The **EMBOSS** Administrator’s Guide

David Martin, EMBnet Norway
Peter Rice, LION Bioscience
Alan Bleasby, HGMP (EMBnet UK)

This guide relates to **EMBOSS** 2.5.0
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\(^1\)http://www.gnu.org/copyleft/fdl.html
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1 Introduction

1.1 About this document
This guide has been written to assist system administrators and developers with the installation and configuration of EMBOSS. If you are reading this to find out how to do bioinformatics then you are wasting your time. You are referred instead to the Resources chapter below where there is a list of more relevant literature and web sites. Experienced users may find this document useful for configuring their own databases and customising their EMBOSS experience.

1.1.1 Credits
The original author of this guide was David Martin\(^1\) at the Norwegian EMBnet node.\(^2\) It is however the result of a team effort. Thanks are due in particular to Johann Visagie for the FreeBSD information. Other contributors are acknowledged in the text.

1.1.2 Reproduction
The obligatory bit of legalese. The first version of this guide was not in the public domain but has been released under the GNU Free Documentation License by the original author. Although ‘Free’ in this license is usually explained as ‘free as in freedom, not as in beer’ the authors are likely to appreciate offers of free drinks should you ever meet them.

1.2 What is EMBOSS?
EMBOSS is a freely available suite of bioinformatics applications and libraries. It can be downloaded via the internet, copied, customised, and passed on under the terms of the various General Public Licenses. EMBOSS has been developed in response to the need for a powerful, adaptable suite of software that can interface readily with many different situations and meet the need of professional bioinformaticists, particularly those needing high throughput and/or scriptable capabilities.

EMBOSS has primarily been developed by those responsible for the public extensions to the GCG package. EMBOSS supercedes much of EGCG and includes far better database interaction. EMBOSS also has the benefit of freely accessible source code so novel applications can be developed rapidly and at minimal cost.

EMBOSS is currently only available for Unix/Linux systems but it has been known to compile and run on Windows NT. This document will only consider the UNIX version and will assume the reader has some familiarity with UNIX system administration.

1.2.1 Where to get it?
EMBOSS is available for download from the primary site at the UK EMBnet node by anonymous ftp.\(^3\) This directory contains the EMBOSS package and several associated packages (collectively known as EMBASSY) that are distributed with EMBOSS. Download these to a suitable location. Documentation is available on the WWW at the EMBOSS web site.\(^4\)

\(^1\)damartin@gmp.mrc.ac.uk
\(^2\)http://www.no.embnet.org
\(^3\)ftp://ftp.uk.embnet.org/pub/EMBOSS/
\(^4\)http://www.uk.embnet.org/Software/EMBOSS
FreeBSD distributions from 4.2 onwards now include **EMBOSS** as an optional package maintained by Johann Visagie.\(^5\) Please see section 2.5 for more information on installation on FreeBSD.

\(^5\)jchann@genetics.com
2 Installation

2.1 Retrieving EMBOSS by anonymous ftp

2.1.1 Interactive FTP

Change directory to the location in which you wish to download the EMBOSS source code. In this example we will download the source to /packages/EMBOSS. Then start your ftp client and point it to ftp.uk.embnet.org.

% ftp ftp.uk.embnet.org
Connected to tantalum.hgmp.mrc.ac.uk.
220 tantalum FTP server ready.
Name (ftp.uk.embnet.org:embuser):

We are using anonymous FTP so type the username anonymous.

Name (ftp.uk.embnet.org:embuser): anonymous
331 Guest login ok, send your complete e-mail address as password.
Password:

Enter your email address here as the password for user anonymous.

Password:

230-######################################################################
230-
230- Welcome to the UK HGMP Resource Centre anonymous ftp service
230-
230- Please contact support@hgmp.mrc.ac.uk regarding
230- any problems with this service
230-
230-######################################################################
230-
230-Please read the file README
230- it was last modified on Wed Aug 13 15:40:25 1997 - 1810 days ago
230 Guest login ok, access restrictions apply.
Remote system type is UNIX.
Using binary mode to transfer files.
ftp>

Move to the EMBOSS directory and list the files. The output has been truncated a little to save space.

ftp> cd /pub/EMBOSS
ftp> ls
200 PORT command successful.
150 Opening BINARY mode data connection for /bin/ls.
total 22334
... 1024 May 26 20:17 .gnu
... 9079913 May 14 21:37 EMBOSS-2.5.0.tar.gz
Now download the source files

ftp> get EMB OSS-latest.tar.gz
200 PORT command successful.
150 Opening BINARY mode data connection for EMB OSS-latest.tar.gz
(9079913 bytes).
...
ftp>

And repeat for each file. Or use mget *gz to download all the files at once. Exit your ftp session with the command bye.

### 2.1.2 FTP using WGET

The program WGET can be used to download a remote directory noninteractively. More details on WGET can be obtained from the Free Software Foundation.\(^1\) Assuming you have WGET installed, use the following command which generates a lot of output on the screen:

```
% wget -m 'ftp://ftp.uk.embnet.org/pub/EMBOSS'
     => 'ftp.uk.embnet.org/pub/.listing'
Connecting to ftp.uk.embnet.org:21... connected!
Logging in as anonymous ... Logged in!
==> TYPE I ... done.  ==> CWD pub ... done.
==> PORT ... done.  ==> LIST ... done.

... many pages truncated
...

FINISHED --15:04:55--
Downloaded: 2,657,366 bytes in 4 files
```

A new directory `ftp.uk.embnet.org` has been created and EMB OSS can be found at `ftp.uk.embnet.org/pub/EMBOSS`. You may wish to create a symbolic link to this from your `/packages` directory for convenience.

\(^1\)http://www.gnu.org
2.2 Unpacking

You will have downloaded the EMBOSS and EMBASSY packages to a suitable directory. For this example we will assume you have downloaded them to /packages so you should now have the following files (or similar) and maybe more packages in EMBASSY.

% ls
EMBOSS-latest.tar.gz
EMBOSS-1.0.5.tar.gz
ESTIM4-1.0.0.tar.gz
HMMER-2.1.1.tar.gz
MEME-2.3.1.tar.gz
MSE-0.0.4.tar.gz
PHYLIP-3.573c.tar.gz
TOPO-0.1.tar.gz

First unpack the EMBOSS distribution

% gunzip EMBOSS-latest.tar.gz
% tar xf EMBOSS-latest.tar

This will create a new directory, EMBOSS-2.5.0 or similar. You may wish to use tar xpf for unpacking EMBOSS.

Enter the EMBOSS directory

% cd EMBOSS-2.5.0

create a directory for the EMBASSY packages

% mkdir embassy

Now move the EMBASSY packages to the EMBASSY directory

% mv .. /MSE-0.0.4.tar.gz PHYLIP-3.573c.tar.gz \  TOPO-0.1.tar.gz embassy

Go into the EMBASSY directory and unpack those packages.

% cd embassy

% gunzip MSE-0.0.4.tar.gz
% tar xf MSE-0.0.4.tar

and so on for each EMBASSY package.

Go back up one directory to the main EMBOSS package directory and prepare to start compilation.

2.3 Graphics Requirements

Depending on your system you may need to explicitly configure the graphics. EMBOSS includes the plplot graphics library and will link to X11 and the recent (non-GIF) releases of the gd graphics library which also require libz and libpng (and possibly libjpeg). Please see the section 'Configuring EMBOSS graphics' below.

To get PLPLOT to produce PNG images you will need to have the z², rgb¹ and gd¹ libraries installed. gd version >= 1.8.4 is recommended. A recent release must be used as older versions

²http://www.info-zip.org/pub/infozip/zlib/
¹http://libpng.sourceforge.net/
¹http://www.boutell.com/gd/
support GIF which is NOT supported in later versions because of software patent problems. If for some reason you do not have the required libraries and your system support group will not update them for the system then install all three latest versions (z, gd, png) to a new directory and then add this new directory to your configure line for EMBOSS: ./configure --with-pngdriver=my_dir where the z, png and gd libraries were each installed using ./configure --prefix=my_dir

??? It may also be helpful to ensure that the LD_LIBRARY_PATH environment variable is set appropriately to include the libraries in the path. ???


These also list the various mirror sites for non UK people.

Alternatively, using ftp -


You can unpack the tar.gz files in any directory, and install them in a common area.

