

A Quick Guide To wEMBOSS

<http://www.wembooss.org>



wEMBOSS (Web EMBOSS) is a WWW interface to the EMBOSS package for sequence analysis. It is being developed by Marc Colet of the Belgian EMBnet node and Martin Sarachu of the Argentinian EMBnet node. Part of the code was taken from Luke McCarty's "EMBOSS GUI". A particularity of wEMBOSS is that it keeps the user's personal data permanently stored on the server side in a classic UNIX directory. The input data and the results of program runs are stored tidily into separate «projects». This guide explains the use of wEMBOSS; it assumes that the reader already has some basic knowledge of EMBOSS (<http://www.embooss.org>).

Logging in

When you start wEMBOSS you need to identify yourself with a user name and password. Your session remains open as long as you do not stop your Web browser. Note: when you log in for the first time in wEMBOSS you are prompted to create a first project.

Legend

1 Current Project Selector (e.g., QuickGuide)

Selector changes the current project.
PM jumps to the Project Management window.

2 Project Management

New creates a new project. Check the subproject box to create a subproject within the current project.
Rename changes the name of the current project.
Move moves the current project (and its contents) into the selected project.

Delete deletes the current project (together with its subprojects and all their contents). Warning, a deleted project with all its content is irrevocably lost, pressing the "back" button of your Web browser does not restore it!

3 Project files

New file creates a new text file. An empty text area will appear below. After clicking "Save as" you will be prompted for a file name.
View displays the content of a file. By default a file is

The screenshot shows the wEMBOSS web interface with the following numbered callouts:

- 1** QuickGuide project (Project Management buttons)
- 2** PROJECT RESULTS (Project Management buttons)
- 3** PROJECT FILES (Project Management buttons)
- 4** Search for programs (Program Selection)
- 5** PROJECT RESULTS (Table of results)
- 6** Search for programs (Program Selection)
- 7** Manual and Hide optional (Project Management)
- 8** INPUT (Sequence(s) and parameters)
- 9** ADVANCED (ATG, TAA, TAG, TGA, etc.)
- 10** Run subproj (Project Management)
- 11** Run subproj (Project Management)
- 12** PLOTORF Output (Sequence alignment plots)

opened in a new browser window or with a helper application depending on the MIME type of the file.

Edit opens the file in a text area for modification.

Copy copies one or more files (select several files with the <ctrl> or <shift> keys) into another project. Note that the destination project becomes the current project.

Delete deletes one or more files.
List-G&G transforms a GCG List File into a List File compatible with both GCG & EMBOSS.

Upload copies a file from your local computer into the project on the remote server. You can type the name of the file (with its path) in the box or use the file browser.

4 Program selection

Top sorted by group or alphabetically; click to expand or collapse the menus.

Bottom search by keyword in the program descriptions.

5 Project results

List of the current result files sorted by date or name.

program displays the result of program.

Files copies the result to your project.

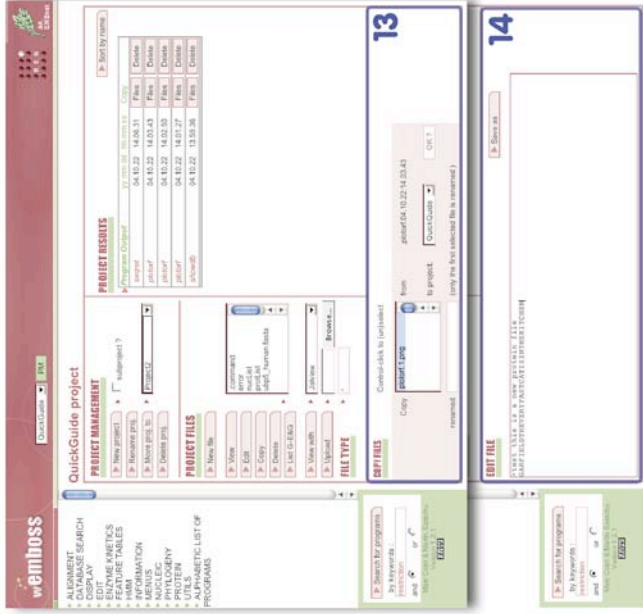
Delete deletes the result file.

6 Program selection (expanded)

program opens the input window of the program.

7 Manual and hide/show buttons

Manual displays the manual pages for the current program.
Hide/Show... hides/displays the optional parameters for the current program.



8 Input parameters

Select the method to be used to enter your input sequence(s):

- from EMBOSS database or project files: you can type in a USA (Universal Sequence Address, e.g., emb1:x91349) as on the command line. However the range specifications (`{n:m:r}`) do not work, but you can use the "begin/end/rev" boxes.
- from files on your local computer: you can type the name of the file directly in the box (e.g. `c:\tmp\my.seq`) or use the "Browse" button.
- from the sequence selector (`nuclList` or `protList`): shortcut to easily run many jobs on the same sequence. You must edit `nucl/protList` files to hold the USA's of the sequences you often use. The content of these special `nucl/protList` files will appear in a selector from which you can choose the files. Note that you cannot select more than one sequence. If you want to operate on several sequences at the same time, you must create separate List Files (with any name you find appropriate); then you can write the USA pointing to such a List File inside `nucl/protList` as `List::xxx`. Note also that some programs (e.g. *fuzznuc* or *texisearch*) output a List File. To work with sequences from this list, you can always rename `nuclList` (to save its content) and then rename your result file `nuclList`.

9 Input parameters (optional)

Select or change the optional parameters; these parameters are different for each program.

10 Run program

Click the "Run program" button to start the program.

11 Batch box

Type in your email if you expect the job to take a long time. You will be warned by email when the program finishes. If you have logged out you can pop up the result from a new wEMBOSS session or from the email itself.

12 Output Window

e.g., PNG graphic of *plotorf* for `emb1:x91349` forward frames.

13 Copy window

Use this window to move files from the results to your project or from a project to another project.

14 New/edit file window

Use this window to create new files or to edit existing files in your project.

MIME attachments

For certain file types wEMBOSS sends them to your Web browser with a MIME label attached. You can configure your browser or system to open such file with the appropriate software running on your local computer as a plug-in. At the time of this writing wEMBOSS supports the following:

file type	file name extension	MIME label
Postscript graphics	.ps	application/postscript
GCG MSF	.msf	chemical/msf
lav file for LALVIEW	.lav	chemical/x-aln2
nested parentheses tree file	.dnd .ph .phb	chemical/x-newhamphire
NEXUS tree file	.tre .treb	chemical/x-nexus

This document was written and designed by Guy Bottu and Robert Herzog from the Belgian EMBnet node, revised by Laurent Falquet of the Swiss EMBnet node and distributed by the P&PR Publications Committee of EMBnet.

EMBnet - European Molecular Biology Network - is a network of bioinformatics support centers situated primarily in Europe. Most countries have a national node which can provide training courses and other forms of help for users of bioinformatics software.

<http://www.ambnet.org/>

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