

Bioconductor

Summary

Bioconductor is a set of scripts written in the [R](#) statistical programming language, useful for calculations on and visualization of biological data. ==

Available on

[Fourierseq](#)

[Phylocluster](#) (with modules

[affy](#), [affydata](#), [affyPLM](#), [annaffy](#), [annotate](#), [Biobase](#), [Biostrings](#), [DynDoc](#), [gcrma](#), [genefilter](#), [geneplotter](#), [hgu95av2.db](#), [limma](#), [marray](#), [matchprobes](#), [multtest](#), [ROC](#), [vsn](#), [xtable](#), [affyQCReport](#), [makecdfenv](#)

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User documentation

- To get started using Bioconductor, check out [the Bioconductor Getting Started page](#). For an overview, go to the main [Bioconductor page](#).

Helpful tips

Start by learning [R](#), which is quite different from most structured programming languages. It is similar to SAS.