By default everything (including EMBOSS) installs in /usr/local but in the examples below we use /home/joe/local

Note: gd does not use a ./configure script, and will fail at the "make install" stage if the installation directory does not have a /bin subdirectory. You can create this directory (e.g. /home/joe/local/bin) if it does not already exist.

2.3.1 zlib

Zlib is available from these sites:


ftp://ftp.infozip.org/pub/infozip/png/png-1.1.3.tar.gz

To install, pick up the sources and then:

% gunzip -c zlib-1.1.3.tar.gz | tar xf -
% ln -s zlib-1.1.3 zlib
% cd zlib
% ./configure --prefix=/home/joe/local
% make
% make install
% cd ..

2.3.2 libpng

Libpng is available from these sites:


ftp://ftp.infozip.org/pub/infozip/png/png-1.1.3.tar.gz

To install, pick up the sources and then:

% gunzip -c libpng-1.2.1.tar.gz | tar xf -
% ln -s libpng-1.2.1 libpng
% cd libpng
% cp scripts/makefile.linux makefile

Libpng has no configure script so you have to do some work by hand. Edit makefile, change prefix to be /home/joe/local and any other places - some files point to ../zlib others use /usr/local/lib and /usr/local/include. On HP-UX this is trickier. CFLAGS has to match the definition for zlib.

Now build using the edited makefile:

\footnote{http://www.mirror.ac.uk/sites/ftp.cdrom.com/pub/infozip/png/}
\footnote{http://www.info-zip.org/pub/infozip/png/}
\footnote{ftp://ftp.infozip.org/pub/infozip/png/png-1.1.3.tar.gz}
\footnote{http://libpng.sourceforge.net/}
\footnote{http://www.mirror.ac.uk/sites/ftp.libpng.org/pub/png/libpng.html}
\footnote{ftp://swrind.nde.swt.com/pub/png/src/libpng.1.2.1.tar.gz}
2.3.3  gd

Gd is available from these sites:

There is no FTP server at this site.
To install, pick up the sources, build zlib and libpng first, and then:

% gunzip -c gd-1.8.4.tar.gz   | tar xf -
% ln -s gd-1.8.4   gd
% cd gd

Now edit Makefile, change the definitions for INCLUDEDIRS, LIBDIRS, INSTALL_LIB, INSTALL_INCLUDE, INSTALL_BIN, and change all /usr/local to /home/joe/local

% make
% make install
% cd ..

If the gd "make install" fails with a warning about the "bin" directory, you need to create it by hand (see above).
To compile with the local version your EMBOSS configure line should now read:

./configure --with-pngdriver=/home/joe/local

This will look for the graphics libraries in your local installation under /home/joe/local instead of a system-wide location
configure keeps a copy of the previous settings. With earlier releases of EMBOSS, or as a developer with an earlier release of autoconf, you may need to delete files config.cache and config.status if configure has been run before.

2.4  Compilation

Building EMBOSS is easy. It follows the usual GNU style of ./configure, make, make install. We’ll take these steps one at a time.

2.4.1  Configure

To accept the default configuration, just type ./configure and let EMBOSS get on with it. You may however want to make some changes to the configuration parameters according to your local policy.
This section will not cover all the possibilities, just some of the more common. The configuration script will attempt to find the necessary components in your system to determine how to successfully build EMBOSS. It typically expects the GNU C compiler (gcc) and several standard libraries that should already be part of your Unix/Linux system. EMBOSS should configure, compile and run on most modern Linux distributions straight out of the box.

11http://www.boutell.com/gd/
Installation directory

You need to have write permission on the directory in which you eventually wish to install EMBOSS. You may also wish to put it somewhere else other than the standard location of /usr/local/emboss.

The installation directory is controlled by the --prefix argument. For example, you can have all third party applications owned by a non-privileged user and installed in a package specific directory under /site/prog/

% ./configure --prefix=/site/prog/emboss

will install EMBOSS under /site/prog/emboss. The binaries will be installed in /site/prog/emboss/bin with shared libraries installed in /site/prog/emboss/lib. System wide data are installed in /site/prog/emboss/share/EMBOSS/data, and the configuration files (ACD files) for the applications will be installed in /site/prog/emboss/share/EMBOSS/acd (or for EMBASSY in directories corresponding to the package name.) Documentation is installed in /site/prog/emboss/share/EMBOSS/doc. The installation directory should be specified using a full path otherwise interesting failures may occur.

The individual directories for installation can be modified with other configuration commands but this is usually not necessary. Run ./configure --help to get more information on the directories that can be changed and other configuration options.

Run ./configure with the options you wish to use. This may take a short time as various messages scroll up the screen.

All should be well with this and configure should exit with a message like this:

... much output skipped

creating ./config.status
creating plplot/Makefile
creating plplot/lib/Makefile
creating nucleus/Makefile
creating ajax/Makefile
creating emboss/Makefile
creating emboss/acd/Makefile
creating test/Makefile
creating test/data/Makefile
creating test/embl/Makefile
creating test/pir/Makefile
creating test/swiss/Makefile
creating test/swnew/Makefile
creating test/wormpep/Makefile
creating emboss/data/Makefile
creating emboss/data/AAINDEX/Makefile
creating emboss/data/CDDON/S/Makefile
creating emboss/data/REBASE/Makefile
creating emboss/data/PRINTS/Makefile
creating emboss/data/PROSITE/Makefile
creating Makefile

Configuration is now complete.

Reconfiguration

If at first you don't succeed, try, try and try again. It is not uncommon to make typos or other mistakes when running ./configure. If you want to run configure again you should run make clean before running ./configure with (hopefully) the correct options. With an earlier EMBOSS release, or as a developer with an earlier release of autoconf, you must first delete the file config.cache but this is no longer produced.
Configuring EMBOSS graphics

The PLplot library can produce output to many devices but requires certain libraries that are NOT distributed with EMBOSS.

To get X-windows based output you must have X installed, or else PLplot will not build the required driver. You may need to specify the location of your X-windows library with the configuration options: $X$-includes=DIR ($X$ include files are in DIR) $X$-libraries=DIR ($X$ library files are in DIR)

To explicitly configure PLplot without $X$-windows, use $X$-windows=without-x.

You can explicitly tell EMBOSS to not include PNG support with $X$-without-pngdriver.

You can tell if configure has found a suitable PNG library by watching for something like the following when running ./configure:

checking if png driver is wanted... yes
checking for inflateEnd in -lz... (cached) yes
caching for gdImageCreateFromPng in -lgd... (cached) yes

This means that the configuration script has located the PNG libraries on your system. If you see a message indicating that configure could not find the libraries or that the version of gd was too old then you should install the latest versions of the libraries yourself and rerun configure with the correct $X$-without-pngdriver value.

When you run an EMBOSS graphical application you can see the list of installed graph devices by giving 'l' as the response to the 'Graph type' prompt.

2.4.2 Configuring for 64 bit systems

EMBOSS configure looks for GCC and uses this of preference when compiling EMBOSS. This is not ideal for those who wish to have a compiled and linked 64bit version of EMBOSS. The current version is NOT 64 bit clean (ie. it does not necessarily use 64 bit representation internally) but will compile and run quite happily on 64 bit systems.

Additional notes are appended below for the various operating systems we have information on.

IRIX 6.5.10

In order to compile for 64 bit on IRIX you have to specify the native compiler in 64 bit mode (cc -64) and the linker in 64 bit mode (/bin/ld -64). The following notes were provided by Jose Ramon Valverde12.

We have succeeded in compiling EMBOSS for IRIX using 64 bit compilation.
It required some tweaking, but works. The recipe for those willing to give it a try is:

- remove 'gcc' from your path
- define COMPILER_DEFAULTS_PATH appropriately (see pe_environ) to look for a compilerdefaults file containing e.g. :abi=64:isa=4:proc=r10k
- ./configure in EMBOSS and all EMBASSY subdirs
- search in all files for 'CC = cc' and substitute it for 'CC = cc -64'
- same for 'LD = /bin/ld' to 'LD = /bin/ld -64'
- make

12jrvalverde@cnb.uam.es
The reason is that compiling depends on the Makefile and on libtool, as well as linking. We didn’t spend much in looking at configure since the above steps where so straightforward. We know we should look into the configure script and add an option for 64-bit-irisx-compile or some such, but that’ll have to wait till we have time for it.

Yes, we know, the search and substitute thing looks tedious, but it isn’t, honest: create a ‘chfile.sh’ out of the EMBOSS source hierarchy containing:

```bash
#!/bin/sh
cp \$1 \$1.orig
mv \$1 tmpfile
sed -e 's/CC="cc"/CC="cc -64"/g' tmpfile |

sed -e 's/CC = cc/CC = cc -64/g' |

sed -e 's/\bin/\bin/ld/\bin/ld -64/g' \$1
rm tmpfile
```

‘cd’ to the emboss directory and run

```
find . -type f -exec /path/to/chfile.sh {} \; -print
```

and you are done with the CC changes. LibTOOL requires special treatment since it uses quotes.

### 2.4.3 Building EMBOSS

Building EMBOSS is a matter of typing ‘make’ and going to find something else to do for the next ten minutes to half an hour depending on the speed of your system. EMBOSS will first build the shared libraries (PLPLOT, AJAX, and NUCLEUS) and then build the applications.

You may see plenty of warnings (especially on SGI systems) complaining about libraries not being used to resolve any symbols. These can be safely ignored.

If all goes according to plan you should have built EMBOSS successfully. If not you will have to try to work out why the build failed. If you can’t work it out yourself, send an email describing the problem to emboss-bug@embnet.org preferably with a copy of the output from the installation.

Assuming that compilation was successful, you can now type ‘make install’. After a few minutes and many pagesful of messages, EMBOSS should be installed where you specified in the --prefix option (or in the default location of /usr/local/emboss if --prefix was not specified).

### 2.4.4 Post compilation setup

You will now need to make a few adjustments to your environment to ensure that EMBOSS runs smoothly. EMBOSS looks for certain environment variables to determine where the libraries and data are found. These instructions assumed you installed EMBOSS in /site/prog/emboss. Adjust these instructions to suit your installation. Insert the following lines at the end of /etc/cshrc (or ~/.cshrc for a personal installation)

```bash
setenv PLPLOT_LIB /site/prog/emboss/lib
set path=( /site/prog/emboss/lib \${path} )
```

Or for bash/ksh/sh users, insert the following at the end of /etc/profile or ~/.bashrc

```bash
PLPLOT_LIB=/site/prog/emboss/lib
PATH=/site/prog/emboss/bin:PATH
export PLPLOT_LIB PATH
```

EMBOSS should now be ready for use.

---

13 You don’t have to do this. You can leave EMBOSS where it is and just add the path to the emboss directory to your PATH.

---
2.4.5 EMBoss data files

EMBOSS will by default install the data files (including those installed with REBASEEXTRACT, PROSEXTRACT PRINTSEXTRACT AINDEXEXTRACT or CUTGSEXTRACT) in the default directory share/EMBOSS/data in the install prefix directory. If EMBOSS is not installed (for example, your own personal installation) the data files are written to emboss/data in the directory where emboss was built.

If you want to place your data files elsewhere, or have a separate set of data files you wish to use, you can set the EMBOSS_DATA variable in emboss.default or, for personal use, in your .embossrc file.

2.4.6 Testing your EMBOSS installation

You can test your EMBOSS installation by trying the program 'wosssname'

% wosssname -auto |more

This should give a long list of programs that are available. Press space to page down through the list. This is just the EMBOSS programs and doesn't include any of the EMBASSY programs, but only because they are not yet installed. (Note: Although wosssname does have a -noembassy option this does not work with installed programs because wosssname can no longer find any difference between EMBOSS and EMBASSY)

2.5 Installing EMBASSY

As well as the base libraries and standard EMBOSS distribution, various extra packages (EMBASSY) are distributed with EMBOSS.

To install an EMBASSY package, go to the relevant directory. For example to install PHYLIP (which was unpacked into /packages/EMBOSS-2.5.0/embassy/PHYLIP-3.573c earlier) go to the relevant directory.

% cd /packages/EMBOSS-2.5.0/embassy/PHYLIP-3.573c
% ./configure --prefix=/site/prog/emboss
... output not shown
% make
... output not shown
% make install
... output not shown

Note. You MUST use the same arguments for ./configure that you used for the installation of the main EMBOSS package. It may be necessary to add other options as required by individual packages (see below).

Repeat as necessary for the other EMBASSY packages. It should also be noted that certain EMBASSY packages may require additional libraries.

You should now find that running WOSSNAME as before lists the EMBASSY programs.

2.5.1 EMBASSY package specific notes

In most cases, EMBASSY packages should build with no problems. Known problems are described below.

Packages with no known problems

So far ESIM4, HMMER, MEME, MSE, PHYLIP and TOPO appear to install without a problem using the same arguments to configure.
EMNU

EMNU requires the curses or n curses libraries that come as standard on most Unix-like systems. In particular EMNU requires two header files form.h and menu.h that are not distributed with all implementations.

If your curses/n curses library is installed in a strange place then you may need to instruct configure with the option

--with-curses=/path/to/curses

2.6 Installing EMBOSS in package format

EMBOSS can be installed on almost all Unix/Linux operating systems using the instructions above, but the package format can be far more convenient. A package is a precompiled set of binaries with installation instructions that can be set up on your system with a minimum of work. In some cases the package will check for the correct libraries and install those as necessary.

Brief instructions are given here for the packages of which we are aware. These are maintained separately from the main source tree and may also install some files in operating system standard locations instead of the locations used by the ‘raw’ EMBOSS distribution. Please read the more detailed instructions that accompany each package.

2.6.1 Installing EMBOSS on FreeBSD

A FreeBSD EMBOSS package has been created by Johann Visagie\textsuperscript{14} of Electric Genetics. This will be distributed on the installation CD’s and through the normal distribution channels from FreeBSD version 4.2 onwards.

For the FreeBSD user with an up-to-date ports tree\textsuperscript{15}, installing EMBOSS reduces to two simple commands (as root):

```
# cd /usr/ports/biology/emboss
# make install
```

The FreeBSD specific parts of the port are that emboss.default is included with the other configuration files under /usr/local/etc as emboss.default.sample, and the EMBOSS documentation is installed in /usr/local/share/doc/EMBOSS instead of the default location. For further information on installation under FreeBSD you are referred to the Resources chapter.

\textsuperscript{14}johann@genetics.com

\textsuperscript{15}FreeBSD users can update their ports tree through a variety of mechanisms. Please see the FreeBSD specific guide produced by Johann for more information

15
3 Configuration

EMBOSS can be readily configured to match your requirements. In a standard installation of EMBoss the configuration directives are looked for in the following locations and in the following search order:

1. A file `emboss.default` in the `share/EMBOSS` subdirectory of your EMBoss installation.\(^1\)
2. A file `embossrc` in the directory specified by the EMBoss environment variable.
3. A file `embossrc` in the users home directory.
4. A file `embossrc` in the current directory.

`emboss.default` and `embossrc` are plain text files that can readily be edited to suit.\(^3\) Redefinitions of configuration parameters will override those previously defined. In the descriptions that follow only `embossrc` will be mentioned but all directives can be placed in `emboss.default` for site wide configuration.

Several aspects of EMBoss can be defined. These are:

- EMBoss environment variables
- EMBoss databases
- Default behaviour of EMBoss programs

Databases are by far the most complex of these.

EMBOSS will ignore blank lines in the `emboss.default` and `embossrc` files. It will also ignore any lines beginning with # or ! allowing comments to illuminate the declarations in the file.

3.1 EMBoss environment variables

EMBOSS environment variables are set with a `env` or a `set` declaration. `env` and `set` are interchangeable. The most important environment variable is the location of the `.acd` files that describe each program.

```
set emboss_acdroot /site/prog/emboss/share/EMBOSS/acd
```

Environment variables are useful for simplifying maintenance of your `embossrc`. For example you may want to specify the location of your databases as an environment variable. Then if you move the databases you only have to update one line in the configuration file.

```
set emboss_database_dir /data/databases/flatfiles
```

This would then be referred to later in `embossrc` as

```
$emboss_database_dir/embl
```

---
\(^1\)This location may have been redefined in installations of EMBoss that have been packaged for specific operating systems. See section 2.5 for further information on OS specific package installations.

