# **Entropy (might do this later)**

https://rdrr.io/github/aet21/SCENT/f/inst/doc/SCENT.Rmd

PPI:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2048726/bin/plntphys\_pp.107.103465v2\_index.ht ml

SCENIC:

http://htmlpreview.github.io/?https://github.com/aertslab/SCENIC/blob/master/inst/doc/SCENIC\_Setup.html

### **How to Calculate Correlation Between Continuous & Categorical Variables**

I.e. correlation between counts/number of features and ploidy/...

Point biserial correlation: <a href="https://www.statology.org/correlation-between-continuous-categorical-variables/">https://www.statology.org/correlation-between-continuous-categorical-variables/</a>

### **Subclustering**

Might be beneficial for clusters with high uncertainty and to avoid cluster names with lots of different cell types

Unsupervised: https://satijalab.org/seurat/reference/findsubcluster

Supervised: e.g. based on specific markers (as they did for distinguishing QC and columella in Denyer paper, fig. 4)

### **GO-enrichment of clusters**

https://cran.r-project.org/web/packages/gprofiler2/vignettes/gprofiler2.html

https://bioconductor.org/packages/release/bioc/html/goseq.html

# Cell-type specific networks:

https://github.com/VIB-PSB/MINI-EX

Single-cell data simulation (could also skip this and start on small cluster)

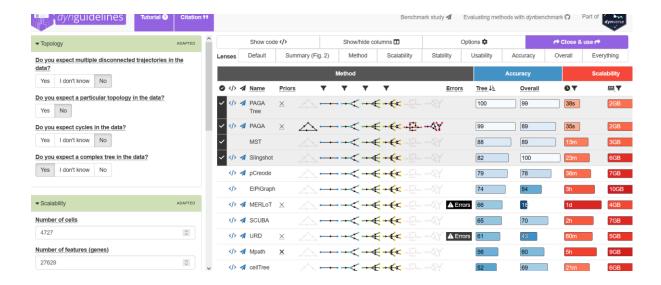
https://github.com/dynverse/dyngen

https://dyngen.dynverse.org/articles/getting started.html

https://dyngen.dynverse.org/articles/showcase\_backbones.html

## **Trajectory inference**

https://github.com/dynverse/dynguidelines



http://bioconductor.org/books/3.13/OSCA.advanced/trajectory-analysis.html

https://bioconductor.org/packages/devel/bioc/vignettes/slingshot/inst/doc/vignette.html

# Differential expression along pseudotime

https://bioconductor.org/packages/release/bioc/vignettes/tradeSeq/inst/doc/tradeSeq.html

https://kstreet13.github.io/bioc2020trajectories/articles/workshopTrajectories.html

https://statomics.github.io/tradeSeq/articles/tradeSeq.html

### **Probabilistic methods**

A descriptive marker gene approach to single-cell pseudotime inference (Campbell et al., 2019): <a href="https://github.com/kieranrcampbell/ouija">https://github.com/kieranrcampbell/ouija</a>

Order Under Uncertainty: Robust Differential Expression Analysis Using Probabilistic Models for Pseudotime Inference (Campbell et al., 2016): <a href="https://github.com/kieranrcampbell/pseudogp">https://github.com/kieranrcampbell/pseudogp</a>