Session 3: Groovy Jalview, and a taste of JalviewLite.

Day 2. Jalview Course, U. Edinburgh, June 27th 2012.

Part 1. Groovy Scripting and Jalview

1. Open the groovy console from the Desktop's Tools menu.

Load and experiment with the following scripts using the example alignment:

2. Printing the alignment's title
http://www.jalview.org/examples/groovy/printtitle.groovy

3. Generating CSV from annotation
http://www.jalview.org/examples/groovy/annotationsascsv.groovy

4. Parsing description strings as alignment annotation (using the 'Extract scores' function)
Example file:
 http://www.compbio.dundee.ac.uk/user/ws-dev1/examples/scanps_out.blc
Script:
http://www.jalview.org/examples/groovy/parseproperties.groovy

6. Manipulating features programmatically
http://www.jalview.org/examples/groovy/removeFeaturesByGroup.groovy

7. Manipulating sequence IDs in alignment
Load some sequences from Uniprot using the sequence fetcher.
Try this script http://www.jalview.org/examples/groovy/stripUniprotPrefixes.groovy

Part 2. Jalview Applet Tutorial

The Jalview applet, JalviewLite is a light-weight version of Jalview designed to run on a web page. It does not include any clients for on-line databases or web services, but otherwise provides the same core visualization and annotation capabilities as the Jalview desktop.

Exercise. The basic steps needed to display alignments with JalviewLite

1. Download and unzip the archive at http://www.jalview.org/training/2012/EdinburghU/June/applet.zip and copy the 'applet' directory on to your desktop.
2. Open the directory and drag the 'applettest.html' file onto a window of your web browser to view it.
    a. You should see a jalview applet button – pressing it will open the applet to display the uniref50.fa alignment in the applet directory.
    b. If you see a black box, try pressing <shift> + F5 to reload the page.
3. Now, open the applettest.html file in a text editor (Notepad will do)
    a. The applet directory contains a newick tree file called 'ferredoxin.nw'. Search the applet parameters page at http://www.jalview.org/examples/appletParameters.html to find out the name of the applet parameter used to load a tree on to the alignment.
    b. Add the parameter after the 'file' parameter in applettest.html like so:
        <param name="file" value="uniref50.fa">
        <param name=".." value="ferredoxin.nw">
    c. Now reload the page in your browser, and click the applet button.
4. Adding annotation to the alignment.
    a. Examine the parameter web page to discover how to add the sequence feature file and alignment annotation file you generated in Exercise 28 and 30 in the manual.
    b. Compare the Sequence Feature Settings dialog box in the JalviewLite and Jalview Desktop
5. JalviewLite and Javascript
    a. Look over the jalview javascript API documented at http://www.jalview.org/examples/jalviewLiteJs.html
    b. Try to create a JalviewLite launch button: http://www.jalview.org/examples/javascriptLaunch.html
    c. JalviewLite supports callbacks, so you can have your own functions called when the user interacts with data shown in Jalview: http://www.jalview.org/examples/linkedapplets_ng.html