\(^3\)EMBOSS will also look in the `emboss` directory under the EMBoss source distribution for `emboss.default.template` and install this as `emboss.default` if no existing file is found under the installation directory.

\(^3\)A sample `emboss.default` is located in `emboss/acd` under the source distribution.
3.1.1 Configuring EMBOSS differently for different groups of users

It may be the case that you have users who need to share a specific setup. Maybe to have access to different sets of databases or need to use a different data directory.

It can be time consuming and error prone to maintain a series of individual `embosrc` files or to cause users to have to work in the same directory or to copy an `embosrc` to each directory they wish to work in. The environment variable EMBOSSRC can be set to point to an arbitrary directory containing an `embosrc` which can then be used to give workgroup specific configuration. Each user then only needs to set EMBOSSRC in their `.cshrc` (CShell) or `.profile` (BASH) to get the workgroup specific setup.

In our case we have several groups of researchers for whom we maintain biological sequence databases. These databases have been made available under restrictive licenses so that we cannot allow researchers outside the groups to access the databases. Using `EMBOSSRC` we can set up a common configuration for the members of each group by defining the databases in the `EMBOSSRC/embosrc` file.

3.2 Databases

3.2.1 Database access modes

EMBOSS offers three modes for accessing databases:

**Single**: EMBOSS retrieves a single sequence indexed by ID.

**Query**: EMBOSS retrieves a set of sequences corresponding to a query that can return more than one entry, including accession numbers or wildcard IDs.

**All**: EMBOSS returns all the sequences in the database in no particular order.

Each database definition can configure one or many of these modes for database access.

Typically EMBOSS uses variations on the EMBLCD system of database indexing to provide rapid access in single and query modes to flat file databases. The EMBLCD method is implemented in a variety of ways depending on the original format of your database. The EMBLCD method assumes that you have one or both of ID and accession number in each record and that they are unique for the whole database index. EMBOSS also provides methods for retrieving sequences via the WWW and three specific methods for interaction with SRS\(^4\) installed locally or through a remote public server. For other non flat file databases or flat file databases in formats not currently supported by EMBOSS you will have to configure an external application to retrieve sequences.

3.2.2 General database configuration.

Each database is configured using a DB declaration.

The generalised form is

```
DB basename [ 
```

Configuration options
```
] 
```

The configuration options are tag/value pairs and must contain at least a description of the access method (using `method:`; or one or more of `methods:`, `methodquery:`, and `methodall:`) and a description of the original format of the sequences (using `format:`). In addition to these tags there will be other tags that are needed for particular methods and other tags that are optional.

\(^4\)http://www.liembioscience.com/solutions/srs
**Database access methods**

The scope of each method is:

**Single mode - s** Supports retrieval of a single sequence.

**Query mode - q** Supports retrieval of a subset of the sequences in the database specified using a wild card query in the USA.\(^5\)

**All mode - a** Supports retrieval of all sequences in the database as a stream of data.

An example entry for each access method is shown.

**APP** Modes: a q s

APP is the same as EXTERNAL.

**BLAST** Modes: a q s

BLAST uses EMBLCD indices created with dbiblast to access databases in BLAST format, created with NCBI’s formatdb program.

Note that the latest 'format version 4' is not yet documented by NCBI. **EMBOSS** will only work with 'format version 3' databases, indexed with:

```
formatdb -A F
```

We hope to support 'format version 4' databases in future. If you pick up a blast database from NCBI (or elsewhere) check the format. If it is in the new format, you will need to pick up the original FASTA format file, and either index it yourself with formatdb, or run dbifasta and use the FASTA file in **EMBOSS** (see EMBLCD access method)

The definition should use format: ncbi because this is what the blast formatdb databases store internally.

```
DB mydb [
#required parameters
  method: "blast"
  format: "ncbi"
  type: "N"
  dir: "\$emboss_db_dir/blas"t
#optional parameters
  fields: "sv des"
  release: "63.0"
  comment: "my comment"
  indexdir: "\$emboss_db_dir/blastindices"
]
```

The index files can be kept in the same directory as the database, but as each EMBLCD index needs its own directory (the filenames are fixed) the indexdir is usually defined.

The EMBLCD index files include the filenames indexed by dbiblast. You can use the file: and exclude: attributes to create file-specific subsets from a single dbiblast generated index, but as blast index files are split only by the number of entries this is not generally useful.

If the database was indexed with additional fields, they can be included in the definition as fields: to allow their use in USAs.

\(^5\)Please see the **EMBOSS** documentation for description of Uniform Sequence Address format
**DIRECT** Modes: a
Direct accesses the flatfile directly. It returns all the database entries, one after the other. It assumes no indexing. Queries are still possible as **EMBOSS** will read each entry and match it against the query, but are slow as the entire database must be read.

```
DB mydb [
  #required parameters
  method: "direct"
  format: "embl"
  type: "N"
  dir: "\$emboss_db_dir/mydb"
  file: "*.dat"
  #optional parameters
  fields: "sv des key org"
  release: "63.0"
  comment: "My own database with no indices"
  exclude: "est*.dat"
]
```

For most cases, it is simpler to use dbiflat for EMBL, Genbank or SwissProt format, or dbifasta to index FASTA or NCBI format files, and to use the EMBLCD access method.

If the file format supports additional fields, they can be included in the definition as fields: to allow their use in USAs.

**EMBLCD** Modes: a q s
EMBLCD uses EMBLCD indices created with dbiflat or dbifasta to access flatfile databases in the original format.

```
DB mydb [
  #required parameters
  method: "emblcd"
  format: "embl"
  type: "N"
  dir: "\$emboss_db_dir/emb"l
  #optional parameters
  fields: "sv des key org"
  file: "*.dat"
  release: "63.0"
  comment: "my comment"
  exclude: "est*.dat"
  indexdir: "\$emboss_db_dir/indice"s
]
```

The EMBLCD index files include the filenames indexed by dbiflat or dbifasta. You can use the file: and exclude: attributes to create file-specific subsets from a single index.

This method can require careful setup. Please read the more specific descriptions below. If the database was indexed with additional fields, they can be included in the definition as fields: to allow their use in USAs.

**EXTERNAL** Modes: a q s
EXTERNAL uses an external application to retrieve sequences. The ID is passed as an argument to the application, either replacing %s in the command string (if present) or as an additional argument (if there is no %s).

EXTERNAL requires the application to return the sequence on STDOUT. If the application writes to somewhere else, simply wrap it in a script that copies the output to STDOUT.

19
DB mydb [  
#required parameters  
method: "app"  
format: "fasta"  
type: "P"  
app: "getfromdb"  
#optional parameters  
comment: "my own protein database with a custom retrieval program"  
app: "getfromdb mydatabase %s"  
]

The first app: definition will use the default call 'getfromdb mydb:id'  
The alternative app: definition will use the %s format and call 'getfromdb mydatabase id'  
Both will pass either the ID or accession from the query, so that USAs mydb-id:x3776 and mydb-acc:x3776 are equivalent.

GCG Modes: a q s  
GCG uses EMBLCD indices created with dbigcg to access databases in GCG format. This method uses the .ref and .seq files created by the GCG suite of programs.

DB mygcgdb [  
#required parameters  
method: "gcg"  
format: "embl"  
type: "N"  
dir: "\$emboss_db_dir/gcge"  
#optional parameters  
fields: "sv des key org"  
file: "*.seq"  
release: "63.0"  
comment: "my comment"  
exclude: "est*"  
indexdir: "\$emboss_db_dir/indices"  
]

The EMBLCD index files include the filenames indexed by dbigcg. You can use the file: and exclude: attributes to create file-specific subsets from a single dbigcg generated index.

SRS Modes: a q s  
SRS returns entries from a local installation of SRS using the -e switch to getz to return entries in the original format.

DB mydb [  
#required parameters  
method: "srs"  
format: "embl"  
type: "N"  
#optional parameters  
dbalias: "embl"  
fields: "sv des key org"  
app: "getz"  
comment: "My srs indexed database"  
release: "63.0"  
]
This access method builds an SRS commandline query to getz. If you have getz installed under another name, define this as app:

The SRS query by default uses the EMBOSS database name. If the database has a different name in SRS, define dbalias: as the database name to pass to SRS.

SRS will return the results using 'getz -e' so the format should match the format of the original data. For some formats this can be tricky (PIR for example), so consider using SRSFASTA although this will lose information that is not included in the FASTA format SRS output.

