H3ABioNet

Bioinformatics Training Unit

H3ABioNet

Pan African Bioinformatics Network for H3Africa

Introduction to Bioinformatics online course: IBT

Multiple Sequence Alignment

Lec5: *Writing sequence alignments*

By

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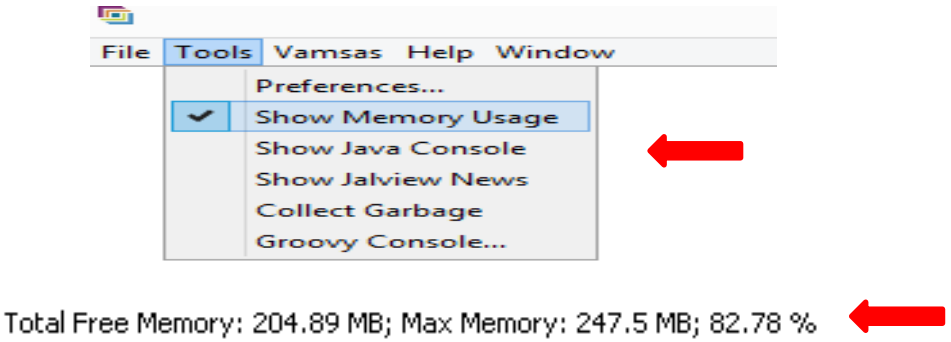
Memory Limits

- ***Jalview is a Java program***. One unfortunate implication of this is that Jalview **cannot *dynamically request additional memory*** from the operating system.
- It is important, therefore, that you **ensure** that you have **allocated enough memory** to work with your **data**.
- On most occasions, Jalview will **warn you** when you have tried to load an alignment that is too **big to fit** in to memory (for instance, some of the PFAM alignments are very large). You can **find out** how much **memory** is **available** to Jalview with the desktop
- ***Tools ⇒ Show Memory Usage*** function



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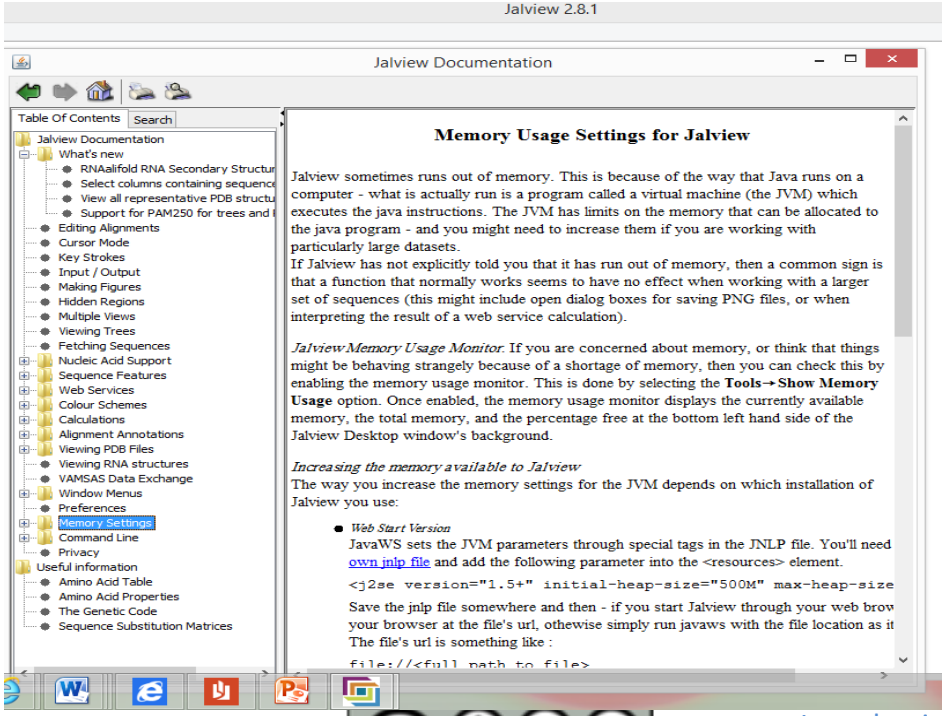
- Should you need to increase the amount of memory available to Jalview, full instructions are given in the built in documentation (***Help ⇒ Documentation***) and on the JVM memory parameters page ***(http://www.jalview.org/jvmmemoryparams.html)***.



