

A Wet Lab Simulation to Enhance the Learning Experience of Undergraduates



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Abstract

JBio Framework is a computer program designed for use in the biochemistry, proteomics, or bioinformatics classroom. The newest upgrade to the program to be released in the coming month will contain simulations of - 2D Electrophoresis, 1D Electrophoresis, Tandem Mass Spectrometry, and Chemical drawing software (Marvin Sketch, available for download here:

<http://www.chemaxon.com/products/marvin/marvinsketch/>). These integrated simulations are designed to teach the concept of proteome analysis of simple organisms. JBio Framework can be used as a freestanding simulation or in conjunction with a wet lab, to introduce proteomics in the undergraduate classroom, and is freely available at <https://sourceforge.net/projects/jbf/>. JBio Framework functions in Mac OSX, Windows, and Linux, ensuring that every student sees a consistent and informative GUI no matter the computer platform they choose. Learning goals have recently been recognized and have been processed through Bloom's Taxonomy. These learning goals are currently an ongoing process and there is work towards implementing these into classrooms for further evaluation in the near future. Planned future applications include Ion Exchange and Reversed Phase Chromatography.

Introduction

What is JBioFramework (JBF)?

- A platform independent program
- A mixture of 2D Electrophoresis, Tandem Mass Spectrometry ,and chemical structures from the Mass Spectrometer
- A program that works with other chemistry resources such as SwissProt, BLAST, and Marvin Sketch.

What can it be used for?

- To teach proteomics to advanced level high school students and college undergraduates.

What will it teach?

- The concepts of peptide sequencing and protein identification.

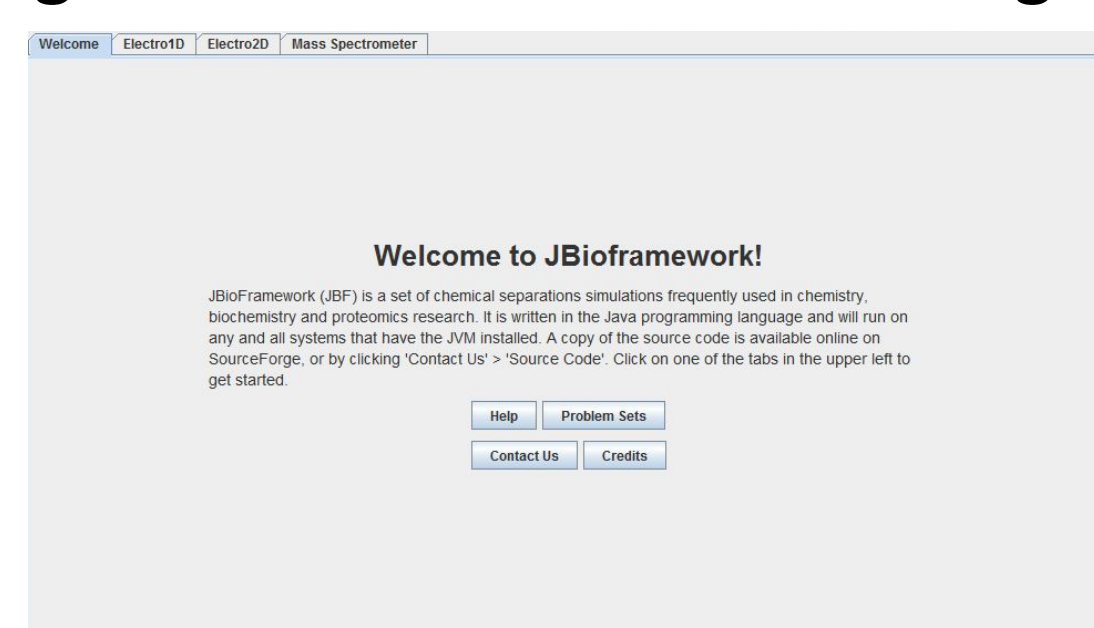


Figure 1: Welcome screen of JBF

Software Development

How was the program made?

