

COMPUTATIONAL METHODS FOR EXPLORING PROTEIN ISOFORMS BASED ON MS DATA

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The complexity of protein isoforms in protein identification and quantification have been addressed in the past with no definitive conclusion. Furthermore, ABRF recently launched a test study for validating the use of MS for identification of Histone proteins which emphasis the importance of the problem. The main issue is the insufficient information provided by MS data in order to achieve a definitive and accurate solution. Currently a number of proposed computational methods for handling protein isoforms identification are available however further developments that provides an optimal probabilistic solution based on the available data are required. To this end a number of novel computational methods have been implemented in the VEMS program. On one hand protein isoforms and homologs present problems for protein identification and quantitation based on MS data but on the other hand it provides valuable information that can be explored for protein sequencing. Novel de novo sequencing strategies that explores the protein homolog information for sequencing proteins based on MS data will be presented.