



## On Mass Spectrometry Based Proteomic Data Processing Using Multiscale Tools

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### ABSTRACT:

Modern technology today allows the collection of biological information at an unprecedented level of detail and in increasingly vast quantities. To reap real knowledge from the mountains of data produced, however, requires interdisciplinary skills—a background not only in biology but also in mathematical tools and statistical techniques of data analysis. Mass spectrometry (MS) has become one of the critical components in medical research. The matrix-assisted laser desorption ionization (MALDI) technique allows the use of MS in applications involving large molecules. In 2002, the Nobel Prize in Chemistry recognized MALDI's ability to analyze intact biological macromolecules. Though MALDI MS has proven to play a key role in the advancement of science with the introduction of new fields such as Proteomics, there are many challenges both in MS data preprocessing and data analysis. In this talk, I'd like to present some recent progress on MS based proteomic data processing using multiscale tools such as wavelets and empirical mode decomposition (EMD) methods.