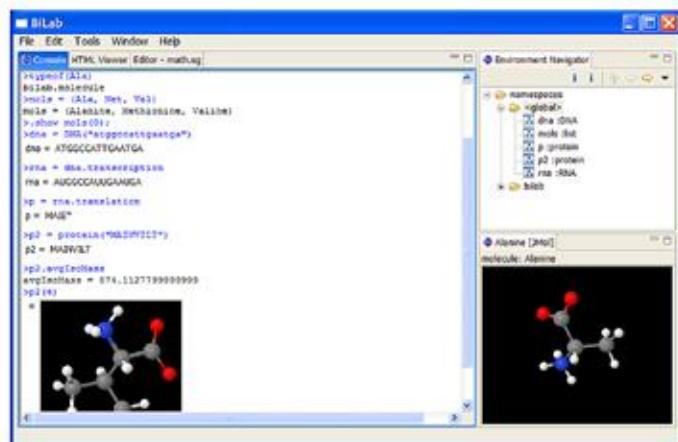


# BiLab – A new Tool that Combines the Ease-of-Use of MatLab and the Power of Multiple Computational Biology Libraries.

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This work is part of the Sandia/ORNL Carbon Sequestration in Synechococcus project ([www.genomes-to-life.org](http://www.genomes-to-life.org))



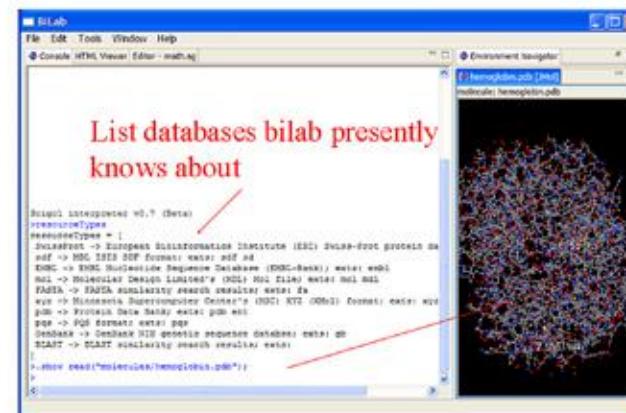
BiLab understands how to manipulate biological objects.

BiLab provides and integrates the functional capabilities from these existing libraries:

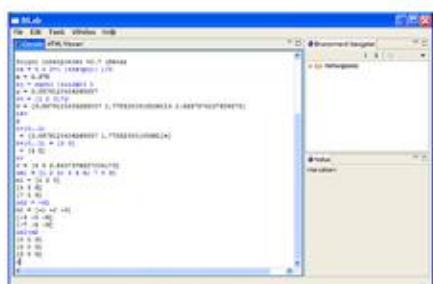
- CDK** – Chemical Development Kit
- biojava** – Biological Java library
- biopython** – Biological Python library
- NCBI tools** – text-based NCBI tools only
- GSL** – GNU Scientific Library C/C++.
- Provides statistics and math functions
- Jmol** – Molecule viewer (structure)
- JaView** – Sequence alignment viewer and editor.

We are developing a new tool called BiLab that has the potential to revolutionize computational biology the way the MatLab revolutionized numerical linear algebra. BiLab presents an easy, intuitive interface similar to MatLab 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. Like MatLab, data can be typed in manually or read in from files. BiLab understands the concept of remote biological databases and is able to dynamically load data from SwissProt, GenBank, FASTA, Protein Data Bank, EMBL, and other databases for analysis and study Just as MatLab can plot math functions, BiLab is able to display 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 cater to different levels of expertise in the users, from biologists who just want a quick way to use existing functions to bioinformatics programmers who want to write sophisticated programs in the BiLab scripting language. We have developed the tool to allow the easy addition of new biological objects and functions. Today BiLab 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. Thus the tool, which now exists as a prototype, is designed to evolve with the Genomics: GTL program.

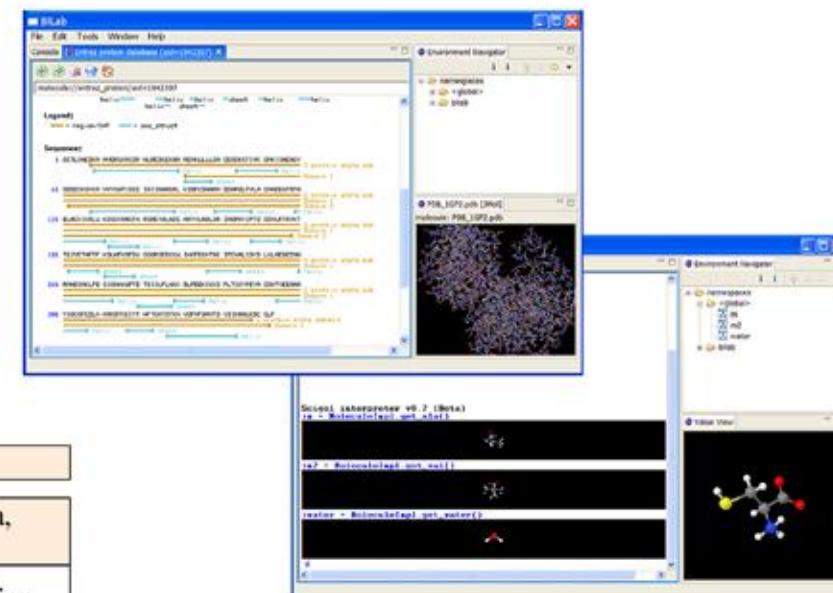
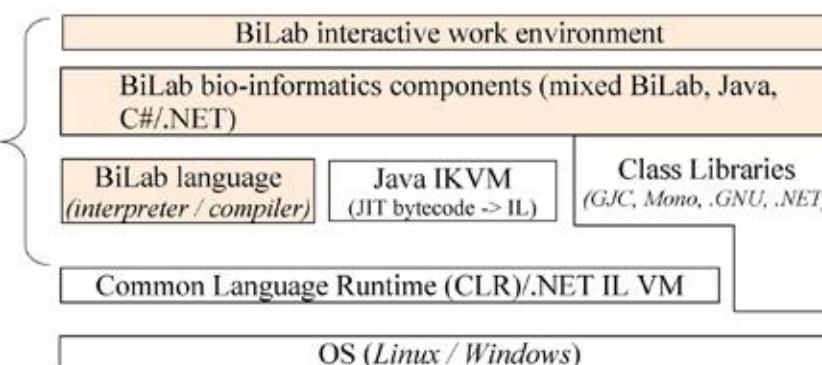


BiLab knows how to dynamically retrieved data from external databases



BiLab script allows easy programming of all the functions it understands.

BiLab's complex CS infrastructure provides flexible means to add new proteomic functions.



BiLab can display results as text or biologically relevant representation