

GenoLogics Case Study: Cell Biology Proteomics Lab at the University of British Columbia

Advancing mass spectrometry-based proteomics through efficient bioinformatics



The Cell Biology Proteomics lab headed by Leonard Foster at the University of British Columbia focuses on applying mass spectrometry-based proteomics methods to topical questions in cell biology. Today's mass spectrometry technology allows laboratories to confidently identify thousands of proteins in extremely complex mixtures, and the resulting knowledge offers insight into how complex systems function. In order to effectively mine the vast amounts of data generated by mass spectrometry-based proteomics methods, labs require effective LIMS solutions that can reliably manage data and support bioinformatics pipelining. The automated pipelining enabled by a lab and data management solution such as GenoLogics' Proteus™ can greatly streamline data analysis processes and accelerate research results.

While quantitative proteomics has yet to be widely applied in mainstream biology, the CBP lab develops and applies quantitative proteomic methods to investigate dynamic changes in organelles and host-pathogen interactions. The lab uses a multidisciplinary approach to investigate cell biological issues, and the knowledge derived from these proteomic investigations is put towards a systems biology approach of in-depth bioinformatic, biochemical, and cell biological analyses to validate the proteomic results. The CBP lab instrumentation includes an LTQ-Orbitrap and an LTQ-FT, both equipped with autosamplers and nESI-interfaced HPLCs.

Projects currently underway in the lab include: finding host targets of effector proteins secreted from pathogenic bacteria, protein interaction network mapping of methicillin-resistant *S. aureus*, exploring why young honeybee larvae are susceptible to invading bacteria but older ones are not, exploring the dynamic composition of lipid rafts, host signal transduction cascades initiated by pathogens, host receptors for pathogenic bacteria, and development of software tools to improve the acquisition, analysis, storage and dissemination of proteomic data.

About two years ago, all the data generated by the lab's research resulted in a pressing need for a scientific data management solution. Although there were a number of generic commercial solutions on the market, Dr. Foster's evaluation determined Proteus™ was the best solution for his lab because it was designed specifically to support proteomics processes using mass spectrometry, and Dr. Foster recalled, "GenoLogics took some of our lab's specific bioinformatics requirements into account while developing Proteus." By February 2006, the lab was producing large volumes of data and Dr. Foster was confident Proteus was the ideal solution for the lab's requirements.

To date, Dr. Foster reports that the Proteus solution has been extremely successful as a scientific data management system. Dr. Foster said Proteus was “malleable enough to be adapted to the lab’s needs,” and the GenoLogics professional services team worked closely with the lab to help them derive the most value from the features that were most relevant to their research. Dr. Foster said, “For instance, while Proteus’ sample tracking feature might be more useful for a core lab, the automatic pipelining capability is very valuable to us, and GenoLogics has helped get this set up and customize it for our own in-house solutions.”

In the beginning of 2007, the lab began working on controlling several third party applications through Proteus in order to take advantage of the solution’s automated pipelining data analysis capability. This has involved collaboration between the lab staff and GenoLogics professional services, and although the lab uncovered some bugs, they were fixed within a day or two of being reported to GenoLogics. Dr. Foster appreciated the real-time pace of addressing issues with GenoLogics, and said, “As soon as an issue is identified, it is fixed, and then the lab can move on.” In addition, the training provided by GenoLogics ensured the solution was very easy for many users to access and use to streamline their day-to-day work through the automation enabled by Proteus. Dr. Foster’s lab has developed a variety of open source software packages, and Proteus currently smoothly integrates with approximately three-quarters of them, which allows staff to use Proteus to simplify interactions with familiar software.

The current Proteus-enabled bioinformatics automated pipelining process includes the following steps: ID proteins from mass spectrometer are automatically converted from mass spec binary data into lists of fragment spectra; spectra are automatically submitted to, then received from, an automated database search system; fractionated samples are analyzed independently; and then the data from each fraction is combined, resulting in the final answer for which proteins are identified. The only step that requires user input is converting the final data into a form Proteus can read, and uploading it into Proteus.

Since installation, Proteus has proven to be very capable of addressing the CBP lab’s bioinformatics needs. Soon, all of the lab staff will start conducting work through automated pipelining, which Dr. Foster expects will save approximately 50% of the time each of the eight team members routinely has to dedicate to data analysis.