

Best Practices for Spatial Transcriptomics Analysis with Bioconductor

2024-09-25

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Welcome

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 \(OSCA\)](#).

Part I

Introduction

1 Introduction

1.1 Overview

This book provides discussion and interactive examples on best practices for computational analysis workflows for spatial transcriptomics data, using the [Bioconductor](#) framework within R.