

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")

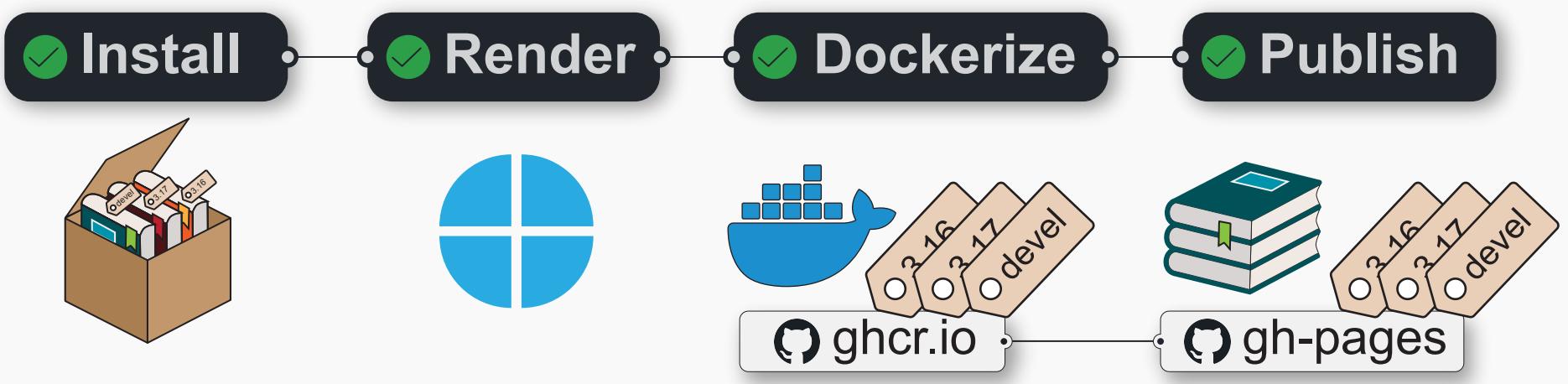
```



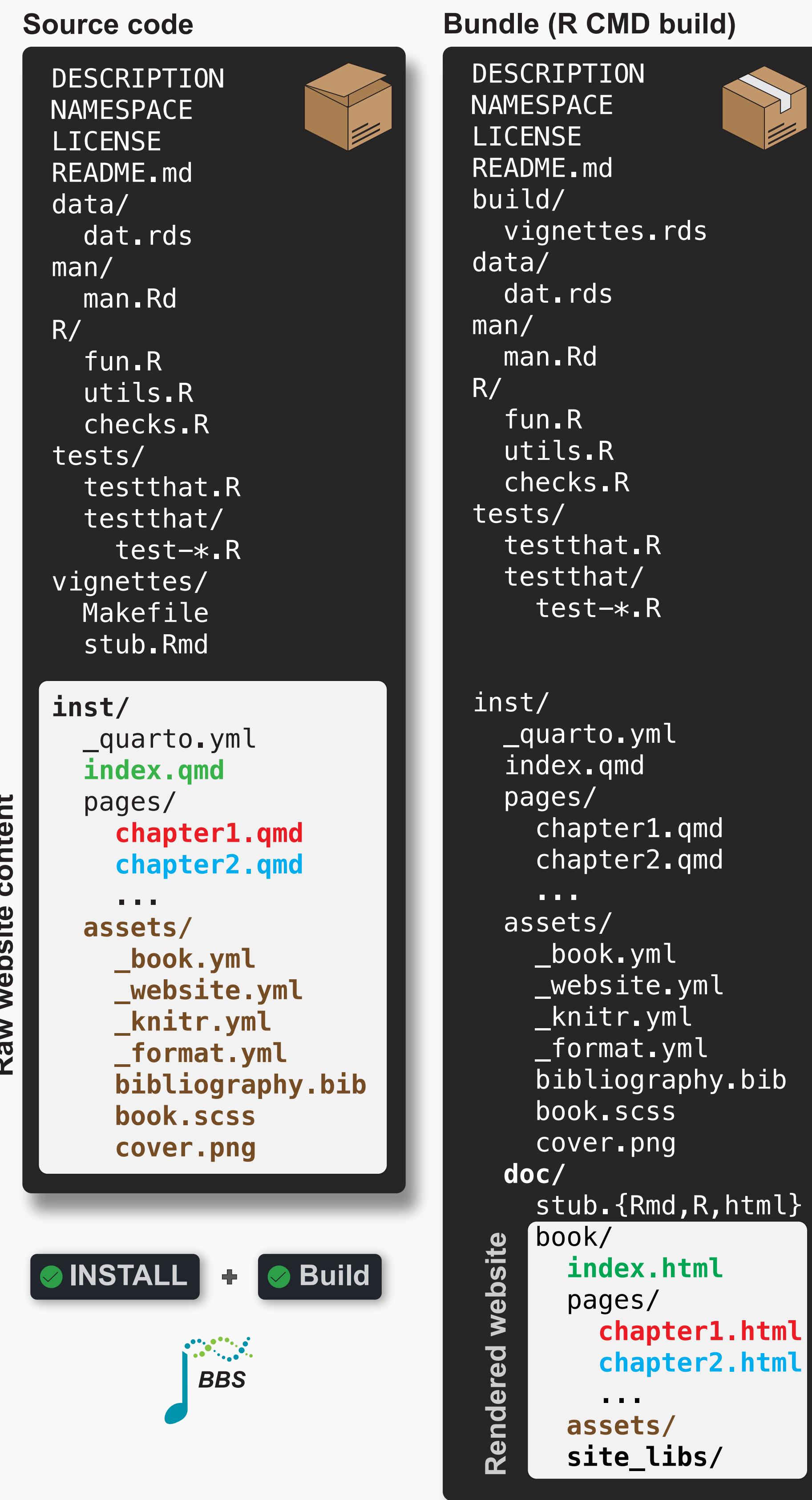
Write, containerize and deploy versioned books (with Bioconductor)

Two preset Github Actions workflows

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



Rendering and deployment by the Bioconductor Build System



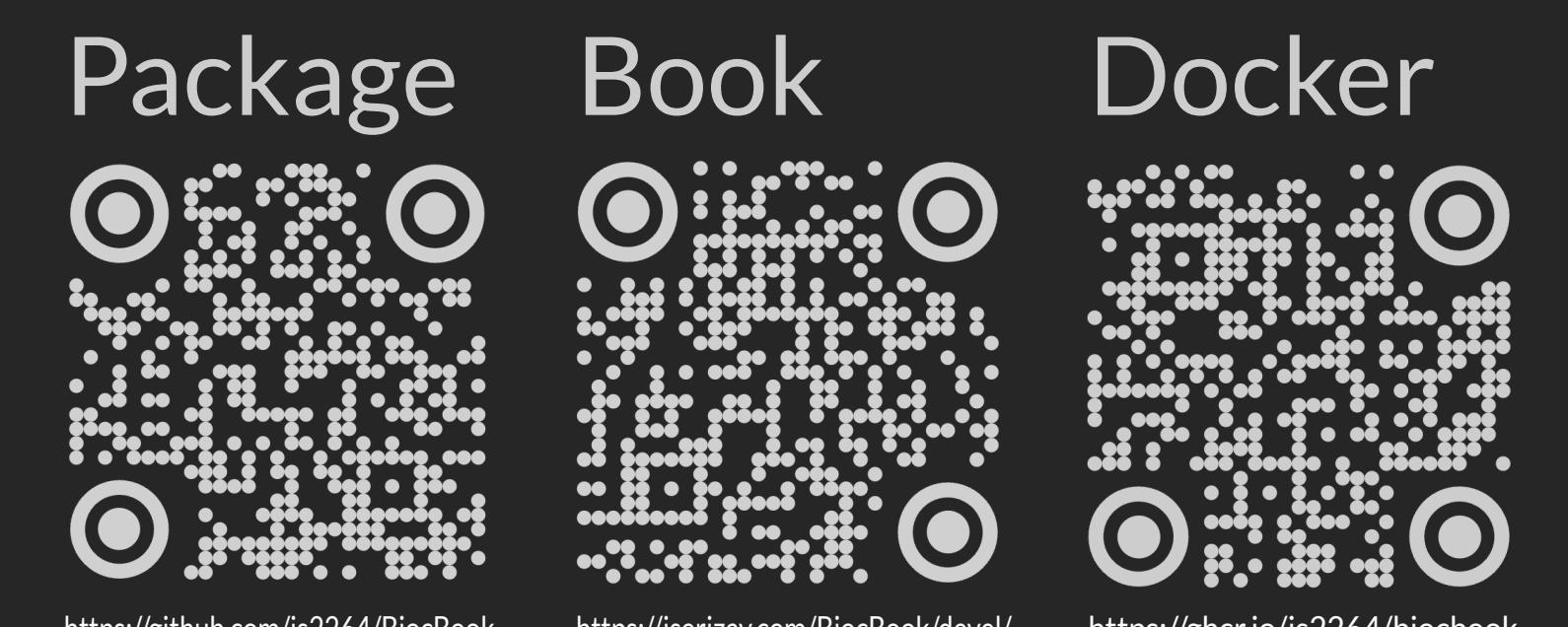
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R developers,
Workshops,
Trainers,
Data scientists,
Communicators,
...

)

- 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 nline book
- Versionize** Deploy an online book to disseminate the compendium
- Use BioC** For its trusted Bioconductor Build System

BiocBook



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