

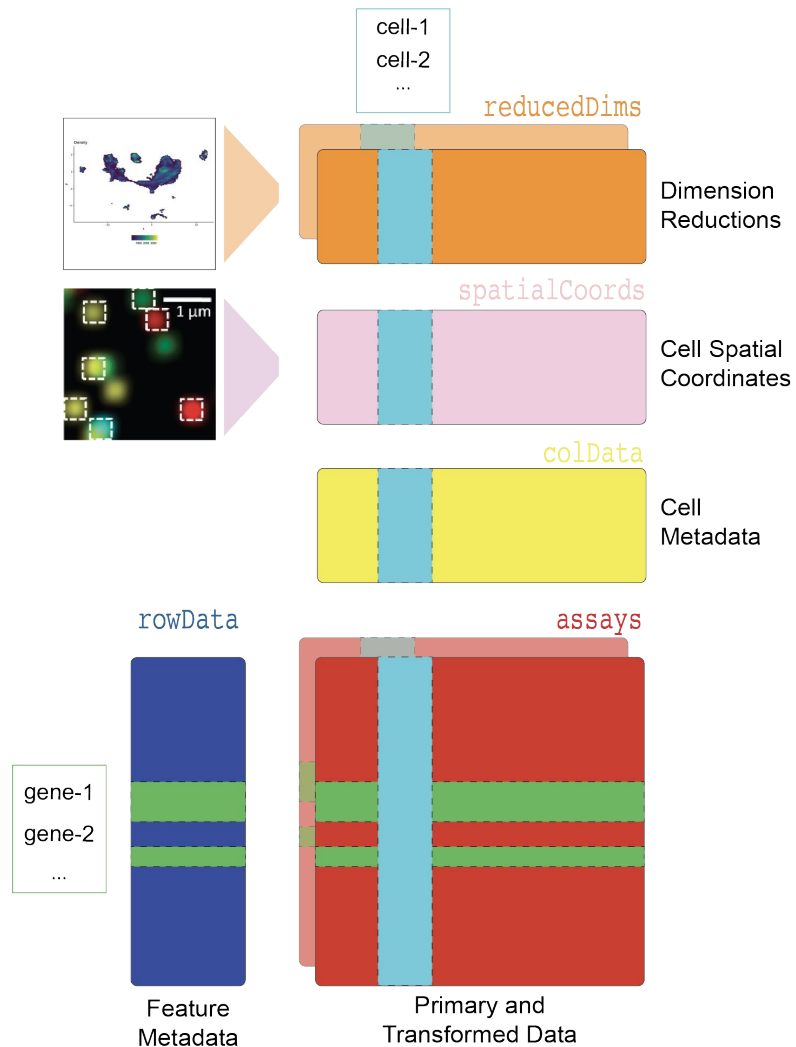
Challenges & Opportunities

Kasper Hansen

SpatialExperiment

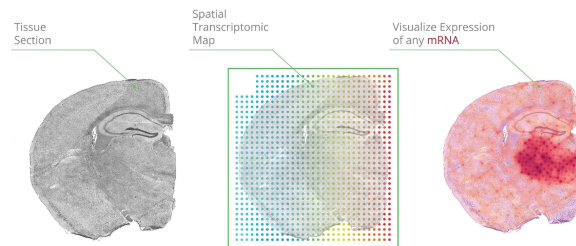
Description:

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



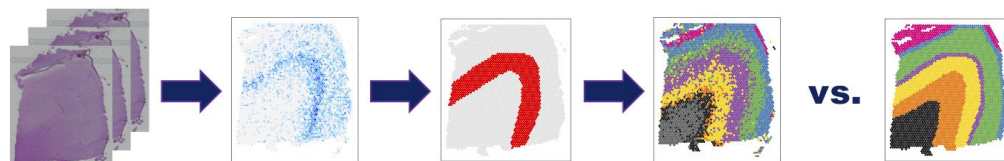
Spatial transcriptomics (10x Visium)

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



<https://spatialtranscriptomics.com/technology/>

Unsupervised analysis pipeline for human prefrontal cortex



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

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

Data resources

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

spatialLIBD

platforms **all** rank **383 / 391** posts **1 / 0 / 0 / 0** build **ok**
updated before release dependencies **181**

DOI: [10.18129/B9.bioc.spatialLIBD](https://doi.org/10.18129/B9.bioc.spatialLIBD)  

LIBD Visium spatial transcriptomics human pilot data inspector

Bioconductor version: Release (3.11)

Inspect interactively the spatial transcriptomics 10x Genomics Visium data from Maynard, Collado-Torres et al, 2020 analyzed by Lieber Institute for Brain Development researchers and collaborators.

