

Best Practices

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Best practices

1. Write organized, consistent *R* code
2. Use version control
3. Document functions
4. Write tests
5. Write vignettes
6. Create a package (!)
7. What about *Rstudio*? Makes this easy!

Example: utilities for working with *GRanges*, e.g., `isSimpleVariant`. See

```
system.file(package="SummerX", "GRangesUtilities.tar.gz")
```

Writing organized, consistent R code

- ▶ Organize frequently used commands into not-too-complicated functions
- ▶ Adopt consistent [coding conventions](#)
 - ▶ Function and variable names
 - ▶ Indentation
 - ▶ Line lengths
 - ▶ ...
- ▶ Organize functions into files, e.g., one-function-per-file

```
|-- GRangesUtilities
  |-- R
    |-- isSimpleVariant.R
    |-- stickFigure.R
  |-- vignettes
    |-- UsingGRangesUtilities.Rmd
```

Using version control

- ▶ Easily keep track of changes as your documents develop, without using confusing file-naming or other conventions.

Software

- ▶ *git* – modern, flexible, easy to use locally (no server required)
- ▶ *subversion* (*svn*) – used by *Bioconductor*, requires central server

Sharing with others

- ▶ Use [github](#), or...
- ▶ Get your IT guys to set up a *git* or *svn* server for your group's use

Using version control – *git*

- ▶ Change into the directory where you've started your project

```
$ cd GRangesUtilities
```

- ▶ Initialize a *git* repository and check the status

```
$ git init
```

```
$ git status
```

- ▶ Create / edit files, directories...; track in git

```
$ git add R/isSimpleVariant.R
```

```
$ git status
```

- ▶ Commit the changes

```
$ git commit
```

- ▶ See the commit log

```
$ git log
```

Document functions

- ▶ Purpose: document how to use *function*
- ▶ `man` directory with 'Rd' files, organized like R files, e.g., `isSimpleVariant.Rd`
- ▶ Alternative: use *roxygen2* package to add 'annotations', e.g., to R code.

Write tests

Unit tests

- ▶ Short tests of specific parts of each function, implemented in a `tests` directory
- ▶ *testthat* framework
- ▶ *RUnit* framework, used in *Bioconductor*

Test-driven development

- ▶ Write unit tests that describe expected functionality *before* implementing the code.

Write vignettes

Why?

- ▶ Purpose: document how to use several functions in an integrated way
- ▶ 'Literate' programming: Text, figures, tables surrounding *R* script

How?

- ▶ Write documents in a directory `vignettes`
- ▶ `Rmd`: 'markdown' and *R* – easy
- ▶ `Rnw`: 'Sweave' combines \LaTeX and *R* to produce PDF documents – flexible

Create a package

- ▶ Why? Easy to re-use, share with others (e.g., lab members)
- ▶ How? – `RShowDoc("R-exts")`

From what we've already done...

- ▶ Add a DESCRIPTION file
- ▶ Arrange for tests to be run when the package is checked

Additional (optional) steps

- ▶ data directory of *R* data objects
- ▶ `inst/script` of *R* scripts

Making a package available to your colleagues

roxygen2-ize to create NAMESPACE, man pages

```
$ R -e "roxygen2::roxygenize('GRangesUtilities')"
```

Build, check, and install the package

```
$ R CMD build GRangesUtilities
```

```
$ R CMD check GRangesUtilities_0.0.1.tar.gz
```

```
$ R CMD INSTALL GRangesUtilities_0.0.1.tar.gz
```

Final step within *R*:

```
install.package("GRangesUtilities_0.0.1.tar.gz",  
  repos=NULL)
```

Windows: create a .zip file for easy installation

```
$ R CMD INSTALL --build GRangesUtilities_0.0.1.tar.gz
```

Use it!

```
library(GRangesUtilities)
?isSimpleVariant
vignette("UsingGRangesUtilities")
example(isSimpleVariant)
```