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Writing sequence alignments

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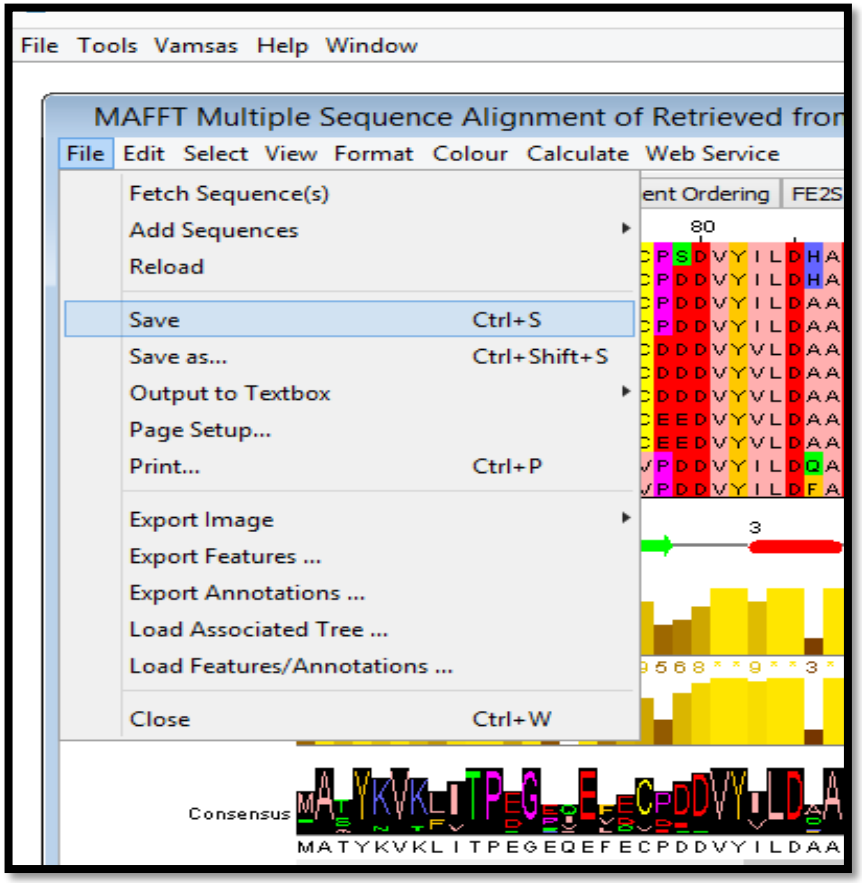
Saving the alignment

Jalview allows the current sequence alignments to be saved to file From the alignment window menu select



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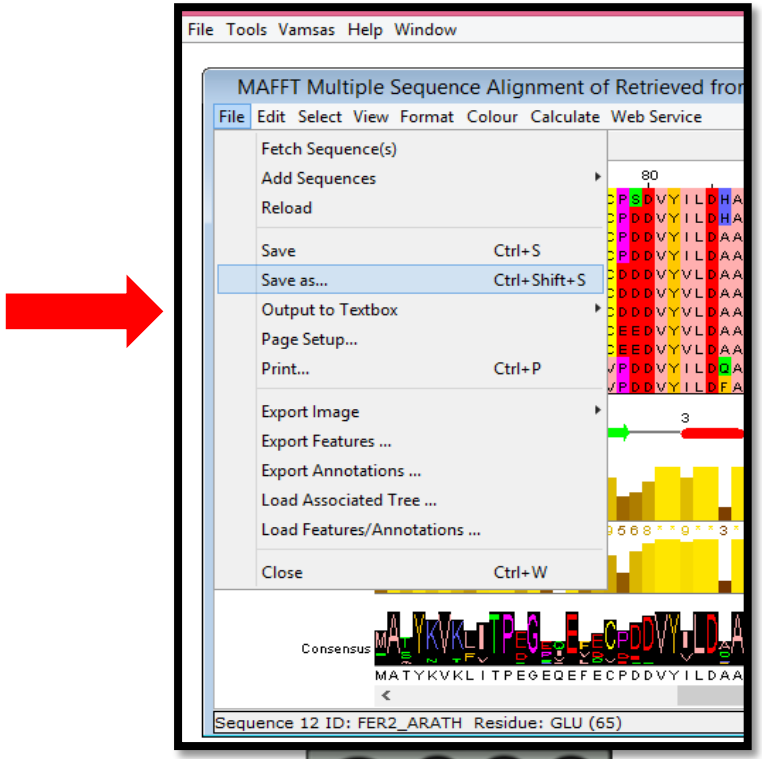
Jalview will remember the last filename and format used to **save (or load)** the alignment, enabling you to quickly save the file during or after editing by using the **File ⇒ Save entry**.



