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# Using entrapment sequences strategy for evaluation of database search engines and quality control methods in shotgun proteomics

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With the advance of mass spectrometry and experimental techniques, proteome research has broken through the bottleneck of data generation and a huge amount of mass spectrometry (MS) data has been accumulated rapidly in the past few years. Meanwhile, the lack of efficient data analysis and quality control methods has greatly hindered proteome development. Target-decoy searching strategy has become one of the most popular strategies to control the false identification in MS/MS data analysis. While this strategy can estimate the false discovery rate (FDR) within a dataset, it cannot directly evaluate the false positive matches in target identifications. In this study, we developed an improved target-decoy strategy: The entrapment sequences method, to set up an objective standard to evaluate the performance of quality control methods and database search tools. Using both standard datasets and experimental datasets, we started with a preliminary study of the size of entrapment sequences and found ten times the sample sequences could be a reasonable size of entrapment sequences. Then, we went on to give a definition and equation of estimated FDR and actual FDR. We found the entrapment sequences method can be a good supplement to target-decoy strategy. So, we evaluated the performance of five quality control methods (BuildSummary, PepDistiller, PeptideProphet, FDRAnalysis and ScoreBased Method) and five database search engines (Mascot, X!Tandem, Comet, MS-GF+ and Tide). We demonstrated that the entrapment sequences method could be an excellent strategy to assess each step of the mass spectrometry data analysis process.

## Biography

Jie Ma has completed her PhD from Beijing Institute of Radiation Medicine. She is now an Assistant Professor at Beijing Institute of Radiation Medicine. She has published more than 10 papers in reputed journals of Proteomics and Bioinformatics.

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