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, von, xtable, affyQCReport, makecdfenv
)

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.