

## **BioFitWeb:** A Comprehensive On-Line Resource for Enzyme Kinetics Researchers second progress report

The goal of the BioFitWeb project is to provide researchers in enzyme kinetics with an easy-to-use tool for doing the always tedious and often mathematically complex analysis required to extract useful information from the data generated by experiments in enzyme kinetics. Software available for researchers in this area suffers from many drawbacks – existing tools are either archaic, expensive, or highly specialized. BioFitWeb will provide an appealing alternative by combining the following features:

- Web-based interface for ease of use, broad availability, and free access.
- Sophisticated and rigorous fitting algorithms available nowhere else.
- Hypertext structure combines availability of extensive references, background information, and decision-aid tools with modularity – undesired features can be ignored.

### **1. Completed Work**

The BioFitWeb site is currently available at <http://156.56.92.83/BioFitWeb.htm>. Presently the site consists of about fifteen HTML pages and perl cgi scripts. Most of the proposed basic tools have been implemented – this involves the ability to dynamically generate forms, upload, parse, echo, process, and store data, and display interactive results. Much of the supporting material for these tools is in place as well, including background, technical documentation, and some references.

The working tools calculate several parameters from either time-course or initial rate enzyme reaction data, including maximum reaction velocity, initial substrate concentration, and the Michaelis-Menten constant for the enzyme, along with the standard errors for each parameter and the chi-square error for the fitting. The results are now displayed graphically using several popular methods for visualization, which the user may choose among. Each graphic is displayed with information about that visualization's advantages and shortcomings. The graphs are generated using GnuPlot, a popular open-source graphing package with excellent

features. Dynamic content including forms and options is generated using javascript. Supporting materials include a derivation for the Michaelis-Menten equation, and a discussion of the quasi-steady-state assumption along with the conditions under which its use is justified. Each tool page also includes extensive background material on the methods used by the tool, and recommendations for the best methodologies to be used in collecting data to be analyzed by the tool. Links to relevant references are also included.

## 2. Current Activities

A database is under development to keep the results of the fittings performed using BioFitWeb and make the results available to other researchers. The database itself has been implemented using MySQL, an open-source implementation of the standard database language SQL. Web interfaces and security are currently in progress.

Some testing of the fitting tools to evaluate their performance has already been done; the initial results are good. The algorithm for fitting initial rate data performs well even given quite noisy data. The time-course fitting algorithms are less robust, but still perform well when noise levels are below 5%, which is high for data of this type.

## 3. Remaining Work

I will continue to add background, technical, and reference material to the site as new tools are brought on-line. The SQL database features remain to be completed.

BioFitWeb must be tested in several ways. The accuracy and utility of the fitting tools must be further evaluated, using real and simulated data. A full comparison of BioFitWeb's capabilities against those of the most-used competing software products must be completed. If possible, a researcher should be found who is willing to use BioFitWeb to evaluate a newly-generated set of experimental data, and then make a parallel analysis using other tools, so that we may compare both accuracy and useability.

The bar below indicates the degree of completion for this project (70 – 75%):