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Maintainer: Leonardo Collado-Torres <lcolladorator@gmail.com>

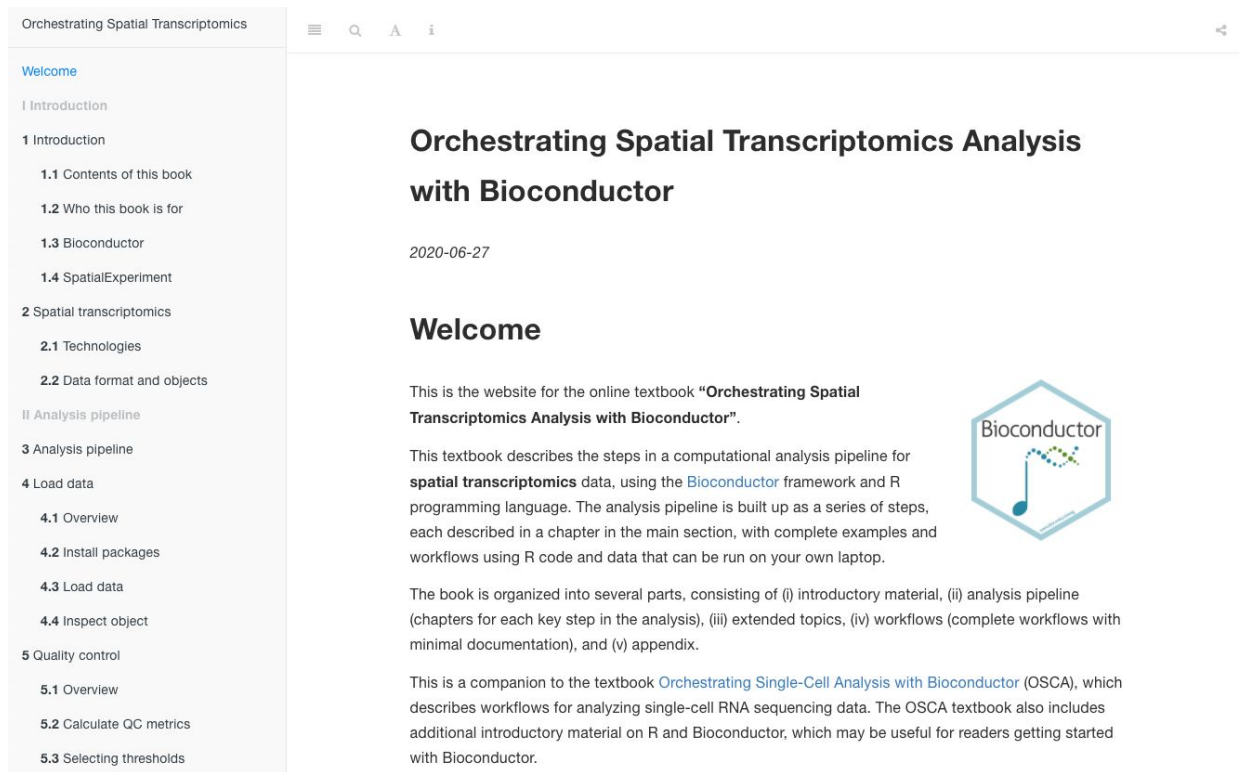
Spatial transcriptomics

Future work:

Orchestrating Spatial
Transcriptomics Analysis
(OSTA)

Pipeline for analyzing
spatial transcriptomics
data using Bioconductor
framework

Work in progress



Orchestrating Spatial Transcriptomics

Welcome

I Introduction

1 Introduction

- 1.1 Contents of this book
- 1.2 Who this book is for
- 1.3 Bioconductor
- 1.4 SpatialExperiment

2 Spatial transcriptomics

- 2.1 Technologies
- 2.2 Data format and objects

II Analysis pipeline

3 Analysis pipeline

4 Load data

- 4.1 Overview
- 4.2 Install packages
- 4.3 Load data
- 4.4 Inspect object

5 Quality control

- 5.1 Overview
- 5.2 Calculate QC metrics
- 5.3 Selecting thresholds

Orchestrating Spatial Transcriptomics Analysis with Bioconductor

2020-06-27


Welcome

This is the website for the online textbook “**Orchestrating Spatial Transcriptomics Analysis with Bioconductor**”.

