LibrAlign — A GUI library for displaying and editing multiple sequence alignments and attached data

Why developing LibrAlign?
Several applications currently developed in our group and by our cooperators deal with multiple sequence alignments (MSA) or associated raw and meta data (e.g., trace files, positions of tandem repeats, hairpins or inversions, ...), and allow the user to view and edit it in a graphical user interface (GUI). Instead of implementing independent solutions for these different tasks, we decided to create a common library that contains powerful and reusable GUI components.

Since this library is open source (GNU GPL 3), it can be used and extended by other researchers, who are then able to focus on the core functionality of their applications, but can still provide a user-friendly GUI.

Features and implementation

LibrAlign is fully interoperable with the BioJava 3 API (Phil et al., 2012), therefore e.g. efficient implementations of the ProxySequenceReader interface of BioJava can be combined with LibrAlign. All components are provided in a native Swing and a native SWT version (the two major GUI frameworks for Java, see also gi), so they can be integrated into nearly all thinkable kinds of Java GUIs, including more complex projects based on the Eclipse Rich Client Platform (http://www.eclipse.org/home/categories/rcp.php) or BioClibse (Spjuth et al., 2009).

LibrAlign source code and binaries are distributed under GNU General Public License Version 3. It is part of the BioInfWeb Software portal and can be downloaded free of charge under the following address:
http://bioinfweb.info/LibrAlign

Software based on LibrAlign
Currently there are a number of software projects available or under development which make use of the LibrAlign API.

Taxonomic editor of the EDIT platform
The EDIT platform is currently extended to support sequence and alignment associated data for the Campanula portal of EDIT. LibrAlign will be used in future version of the EDIT software to display such data.

AlignmentComparator
AlignmentComparator is an application to visualize differences between alternative automatic and manual alignments, which we currently use in study investigating the influence of manual alignment corrections on phylogenetic studies.

HIR-Finder
This application locates microstructural mutations like tandem repeats possibly associated with hairpins in single sequences and visualizes its findings in a special data area (see also fig. 4). LibrAlign is especially useful for the future development of HIR-Finder because it is planned to additionally locate similar patterns that can only be identified when looking at an alignment of homologue sequences.

PhyDE - Phylogenetic data editor
PhyDE is a multiple sequence alignment editor that is part bioinfweb and provides functions especially useful for phylogenetic purposes that are still not sufficiently covered by a single other editor. Future versions will be based on LibrAlign.

Compatibility

Citations: