EMBOSS: European Molecular Biology Open Software Suite

EMBOSS is a joint development by the institutes on the Hinxton Genome Campus. EMBOSS is licensed under GPL, includes over 300 applications and has comprehensive libraries for rapid code development. EMBOSS has been installed at more than 10,000 sites, and has been used by thousands of registered users at the Rosalind Franklin Centre for Genomics Research.

EMBOSS is aimed at providing all the common sequence analysis functions, and related applications, using local and remote sequence data sources. Sequence databases can be shared with other software, as EMBOSS includes access methods for most common sequence database formats. Databases and other resources are defined in site-wide and personalised user resource files.

A key feature of EMBOSS is the use of "ACD files" to completely define the interface between the code and the user. By building an ontology around these ACD files, and by converting them into various alternative representations, EMBOSS has been automatically transformed into web interfaces, GUIs, and web services (a total of more than 50 known interfaces). The ACD "standard" has also been extended to define various third party applications and packages.

The new release of EMBOSS (3.0.0) provides advanced features for application integration into GUI and web interfaces, and for web service and grid service providers.

The focus of EMBOSS now extends beyond sequence analysis to include phylogenetics, structural biology and other non-sequence data types. These will continue to expand in future releases.

The demonstration will cover:

- A brief introduction to EMBOSS
- An overview of EMBOSS interfaces
- Using EMBOSS through the JEMBOSS GUI
- Linking EMBOSS applications in Taverna a workflow
- Rapid application development

EMBOSS is available from http://emboss.sourceforge.net/