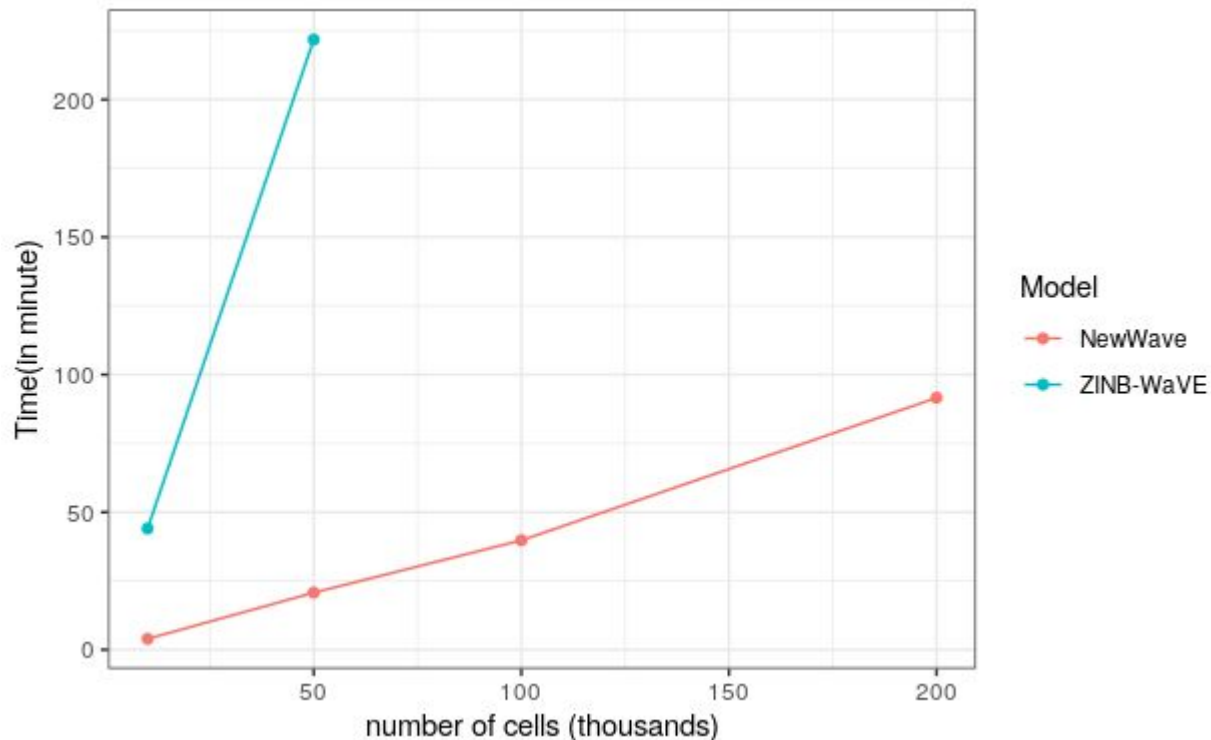
This textbook describes the steps in a computational analysis pipeline for **spatial transcriptomics** data, using the [Bioconductor](#) framework and R programming language. The analysis pipeline is built up as a series of steps, each described in a chapter in the main section, with complete examples 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

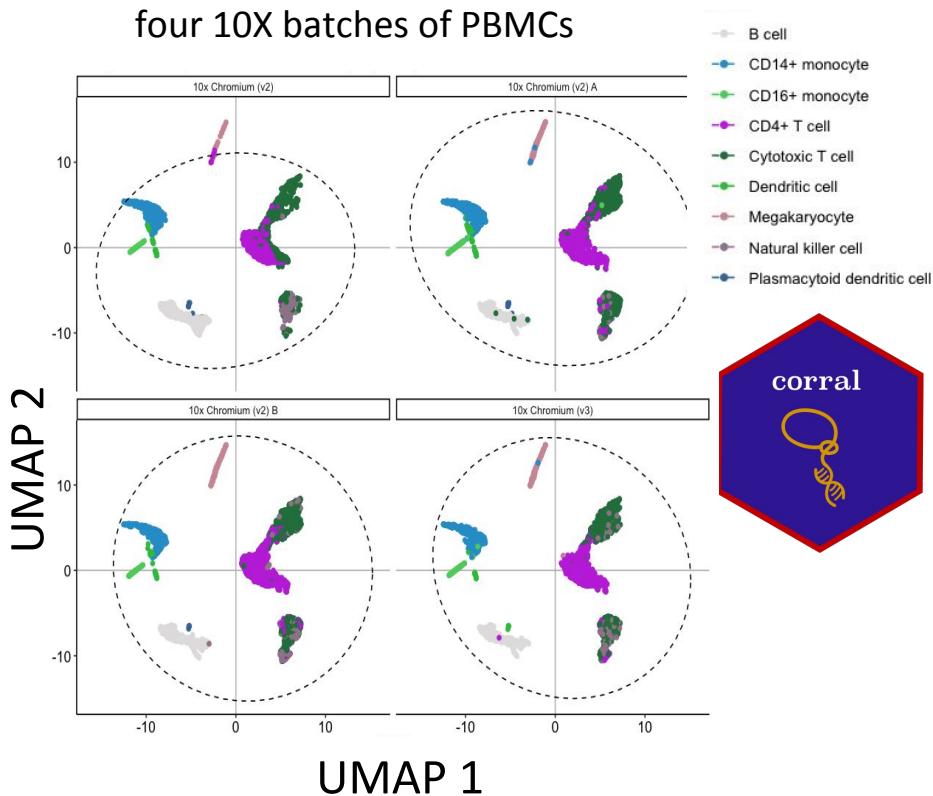
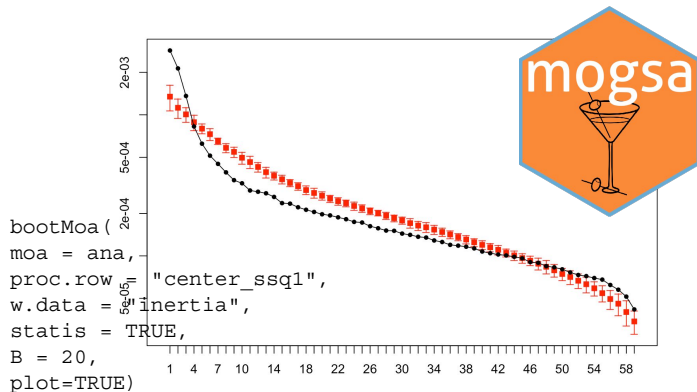


