See this [link](https://contributions.bioconductor.org/bioconductor-package-submissions.html); this is general instruction

General:

* full documentation and vignettes
* fully evaluated code
* Nowhere in the code ( code, man pages, vignettes, Rmd files) should someone try to install or download system dependencies, applications, packages, etc.

Package name:

* On github make dedicated repo for the package:
* package name should match the GitHub repository name and is case-sensitive
* legacy package name. mail to inquire about using a legacy package name on the [bioc-devel@r-project.org]

Checks to pass (see the ***BiocCheck*** package):

* R CMD build (also, should not be more than 5MB and not take longer than 10 min)
* BiocCheck::BiocCheckGitClone() and
* BiocCheck::BiocCheck('new-package'=TRUE)

Including data:

* Should be via mentioned standards on bioncudctor (see [link](https://contributions.bioconductor.org/data.html#data))
* CAN work via dedicated environment in data/ directory (see 13.2.1)

DESCRIPTION file:

* Requires a dedicated “biocViews:” part including keywords to describe the package. See (4.1)

Vignette: (see [link](https://contributions.bioconductor.org/docs.html#vignettes))

* Introduction
* Installation
* Table of contents
* Evaluated code chunks
* Session information
* Other directories
* References

Man pages; ( think roxygen; check [link](http://cran.fhcrc.org/doc/manuals/R-exts.html#Rd-format'))

* Package-level documentation
* Functions and classes
* Data
* Examples

The inst/script/ directory

* It should include source URLs and any key information regarding filtering or processing.
* It can be executable code, sudo code, or a text description.

README file:

* installation instructions, those instruction should also include Bioconductor installation instructions.

INSTALL file:

* see <https://contributions.bioconductor.org/sysdep.html#sysdep>