To query using the additional fields SRS supports, add them as fields:

**SRSFASTA** Modes: a q s
As SRS but returns the sequences in FASTA format. The definition must include format: fasta so that EMBOSS will read the results in FASTA format.

```bash
DB mydb [  
# required parameters  
  method: "srsfasta"  
  format: "fasta"  
  type: "N"  
#optional parameters  
  dbalias: "embl"  
  fields: "sv des key org"  
  app: "getz"  
  comment: "My srs indexed database"  
  release: "63.0" ]
```

This access method builds an SRS commandline query to getz. If you have getz installed under another name, define this as app:

The SRS query by default uses the EMBOSS database name. If the database has a different name in SRS, define dbalias: as the database name to pass to SRS.

SRS will return the results using 'getz -e' so the format must be 'fasta'.

To query using the additional fields SRS supports, add them as fields:

**SRSWWW** Modes: a q s
As URL, but specific to an SRS web server. This method takes a base URL (up to wgetz) for an SRS server, and builds the rest of the URL as a valid SRS query.

By building the URL, SRSWWW access can query both ID and accession number, and can query additional fields 'sv', 'des', 'key' and 'org' if they are allowed with a fields definition.

```bash
DB mydb [  
# required parameters  
  method: "srswww"  
  format: "genbank"  
  type: "N"  
  url: "http://www.infobiogen.fr/srs5bin/cgi-bin/wgetz?"  
#optional parameters  
  dbalias: "genbank"  
  fields: "sv des key org"  
  comment: "Genbank by SRS from InfoBiogen"  
  proxy: ""  
  httpversion: "1.0" ]
```

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Because queries for such fields to a remote server can find a very large number of hits, and EMBOSS will load the entire output into memory to process the HTML, many EMBOSS administrators choose not to define these fields for an SRSWWW server.

If there is sufficient demand, it should be possible to rewrite the HTML preprocessing to avoid buffering in memory.

SRSWWW support the proxy and httpversion settings described under access method URL.

**URL**

Modes: s

URL uses a defined web server to retrieve a specific entry. EMBOSS may fail if the HTML causes complications with parsing of the entry.

```plaintext
DB mydb [
  # required parameters
  method: "url"
  format: "genbank"
  type: "N"
  url: "http://www.infobiogen.fr/srs5bin/cgi-bin/wgetz?-e+[genbank-id:%s]"
  #optional parameters
  comment: "Genbank by ID from InfoBiogen"
]
```

The %s in the URL string indicates where EMBOSS will insert the identifier portion of the USA.

At many sites, remote HTTP access is controlled by a proxy server. EMBOSS uses a proxy server defined as EMBOSS_PROXY with a value in the format domain.address:port, for example:

```
set emboss_httpversion 'proxy.mydomain.org:8080'
```

This is a global definition. For selected databases (local web-based services, for example) you can turn off the proxy inside the database definition with:

```plaintext
DB [...] proxy: ":";
]
```

HTTP access by default used HTTP protocol version 1.0. EMBOSS can also support version 1.1, which provides chunked HTML results to improve improve network performance. The HTTP version is controlled by a variable EMBOSS_HTTPVERSION and by a DB attribute, for example:

```
set emboss_httpversion "1.1"
```

or

```
DB [...] httpversion: '1.1'
]
```

### 3.2.3 Mixed access methods

For any given method: declaration, EMBOSS will use that method for those access modes supported by the method.

If you wish to specify which access mode (all, query or single) should be handled by which database retrieval method then the method single:, method query: and method all: declarations should be used instead of method:
DB mydb [
  methodsingle: app
  format: fasta
  app: "customapp myproteindb"
  methodall: direct
dir: \$emboss_db_dir/myproteindb
file: myproteindb.dat
type: P
comment: "single and all access for myproteindb"
]

You can mix these, for example, to use a script to query a file, and direct access to read all entries,

  methodall: 'direct'
  methodquery: 'external'

3.2.4 Indexing and configuring flatfile databases

Flatfile databases are plain text files in a defined format such as those released by EMBL, Swissprot and so on. The EMBOSS program DBIFLAT is used to generate EMBLCD indices that can be used for all types of database access. DBIFLAT can process databases in EMBL, SWISSPROT and GENBANK format. Pseudo EMBL format databases which do not have unique ID and AC entries may cause DBIFLAT to do mysterious things and should be avoided.

DBIFLAT (and the EMBLCD access method) requires the databases to be uncompressed. The examples given here will not probe the deeper secrets of DBIFLAT (for which the reader is referred to the documentation, or failing that the source code) but will show a typical installation for a common database.

We assume that EMBOSS has been installed and works. This can be tested with the command vossname -auto which should list all the programs available.

In this example we will index and configure the EMBL database for use with EMBOSS.

First download and unpack the EMBL database. This will require a considerable amount of disk space. If you do not have sufficient space available then just download a subset of the database.

Use cd to move the directory in which you have unpacked EMBL. This should look something like this when you run ls:

  % ls
  est_fun.dat
  est_hum1.dat
  est_hum10.dat

  Output truncated

  syn.dat
  unc.dat
  vrl.dat
  vrt.dat

  Run DBIFLAT to create the EMBLCD indices.

  % dbiflat

Index a flat file database

  EMBL : EMBL
  SWISS : Swiss-Prot, SpTrEMBL, TrEMBLnew
  GB : Genbank, DDBJ
Entry format [SWISS]: EMBL
Database name: embl
Database directory [-]:
Wildcard database filename [*.dat]:
Release number [0.0]: 63.0
Index date [00/00/00]: 31/07/00

DBIFLAT should happily chug away for some considerable time (up to a few hours depending on
the speed of your machine) and will generate (eventually) the following index files:

% is
acnum.hit
acnum.trg
division.lkp
entrynam.idx

Now we create an entry in the EMBOSS configuration files to access the database. It is probably
a good idea to try new database definitions in your local configuration file first.

Put the following entry in your .embossc

DB embl [
  type: N
  method: emblcd
  format: embl
  dir: \$emboss_db_dir/embl
  file: "*.dat"
  release: "63.0"
  comment: "EMBL release 63.0"
]

you will have needed to predefine $emboss_db_dir using a directive such as

set emboss_db_dir /path_to_databases

somewhere in your emboss.default or .embossc.

Save .embossc and try showdb. You should see a line that looks like:

% showdb
.. output deleted
embl    N  OK  OK  EMBL release 63.0
.. output deleted

3.2.5 Fine tuning the installation:

It is probably a good idea to set up subsections of the database so that end users can search just
the regions they wish to search. This section applies to all access methods that use EMBLCD style
indexes and probably to others as well.

Files can be included with the declaration file: or excluded with the declaration exclude:. It
is a good idea to put the wildcard directory specifier (*/*) in front of the filename to ensure that
any path that may be included in division.lkp will be matched. Please note especially the notes for
GCG formatted databases indexed with DBIGCG.

In order to just take the EST files in our EMBL database try the following:

DB emblest [
  type: N
  method: emblcd
format: embl
dir: \$emboass_db_dir/embl
file: "est*.dat"
release: "63.0"
comment: "EMBL release 63.0"
]

Files can also be given as a space separated list enclosed in quotes. For example to set up a
database of all mammalian sequences (except genomes) try the following:

DB emblallmam [
  type: N
  method: emblcd
  format: embl
  dir: \$emboass_db_dir/embl
  file: "rod*.dat hum*.dat mam*.dat"
  release: "63.0"
  comment: "EMBL release 63.0"
]

As you can see from these two examples, the file: tag takes a space delimited list of filenames
enclosed in quotes that can contain normal wildcard (??) characters.

It can be quite tedious to set up a long list of sequences to search. In many cases you can use
the exclude: tag to make things easier.

DB emblnoest [
  type: N
  method: emblcd
  format: embl
  dir: \$emboass_db_dir/embl
  file: "*.dat"
  exclude: "est*.dat"
  release: "63.0"
  comment: "EMBL release 63.0"
]

This configures the emblnoest database to contain all of EMBL except the EST’s.

### 3.2.6 Indexing and configuring GCG format databases

**EMBOSS** can access GCG formatted databases, thus avoiding having multiple copies of the same
databases in different formats for those who still use GCG alongside the flatfiles. **EMBOSS** creates
EMBLCD like indices for the GCG format databases using the program DBIGCG. This runs in much
the same way as DBIFLAT. You will need the GCG format .seq and .header files in order to create
an EMBLCD indexed database.