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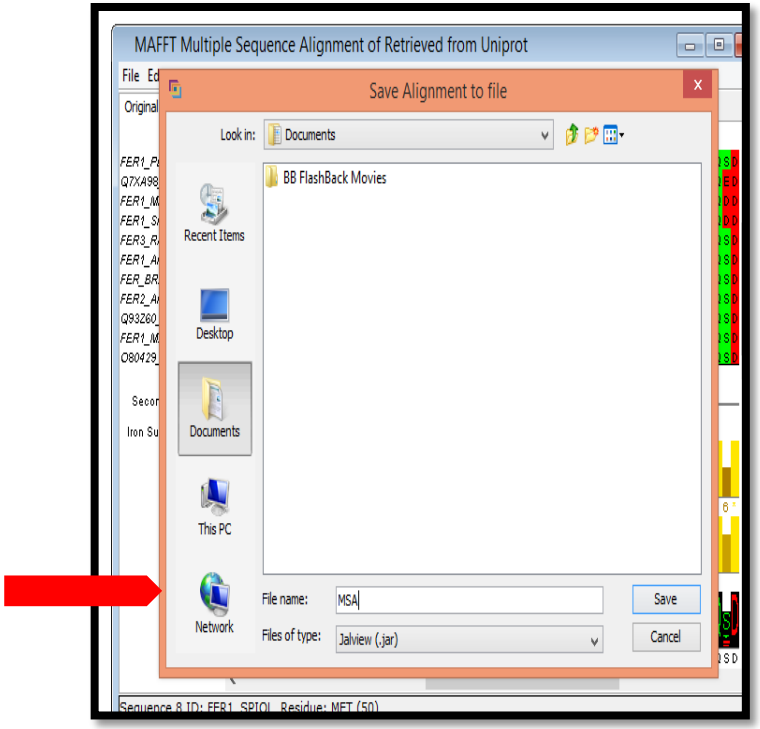
Jalview offers several different formats in which an alignment can be saved. The **jalview format (.jar)** is the only one which will **preserve** the **colors**, **groupings** and **similar information** in the alignment.