- The program is written using Java utilizing the programs Eclipse or IntelliJ to compile the code.
- The compiled java runs on the JVM (Java Virtual Machine) allowing it to perform across platforms.
- Revisions between programmers are compiled using Git.

What is included in the software?

- 1D Electrophoresis
- 2D Electrophoresis
- Tandem Mass Spectrometry
- Chemical Drawing Software (Marvin Sketch)

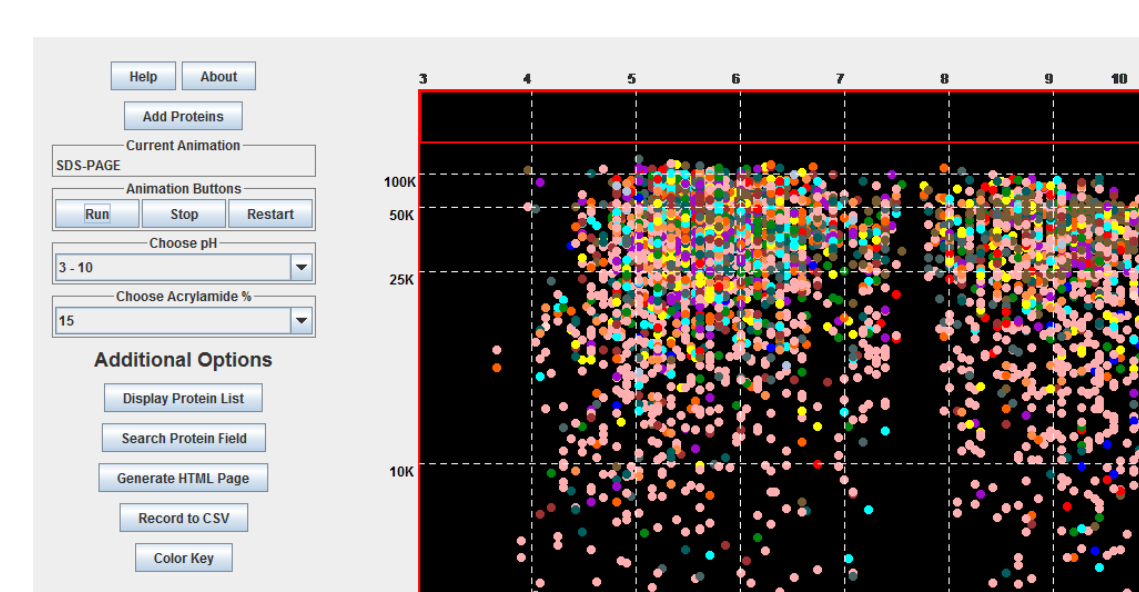


Figure 2: SDS-Page on the 2DE Application.

What's happened recently?

- Our most recent work has been on creating a website for our users. It provides the team names and contact info as well as having the learning questions available for teachers use. There is also a section for users to find all downloads related to our software.

What will be released next?

- Our next release (Helium) will include 2DE, Tandem Mass Spectrometry and (for the first time) Chemical Drawing with MarvinSketch.
- Future additions (Lithium release) will include Ion Exchange and Reverse Phase LC.



Figure 3: The newest JBF Logo

Software Testing

Students tested the software and were recorded using Camtasia.

Majors of Students Tested:

- Chemistry, Biochemistry, and Biotechnology.

What was found?

Chemistry Students Tested

- Didn't feel as though they learned much
- Had difficulty using the databases.
- Program was easy to use.
- Had more interest in the Mass Spectrometer.
- Did not test as well as the Biotechnology student

Biotechnology Students Tested

- Felt like they learned a lot in the simulation.
- Program implemented what they had learned in lab previously.
- Easier way to use databases and search them.
- Visually Stimulating.
- Had an overall easier time using the program and had more correct answers.