- New implementation of the *ZINB-WaVE* model
- Negative binomial to work with UMI data
- Explicit use of shared memory for faster computations

Federico Agostinis, Davide Risso

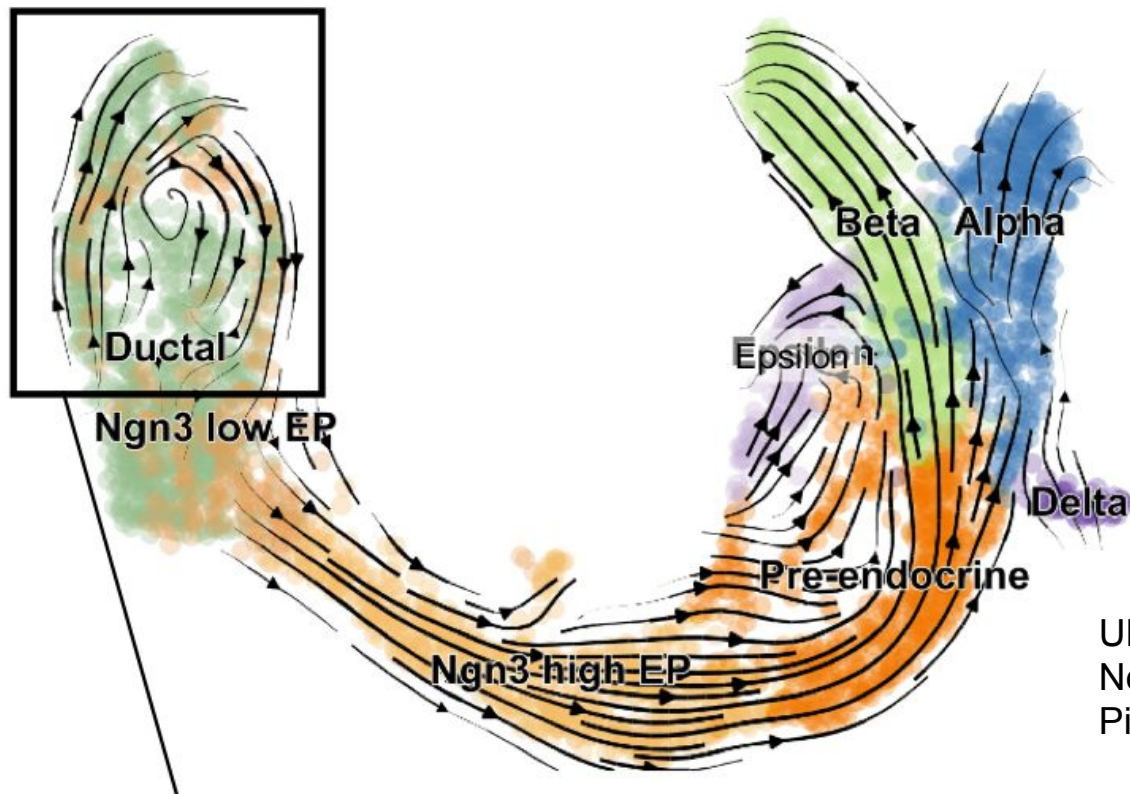
Multi-table SVD for alignment, integration of scData

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



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

RNA velocity



UMAP with velocity predictions
Neurogenesis in the dentate gyrus
Picture from Bergen (2019, bioRxiv)

RNA velocity, methods

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

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 !