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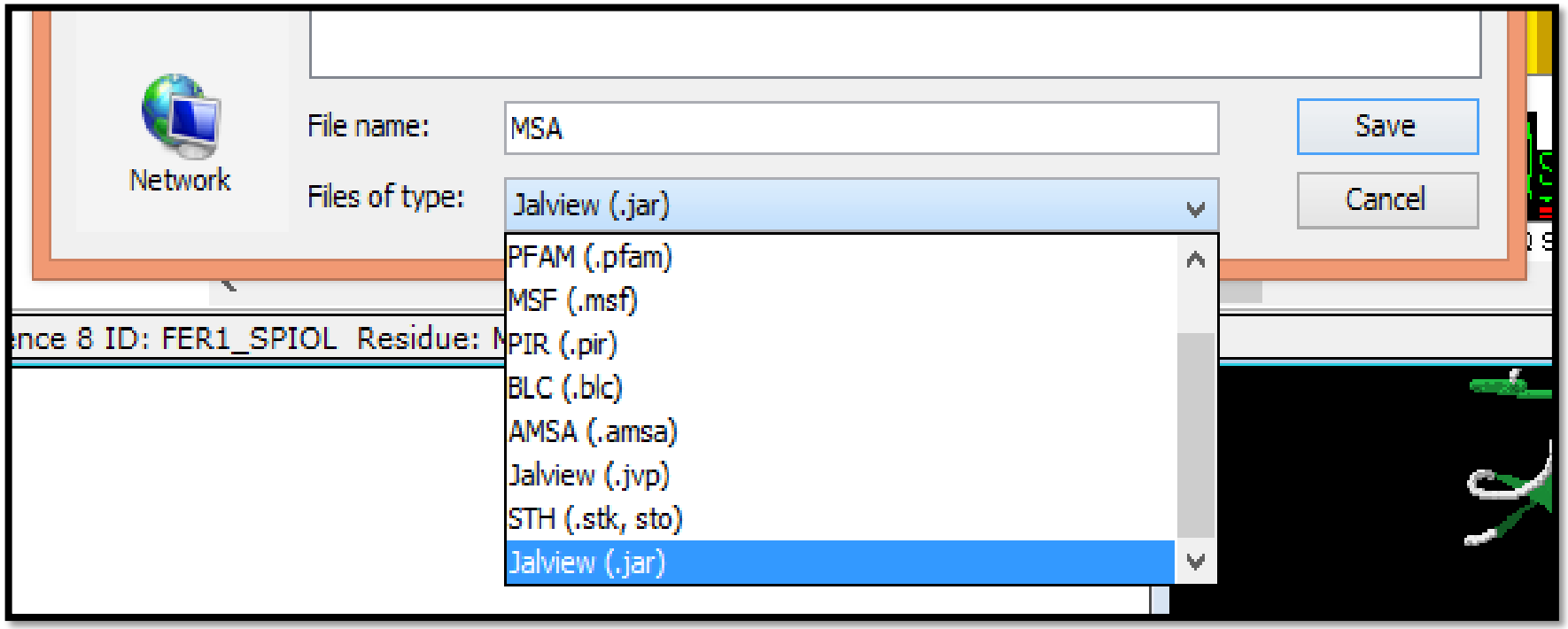
The other formats produce text files containing just the sequences with no visualization information. Unfortunately, only Jalview can read Jalview files.



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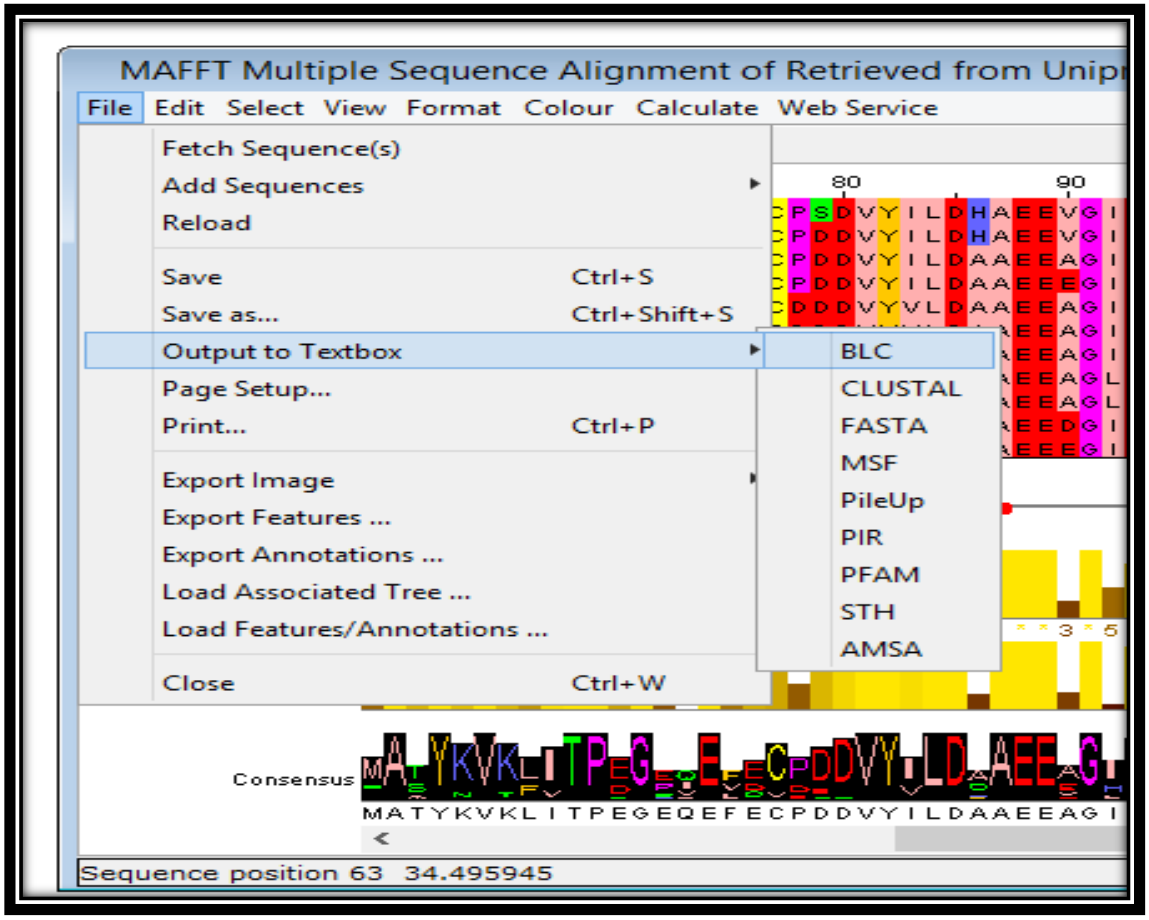
The ***File ⇒ Output To Textbox*** menu option allows the alignment to be copied and pasted into other documents or web servers.



