

wEMBOSS and wrappers4EMBOSS

Volunteers asked to join the maintenance and development team

wEMBOSS is a Web interface for EMBOSS that provides the user with a personal data space server-side, where he can manage his data and analysis results in projects [1]. The companion package wrappers4EMBOSS allows to integrate under EMBOSS 3th party software like BLAST, fastA and CLUSTAL and to use MRS as sequence databank access method.

The wEMBOSS+wrappers4EMBOSS development team consisted of Martin Sarachu from the Argentinian EMBnet Node, and Marc Colet and Guy Bottu from the Belgian EMBnet Node. Unfortunately, Martin Sarachu tragically died from cancer on 9 September 2007. At the Belgian side Marc Colet retired as professor at the University of Brussels on 1 October 2008 and Guy Bottu is not working for BEN anymore since 1 May 2009, because the Belgian Federal Science Policy Office decided to cut the financing of BEN. Marc is not willing to continue working on the project and Guy is unsure whether he will continue to have

time to spend. Marc and Guy however do not want to see this useful software lost for the bioinformatics community.

Therefore they are searching volunteers to take over the development. The idea is that the new member(s) should join the project at SourceForge and start working on wEMBOSS. To make the take-over easy Marc has recently released a version of wEMBOSS maintained as project under Eclipse and with an as much as possible cleaned up and debugged code. During the first six months Marc Colet will remain available for advice, but will ultimately leave the team. Guy will keep working on wrappers4EMBOSS as long as possible, but in the medium term the new member(s) should also collaborate on/take over the development of wrappers4EMBOSS.

For any further details please contact Marc Colet (marccolet@gmail.com).

References

Martin Sarachu and Marc Colet. wEMBOSS: a web interface for EMBOSS. *Bioinformatics* 2005, 21(4):540-541.

The screenshot shows the wEMBOSS website with a red header containing the logo and navigation links: "Download - Screenshots - Mailing lists - News". On the right side of the header is the EMBnet logo. The main content area has a light yellow background and includes the following sections:

- wEMBOSS** is a web interface to the popular **EMBOSS** software package for biological sequence analysis. wEMBOSS started as a coordinated effort from Martin Sarachu¹ of the Argentinian EMBnet Node and Marc Colet from the Belgian EMBnet node.
- Features**
 - Results from program runs remain stored permanently on the server.
 - Each user has a personal workspace and can create project folders, nested at any depth, to manage rationally his data and results.
 - Each program has a panel with dynamic hiding/unhiding of available options.
 - On-line access to program manuals and a program search facility
 - The site administrator can exclude EMBOSS programs from wEMBOSS.
 - Some program outputs can be automatically opened with applets or plug-ins.
- Requirements** (most come included in any Linux distribution)
 - Linux or another UNIX variant
 - Perl and some modules (see INSTALL file)
 - A C compiler
 - A Web server
 - EMBOSS
- The wEMBOSS developers team presently consists of :
 - [Marc Colet](#)
 - [Guy Bottu](#)
- wrappers4EMBOSS** allows to integrate under EMBOSS a number of popular bioinformatics software suites and databanks like [BLAST](#), [fastA](#), [CLUSTAL](#), [MUSCLE](#), [PROSITE](#), [InterPro](#), [PhyML](#), [ModelGenerator](#), [CODEHOP](#) and some selected [EBI Web Services](#), as well as to use [MRS](#) as EMBOSS sequence access tool. wrappers4EMBOSS is included in the wEMBOSS release and is also distributed as a stand-alone package for people who prefer to run EMBOSS at the command line or under some other GUI.

At the bottom, it says: "You can use the mailing list [wemboss-users](#) to post your questions and suggestions. Thank you for your interest and feedback."

Latest news

- wrappers4EMBOSS-2.3.0 released**
2009-08-24 16:08 - [wEMBOSS](#)
It contains support for EMBOSS 6.1.0, MRS 4, PhyML 2, CLUSTAL 2 and InterProScan 4.5.
[Read More »](#)
- wEMBOSS version 2**
2009-06-29 09:01 - [wEMBOSS](#)
In order to make further development easier, wEMBOSS has been reorganized from the developer and manager point-of-view. It is now developed using Eclipse and the Epic plug-in. The development version is called wEMBOSSDEV. From this distribution versions can be regularly generated ; they are called wEMBOSSDIST, followed by some version number.
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Figure 1. <http://wemboss.sourceforge.net/>.