

-- OliverVoigt - 15 Mar 2012

SeaView alignment editor

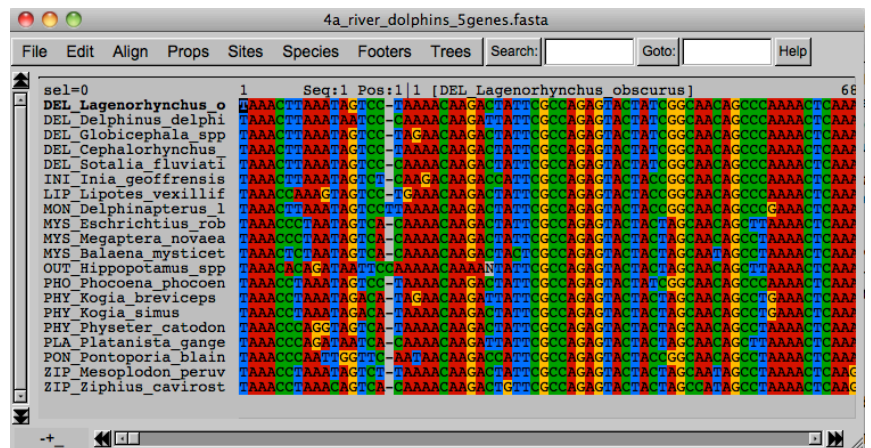
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Seaview is an editor for multiple alignments developed by Manolo Gouy. It is available for Linux, Mac OS X and MS Windows and can be downloaded at <http://pbil.univ-lyon1.fr/software/seaview.html>. SeaView is able to read and write various alignment formats (NEXUS, MSF, CLUSTAL, FASTA, PHYLIP, MASE). It allows running the alignment programs clustalW and MUSCLE and basic phylogenetic analyses. **Note that**

SeaView does not have an "Undo" function- therefore you should save the alignment you are working on frequently!



Creating a new alignment in SeaView

A new alignment can be created in different ways:

1. Add single sequences

Use "Edit>Load sequence" to paste and name a sequence. Numbers and gap characters can be removed.

2. Add sequences in a text editor (e.g. to an existing alignment)

Sequences can be pasted in the correct format into an existing or new text file. This is easily possible for the following formats:

Fasta format

The sequence identifier line is specified by beginning with ">". The following lines contain the sequence:

```
>Sequence_1
AGTCAGGCTCACCAACAATTCGATC
>Sequence_2
AGTCAGGCTCACCACCGTAATTCGATC
. . . .
```

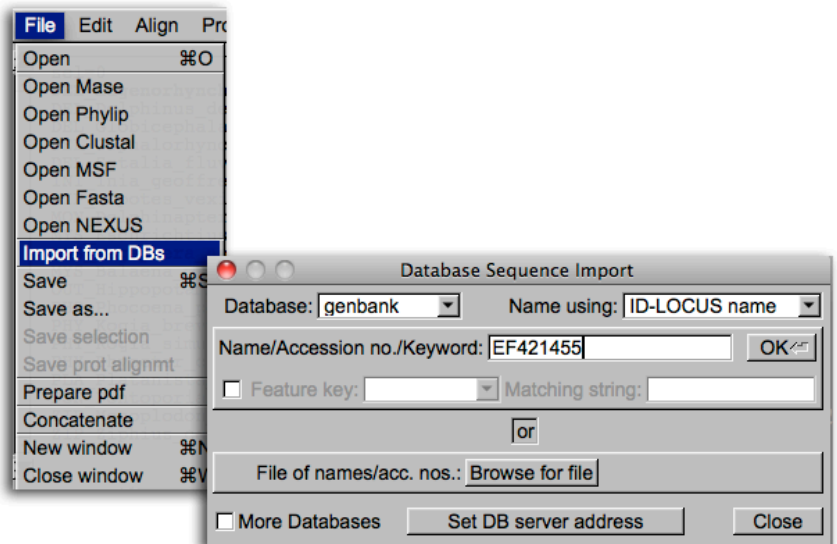
MASE format

This is the [SeaView](#) -sequence format. In addition to sequences, other information can be stored in a mase file (see below). Every sequence in a mase-file can have several comment lines. These are specified by beginning with ";". At least one "empty comment line" has to appear above the sequence identifier, because the sequence identifier line is defined the first line after the last comments (at least one empty comment line is necessary). The following line(s) contain(s) the sequence.

```
;
Sequence 1
AGTCAGGCTCACCAACAATTCGATC
;similar to Sequence 3
;good sequence
Sequence 2
AGTCAGGCTCACCAACGTAATTCGATC
....
```

