

BiLab – A new Tool that Combines the Ease-of-Use of MatLab and the Power of Multiple Computational Biology Libraries.

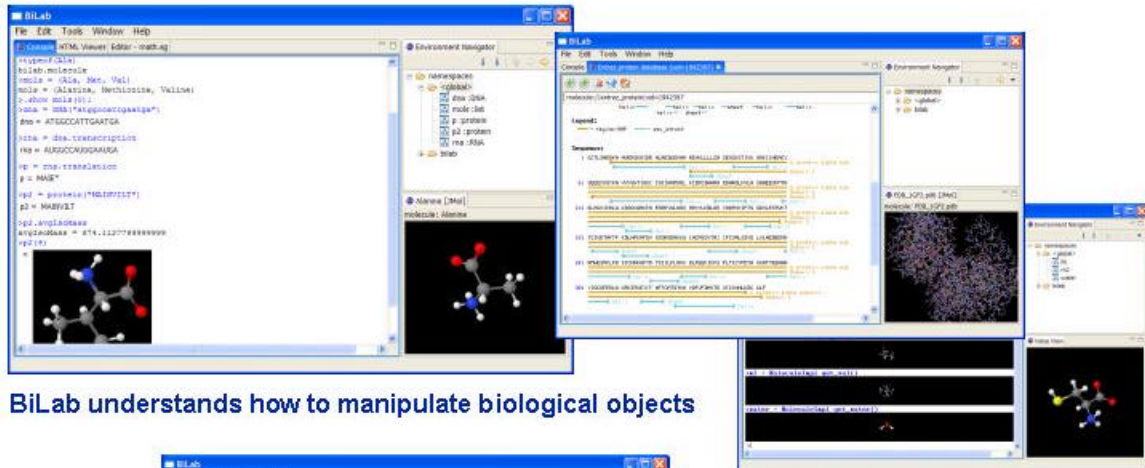
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As part of the Sandia National Laboratories-Oak Ridge National Laboratory Genomics:GTL project “Carbon Sequestration in *Synechococcus* Sp.: From Molecular Machines to Hierarchical Modeling,” we are developing a new tool called BiLab that we hope will revolutionize computational biology the way MATLAB[®] revolutionized numerical linear algebra. MATLAB is a scripting language that provides easy access to the robust linear algebra functions in the LAPACK library. It is simple enough for new users and powerful enough for sophisticated users and is widely used to do analysis, develop new algorithms, and teach students. BiLab takes a similar approach, except instead of only understanding matrices and doing linear algebra, BiLab understands biological objects, such as DNA, proteins, and molecules and is able to manipulate them through any of the functions in a half-dozen standard computational biology libraries. BiLab displays results in biologically relevant form, for example, a protein may be displayed as a molecule, a sequence alignment as stacked sequences.

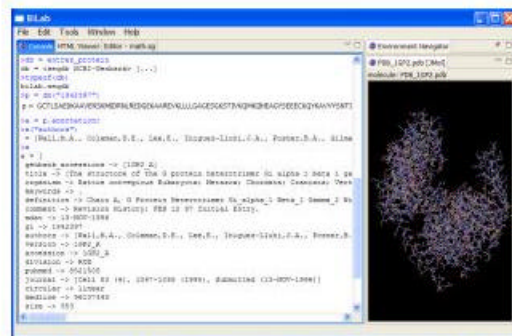
We developed the BiLab scripting language to support different levels of expertise in the user, from biologists who want a quick way to use existing functions to bioinformatics programmers who want to write sophisticated programs in the BiLab scripting language. BiLab allows the easy addition of new biological objects and functions and currently provides access to all the functions in bioJava, bioPython, the text based NCBI tools, Jmol, JalView, and CDK. Developers can extend the scripting language to understand new biology. This tool is designed to evolve with the Genomics: GTL program. The Systems Biology Workbench group is collaborating with us to integrate all their tools into BiLab.

Like MATLAB, data can be typed in manually or read in from files. BiLab understands the concept of remote biological databases and the prototype is able to dynamically load data from SwissProt, GenBank, FASTA, Protein Data Bank, EMBL, and other databases for analysis and study.

Acknowledgement: This project is supported by the U.S. Department of Energy’s Genomes to Life Program under project “Carbon Sequestration in *Synechococcus* Sp: From Molecular Machines to Hierarchical Modeling” (<http://www.genomes-to-life.org>)



BiLab understands how to manipulate biological objects



BiLab knows how to dynamically retrieve data from external databases

BiLab can display results as text or biologically relevant representations