

BestPracticesSTBiocBook

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Welcome

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This is the website for the online book ‘**Best Practices for Spatial Transcriptomics Analysis with Bioconductor**’.

This book provides discussion and interactive examples on best practices for computational analysis workflows for spatial transcriptomics data, using the [Bioconductor](#) framework within R. The chapters contain details on individual analysis steps as well as complete example workflows, with interactive example datasets and R code.

The book is organized into several parts, including introductory materials, analysis steps, and example workflows.

Additional details on analysis workflows for non-spatial single-cell data as well as further introductory materials on R and Bioconductor can be found in the related book [Orchestrating Single-Cell Analysis with Bioconductor \(OSCA\)](#).

Docker image

A Docker image built from this repository is available here:

ghcr.io/lmweber/bestpracticesstbiocbook

Get started now

You can get access to all the packages used in this book in < 1 minute, using this command in a terminal:

Listing 0.1 bash

```
docker run -it ghcr.io/lmweber/bestpracticesstbiocbook:devel R
```

RStudio Server

An RStudio Server instance can be initiated from the **Docker** image as follows:

Listing 0.2 bash

```
docker run \  
  --volume <local_folder>:<destination_folder> \  
  -e PASSWORD=0HCA \  
  -p 8787:8787 \  
  ghcr.io/lmweber/bestpracticesstbiocbook:devel
```

The initiated RStudio Server instance will be available at <https://localhost:8787>.

Session info

 Click to expand

1 Introduction

1.1 Overview

[Bioconductor](#)

1.2 Contents

-
-
-
-

1.3 Scope and who this book is for

[Preprocessing](#)

[Visium Data](#)

1.4 Bioconductor

[Bioconductor](#)

1.5 Additional resources

- [Orchestrating Single-Cell Analysis with Bioconductor \(OSCA\)](#)
- [R for Data Science](#)
- [Data Carpentry](#) [Software Carpentry](#)

- [detailed guide](#)
[YouTube videos](#)
- [Visium Data Preprocessing](#)

1.6 Contributions

[GitHub issues](#)

References

2 Spatial transcriptomics

2.1 Overview

of the Year 2020

Method

2.2 Sequencing-based platforms

2.2.1 10x Genomics Visium

10x Genomics Visium

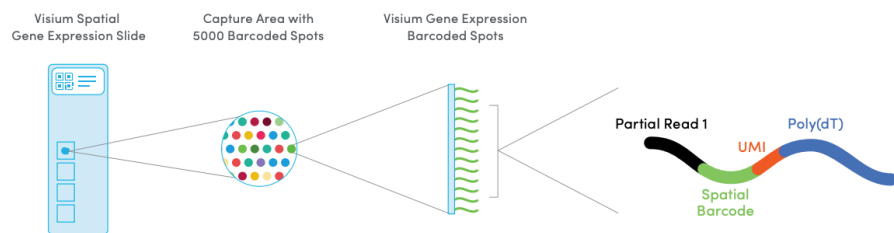


Figure 2.1: Schematic illustrating the 10x Genomics Visium platform. Source: [10x Genomics Visium](#)

2.2.2 10x Genomics Visium HD

[10x Genomics Visium HD](#)

2.2.3 Curio Seeker

[Curio Seeker](#)

2.3 Molecule-based platforms

2.3.1 10x Genomics Xenium

[10x Genomics](#)

2.3.2 Vizgen MERSCOPE

[Vizgen](#)

2.3.3 NanoString CosMx

[NanoString](#)

References

3 Bioconductor data classes

3.1 Overview

3.2 SpatialExperiment class

[SpatialExperiment](#)

[SingleCellExperiment](#)

[Bioconductor vignette](#)

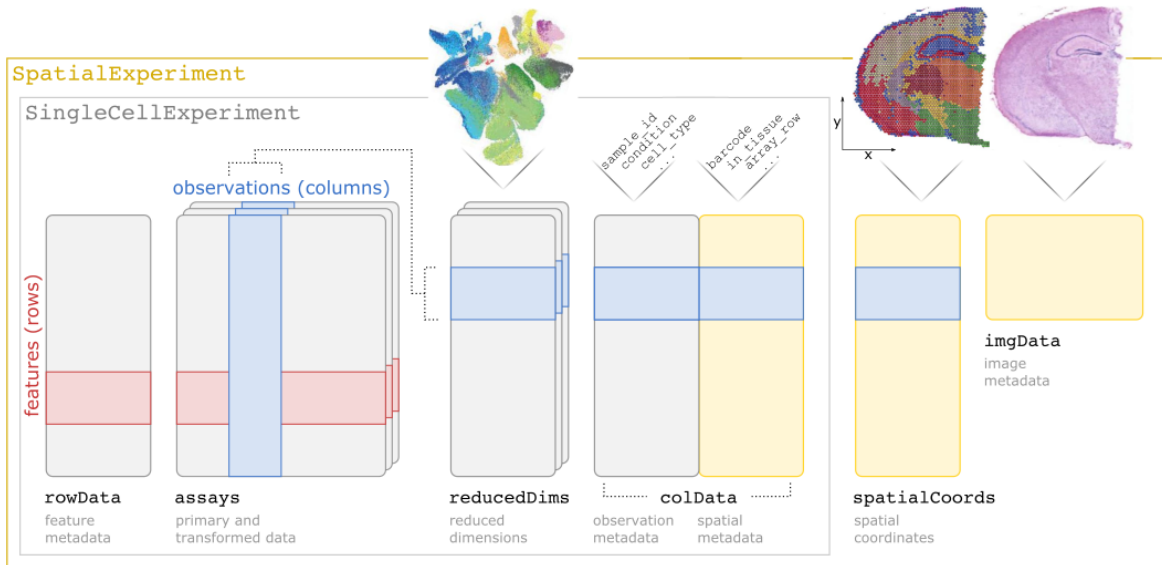


Figure 3.1: Overview of the **SpatialExperiment** data class for storing and manipulating spatial transcriptomics datasets within the Bioconductor framework.

3.3 Molecule-based data

3.3.1 MoleculeExperiment

[Bioconductor package](#)

3.3.2 SpatialFeatureExperiment

[Bioconductor package](#)

References