3.Import sequences from databases

It is also possible to directly download data from [GenBank](#) into seaview. Use File import from db, choose genbank. The search function is however somewhat limited and works best if you provide the accession numbers. If you have a set of accession numbers, you can create a text file with each of these, separated by linebraks and use this file to receive the data via seaview. It is possible to choose the sequence name that seaview will give the sequences ("**Name using**" in the "**Database Sequence Import**" menu), in our case, "Species name" is the best choice.



Aligning sequences in [SeaView](#)

Automated alignment with [ClustalW](#) or [MUSCLE](#)

It is possible to run clustal w and MUSCLE on your alignment file in [SeaView](#). The alignment applications are started externally. It is also possible to align only parts of an alignment or only a set of sequences (see below).

Manual alignment

Single sequences or groups of sequences can be moved by using "space" or "-". If you want to add several gaps at once, you can enter a number (which appears in the left down corner of the editor window) before pressing "space" or "-". The corresponding number will be added to the sequences. Deleting gaps works similarly with "backspace" or "del". Note: as default, [SeaView](#) secures your sequences, so you cannot accidentally delete nucleotides in your

alignment. If for some reason you want to delete characters in a sequence, choose "Props" and check "Allow sequence editing". **BE EXTREMELY CAREFUL WHEN USING THIS OPTION- YOU MAY DELETE PARTS OF YOUR DATA!**

Keys for manual alignment:

"-" or "space" : Adds one gap (or several, if a number is entered).

"+" : Adds one (or several) gap(s) to every sequence **EXCEPT OF** the marked sequence(s).

"shift" & "-" : Deletes one (or several) gap(s) to every sequence **EXCEPT OF** the marked sequence(s).

Working in SeaView

Moving sequences vertically

To move a "sequence A" to a position above "sequence B", mark "sequence A", then hold "ctrl" and click on sequence B.

Additional information that can be included in mase-files and nexus-format

Additional information can be stored in the mase format. The information is stored at the beginning of the file in lines starting with ";;", which you can see in a text editor. It is important that if you add new sequences into a mase file in a text-editor to put them at the end of the file. Otherwise previously defined groups will change.

Groups of sequences ("Species")

To create a group of sequence, mark the corresponding sequences and choose "**Species>Create group**". You can now enter a group name. After defining different groups, you can easily switch between them to simultaneously edit all sequences in a group (add or delete gaps).

Sets of characters of the alignment

This option can be used, if you want to use only certain parts of the alignment for the phylogenetic analysis. Use "**Sites>Create set**" to create a new set. A new line with the name of your new set is displayed beneath the sequences. Here you can choose sites you want to include by clicking on them, sites included are shown as "x" (and shaded, if you choose "Props>Colors" and uncheck "inverted colors"). When pressing "ctrl" before choosing a site, all sites between the last 5' chosen position and that click are marked. The sites can be exported "File>Save selection"; if no sequence is chosen in that operation, the corresponding sites of all sequences are exported. Otherwise, only the sites of marked sequences are exported.

Phylogenetic Trees

SeaView can be used to calculate phylogenetic trees using Distance, Parsimony and Maximum Likelihood (with the external software PHYLIP) methods. Phylogenetic analyses will be carried out on the complete dataset or, if chosen, of the selected taxa and sites only.

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Assignment 3: Working with SeaView

I	Attachment	Action	Size	Date	Who	Comment
	accessions_hydra.txt	manage	0.1 K	20 Mar 2012 - 22:25	OliverVoigt	
	course.fasta	manage	14.8 K	21 Mar 2012 - 10:29	OliverVoigt	
	genbank_import.png	manage	94.1 K	15 Mar 2012 - 10:20	OliverVoigt	
	hydra.jpg	manage	31.2 K	20 Mar 2012 - 22:23	OliverVoigt	
	seaview.png	manage	90.2 K	15 Mar 2012 - 10:04	OliverVoigt	

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