

The Bioconductor 2018 Workshop Compilation

Contents

1	Introduction	5
1.1	For Everyone	5
1.2	For Workshop Authors	5

Chapter 1

Introduction

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1.1 For Everyone

This book contains workshops used in *R / Bioconductor* training. The workshops are divided into 3 sections:

- **Learn** (100-series chapters) contains material for beginning users of *R* and *Bioconductor*. The *Bioconductor*-related material is relevant even for experienced *R* users who are new to *Bioconductor*.
- **Use** (200-series chapters) contains workshops emphasizing use of *Bioconductor* for common tasks, e.g., bulk RNA-seq differential expression, ChIP-seq, single-cell analysis, gene set enrichment, and annotation.
- **Develop** (500-series chapters) contains workshops to help expert users hone their skills and contribute their domain-specific knowledge to the *Bioconductor* community.

1.2 For Workshop Authors

To contribute a new workshop, open a BiocWorkshops issue asking to be added as a collaborator.

Write your workshop as a stand-alone markdown document, using the `_template.Rmd` file as a starting point. Follow the numbering scheme for classifying your workshop.

Also update the DESCRIPTION file adding packages utilized in your workshop to the Imports field. Please be kind and don't remove anyone else's packages from the DESCRIPTION as this is a shared file for all workshops.

See bookdown instructions for authoring documents; we are using the 'knit-then-merge' strategy. You'll need to install the bookdown package from CRAN, as well as pandoc. Render your chapter with the `preview=` option to `render_book()`, e.g.,

```
Rscript -e "bookdown::render_book(
  'xxx_Your_Workshop.Rmd', 'bookdown::gitbook', preview=TRUE \
)"
```

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As this is a shared space for all workshop contributors, in order to use the above command in the BiocWorkshops directory, the index has to be built at least once, which can be time consuming depending on how many workshops have already been submitted.

```
Rscript -e "bookdown::render_book(
  'index.Rmd', 'bookdown::gitbook')"
```

To avoid having to build all workshops but still be able to preview your individual workshop we recommend creating a soft link to your .Rmd file. We recommend having the file in the **BiocWorkshop/** and the soft link in any other directory on your system. By default, this will generate an html file in **_book/** wherever this command is run.

```
mkdir tmp
cd tmp/
ln -s ../xxx_Your_Workshop.Rmd
Rscript -e "bookdown::render_book(
  'xxx_Your_Workshop.Rmd', 'bookdown::gitbook', preview=TRUE \
)"
```

Push **only** your .Rmd file to the BiocWorkshop repository; the book will be rebuilt manually or automatically. Eventually the output will be available for end-users at <https://bioconductor.github.io/BiocWorkshops>