

What is MSEIP?

The **Minority Science and Engineering Improvement Program** is designed to improve the quality of science and engineering education as well as open doors for underrepresented groups in science and engineering career fields and educational opportunities.

What are the goals for **MSEIP** at HT?

- To revise biology courses through the integration of computational and technological applications.
- To retain students who are not completing degrees in live sciences

Expected Outcomes

Enhancement of integrative problem solving and process thinking skills; thus better prepare students to pursue post baccalaureate careers/graduate degrees in interdisciplinary fields such as:

- bioinformatics
- biomechanics
- biotechnology
- forensic science

Objectives

- Revise all courses in the main biology curriculum to reflect mathematical and computer science applications germane to current applications.
- Update the knowledge of STEM faculty in interdisciplinary mathematics and computer science.
- Establish an interdisciplinary advisory group of STEM faculty and consultants who will advise on curricular quality relative to current practice.
- Update available software and equipment to support revised courses.

BIOCOMP2010 <http://biocomp2010.htu.edu>

Introduction

The Huston-Tillotson University (HT) Minority Science and Engineering Improvement Program (MSEIP), funded by the U.S. Department of Education, provides a significant means by which the biology curriculum at HT can be made more viable and “cutting edge” in support of student learning. The main purpose of this web page is to share information with HT faculty, students, and staff and external organizations.

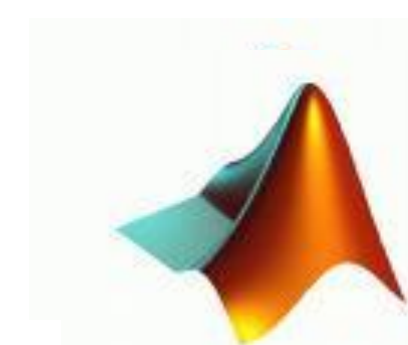
Sample Lab Activity

LAB 1 TECHNIQUES: USING THE SPECTROPHOTOMETER, PRODUCING ABSORPTION SPECTRA AND STANDARD CURVES

A stock solution of a dye called Safranin O is available for your use. It was prepared to give a concentration of one gram/liter or an equivalent 1000 milligrams/liter. You will be transferring 1 ml of this stock solution to a clean 100 ml flask and make up to volume using distilled water.

Label your flask solution A and label 6 other flasks 1-6. Carefully make up the following dilutions for each of the other flasks calculating their concentrations.

In the computer lab, you will log on to a computer to calculate the concentration using MATLAB®. Click on the MATLAB icon, which looks like this:

