

**Friend, an Integrated Front-end Environment for Bioinformatics**  
*Ilyin, Valentin, Abyzov, Alex, Errami, Mounir, Leslin, Chesley*  
Northeastern University, Boston, MA, USA



We present an integrated application, Friend, as a front-end user interface for visual and analytical analysis of multiple sequences and multiple structures in real time. Both structure and sequence data are linked to local and remote databases allowing researchers to analyze the comprehensive picture about related protein structures and sequences. Friend can visualize and manipulate hundreds of spatial structures of proteins, it can manipulate thousands of protein or DNA/RNA sequences providing easy to use alignments, clustering and phylogeny analysis.

Friend is stand-alone web-related application. The core module consists of a powerful multiple structure viewer integrated with an extended multiple sequence alignment viewer/editor. There are also several extension modules including: an internal bridge to multiple sequence alignments, libraries to calculate structural superimpositions based on internal and external modules, and the ability to calculate structural alignments using the novel, in-house developed Partial Spatial Volume algorithm. Friend also allows the user to add their own external modules to fulfill their specific needs. As an example, we present the *libHydro* library to calculate the positions of hydrogen atoms and evaluate the energy of the hydrogen bonds to analyze the protein stability.

Another powerful feature of the Friend application is the ability to provide a database interface to various sequence and structure databases. Internal integrated client modules allow Friend to query sequence and structure databases including BLAST and pattern searches, and an interface to the in-house structural exon database, SEDB. We present current implementation of Friend user interface to several databases.

Friend is available from <http://mozart.bio.neu.edu>.