

## HERMES

### **Introduction:**

The open source laboratory information management system <sup>3</sup>Proteome Research Information Management Environment<sup>2</sup> or PRIME developed at the University Of Michigan is integrated with the following search engines, MASCOT, XTandem, and Protein Prospector. The subsystems responsible for handling the MASCOT search engine have been re-engineered as a stand-alone software system named <sup>3</sup>Hermes<sup>2</sup>. The source code can be found at [Proteomecommons.org](http://Proteomecommons.org) and is openly available under the Apache licensing agreement (<http://www.apache.org/licenses/>). Because it is integrated with the open source project IOFramework that can also be found at [Proteomecommons.org](http://Proteomecommons.org) it is able to receive spectra in various formats and convert them to MASCOT mgf formats.

**Download:** Hermes binary and source code can be downloaded from <https://www.prime-sdms.org/prime/index.htm>.

### **Methods:**

<sup>3</sup>Hermes<sup>2</sup> is an open source application written in Sun JAVA. It can be viewed as comprising of several processes linked together to form a pipeline. Once a spectrum file is copied to the directory monitored by Hermes, it is converted to a MASCOT pmf or mgf file and passed to a separate process responsible for handling the management of MASCOT. Upon completion, the dat file is collected and moved to an archive directory. Parameters for the conversion of the spectra and for the criteria used for searches are located in xml formatted files. A utility with a dynamic user interface configurable from an XML file is provided to aid with the update of the xml files associate with MASCOT searches.

### **Preliminary Data:**

Currently, Hermes is implemented in the Protein Center at Memorial Sloan-Kettering Cancer Center. It has been installed on a Mac Xserve that also works as the data repository for the laboratory's LC-MS runs. The sub-system of Hermes responsible for converting wiff files – with the aid of Andreas Boehm's (<http://www.protein-ms.de>) wiff2dta converter and the IOFramework – was installed on the same computer that has the Applied Biosystems Analyst software. The converted data is sent to through a socket to the Hermes sub-system responsible for handling the MASCOT management.

Then Hermes sends the data to Mascot and waits for the search to finish. Upon completion, Hermes copies the appropriate Mascot dat file to an archive location.

The use of Hermes instead of Mascot Daemon confers upon the user many advantages. First, Hermes is cross-platform whereas Mascot only works in Windows. Hermes is open-source, allowing others to modify the code as desired. Hermes is flexible: it can be modified to work with any search engine. Thus instead of a user needing to learn several interfaces for various search engine, Hermes can be the one consistent gateway. Hermes can also work with various LIMS systems as since it only works with directories. An existing LIMS system can be configured to monitor the location where Hermes deposits the results of a search. Hermes also uses the same pipeline (but different configuration files) to process MS1 data or MS/MS data.