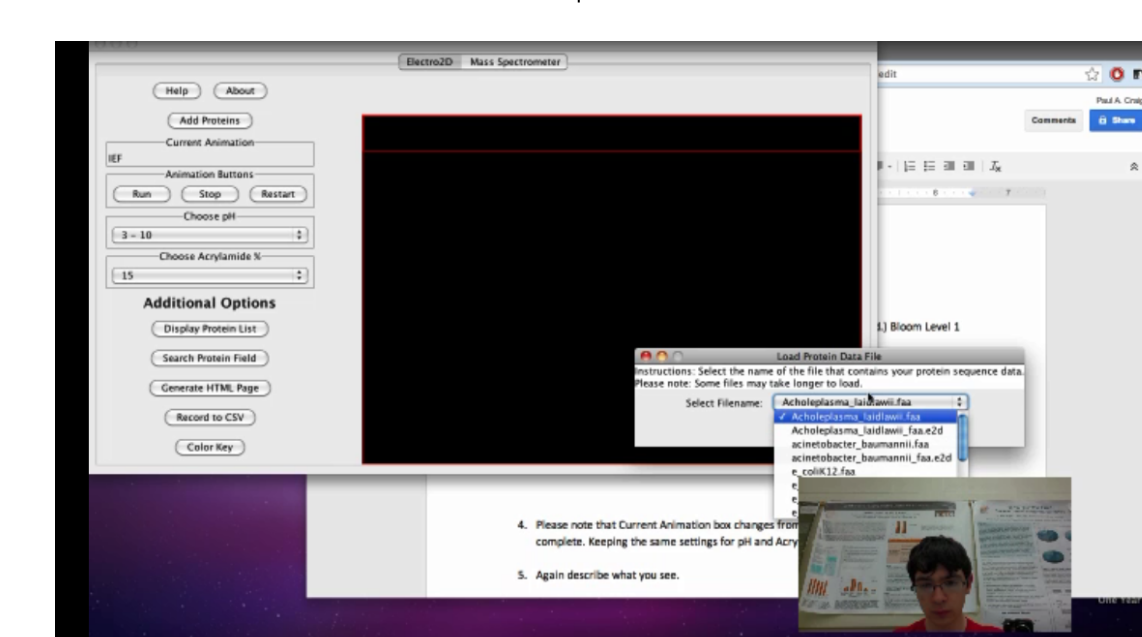


Figure 4: Camtasia recording a student's work.

Learning Goals

How the process began:

To create the learning goals, we first identified some of the larger topics that we wanted students to learn and be able to expand upon.

Those included:

- To prepare students for using the actual instruments
- To connect to basic Chemistry and Biochemistry
- To understand and interpret data from 2DE and MS
- To explain the purpose of each instrument

What happened next?

Each of the learning goals were "Bloomed out" to create questions that enhanced student learning.

Knowledge	Comprehension	Application	Analysis
Define important terms in chemistry and biochemistry that are used in the program eg: Protease, pI, amino acid, Molecular Weight.	Identify the role of each of these components in 2DE-TMS: SDS, Dithiothreitol, Urea.	Given the following protein sequence, predict the fragments that would form following digestion with Trypsin.	Infer why Leucine and Isoleucine are ambiguous on a mass spectrum.
Synthesis Using the tools of the 2DE-MS simulation, compose a list of proteins that share sequence similarity or function similarity than align those sequences using Clustal Omega.		Evaluation Using Swiss- 2D Page, compare the MW and pI for dihydrofolate reductase on the simulated and actual gel. Why are they different?	

Crowe, A., et al. Biology in Bloom: Implementing Bloom's Taxonomy to Enhance Student Learning in Biology. *CBE-Life Sciences Education* 7(4):368-381; 2008.

Conclusion

Based on what was found through student testing and our own evaluation of the software, we decided that once the learning goals are fully developed, the software should be tested in a classroom setting. At RIT classes that could benefit from the software include Bioinformatic Analysis of Macromolecules, Chemical Separations, Biological Separations: Principles and Practices, and Biochemistry I with their associated labs. With the learning goals in mind we will be able to test the software regarding specific goals and be able to help the software to evolve into a better learning tool regarding specific topics of study and to help it fit better into different classroom environments.

Acknowledgements

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