A Quick Guide To EMBOSS
http://www.emboss.org

This is a Quick reference Guide for EMBOSS version 2.8.0

Introduction
EMBOSS (European Molecular Biology Open Software Suite) is a freely available suite of programs and libraries for sequence analysis. It incorporates many tools originating from the EGGCG package created in 1988. All EMBOSS programs are designed to run on a UNIX command-line or behind graphical interfaces (e.g., Jemboss, wEMBOSS).

Obtaining EMBOSS

Graphical User Interfaces
There are a number of graphical interfaces to EMBOSS: http://www.bioinformatics.nl/cgi/plink/EMBOSS/Interfaces.html

Jemboss is a java interface and is distributed with EMBOSS. If you are installing with the Jemboss interface you should use the installation script in the EMBOSS-x.x.x/jemboss/utils directory. Instructions for Jemboss installation are given at: http://www.bioinformatics.nl/cgi/plink/EMBOSS/Jemboss

Support and Mailing lists
The mailing list emboss@embnet.org is used for discussions of user problems. To subscribe to this list, send a mail to majordomo@embnet.org with the message text: subscribe emboss. The mailing list archive is: http://www.bioinformatics.nl/cgi/plink/EMBOSS/HYPERMAIL/emboss

Please send bug reports to emboss-bug@embnet.org

Help on a program
A program can be found using a keyword search of the description of all the programs by running the EMBOSS application wasename.

wasename keyword displays list of all programs with keyword in description

wasename -alphabetio -auto displays a list of all programs
programname -help gives the available parameters for the programname
tfm programname displays the documentation of programname
Documentation is also given online at:
http://www.bioinformatics.nl/cgi/plink/EMBOSS/Apps

Sequence formats
Sequences are stored in databases or in files as simple text. EMBOSS does not support sequences in word-processor files!

The default sequence file format is fasta. This format has an initial title line consisting of a ‘>’ followed by the sequence description on the first line. The second and subsequent lines contain the sequence, e.g.:

>fu Human FAU gene fragment
GNCGCCAGAAACCGGATGAGCTACTGGAATGGATGAG

EMBOSS currently supports 2 formats, including Clustal, EMBL, GCG, Genbank, PIR, MSF, Phylip, SwissProt, Text (raw).

The default output can be altered for all programs by an environment setting:
setenv EMBOSS_OUTFORMAT format

Alignment Formats
Several formats have been written or adopted for EMBOSS output.

Multiple Alignment
simple Displays names, positions and sequences, mark up line underneath [default]
fasta Standard fasta display. Gaps displayed as ‘-’
msf Standard MSF format. Gaps displayed as ‘-’
for intrinsic and for terminal ones
srs Similar to simple. No mark up line
trace Verbese form for de-bugging

Pairwise Alignment
pair Simple format for pairwise output [default]
mark Standard output from FASTA program suite
srpair Similar to pair format
score Score output. No sequence display

Any program derived from Bill Pearson FASTA suite of programs has a markx default format.

-aformat Alters output format
-awidth Displays alignment width
-ahasshow Displays the full USA (see below) in the alignment

Feature Formats

<table>
<thead>
<tr>
<th>Format</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gff</td>
<td>General Feature format defined by the Sanger Institute [default]</td>
</tr>
<tr>
<td>embl</td>
<td>Feature table used by EMBL database (em)</td>
</tr>
<tr>
<td>swissprot</td>
<td>Feature table used by SwissProt database (swiss) (sw)</td>
</tr>
<tr>
<td>-fuffu</td>
<td>UFO (uniform features object) features</td>
</tr>
<tr>
<td>-fformat</td>
<td>Opens features format</td>
</tr>
</tbody>
</table>

These flags can be applied to the output by using “-o” as a prefix, e.g., -oufo

-ffbegin Specifies first position
-ffend Specifies final position
-ffreverse Reverses features (DNA only)

Graphic Formats

<table>
<thead>
<tr>
<th>Format</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-graph</td>
<td>Static graphics using PLP plot. Output as X11 [default], PNG, ps, tektronix amongst others</td>
</tr>
</tbody>
</table>

Sequence Databases
Your local EMBOSS installation may have many sequence databases set up. The program showdb will indicate the available databases.

Uniform Sequence Address (USA)
A USA is an unambiguous means of specifying sequences in EMBOSS. It has the following syntax:

format:database:entry

Only raw (text) or IntelliGenetics format need to be specified. EMBOSS identifies the rest automatically.

You may also use:

- filename all sequences in a file
- filename:entry an entry in a file
- list:filename a list file (see below)
- asis:ACGTACGCGG a specific short sequence

The entry can include ‘*’ characters for wildcard matches of several entries and sequence may be specified by adding [starts:ends] positions to the USA. The rev keyword will reverse complement a DNA sequence. Command lines using these characters must be enclosed in double quotes:
A part of the sequence can be specified by adding the range:

```
e.g.  seqret "emb1hsau[1:571]"
```

The last 100 bases of a sequence can be specified by a negative start:

```
e.g.  seqret "emb1hsau[-100:1]"
```

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**List Files**

A list file contains a list of USAs (one per line). The list file input is @listfile. A list file may be read in wherever a program can read multiple sequences. Blank lines and USAs starting with a `#` character are ignored. There is no limit on different sequence formats within one list file.

**Format Conversion**

The format of an output sequence file can be specified. `seqret` can read in sequences in one format and write them in the other format, for example to convert a sequence to GCG format:

```
seqret in.seq gcg::out.seq
```

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**The command line and parameters**

EMBOSS programs are designed to be run from the command-line, as well as within scripts. To customise their behaviour, each has a distinct set of parameters, also known as options or flags.

There are 3 classes of parameters: standard, additional, advanced. Information on allowable flags for each program is given in the help files.

If values for standard (mandatory) parameters are not specified, the programs will prompt for them.

If additional (optional) parameters are missed out, default values will be used unless you put options (or opt) on the command line.

EMBOSS programs never prompt for advanced parameters; these must be explicitly specified. They are defined in the program documentation.

**General qualifiers**

These can be used with any program:

- `-auto` Turns off prompts and descriptions. Used when in running programs scripts.
- `-stdout` Writes to standard output (screen) by default.
- `-stdin` Reads from standard input (keyboard), writes to standard output (screen) by default.
- `-options` Prompts for all required and additional values.
- `-debug` Writes debug output to the file `programname.dbg`.
- `-help` Reports command line options. Or help verbose for more information on associated and general qualifiers.
- `-warning` Reports warnings.
- `-error` Reports errors.

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**Tools (examples)**

`seqret` Reads and writes (returns) sequences.

`emb2genome` Aligns EST and genomic DNA sequences.

`needle` Needleman-Wunsch global alignment.

`water` Smith-Waterman local alignment.

`dotmatcher` Displays a thresholded dotplot of two sequences.

`remap` Displays a sequence with restriction cut sites, translation etc.

`prettyplot` Displays simple sequence with colouring and boxing.

`extractseq` Extracts aligned sequences, with colouring and boxing.

`reverse` Reverses and complements a sequence.

`plotref` Plots regions from a sequence.

`and many other` Utilities for various tasks.

**Utils Misc**

`embossdata` Finds or fetches the data files read in by the EMBoss programs.

`embossversion` Writes the current EMBoss version number.

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This document was written and designed by Lisa Mullan from the UK EMBnet node and being distributed by PPR Publications Committee of EMBnet.

EMBnet - European Molecular Biology Network - is a bioinformatics support 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.

You can find information about your national node from the EMBnet site:


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