

What is Bioconductor

April 11, 2014

Prerequisites

Bioconductor is a project to develop innovative software tools for use in computational biology. It is based on the R language (www.r-project.org). You should already be quite familiar with R before using Bioconductor. There are several on-line resources that can help you get started using R. They can be found from the R website. Some users find this a very steep learning curve; your experience may be similar.

Bioconductor packages provide flexible interactive tools for carrying out a number of different computational tasks. They are generally not as fast as other analysis tools (since they are interactive) and often reflect current ideas. Most can be improved and interested users should file bug reports and feature requests on the Bioconductor mailing list.

Bioconductor welcome collaboration in many different forms. These include new packages, fixes or additions to existing packages and help on different projects that are currently underway. Please see the *Current Projects* web page to see if there are any projects that are interesting to you.

How to report a bug

Please provide enough information for us to help you. This typically includes the platform (windows, Unix, Macintosh) that you are using as well as version numbers for R and for the package that seems to be working incorrectly.

Include a small complete example that can be run and demonstrates the problem. In some cases it is also important that you describe what you thought you should get.

Please note:

- bugs in R should be reported to the R community
- missing features are not bugs – they are feature requests.

1 Bioconductor Design

Bioconductor relies on the R package system to distribute code and data. Most packages use S4 methods and classes (as described in *Programming with Data* by J. M. Chambers). This adherence to object oriented programming makes it easier to build component software and helps to deal with the complexity of the data.

One of the important Bioconductor packages is *annotate*. This package provides access to various genomic annotation data. This package makes use of various web resources and precompiled data packages to provide tools for exploring biological data.

2 Session Information

The version number of R and packages loaded for generating the vignette were:

R version 3.1.0 (2014-04-10)

Platform: x86_64-unknown-linux-gnu (64-bit)

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] parallel stats graphics grDevices utils datasets
[7] methods base
```

other attached packages:

```
[1] Biobase_2.24.0 BiocGenerics_0.10.0
```

loaded via a namespace (and not attached):

```
[1] tools_3.1.0
```