

# BioJava 1.5 beta released



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## Keywords

Biology, Java, Biojava

## Abstract

Martin Szugat reported that a beta for BioJava 1.5 has been released. New features include: a new biojavax package with extension on the basic functionality, such as the RichSequence.IOTools and the RichSequence object; a genetic algorithm library; features that allow manipulation of 3D structure files and objects; and non-HMM implementations of the NW and SW alignment algorithms.

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[Martin Szugat reported](#) that a beta for [BioJava 1.5](#) has been released. New features include: a new [biojavax](#) package with extension on the basic functionality, such as the `RichSequence.IOTools` and the `RichSequence` object; a [genetic algorithm library](#); features that allow manipulation of 3D structure files and objects; and non-HMM implementations of the NW and SW alignment algorithms. The announcement also mentions a new package for handling external processes (`org.biojava.utils.process`); I am wondering what that is about. I will upload this beta to Bioclipse [trunk/bc\\_biojava/](#) shortly, so that we can play with it.