

A method to identify mass spectra of proteins containing post-translational modifications

Proteins are complex substances consisting of amino acid residues, and essential biological compounds. After proteins are decoded from DNA and synthesized by the ribosome, chemical modifications known as post-translational modifications (PTMs) often occur. These modifications change the structure and function of proteins, and are therefore important to study and understand. Tandem mass spectrometry (MS/MS) has become the major tool in the identification of proteins, and consequently in the search for PTMs. In MS/MS, peptides are broken into mainly b-ions and y-ions, and the masses and intensities of these resulting ions can be used to reconstruct the original peptide. Currently, the most popular method of identifying known PTMs is to use a database search algorithm such as Sequest, which compares theoretical mass spectra created from a database to the experimental mass spectra data. However, searching for possible PTMs greatly increases computational expense, which is especially unnecessary for spectra which do not contain PTMs. A method to identify the mass spectra that are most likely to contain PTMs could be useful in improving PTM searching capabilities. The research involves constructing a PTM-filter program that quickly scans mass spectra for possible signs of modified proteins. The recently developed Probability Profile Method (PPM) is used to reliably identify b-ions and y-ions in the mass spectrum. PTM-filter performs a de novo search for any of these ions that are separated by the mass of modified amino acids, and then reports whether the spectrum is a possible candidate for further PTM analysis. The filter can be adjusted to minimize either "false negatives" or "false positives" among the reported spectra. This filter will allow later PTM searches to be focused only on the mass spectra most likely to contain PTM information, helping to streamline the entire PTM search process.

Student's name:	Rashida E. Askia
School student attends:	Fisk University
Name(s) of mentor(s):	Dr. Michael Leuze and Dr. Andrey Gorin
Division:	Computer Science and Mathematics
Program:	Research Alliance in Math and Science (RAMS)