8 Input parameters
Select the method to be used to enter your input sequence(s):
• from EMBL-EBI database or project file: you can type in a USA (Universal Sequence Address, e.g., emb1:x291349) as on the command line. However, the range specifications (begin/end/rev) 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., crv/cmpn/my.msp) or use the "Browse" button.
• from the sequence selector (nuc.list or prot.list): shortcut to easily run many jobs on the same sequence. You must edit nuc/prot.list files to hold the USA's of the sequences you often use. The content of these special nuc/prot.list 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 nuc/prot.list as list:<name>. Note also that some programs (e.g., fixmate or textsearch) output a List File. To work with sequences from this list, you can always rename nuc.list (to save its content) and then rename your list file nuc.list.

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:x291349 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:

<table>
<thead>
<tr>
<th>file type</th>
<th>file name extension</th>
<th>MIME label</th>
</tr>
</thead>
<tbody>
<tr>
<td>PostScript</td>
<td>.ps</td>
<td>application/postscript</td>
</tr>
<tr>
<td>SGK MSG</td>
<td>.msg</td>
<td>chemical/x-sig2</td>
</tr>
<tr>
<td>nucleotide file</td>
<td>.nucl</td>
<td>chemical/x-nucleic</td>
</tr>
<tr>
<td>FASTA tree file</td>
<td>.tre</td>
<td>chemical/x-nucleic</td>
</tr>
<tr>
<td>tree file</td>
<td>.tree</td>
<td>chemical/x-nucleic</td>
</tr>
</tbody>
</table>

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

EMNet - 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.embnet.org/
A Quick Guide To wEMBOSS
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