Bioclipse 2: towards integrated biocheminformatics

Ola Spjuth* and Jonathan Alvarsson

Department of Pharmaceutical Biosciences, Uppsala University, Uppsala, Sweden

* Corresponding author
email: ola.spjuth@farmbio.uu.se

Introduction and history
Bioclipse [1] is a free and open source workbench for the life sciences with advanced functionality in bioinformatics and chemoinformatics. It allows users to work with resources and entities in the life sciences, such as chemical structures, sequences, spectra, and alignments. Bioclipse 2, which was released in July 2009, constitutes a complete rewrite of the Bioclipse version published on EMBnet.news in 2007 [2] and provides more features and new graphical components that simplifies integrated life science research and development. The Bioclipse project has as of July 2009 accumulated over 28,000 downloads since its original release in 2007, and also been awarded 3 international prizes for its innovative architecture and intuitive interface.

Architecture
Bioclipse is built on Eclipse (http://www.eclipse.org), which is an open source framework that evolved from being an Integrated Development Environment (IDE) into a universal platform for constructing software applications. This provides Bioclipse with advanced plugin architecture, where all functionality is contributed via plugins. Bioclipse defines common interfaces for biological and chemical entities, such as IMolecule for chemical structures, and ISequence for biological sequences. Other plugins can operate on these entities without being aware of each other’s existence, for example a tool that visualizes sequences graphically.

In Bioclipse, all functional source code contributed by plugins is collected in Bioclipse Managers; e.g. BioJava [3] contributes functionality via a
BioJavaManager. The Manager objects are built with the help of Spring (http://www.springframework.org) and published into the scripting environment. Hence, the same objects that are called from the GUI are also reachable from scripts (see Figure 1), which is named Bioclipse Scripting Language (BSL). The reference BSL is based on JavaScript, and users can invoke all functionality in Bioclipse by typing commands in the JavaScript Console. A JavaScript Editor is also included, which allows for scripting entire analyses. It is already an appreciated feature to use the graphical editors of Bioclipse together with the scripting language to solve biological problems.

Bioinformatics
The core framework for Bioinformatics in Bioclipse 2 is primarily based on BioJava [3], which is available from the BioJavaManager. Figure 2 shows some examples on how to create and read sequences on the JavaScript Console.

Bioclipse also has bioinformatics plugins that take advantage of remote functionality, such as Web services. Examples include WSDbfetch for retrieving data from public repositories, and Kalign for sequence alignments [4].

Conclusions
The Bioclipse project aims at providing a workbench with the commonly needed features in chem- and bioinformatics, and also to enable scientific research and development spanning multiple fields. There are ongoing projects to further develop the platform and existing features, but also many new initiatives that widen
the scope of Bioclipse into more fields. The list includes toxicity assessment, site-of-metabolism predictions, integrated local and networked databases, and QSAR analysis. Social features such as integration with MyExperiment [6] are already available, as are features for working with semantic technologies like RDF/OWL. The Bioclipse Wiki (http://www.wiki.bioclipse.net) and the Bioclipse Blog (http://bioclipse.blogspot.com) holds the most recent information regarding the Bioclipse development.

License and Availability
Bioclipse 2 is released under the Eclipse Public License (EPL), a flexible open source license that allows additional plugins to be of any license. Bioclipse 2 is implemented in Java and supported on all major platforms. Source code and binaries are freely available at http://www.bioclipse.net and development versions are available from http://pele.farmbio.uu.se/bioclipse-devel/.

References