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Peptide Identification by Tandem Mass Spectrometry Data Interpretation

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Proteomics, or direct analysis of the expressed protein components of a cell, is critical to understand the cellular biological processes in normal and diseased tissue. A key requirement for its success is the ability to identify the proteins in complex mixtures. Recent technological advances in tandem mass spectrometry, has made it a method of choice in high-throughput identification of proteins. The automatic interpretation of mass spectrometry data is becoming increasingly important in protein identification.

In this work, we present the two major classes of algorithms which are used in interpretation of the tandem mass spectrometry data.