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Jalview Projects

If you wish to save the complete Jalview session rather than just one alignment (e.g. because you have calculated trees or multiple different alignments) then your work should be saved as a Jalview Project file.

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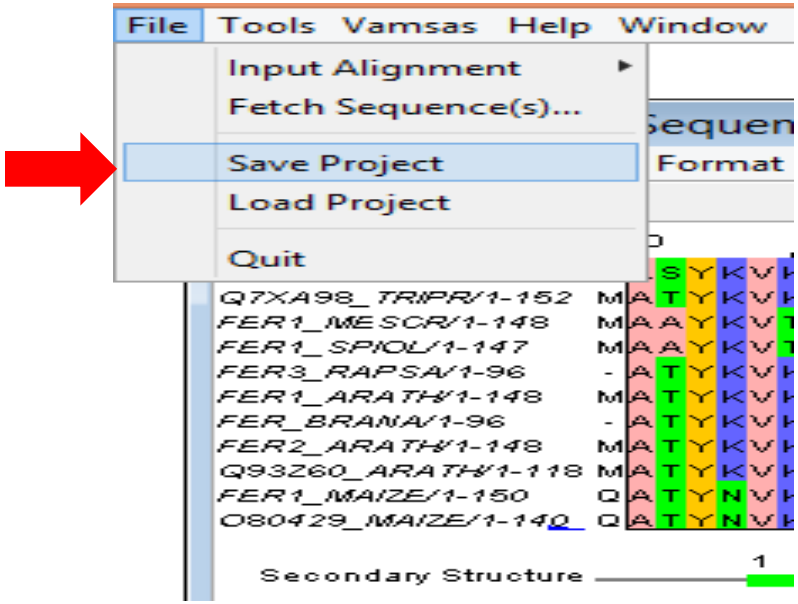
From the main menu select ***File ⇒ Save Project*** and a file save dialog box will appear. Loading a project will restore Jalview to exactly the view at which the file was saved, complete with **all alignments, trees, annotation and displayed structures rendered appropriately**



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Exercise : Saving Alignments

"to try on your own time"

a. Start Jalview, close all windows and load the ferredoxin alignment from PFAM (**PFAM seed** accession number **PF03460** (see Exercise 3).

b. Select ***File⇒Save*** *As* from the alignment window menu. Choose a location into which to save the alignment and select a format.

"All formats except *Jalview* can be viewed in a normal text editor (**e.g. Notepad**) or in a **web browser**. Enter a file name and click *Save*. Check this file by closing all windows and opening it with Jalview or by browsing to it with your web browser.

c. Repeat the previous step trying different file formats".

d. Select ***File ⇒ Output to Textbox ⇒ FASTA***. You can select and copy this alignment to the clipboard using the textbox menu options ***Edit ⇒ Select All*** followed by ***Edit ⇒ Copy***. The alignment can then be pasted into any application of choice, **e.g. a word processor or web form**.

e. Ensure at least one alignment window is shown in Jalview. Open the **overview** window and scroll to any part of the alignment. Select ***File⇒Save*** *Project* from the main menu and save in a suitable place.

F. Close all windows and then load the project *via* the ***File ⇒ Load Project*** menu option. **Note how all the windows and positions are exactly as they were when they were saved.**

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