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Poster presentation

Jalview: Visualization and Analysis of Molecular Sequences, Alignments, and Structures

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Jalview is a Java application for editing and viewing sequence alignments, originally developed by Michele Clamp in 1997. It has facilities for assessing alignment quality, visualizing residue property conservation, and constructing and viewing sequence clusters through tree and principle components based algorithms. After eight years, it now has over 15,000 hits on Google, indicating wide usage as both a stand alone application, and applet based viewer for alignments derived from SRS, PFAM, and Interpro.

Jalview is now being redesigned to take advantage of the many new analysis and alignment tools available, and circumvent the technical obstacles presented by complex sequence analysis tasks. Improvements have been made to the user interface and display for handling many alignments with large number of sequences, and generate fully annotated diagrams for publication.

Jalview is also able to access web based alignment, secondary structure prediction and sequence database services provided by the the European Bioinformatics Institute (EBI), and the University of Dundee. Web services employed by Jalview are being developed as part of the Visualization and Analysis of Molecular Sequences, Alignments, and Structures (VAMSAS) project, funded by the BBSRC.

VAMSAS is an open framework that facilitates the interoperation of advanced tools for phylogenetics, sequence analysis, and structural bioinformatics, by providing a common model for bioinformatic data exchange, web service discovery and interaction. The other tools in this project are AV@EBI – a version of the Astex Viewertm for

molecular structure developed by the EBI's Macomolecular Structure Database group, and TOPAli – a tool for phylogenetic and recombination analysis which is developed at the Scottish Crop Research Institute. More information can be found at http://www.jalview.org.