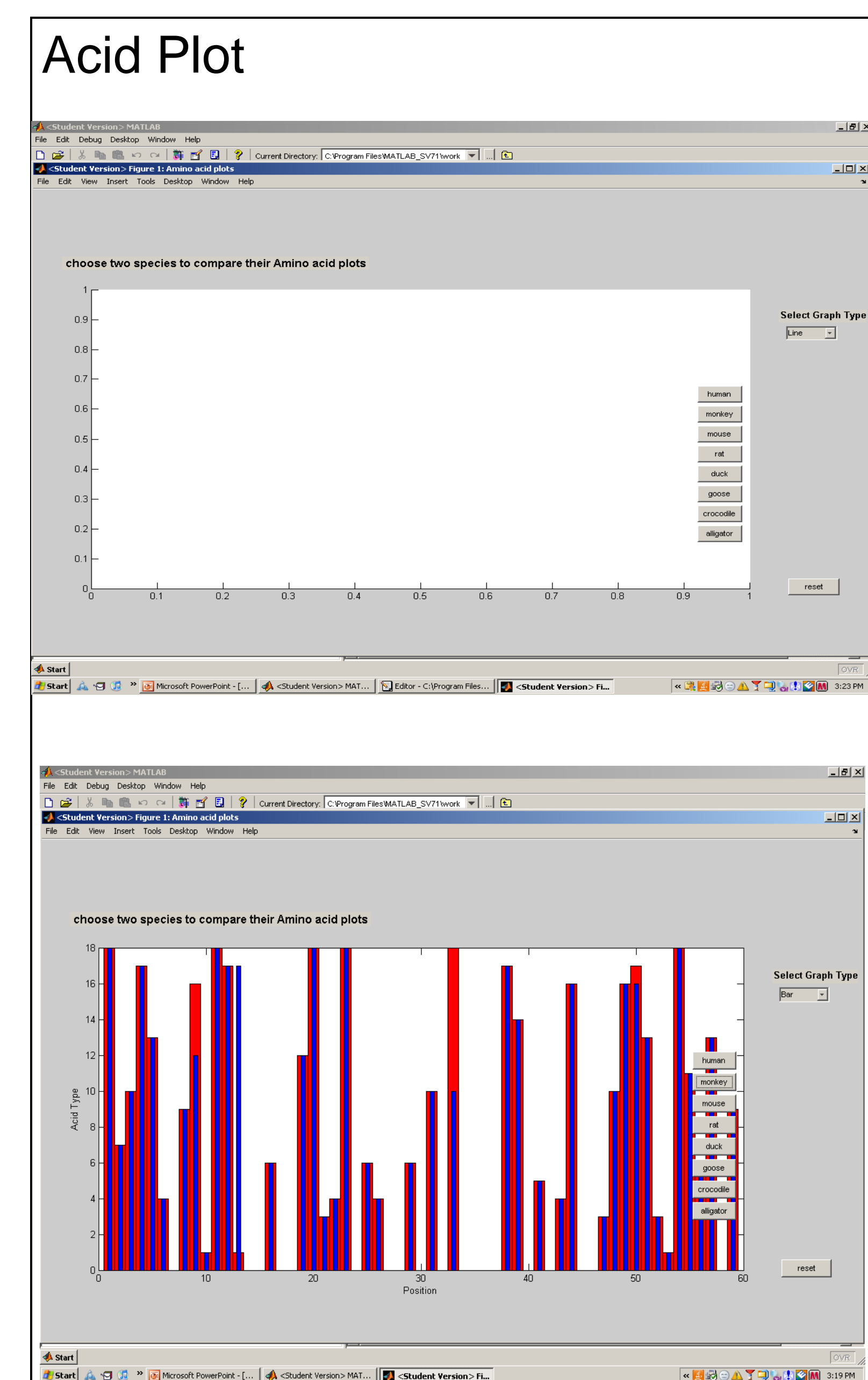
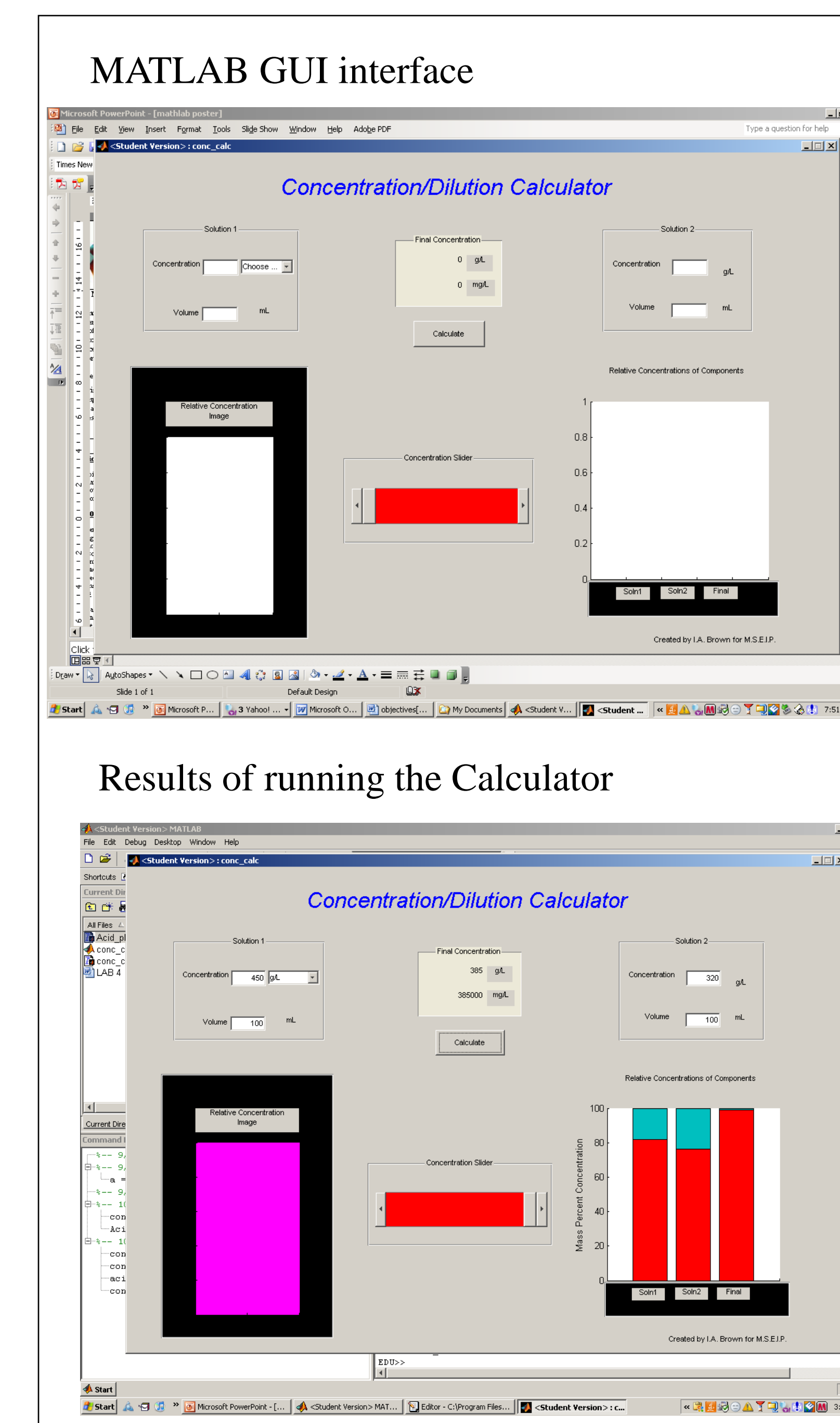


