Release Notes

APEX Quantitative Proteomics Tool, v. 1.1.0

03.20.2010

Overview

The APEX Quantitative Proteomics Tool is designed to generate APEX scores, Absolute Protein Expression Estimates, according to the technique described in:

Peng Lu, Christine Vogel, Rong Wang, Xin Yao, Edward M. Marcotte. Absolute Protein Expression Profiling Estimates the Relative Contributions of Transcriptional and Translational Regulation. Nature Biotech. 25(1):117-124, 2007.

A full description of the tool is described in:

John C Braisted, Srilatha Kuntumalla, Christine Vogel, Edward M Marcotte, Alan R Rodrigues, Rong Wang, Shih-Ting Huang, Erik S Ferlanti, Alexander I Saeed, Robert D Fleischmann, Scott N Peterson, Rembert Pieper. The APEX Quantitative Proteomics Tool: Generating protein quantitation estimates from LC-MS/MS proteomics results. BMC Bioinformatics 9:529. 2008.

The APEX technique uses a modified spectral counting technique that utilizes machine learning techniques to arrive at protein abundance values with improved accuracy over traditional spectral counting techniques. The APEX Tool provides computational support for this technique through a set of interfaces designed to guide the user through the process of generating APEX protein abundance estimates.

What's New

- Improved support for selecting proteins for classifier training data At the Training Data Building stage, the list of accessions for training proteins can be collected in two ways:
 - (1) By supplying a Protein Accession List File (as in version 1.0.0)
 - (2) By selecting proteins from a previous MS result (prot.XML File)

If proteins are selected from a previous MS result file (2), proteins will first be filtered on protein identification probability to produce a list of candidate proteins. From this candidate list, a selection of proteins can be made to build the peptide training data set.

• New and customizable proteolytic enzyme options – Digestion Scheme is expanded to include both trypsin and chymotrypsin digestions. Five default digestion options are presented for selection. Users can modify enzyme digestion rules (targets) and can define new enzyme digestion schemes or rule sets that match enzymes use in the lab.

• New Utilities & Analysis feature: Attribute Evaluation

This new utility provides users methods to evaluate which peptide attributes (peptide physicochemical properties) appear to be most critical in predicting peptide observation by MS for a user's lab protocol and instrumentation.

System Requirements

Java

The APEX Tool was written in the Java programming language which means that the program will run on computers running MicrosoftTM Windows® (2000, XP or Vista), Linux®, and Mac® OSX (1.4 or 1.5) operating systems. APEX requires a Java Runtime Environment (JRE) installation of version 1.5 or greater. Most computers will have an installation of Java but if Java has not been installed it can be downloaded and installed from http://java.sun.com/downloads. You can determine your JRE version using the command 'java –version' on the command prompt in a dos window or in a terminal window (Mac and Linux).

Hardware

Being developed in Java, the APEX Tool is compatible with Windows, Linux, and Mac operating systems. APEX has been tested on machines with as little as 256MB of RAM however, 512MB to 1GB of memory is recommended. The processor speed will impact the time required to complete tasks. APEX has been tested on machines with processor speeds below 1 GHz but faster processors that run above 2 GHz will help speed processing.

Disclaimers

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