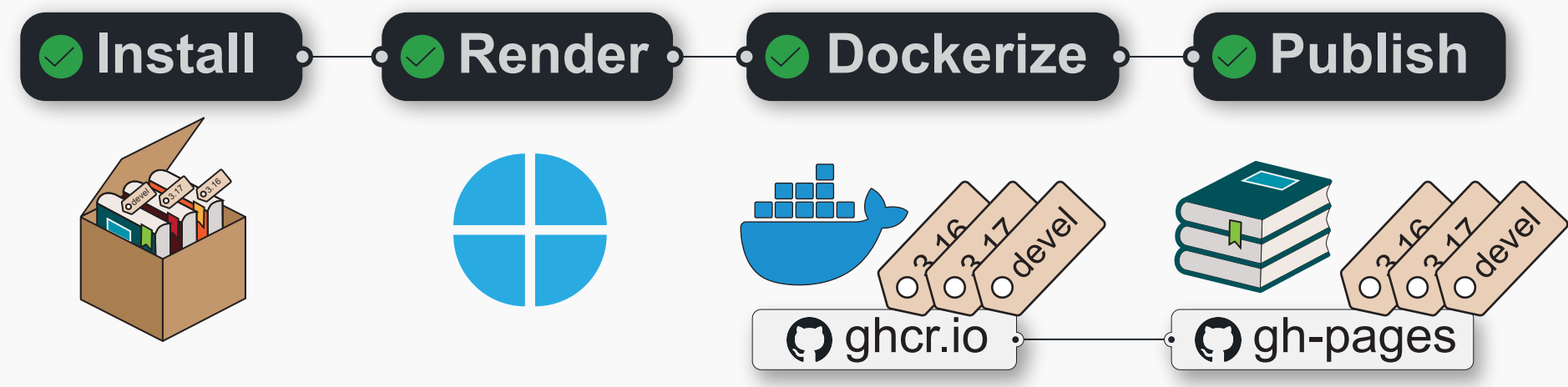


A streamlined set-up for writing books

```
1 library(BiocBook)
2
3 ## Make sure you have set up a Github token
4 gh:gh_whoami()
5
6 ## Create a new BiocBook
7 init("myBook")
8
9 ## Open the new BiocBook
10 bb <- BiocBook("./myBook")
11
12 ## Add pages
13 add_preamble(bb)
14 add_chapter(bb, title = "Chapter 1")
15 add_chapter(bb, title = "Chapter 2")
16
17 ## Preview
18 preview(bb)
19
20 ## Publish to Github
21 publish(bb, message = "🚀 Publishing")
```

Two preset Github Actions workflows

- neurogenomics/rworkflows
- build-docker-deploy.yml



Rendering and deployment by the Bioconductor Build System

Source code

DESCRIPTION
NAMESPACE
LICENSE
README.md
data/
 dat.rds
man/
 man.Rd
R/
 fun.R
 utils.R
 checks.R
tests/
 testthat.R
 testthat/
 test-*.R
vignettes/
 Makefile
 stub.Rmd

inst/
 _quarto.yml
 index.qmd
pages/
 chapter1.qmd
 chapter2.qmd
 ...
assets/
 _book.yml
 _website.yml
 _knitr.yml
 _format.yml
 bibliography.bib
 book.scss
 cover.png

Bundle (R CMD build)

DESCRIPTION
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 testthat.R
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Raw website content

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pages/
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 chapter2.qmd
 ...
assets/
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 _website.yml
 _knitr.yml
 _format.yml
 bibliography.bib
 book.scss
 cover.png

Rendered website

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INSTALL + Build

BBS

Write, containerize and deploy versioned books (with Bioconductor)

for c(R developers, Workshops, Trainers, Data scientists, Communicators, ...)

- Code Leverage package development toolkit
- Write Compile a body of biological and/or bioinformatics knowledge
- Render Automatically generate high-quality online book
- Containerize Provide Docker images to reproduce examples illustrated in the online book
- Versionize Deploy an online book to disseminate the compendium
- Use BioC For its trusted Bioconductor Build System

BiocBook

Package

<https://github.com/js2264/BiocBook>

Book

<https://jsrizay.com/BiocBook/devel/>

Docker

<https://ghcr.io/js2264/biocbook>

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