Move to the GCG database directory containing your data and run DBIGCG

Index a GCG formatted database

    EMBL : EMBL
    SWISS : Swiss-Prot, SpTrEMBL, TrEMBLnew
    GB : Genbank, DDBJ
    PIR : NBRF

Entry format [EMBL]:
Database name: embl
Database directory [.]:
Wildcard database filename [*.seq]:
Release number [0.0]: 63.0
Index date [00/00/00]: 31/07/00

The program will chug along for a while and will then generate the EMBLCLD index files for the GCG format database.

When DBIGCG prompts for the entry format (Entry format [EMBL]:) you should enter the original database format before you ran EMBLTOGCG or similar to generate the GCG databases.

The following entry should be put in your .embossrc

DB gcgembl [  
type: N  
method: gcg  
format: embl  
dir: \$emboss_db_dir/embl  
file: "*.dat"  
release: "63.0"  
comment: "EMBL release 63.0"
]

SHOWDB should show your newly configured database.

You can configure subsets of the databases in the same way as for the original format databases, described in section 3.2.4 above. One difference to DBIFLAT indexing is that both the .seq and .header files are listed in the division.lkp file. file: and exclude: directives should therefore be of the form exclude: */em_est*. instead of just */em_est*.seq.

3.2.7 Indexing and configuring BLAST databases

BLAST format databases are generated for efficient homology searching using the BLAST programs. It can be convenient to avoid redundant copies of databases so EMBASS provides a mechanism for accessing these databases.

BLAST format databases are those generated using the tools distributed with NCBI-BLAST or with WU-BLAST.

For indexing of one BLAST database, move to the directory containing your BLAST format databases and run DBIBLAST

Index a BLAST database
Database name: blastsw
Database directory [.]:
database base filename [blastsw]:
Release number [0.0]:
Index date [00/00/00]:
N : nucleic
P : protein
? : unknown
Sequence type [unknown]: p  
1 : wublast and setdb/pressdb  
2 : formatdb  
0 : unknown
Blast index version [unknown]: 2

The program will chug along for a while and will then generate the EMBLCLD index files for the BLAST format database.

The following entry (or one like it that is more appropriate to your particular installation) should be put in your .embossrc

26
DB blastsw [
    type: P
    method: blast
    format: ncbi
    dir: %emboss_db_dir/blastw
    file: "blastsw"
    release: "38.9"
    comment: "BLAST format Swissprot"
]

SHOWDB should show your newly configured database.

Because of the way BLAST works, many sites may group their BLAST databases in the same
directory. You can index these in situ with DBIBLAST but this may require some extra steps if your
databases are not of the same type as generation of subsequent index files will overwrite those that
already exist. To avoid overwriting of index files you can index many databases with one set of index
files, or you can use the indexdir options to place the indices in a different directory.

There are two requirements for indexing several databases together in one index. The first is that
the databases are the same type (protein/nucleic acid) and generated with the same tool (pressdb
or formatdb); the second is that all the ID and accession numbers in the combined databases are
unique.

Run DBIBLAST as before but specify all the databases you wish to be included when prompted
for the database filename.

Index a BLAST database
Database name: alldBs
Database directory [.]:
database base filename [alldBs]: dbone dbtwo dbthree dbfour
Release number [0.0]:
Index date [00/00/00]:
    N : nucleic
    P : protein
    ? : unknown
Sequence type [unknown]: p
    1 : wblast and setdb/pressdb
    2 : formatdb
    0 : unknown
Blast index version [unknown]: 2

These can then be configured as described in section 3.2.4 above by using the 'file:' and
exclude:' tags as appropriate.\(^6\)

When you have databases of different types, generated with different programs or where the
ID/accession numbers are duplicated between databases the preferred strategy is probably to keep
the source data for the individual databases in separate directories and index them there.\(^7\)

Alternatively you can place the index files in a separate directory. This requires that you run
DBIBLAST with the -indexdirectory option and set the indexdir: tag in the database configuration
to point to the correct database. The example below illustrates database configuration using the
indexdir options.

\(^6\)There is one difference to the standard EMBOSS access method in that the database indexes will not allow
the generation of exclusive subsections of the combined database. If an ID or accession number is specified that is present
in the index then the sequence will be returned irrespective of which database it is in.

\(^7\)Keeping one directory with symbolic links for your BLAST installation will ensure that BLAST continues to
function correctly if you set BLASTDB to point to the directory containing the symbolic links. The EMBOSS indices
can be placed wherever you wish as long as you remember to run DBIBLAST with the appropriate options and put an
appropriate indexdir tag in the DB configuration in your /embossrc.
% dbiblast -indexdir=/databases/indices/mydb
Index a BLAST database
Database name: mydb
Database directory [.]:
database base filename [mydb]:
Release number [0.0]:
Index date [00/00/00]:
N : nucleic
P : protein
? : unknown
Sequence type [unknown]: p
1 : wblast and setdb/pressdb
2 : formatdb
0 : unknown
Blast index version [unknown]: 2

The corresponding entry in /embossp (or emboss.default) would look like:

DB mydb [
type: P
method: blast
format: ncbi
dir: \$emboss_db_dir/blastsw
indexdir: /databases/indices/mydb
file: mydb
release: "1.0"
comment: "My BLAST DB with an index in a different directory"
]

Again, multiple indices cannot coexist in the same directory so care should be taken when using
the indexdir options that an existing database index is not overwritten.

3.2.8 Indexing and configuring FASTA databases

The FASTA specifications just define the sequence file as a header line that begins with > and
subsequent lines containing the sequence. The header line can be present in an almost infinite number
of formats, several of which can be processed by EMBASS. EMBASS attempts to determine the
accession number and/or ID for each sequence. For indexing purposes there is no semantic difference
between an accession number and an ID. In the real world, accession numbers are immutable, i.e. they
do not change with subsequent releases of the database, but ID’s may change. In any case IDs and
accession numbers are unique, and that is all that matters for database indexing EMBASS.

The program used to process FASTA format databases is DBIFASTA. It can recognise the following
header line formats, specified on the command line:

<table>
<thead>
<tr>
<th>simple</th>
<th>&gt;id ...</th>
</tr>
</thead>
</table>
| idacc    | >id accno ...
| gcgid    | >db:id ... |
| gcgiddacc| >db:id acc ...
| dbd      | >db id ... |
| ncbi     | ...[accno]id ...

*db is one word
*The ID is always taken to be the characters after the last bar (|). The previous field is also indexed but ONLY
if it looks like an accession number (e.g. AC00001).
Other header formats will not be recognised by DBIFASTA and will cause indexing and/or database lookup to fail. If you have a different header format that DBIFASTA cannot yet handle you have two options:

1. (The preferred option) Get a C programmer to modify the source code for DBIFASTA and recompile. If you are a community spirited person you will also contribute these changes to the main EMBOSS source tree. (email emboss-dev@embnet.org for more information on contributing changes to the EMBOSS source code and/or read the EMBOSS developers documentation)

2. (The quick hack) Write a custom script (using e.g. BioPerl\(^{10}\)) to access your database and use method: **external** to configure it. This is less desirable as you may be limited in the access modes you can use.

To index a FASTA format database, run **DBIFASTA**.

\%
\*dbifasta
\*Index a fasta database
\* simple : >ID
\* idacc : >ID ACC
\* gcgid : >db:ID
\* gcgidacc : >db:ID ACC
\* ncbi : >blah...[ACC]|ID
\* ID line format [idacc]:
\* Database name: mydb
\* Database directory [.]:
\* Wildcard database filename [* .dat]: mydb.fasta
\* Release number [0.0.]:
\* Index date [00/00/00]:

**DBIFASTA** will chug along for a little while and will produce the index files. You can use the same indexdir options as for **DBIFLAT,DBIGCC** and **DBIBLAST** to place the indices in a different directory.

Place the following entry in your **embossrc**

```
DB mydb [
    type: P
    method: emblcd
    format: fasta
    dir: \$emboss_db_dir/mydb
file: mydb.fasta
    comment: "My database"
]
```

format: should be dbid,ncbi or fasta (for every format except dbid or ncbi. The same file: and include: tags can be used as for the other database indexing programs.

