Packages must satisfy the following checklist:

|  |  |
| --- | --- |
| Pass R CMD build, R CMD check, and R CMD BiocCheck (see the [R CMD check](http://r-pkgs.had.co.nz/check.html) cheatsheet and the[BiocCheck](https://www.bioconductor.org/packages/devel/bioc/html/BiocCheck.html) package) on all supported platforms (Windows, Macintosh, Linux) with no errors or warnings, using an appropiate version of R. To work out which version that is, see [useDevel](https://www.bioconductor.org/developers/package-submission/how-to/useDevel). | OK |
| The result of R CMD build must be less than 4MB; | OK |
| R CMD check must complete within 5 minutes. | OK |
| Contain a DESCRIPTION file with valid contact information, an informative title and description, correct license specification, appropriate biocViews terms, valid version number. | OK |
| Set Version: 0.99.0 in the DESCRIPTION. Subsequent versions created during the review process will be numbered 0.99.1, 0.99.2, etc. When released, your package’s version number will be automatically incremented to 1.0.0. | OK |
| Contain a NAMESPACE that imports all symbols used in the package, and exports just those symbols the package author identifies as appropriate. Use of a NAMESPACE implies that appropriate packages are mentioned in the Imports: field of the DESCRIPTION file. | OK |
| Contain a vignette that illustrates the major uses of the package. The vignette must be *evaluated*during package installation; a static vignette is not acceptable. | OK |
| Contain comprehensive help pages. This includes accurate description of function parameter and return values, and meaningful examples. | OK |
| Make use of appropriate existing packages (e.g., biomaRt, AnnotationDbi, Biostrings) and classes (e.g., ExpressionSet, AnnotatedDataFrame, RangedData, Rle, DNAStringSet) to avoid duplication of functionality available in other Bioconductor packages. | OK |
| Contain no extraneous files (e.g., ‘.DS\_Store’, ‘.project’, ‘.svn’, etc.), files with invalid names (e.g., differing only in case), or code that cannot be distributed under the license specified by the author. | OK |
| Packages should have a descriptive name that is not already in use. See if it is by running biocLite("myPackageName"). You cannot have a package name that is case-insensitively equal to an existing package name in CRAN or Bioconductor. | OK |
| Follow the [Package Guidelines](https://www.bioconductor.org/developers/package-guidelines/) for details on appropriate use. | OK |
| Include an inst/NEWS file for providing users with information on package updates. | OK |

**Submission**

* Submit by opening a new issue at the Bioconductor [Contributions](https://github.com/Bioconductor/Contributions/issues/new) repository.
* Read the [Contribution Guidelines](https://github.com/Bioconductor/Contributions/blob/master/CONTRIBUTING.md) for full instructions.
* Assuming your package is in a [GitHub Repository](https://help.github.com/articles/create-a-repo/), under a default ‘master’ branch, add the link to your repository to the issue you are submitting.

*Note - your DESCRIPTION file will be automatically attached the issue you create, as a convenient summary of your package.*

**Experiment Data Packages**

Experimental data packages contain data specific to a particular analysis or experiment. They often accompany a software package for use in the examples and vignettes and in general are not updated regularly. If you need a general subset of data for workflows or examples first check the AnnotationHub resource for available files (e.g., BAM, FASTA, BigWig, etc.).

If you have an associated data package for your software package, please do *NOT* create a separate issue in our tracker repository for that. Instead, please add the data package repository to the same issue as the software package. The process for doing this is documented [here](https://github.com/Bioconductor/Contributions/blob/master/CONTRIBUTING.md#submitting-related-packages).

**Annotation Packages**

Annotation packages contain lightly or non-curated data from a public source and are updated with each Bioconductor release (every 6 months). They are a source of general annotation for one or many organisms and are not specific to a particular experiment. When possible, they should support the select() interface from AnnotationDbi.

Annotation packages should *NOT* be posted to the tracker repository. Instead send an email to [packages@bioconductor.org](mailto:packages@bioconductor.org) with a description of the proposed annotation package and futher instructions of where to send the package will be provided.

Review Process

After you submit a GitHub repository, a human will intervene to allow the package to build. A reviewer will be automatically assigned. Then a comment will be posted to the issue you created, with the result of R CMD build, R CMD check and R CMD BiocCheck on all three platforms. Please address all the Warnings from R CMD check and all ‘Required’ and ‘Recommended’ issues from R CMD BiocCheck. Your assigned reviewer will address your concerns and help you through the review process. The entire review process typically takes between 2 and 5 weeks.

A typical review works as follows.

* The package developer submits first version of the package (0.99.0).
* Build system returns check results.
* The package developer fixes any issues found, runs R CMD build, R CMD check and R CMD BiocCheckon their local machine, and pushes the new version (0.99.1).
* A reviewer is assigned to the package.
* A detailed package review is returned to the developer within a few weeks.
* The package developer updates their package incorporating the reviewer comments, runs R CMD build, R CMD check and R CMD BiocCheck on their local machine, and pushes the new version (0.99.2).
* The process is repeated, with appropriate version bumps, until the package is accepted to Bioconductor.

Following acceptance of a package:

* Packages accepted on the tracker repository are added to the ‘devel’ branch of the Bioconductor SVN repository, with the current version number of the accepted package.
* Packages are then built by the Bioconductor nightly build process. If the build is successful, the package has its own ‘landing page’ created, and the package is made available to users of the ‘devel’ branch of Bioconductor via biocLite().
* Developers may continue to make changes to their package, but now do so to the version in the subversion repository, or by using [Bioconductor Git Mirrors](https://www.bioconductor.org/developers/how-to/git-mirrors/).
* Developers should bump the z portion of their version number every time they commit changes to their package, following the [Version numbering](https://www.bioconductor.org/developers/how-to/version-numbering/) guidelines. If developers don’t bump the version, the changes made to their package *do not propagate* to the Bioconductor web site and package repository.