# Mebitoo - A Bioinformatics Sequence Analysis Toolbox

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We present Mebitoo, a bioinformatics software tool to embrace sequence analysis methods within a uniform graphical user interface. Since a number of departments provide methods such as the prediction of structure, function, and interactions, we developed a framework that is intended to simplify both the development of new methods and the workflow when assessing large sequence sets. The software is able to incorporate various different methods that may or may not depend on each other.
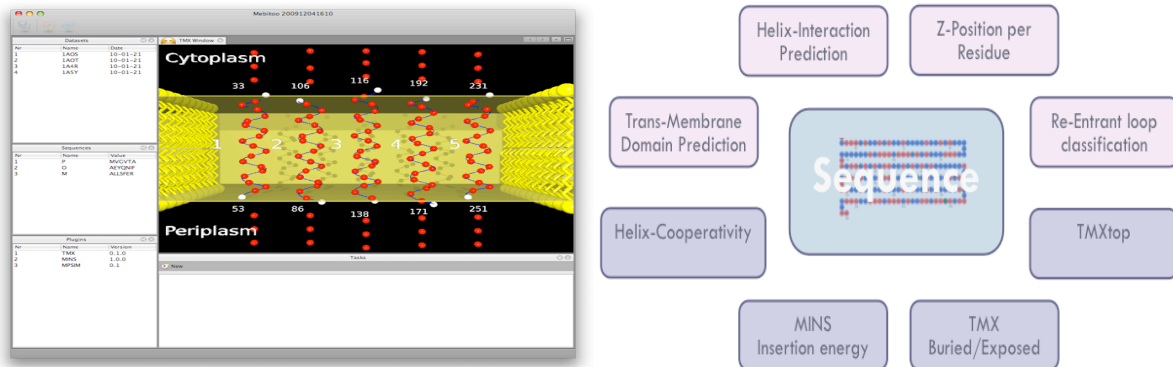
Mebitoo is a platform-independent desktop application written in Java. The software allows to import sequences persistently into an incorporated database engine, namely HSQL. A combined storage concept based on XML-files enables software extensions – plugins – to archive information in customized data structures.

To provide additional functionality, plugins can be deployed as independently developed software extensions, which are mounted dynamically by a plugin loading framework during start-up. Automated data processing using those extensions can be invoked using a task execution interface, which enables to queue multiple operations and process multiple datasets in parallel. A data viewer allows for visual representation of both stored sequence data and information that has been computed by third-party plugins. The core software provides fundamental storage and graphical interface methods, such as conversion of tables and plotting, to ease the development of plugins.

The software has been engineered deliberately in order to accomplish the aimed functionality, and the application couples various frameworks for both frontend and backend realization, database storage, extensibility by plugins, concurrent task processing, and flexible data exchange using XML.

We started to incorporate our own existing prediction methods *TMX* [1] and *MINS* [2] as well as upcoming tools to predict helix cooperativitiy, and the HMM-based Beta-Barrel TMX (BTMX). We aim to release the software including these tools combined with fundamental utilities like PFAM-based sequence alignments and visualization with *TopoView* and *JMol*.

[1] Y. Park, S. Hayat, V. Helms, *BMC Bioinformatics*, **2007**, *8:302* .
[2] Y. Park, V. Helms, *Bioinformatics*, **2008**, *Vol. 24 no. 16, 1819–1820*