The Bioconductor 2018 Workshop Compilation

Contents

Chapter 1

Introduction

Author: Martin Morgan[1]. Last modified: 22 May, 2018.

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 elses 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 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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[1]Roswell Park Comprehensive Cancer Center, Buffalo, NY

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

Chapter 2

Lori's Test Workshop

Authors: Lori Shepherd[1]. Last modified: 22 May, 2018.

2.1 Overview

2.1.1 Description

Along with the topic of your workshop, include how students can expect to spend their time. For the description may also include information about what type of workshop it is (e.g. instructor-led live demo, lab, lecture + lab, etc.). Instructors are strongly recommended to provide completely worked examples for lab sessions, and a set of stand-alone notes that can be read and understood outside of the workshop.

2.1.2 Pre-requisites

List any workshop prerequisites, for example:

- Basic knowledge of R syntax
- Familiarity with the GenomicRanges class
- Familiarity with xyz vignette (provide link)

List relevant background reading for the workshop, including any theoretical background you expect students to have.

- List any textbooks, papers, or other reading that students should be familiar with. Include direct links where possible.

2.1.3 Participation

Describe how students will be expected to participate in the workshop.

2.1.4 *R / Bioconductor* packages used

List any *R / Bioconductor* packages that will be explicitly covered.

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[1]Roswell Park Comprehensive Cancer Center, Buffalo, NY

2.1.5   Time outline

An example for a 45-minute workshop:

Activity	Time
Packages	15m
Package Development	15m
Contributing to Bioconductor	5m
Best Practices	10m

2.1.6   Workshop goals and objectives

List "big picture" student-centered workshop goals and learning objectives. Learning goals and objectives are related, but not the same thing. These goals and objectives will help some people to decide whether to attend the conference for training purposes, so please make these as precise and accurate as possible.

Learning goals are high-level descriptions of what participants will learn and be able to do after the workshop is over. *Learning objectives*, on the other hand, describe in very specific and measurable terms specific skills or knowledge attained. The Bloom's Taxonomy may be a useful framework for defining and describing your goals and objectives, although there are others.

2.1.7   Learning goals

Some examples:

- describe how to...
- identify methods for...
- understand the difference between...

2.1.8   Learning objectives

- analyze xyz data to produce...
- create xyz plots
- evaluate xyz data for artifacts

2.2   Workshop

Divide the workshop into sections (`## A Section`). Include fully-evaluated R code chunks. Develop exercises and solutions, and anticipate that your audience will walk through the code with you, or work on the code idependently – do not be too ambitious in the material that you present.

```r
vec <- 1:20
plot(1:20, col="red")
```