### 3.2.9 Configuring EMBOSS to use SRS for database lookup.

**method**: srs is really a special case of **method**: **external** with some additional features.

SRS is a powerful database querying system that can cross reference between different databases, launch applications and so on. SRS can be run either through a web interface (see the description of the URL method above for an example) or via the command line program **GETZ**. Indexing and configuring databases for SRS is outside the scope of this document which will describe how to connect to preconfigured and indexed SRS databases. If **GETZ** is already in your PATH environment variable then insert the following (or similar) in your **embossrc**:

\(^{10}\)http://www.bioperl.org

\(^{11}\)For information on configuring and indexing SRS databases please look at the SRS administrators guide www/doc/srsadmin.pdf in your SRS 6 installation.
DB emblgetz [
  type: N
  method: srs
  release: "63"
  format: embl
  comment: 'EMBL using getz'
  dbalias: embl
  app: getz
]

This will provide access to the SRS database 'embl' as emblgetz:acc. If the SRS database has a different name to the EMBOSs database (as is the case here) then the dbalias: tag should be used to access the correct SRS database.

This configuration can be extremely slow for the all access mode. It is probably a better idea to set up the database as follows:

DB emblgetz [
  type: N
  methodquery: srs
  release: "63"
  format: embl
  comment: 'EMBL using getz'
  dbalias: embl
  app: getz
  methodall: direct
  file: "*.dat"
  dir: \\$emboss_db_dir/embl
]

which will use method: srs for the query access mode but will use method: direct for the all access mode, thus speeding up reading of the whole database.

The SRSFASTA access method is identical to the normal SRS method except that it returns the sequence in FASTA format and so does not need a format: tag.

3.2.10 Indexing and configuring other databases

Many institutions may have local databases set up in their own Laboratory Information Management System. EMBOSs provides a simple mechanism for interfacing with such systems.

As long as a program is available that can be called noninteractively and returns the specified sequence on standard output, EMBOSs can interface with it. Use method: app or external (the two are equivalent) and app: "program command". The ID given in the USA will be appended to the command used to run the program. It is probably best to specify the methods available using the method subsets, methodall:, methodquery: and methodsingle: rather than using the generic method: tag.

3.3 Other data

EMBOSs can be integrated with some common biological databases. These are described in this section.

3.3.1 REBASE

Rebase is the restriction enzyme database maintained by New England Biolabs. It is needed for programs such as remap and restrict.
The latest version of Rebase can be obtained by anonymous FTP.\textsuperscript{12} \textbf{EMBOSS} needs the \texttt{withrefm} file. The data is extracted for \textbf{EMBOSS} with the program \texttt{REBASEEXTACT}.

\begin{verbatim}
% mkdir /site/prog/emboss/data/REBASE
% rebaseextract
Extract data from REBASE
Full pathname of WITHREFM: /data/rebase/withrefm.208

Rebase is now installed and ready to use.
\end{verbatim}

3.3.2 TRANSFAC

Transfac is the transcription factor binding site database. It is available by anonymous FTP.\textsuperscript{13} Unpacking the distribution reveals a file called site.dat. This is the one \textbf{EMBOSS} needs.

Run \texttt{TFEXTRACT} to extract the data from TRANSFAC.

\begin{verbatim}
% tfextract
Extract data from TRANSFAC
Full pathname of transfac SITE.DAT: /databases/transfac/site.dat

TFSCAN can now access the TRANSFAC database.
\end{verbatim}

3.3.3 PROSITE

Prosite is a database of regular expressions that match potentially diagnostic regions for structural/functional classification of proteins. \textbf{EMBOSS} needs this database for the patmatmotifs program.

\textbf{PROSITE} can be obtained via anonymous FTP.\textsuperscript{14} You may need to create a PROSITE subdirectory under data in the \textbf{EMBOSS} installation directory.

Then run \texttt{PROSEXTACT} to build the \textbf{EMBOSS} Prosite database.

\begin{verbatim}
% prosextact
Builds the PROSITE motif database for patmatmotifs to search
Enter name of prosite directory: /data/prosite

PROSITE is now integrated into your EMBOSS installation.
\end{verbatim}

3.3.4 PRINTS

Prints is a database of diagnostic patterns of blocks of sequence homology in protein families. The PRINTS database can be searched using the \textbf{EMBOSS} program \texttt{PSCAN}.

PRINTS can be obtained via anonymous FTP.\textsuperscript{15} The database is made available as compressed files which should be uncompressed using \texttt{GZIP} before integrating them into \textbf{EMBOSS}

PRINTS is integrated with \textbf{EMBOSS} using the program \texttt{PRINTSEXTRACT}

\begin{verbatim}
% printsextract
Extract data from PRINTS
Input file: /data/prints/prints27_0.dat

The PRINTS database is now integrated with \textbf{EMBOSS}.
\end{verbatim}

\textsuperscript{12}\url{ftp://ftp.ebi.ac.uk/pub/databases/rebase}
\textsuperscript{13}\url{ftp://transfac.gbf.de/pub/transfac/ascii/}
\textsuperscript{14}\url{ftp://ftp.ebi.ac.uk/pub/databases/prosite}
\textsuperscript{15}\url{ftp://ftp.ebi.ac.uk/pub/databases/prints}
3.3.5 **AAINDEX**

An amino acid index is a set of 20 numerical values representing any of the different physicochemical and biological properties of amino acids. The AAIxex1 section of the Amino Acid Index Database is a collection of published indices together with the result of cluster analysis using the correlation coefficient as the distance between two indices. This section currently contains 437 indices in release 4.0 of the database.

The **EMBOSS** programs **PEPWINDOW** and pepwindowall plot hydrophobicity using the data from an Aaindex entry. If Aaindex is installed these programs can plot the other amino acid properties.

Aaindex can be obtained via anonymous FTP:  
Aaindex is integrated with **EMBOSS** using the program AAINDEXEXTRACT

% aaindexextract  
Extract data from AAINDEX  
Full pathname of file aaindex1: /data/aaindex/aaindex1

The AAINDEX database is now integrated with **EMBOSS**.

3.3.6 **CUTG**

The CUTG database contains a series of codon usage tables calculated from GenBank.

CUTG can be obtained via anonymous FTP.  
CUTG is integrated with **EMBOSS** using the program CUTGEXTRACT which writes files to the CODONS data directory.

% cutgextract  
Extract data from CUTG  
CUTG directory [.] : /data/cutg/

The CUTG database is now integrated with **EMBOSS**.

3.3.7 **Miscellaneous data files**

Other data files should be kept in the data directory under the main **EMBOSS** installation. Individual users personal data files can be kept in the current working directory, a subdirectory .embossdata of the current directory, their home directory or a subdirectory .embossdata of their home directory. **EMBOSS** will search these locations in this order and will stop as soon as it finds a matching file. If the personal directories do not contain the desired file, **EMBOSS** will search the system wide data directory, /site/prog/emboss/data in this example.

Apparently inexplicable errors when running **EMBOSS** programs may be caused by the system not using the data files one expects. The search path can be displayed in search order using the command **EMBOSSDATA**.

3.4 **Default program settings**

As with many other areas, the default behaviour of programs can be controlled by setting appropriate values in .embossrc.

All general qualifiers can be specified as

set embossQualifier 1

---

16 ftp://ftp.genome.ad.jp/pub/db/genomenet/aaindex/aaindex1  
18 See the **EMBOSS** Quick Guide or the web documentation (or use wssname -help -verbose) for an overview of general qualifiers.
where QUALIFIER is one of the general qualifiers and the value can be 1 or 1 for true, or 0 or N for false.

Setting the qualifier value to true has the effect of running every program with that qualifier set. Qualifiers can be set and will work in the same way as if you set them when running the program. For example you can set emboss_verbose Y and the program will run normally, but when the program is run with the -help qualifier, the output will be in verbose form.

There is no point in globally setting options that are there for producing help output.
Qualifiers that can be set:

**VERBOSE** Causes -help to print verbose text.

**STDOUT** Causes all output to go to STDOUT as default. Programs will usually build a default output file name form the input sequence and the program name.

