BestPracticesSTBiocBook

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Welcome

Package: BestPracticesSTBiocBook **Authors:** First Last [aut, cre] **Compiled:** 2024-09-25 **Package version:** 0.98.0 **R version:** R version 4.4.1 (2024-06-14) **BioC version:** 3.20 **License:** MIT + file LICENSE

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`
>
> ```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`

```bash
docker run \
    --volume <local_folder>:<destination_folder> \
    -e PASSWORD=OHCA \
    -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