proteiNorm – A user-friendly tool for normalization and analysis of TMT and label-free protein quantification

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ABSTRACT

The technological advances in mass spectrometry allow us to collect more comprehensive data with higher quality and increasing speed. With the rapidly increasing amount of data generated, the need for streamlining analyses becomes more apparent. Proteomic data is known to be often affected by systemic bias from unknown sources and failing to adequately normalize the data can lead to erroneous conclusions. To allow researchers to easily evaluate and compare different normalization via a user-friendly interface, we have developed “proteiNorm”.

The current implementation of proteiNorm accommodates some preliminary filter on peptide and sample level, followed by an evaluation of several popular normalization methods and identification of missing value pattern. The user then selects an adequate normalization method and one of several imputation methods used for the subsequent comparison of different differential abundance/expression methods and estimation of statistical power. The application of proteiNorm and interpretation of results is demonstrated on a Tandem Mass Tag mass spectrometry example, where the proteome of three different breast cancer cell lines was profiled.

With proteiNorm, we provide a user-friendly tool to identify an adequate normalization method and to select an appropriate method for a differential abundance/expression analysis.

KEYWORDS: Proteomics, Normalization, Differential analysis