Challenges & Opportunities

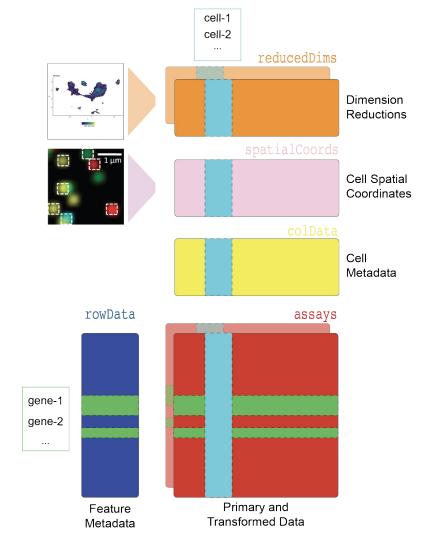
Kasper Hansen

SpatialExperiment

Description:

- SingleCellExperiment inheritance
- Puts the basis for spatial experiments analysis
- <u>spatialCoords</u>: samples spatial coordinates
 (Typically x and y)
- <u>coerce</u>: coercing SpatialExperiment for working with external developed tools (i.e. Giotto)





Spatial transcriptomics (10x Visium)

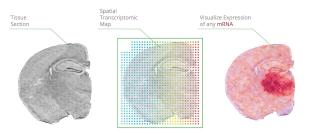
Transcriptome-wide expression at spatial resolution on the order of single cells

Unsupervised analysis pipeline for human prefrontal cortex

Maynard & Collado-Torres et al. (2020 bioRxiv)

Data resources

- Bioconductor package: http://bioconductor.org/packages/ spatialLIBD
- Shiny web application: http://research.libd.org/spatialLIBD/



https://spatialtranscriptomics.com/technology/



Maynard & Collado-Torres et al. (2020), Fig. 7





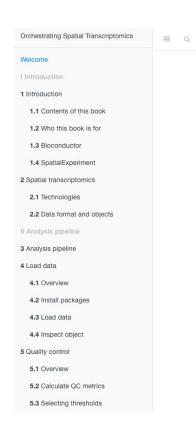
Spatial transcriptomics

Future work:

Orchestrating Spatial Transcriptomics Analysis (OSTA)

Pipeline for analyzing spatial transcriptomics data using Bioconductor framework

Work in progress



Orchestrating Spatial Transcriptomics Analysis with Bioconductor

2020-06-27

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Welcome

This is the website for the online textbook "Orchestrating Spatial Transcriptomics Analysis with Bioconductor".

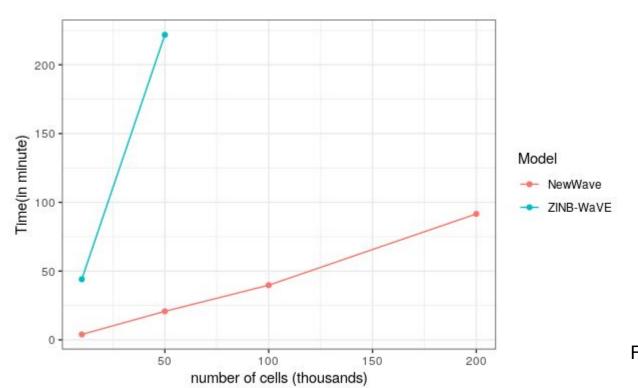
This textbook describes the steps in a computational analysis pipeline for spatial transcriptomics data, using the Bioconductor framework and R programming language. The analysis pipeline is built up as a series of steps, each described in a chapter in the main section, with complete examples and workflows using R code and data that can be run on your own laptop.



The book is organized into several parts, consisting of (i) introductory material, (ii) analysis pipeline (chapters for each key step in the analysis), (iii) extended topics, (iv) workflows (complete workflows with minimal documentation), and (v) appendix.

This is a companion to the textbook Orchestrating Single-Cell Analysis with Bioconductor (OSCA), which describes workflows for analyzing single-cell RNA sequencing data. The OSCA textbook also includes additional introductory material on R and Bioconductor, which may be useful for readers getting started with Bioconductor.

NewWave: scalable factor analysis for negative binomial data

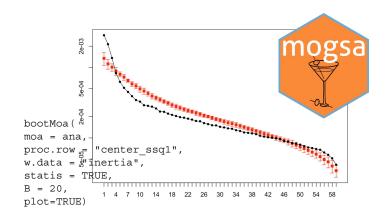


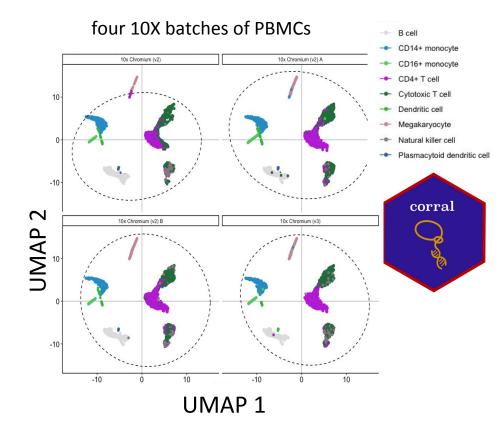
- New implementation of the ZINB-WaVE model
- Negative binomial to work with UMI data
- Explicit use of shared memory for faster computations

Federico Agostinis, Davide Risso

Multi-table SVD for alignment, integration of scData

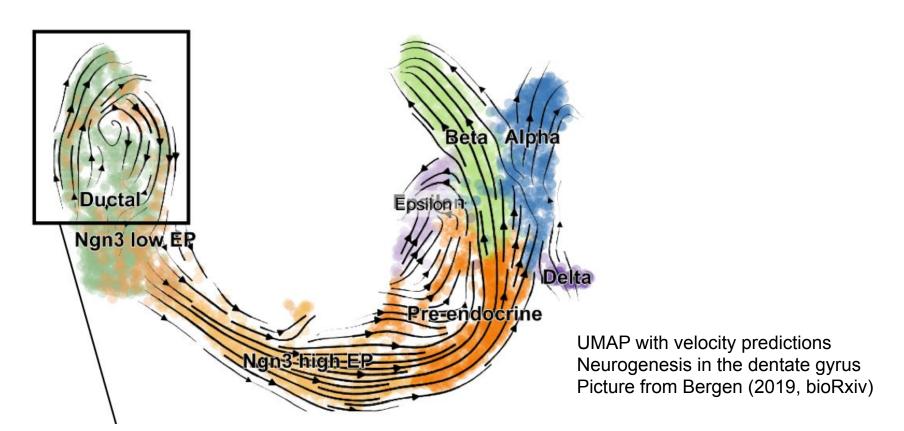
- SVD for Multi-table integration
 - Compare CCA, MFA, MCIA
 - Selection # component
 - QC of components (arch)
 - Layer annotation (Gene Sets)





RNA velocity

La Manno (2018, Nature) Bergen (2019, bioRxiv)



RNA velocity, methods

La Manno et al (2018, Nature) [steady-state model] Implemented in velocyto

Bergen et al (2019, bioRxiv) [dynamical model] Implemented in scVelo

Soneson et al (2020 bioRxiv) finds that "preprocessing choices affect RNA velocity"

Velociraptor from Rue / Lun / Soneson uses basilisk to embed scVelo in R/Bioc: https://github.com/kevinrue/velociraptor Works great !