHeatmap::Heatmap(t(scale(t(yhatSmooth))),
      cluster_columns = FALSE,
      show_row_names = T,
      show_column_names = F)

#tidyHeatmap::save_pdf(Heatmap_same_Genes, "Heatmap_same_Genes.pdf", width = 20, height = 65, units = "cm")
```

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.6 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=fr_BE.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=fr_BE.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=fr_BE.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_BE.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
##  [1] parallel stats4 grid stats graphics grDevices utils
##  [8] datasets methods base
##
## other attached packages:
##  [1] formatR_1.14              SingleCellExperiment_1.12.0
##  [3] SummarizedExperiment_1.20.0 Biobase_2.50.0
##  [5] GenomicRanges_1.42.0      GenomeInfoDb_1.26.7
##  [7] IRanges_2.24.1            S4Vectors_0.28.1
##  [9] BiocGenerics_0.36.1       MatrixGenerics_1.2.1
## [11] matrixStats_0.63.0        ComplexHeatmap_2.6.2
## [13] tradeSeq_1.4.0            ggplot2_3.4.0
## [15] slingshot_1.8.0           prncurve_2.1.6
## [17] patchwork_1.1.2           SeuratObject_4.1.3
## [19] Seurat_4.3.0              dplyr_1.0.10
##
## loaded via a namespace (and not attached):
##  [1] circlize_0.4.15          VGAM_1.1-7                plyr_1.8.8
```

| | | | |
|----------|-----------------------|------------------------|-----------------------|
| ## [4] | igraph_1.4.1 | lazyeval_0.2.2 | sp_1.6-0 |
| ## [7] | splines_4.0.3 | BiocParallel_1.24.1 | densityClust_0.3.2 |
| ## [10] | listenv_0.9.0 | scattermore_0.8 | fastICA_1.2-3 |
| ## [13] | digest_0.6.31 | htmltools_0.5.4 | magick_2.7.3 |
| ## [16] | viridis_0.6.2 | fansi_1.0.4 | magrittr_2.0.3 |
| ## [19] | tensor_1.5 | cluster_2.1.0 | ROCR_1.0-11 |
| ## [22] | limma_3.46.0 | globals_0.16.2 | docopt_0.7.1 |
| ## [25] | spatstat.sparse_3.0-0 | colorspace_2.1-0 | ggrepel_0.9.2 |
| ## [28] | xfun_0.37 | crayon_1.5.2 | sparsesvd_0.2-2 |
| ## [31] | RCurl_1.98-1.10 | jsonlite_1.8.4 | progressr_0.13.0 |
| ## [34] | spatstat.data_3.0-0 | survival_3.2-7 | zoo_1.8-11 |
| ## [37] | ape_5.6-2 | glue_1.6.2 | polyclip_1.10-4 |
| ## [40] | gtable_0.3.1 | zlibbioc_1.36.0 | XVector_0.30.0 |
| ## [43] | leiden_0.4.3 | GetoptLong_1.0.5 | DelayedArray_0.16.3 |
| ## [46] | shape_1.4.6 | future.apply_1.10.0 | abind_1.4-5 |
| ## [49] | scales_1.2.1 | pheatmap_1.0.12 | edgeR_3.32.1 |
| ## [52] | DBI_1.1.3 | spatstat.random_3.1-3 | miniUI_0.1.1.1 |
| ## [55] | Rcpp_1.0.10 | viridisLite_0.4.1 | xtable_1.8-4 |
| ## [58] | clue_0.3-64 | reticulate_1.27 | htmlwidgets_1.6.1 |
| ## [61] | httr_1.4.5 | FNN_1.1.3.1 | RColorBrewer_1.1-3 |
| ## [64] | ellipsis_0.3.2 | ica_1.0-3 | pkgconfig_2.0.3 |
| ## [67] | uwot_0.1.14 | deldir_1.0-6 | locfit_1.5-9.4 |
| ## [70] | utf8_1.2.3 | tidyselect_1.2.0 | rlang_1.0.6 |
| ## [73] | reshape2_1.4.4 | later_1.3.0 | munsell_0.5.0 |
| ## [76] | tools_4.0.3 | cli_3.6.0 | generics_0.1.3 |
| ## [79] | ggridges_0.5.4 | evaluate_0.20 | stringr_1.5.0 |
| ## [82] | fastmap_1.1.1 | yaml_2.3.7 | goftest_1.2-3 |
| ## [85] | knitr_1.42 | fitdistrplus_1.1-8 | DDRTree_0.1.5 |
| ## [88] | purrr_1.0.1 | RANN_2.6.1 | pbapply_1.7-0 |
| ## [91] | future_1.32.0 | nlme_3.1-162 | mime_0.12 |
| ## [94] | monocle_2.18.0 | slam_0.1-50 | compiler_4.0.3 |
| ## [97] | rstudioapi_0.14 | plotly_4.10.1 | png_0.1-8 |
| ## [100] | spatstat.utils_3.0-1 | tibble_3.1.8 | stringi_1.7.12 |
| ## [103] | lattice_0.20-41 | Matrix_1.5-3 | HSMMSingleCell_1.10.0 |
| ## [106] | vctrs_0.5.2 | pillar_1.8.1 | lifecycle_1.0.3 |
| ## [109] | GlobalOptions_0.1.2 | combinat_0.0-8 | spatstat.geom_3.0-6 |
| ## [112] | lmtest_0.9-40 | RcppAnnoy_0.0.20 | data.table_1.14.8 |
| ## [115] | cowplot_1.1.1 | bitops_1.0-7 | irlba_2.3.5.1 |
| ## [118] | httpuv_1.6.9 | R6_2.5.1 | promises_1.2.0.1 |
| ## [121] | KernSmooth_2.23-20 | gridExtra_2.3 | parallelly_1.34.0 |
| ## [124] | codetools_0.2-19 | MASS_7.3-53 | assertthat_0.2.1 |
| ## [127] | rjson_0.2.21 | withr_2.5.0 | qlcMatrix_0.9.7 |
| ## [130] | sctransform_0.3.5 | GenomeInfoDbData_1.2.4 | mgcv_1.8-33 |
| ## [133] | tidyr_1.2.1 | rmarkdown_2.19 | Cairo_1.6-0 |
| ## [136] | Rtsne_0.16 | spatstat.explore_3.0-5 | shiny_1.7.4 |