

## Application Note:

# JSAV: JavaScript Sequence Alignment Viewer

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### ABSTRACT

**Summary:** JSAV is designed as a simple-to-use JavaScript component for displaying sequence alignments on web pages. The display of sequences is highly configurable with options to allow alternative colouring schemes, sorting of sequences, 'dotifying' repeated amino acids. An option is also available to submit selected sequences to another web site or to other JavaScript code.

**Availability and Implementation:** JSAV is implemented purely in JavaScript making use of JQuery and JQuery-UI. It does not use any HTML5 specific options to help with browser compatibility. The code is documented using JSDOC and is available from <http://www.bioinf.org.uk/software/jsav/> or from GitHub <http://www.github.com/AndrewCRMartin/JSAV/>

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## 1 INTRODUCTION

Viewing multiple sequence alignments (MSAs) is a fundamental requirement in the analysis of protein sequences. MSAs allow us to visualize conservation across protein families as well as unusual features of particular sequences. As a result, there are a plethora of tools for viewing sequence alignments. These range from tools which provide attractive printed output, through standalone tools — either operating-system dependent, or independent — to web-based viewers.

Two of the earlier such tools are HOMED? and MALIGNED? written for VAX/VMS workstations. Neither seems to be actively maintained or easily available any more. Other early viewers include GeneDoc?, BioEdit and Seaview?.

RnaViz?, a program for visualizing RNA secondary structure contains DCSE?, an interactive sequence alignment viewer and editor which can be used for protein sequence alignments, but is targeted at the examination of RNA. A major problem in writing graphical software is the operating-system dependency of many graphics libraries. CINEMA? was probably the first sequence alignment viewer and editor implemented in Java, a platform independent programming language allowing graphical interfaces to run on any operating system. More recent software includes MPSA? and ANTHEPROT?. ClustalX? is a graphical user interface (GUI) for the ClustalW multiple sequence alignment program providing an integrated environment for aligning sequences and analyzing

the results. It is available for Linux, Mac and Windows platforms. Clustal Omega is the most recent addition to the Clustal family, but at the time of writing only has a command line interface — a beta version of a GUI is due to be released soon.

More recent developments include the Protein Family Alignment Annotation Tool (PFAAT)? designed specifically for family analysis and incorporating residue annotation tools as well as integration with Jmol for protein structure display. Like CINEMA, PFAAT is implemented in Java for operating system independence. CLC viewer is a recent free package written in Java for Linux Mac and Windows. It contains a number of integrated tools and acts as a core product for adding other features through a commercial version of the software. A more complete list is available on the web at [http://en.wikipedia.org/wiki/List\\_of\\_alignment\\_visualization\\_software](http://en.wikipedia.org/wiki/List_of_alignment_visualization_software).

Probably the most popular of the available tools is Jalview from Geoff Barton's group in Dundee. Jalview is available in two versions: a standalone Java application which is operating system independent and provides many tools and facilities, and as a 'light' version (JalviewLight) — a Java applet that can be embedded in a web page. The latter responds to the need for web site developers to be able to embed sequence alignment visualization tools into web pages.

However, in recent years there has been a gradual move away from using Java applets in web pages. New HTML features such as the HTML5 Canvas and powerful JavaScript libraries such as Bootstrap, JQuery and JQuery-UI that provide an easier syntax for accessing elements of a web page together with new widgets such as sliders and drag-and-drop support, have overtaken Java as the method of choice for creating interactive web sites with complex requirements. Such features are used widely by commonly used popular web sites such as Google Mail, Google Docs and Facebook.

To our knowledge, while there is an intention to port JalviewLight to JavaScript, there are currently no JavaScript based sequence alignment viewers available. To address this, we have developed JSAV (JavaScript Sequence Alignment Viewer). JSAV is designed to be a lightweight component that can easily be dropped into a web site to display and manipulate a sequence alignment. It does not offer the ability to edit the alignment, but does allow sorting and removing sequences as well as integration with other web pages and local JavaScript code.

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**Fig. 1.** Example code illustrating the creation of a JavaScript array of sequence objects, the options and the call necessary to create the alignment viewer.

## 2 IMPLEMENTATION

JSAV is implemented purely in JavaScript. JSAV employs the JQuery library to ease access to elements of the HTML that it generates and uses JQuery-UI to implement a two-value slider that is used to specify a range of positions in the alignment.

As input, the code requires an array of JavaScript objects which contain two elements: a unique identifier for a sequence and the

sequence itself — all sequences must be pre-aligned. Secondly a set of options can be provided. These control the display and facilities available to the end user of a web site. A brief piece of example code is shown in Figure 1 and available options are described in Table ??.

## 3 AVAILABILITY

The software may be downloaded from <http://www.bioinf.org.uk/software/jsav/> or from <http://www.github.com/AndrewCRMartin/JSAV/> and used freely. The web site provides demonstrations and full documentation.