When MATLAB opens, in the right hand screen type in:

`conc_calc` and press the **ENTER** key

This will give you a Concentration/Dilution Calculator. Enter the initial concentration in the top left box, the amount that will be used in the box directly beneath it. In the top right box, enter the concentration of water (0) and the amount of water that you will be using. Then click on “Calculate”. This will give you the calculation needed. Do the same for the other concentrations in your table.

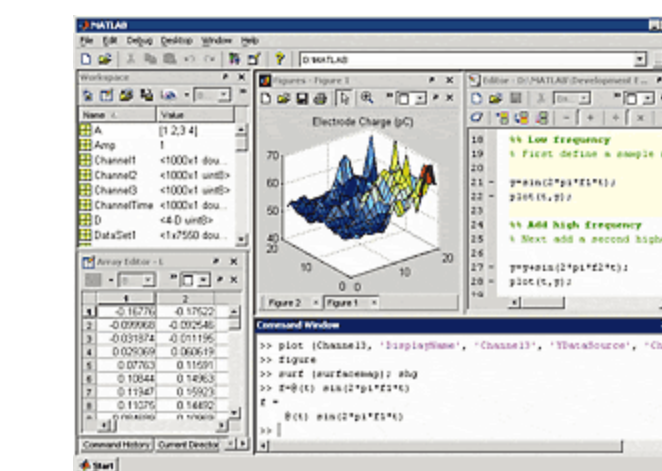
This laboratory is modified from one offered at the 1998 ABLE meetings in Tallahassee, Florida. The laboratory was submitted by Gilbert Ellis, School of Natural and Health Sciences, Barry University, Miami Shores, FL. “Spectrophotometry and Hemoglobinometry”.



Huston-Tillotson University M.S.E.I.P. Project Software Update

The Huston-Tillotson University MSEIP Project Staff and Advisory Committee have selected MATLAB® by MathWorks as the foundational software tool for our use in the classroom as well as on the faculty research workstations. “MATLAB® is a high-level technical computing language and interactive environment for algorithm development, data visualization, data analysis, and numeric computation. Using MATLAB®, you can solve technical computing problems faster than with traditional programming languages, such as C, C++, and Fortran.”

The MATLAB development environment lets you develop algorithms, interactively analyze data, view data files, and manage projects.



Some of the key features of MATLAB® include:

- High-level language for technical computing
- Development environment for managing code, files, and data
- Interactive tools for iterative exploration, design, and problem solving
- Mathematical functions for linear algebra, statistics, Fourier analysis, filtering, optimization, and numerical integration
- 2-D and 3-D graphics functions for visualizing data
- Tools for building custom graphical user interfaces
- Functions for integrating MATLAB based algorithms with external applications and languages, such as C, C++, Fortran, Java, COM, and Microsoft Excel

In addition to the MATLAB® foundation, we selected the Bioinformatics Toolbox as our primary research and training software tool for biological applications. This Bioinformatics Toolbox will allow our researchers and students to develop custom algorithms to investigate new ways to teach and better understand current advances in the areas of genetic engineering and other genomics and proteomics. Some of the key features of this software include:

- Genomic, proteomic, and gene expression file formats
- Internet database access
- Functions for pairwise and multiple sequence alignment
- Sequence analysis tools
- Phylogenetic tree analysis tools
- Capabilities for microarray data analysis and visualization
- Support for mass spectrometry preprocessing and analysis
- Statistical learning functionality

We have also selected the Neural Network and the Statistical Toolboxes as ancillary software tools. The Neural Network Toolbox will allow our students and researchers the ability to explore complex, non-linear, multivariable functions with relative ease. This includes the ability to build artificially intelligent systems that the students can “train” to recognize complex patterns in data that the human eyes would normally overlook. The Statistical Toolbox will allow our students to perform complex statistical tests on the data quickly and efficiently. The foundational statistical concepts taught in our stats classes will be reinforced with real laboratory data.

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