**DEBUG** Writes debugging output to a file. Useful for finding bugs as a command line option.

**OPTIONS** Enable prompting for optional parameters.

**FILTER** Take input from STDIN and send it to STDOUT, and turn on -auto

**AUTO** Do not prompt for any options but accept the defaults if no values are given.

**WARNING** Print warning messages to STDERR (default is true)

**ERROR** Print error messages to STDERR (default is true)

**FATAL** Print fatal messages to STDERR (default is true)

**DIE** Print crash messages to STDERR

These general qualifiers are typically used by advanced users (-options, -verbose) or by developers (-debug, -acmdlog).

Other program options that can be set are emboss_format, emboss_acdroot, and emboss_data. The value of emboss_format determines which default sequence format to use for output. For example, if you are running EMBOSS alongside GCG you may wish to have the following entry in your .EMBOSSRC

set emboss_FORMAT gcg
set emboss_OUTFORMAT gcg

which has the effect of using GCG format by default. 20

emboss_acdroot /path/to/acd can be set if you wish to use a different directory for the ACD files, and emboss_data /path/to/data if you wish to use a separate data directory.

### 3.5 Logging

Many system administrators may wish to make use of the logging facilities of EMBOSS. Setting the variable emboss_logfile in emboss_default or .embossrc allows the system to keep a log of which programs are used when and by whom.

set emboss_logfile /site/log/emboss.log

The log file structure is very simple. Three tab separated fields are stored, program name, user name, and the date and time.

---

19 You can specifically unset it by using the -noQUALIFIER command line option

20 This can of course be overridden using the -sformat and -esformat associated qualifiers. See the EMBOSS ACD Syntax documentation or the EMBOSS Quick Guide for more information.
The file defined in emboss_logfile should be world writable. The following command ensures logging can occur.

```
chmod +w /site/log/emboss.log
```

All settings can be overridden in a users .embossrc files by redefining the relevant variables. So to prevent our system usage being logged we can redefine emboss_logfile by putting the following entry in our .embossrc file.

```
set emboss_logfile /dev/null
```

This behaviour may change in the future to prevent users redefining some system settings.
4 Graphical interfaces to EMBOSS

This chapter needs to be written. It will be written when the available GUIs are stable enough to document.
5 Resources

5.1 Web sites

5.1.1 Programs

EMBOSS source code ftp://ftp.uk.embnet.org/pub/EMBOSS

EMBOSS Documentation http://www.uk.embnet.org/Software/EMBOSS

BLAST tools Tools for generating BLAST format databases are contained in the NCBI toolkit which can be obtained from NCBI at:

SRS software The SRS software can be obtained from Lion Bioscience. This is a commercial package but at the time of writing is available free of charge to academic institutions.

wget Various useful utilities including the wget program are available from the Free Software Foundation.

5.1.2 Databases

Most of the databases mentioned in the text along with many others can be obtained via anonymous ftp from the European Bioinformatics Institute (EBI) at:
ftp://ftp.ebi.ac.uk/pub/databases

Please use a mirror site where possible to avoid overloading of the EBI’s resources.

Other databases can be obtained from NCBI (Genbank,UniGene etc.)

5.1.3 Other Documentation

Please review the EMBOSS documentation available on the WWW at the URL above.

The EMBOSS Quick guide A pocket reference guide to using EMBOSS.

The EMBOSS Tutorial A tutorial to give an introduction to using EMBOSS for bioinformatics users.

The updated ABC guide This is a series of bioinformatics practicals based predominantly on EMBOSS.

EMBOSS-FreeBSD-HOWTO Detailed documentation on installation of EMBOSS on FreeBSD.

1http://www.lionbioscience.com/solutions/srs
2http://www.gnu.org
3ftp://ftp.ebi.ac.uk/pub/EMBOSS-extra/emboss-qg.ps
4http://www.hgmp.mrc.ac.uk/Registered/Option/emboss.html
5ftp://ftp.no.embnet.org/pub/ABC
5.2 Maintainance of your EMBOSS installation

EMBOSS is a rapidly evolving software packages. It is constantly being improved, new features added and 'issues' resolved. In addition there are new applications added and you probably want to make use of these.

5.2.1 Automated installation of EMBOSS and EMBASSY

Once you have installed EMBOSS and got it to work you have solved the hardest part of the struggle. Updating EMBOSS as new releases appear\(^7\) can be quite tedious. UNIX is designed for the lazy, so here is our lazy man’s guide to always having an up to the minute EMBOSS installation.

The following script can be run manually (it should probably be ‘sourced’ rather than executed directly) or can be fired off with cron (in the early hours of the morning is a good time). It assumes you are installing EMBOSS outside the source directory and have write permissions to do so.

EMBOSS will update EMBOSS distributed files but will not alter or overwrite your own datafiles\(^8\) or your emboss default.

# This script should be sourced, not run.
# EMBOSS UPDATE.
# it assumes \$packages_dir/EMBOSS is a symbolic link to
# \$mirror_dir/ftp.uk.embnet.org/pub/EMBOSS
#

#site specific variables: season according to taste..

set mirror_dir=’/ftp/mirrors’
set packages_dir=’/site/newprog’
set emboss_config_options=\n(’--prefix=/site/prog/emboss --with-pngdriver=/site/lib’)

# Now the script proper

set oldpwd=’pwd’

cd \$mirror_dir
echo ’ updating EMBOSS’
if ( ’wget -m ’ftp://ftp.uk.embnet.org/pub/EMBOSS’ | & \
tail -1 | awk ’/\"Downloaded:/\{print \$5\}’ != "0" ) then

   cd \${packages_dir}/EMBOSS
   echo ’ new EMBOSS programs found .. installing’
   set latest_emboss=’ls -t EMBOSS*|head -1’

   cd \$packages_dir
   rm -Rf EMBOSS-*
   tar zxf EMBOSS/\$latest_emboss
   set emboss_dir=’ls -dt EMBOSS-*[^z]|head -1’

# the next line is necessary on our system but may not be for yours.
   setenv LD_LIBRARYPATH /site/lib

---

\(^7\)EMBOSS is rebuilt nightly from CVS, tested, and, assuming it passes the compilation tests, the latest version is posted to the EMBOSS FTP server.

\(^8\)Assuming of course that you haven’t overwritten EMBOSS datafiles with your own to begin with.
cd \$emboss_dir

# If you have any site specific changes to the source code
# that you want to include, copy them in here

./configure \$emboss_config_options &\$
make &\$
make install

# Now unpack and build EMBASSY

mkdir embassy
cd embassy

# Unpack and build each package one at a time

foreach embassadir ( 'ls ../EMBOSS/*gz |grep -v EMBASSY' )
tar zxf \$embassadir
set embassadir_arch=\$embassadir:t
set embassadir_root=\$embassadir_arch:r
cd \$embassadir_root:r
./configure \$emboss_config_options &\$
make &\$
make install
cd ..
  end
else
  echo 'No new version of EMBOSS available'
endif
cd \$oldpwd

5.2.2 Automated database updating

In the same way, scripts can be written to automatically update the biological databases. An example is given here for REBASE. As all the parameters for EMBOSS programs can be specified on the command line it is a trivial matter to include index generation in your nightly update scripts. The management of a bioinformatic resource is beyond the scope of this document, though EMBOSS goes a long way towards easing the burden of management.

Automated update of REBASE

This script will look for a new version of REBASE and install it in EMBOSS using REBASEEXTRACT.

# This script should be sourced, not run.
# REBASE UPDATE. Should be run just after the beginning of the month.
set mirrors_dir=('/ftp/mirrors')
set oldpwd='pwd'
cd \$mirrors_dir
if (`wget -m 'ftp://ftp.ebi.ac.uk/pub/databases/rebase/*' |& \
  tail -1 | awk '/Downloaded:/{print "$5"}'' != "0"`) then
  cd ftp.ebi.ac.uk/pub/databases/rebase
  cp 'ls -t withrefm.*Z|head -1' withrefm.Z
  uncompress withrefm.Z
  rebaseextract \n  \
  \${mirrors_dir}/ftp.ebi.ac.uk/pub/databases/rebase/withrefm
  rm withrefm
endif

  cd \$oldpwd
  
  We make no guarantees that these scripts will work correctly on your system. If it deletes all your files, spams your associates, scratches your CD's and initiates a nuclear strike on a small unpopulated pacific island it is NOT OUR FAULT. It just happens to work for us.
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