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Peptide tandem mass spectra can be analyzed by a number of means. They can be compared against predicted spectra of peptides derived from genome sequences, compared against previously acquired and identified spectra, or - sometimes - sequenced de novo. We recently introduced another method which compares spectra between liquid chromatography/tandem mass spectrometry (LC/MS/MS) datasets to determine the shared spectral content, and demonstrated how this can be applied in a molecular phylogenetic study using sera from human and non-human primates. We will here explore if such a method have other, serendipitous uses. We used the existing compareMS2 algorithm without modification on a diverse set of experiments. First we conducted a small phylogenetic study, using (mammalian) bone samples to study old material, and human pathogens aiming to distinguish clinically important strains. Although not as straightforward as primate sera analysis, the method shows significant promise for all these applications. We also used the algorithm to compare 24 different protocols for extraction of proteins from muscle tissue. The results provided useful information in comparing protocols. Finally, we applied compareMS2 aiming for quality control of two traceable protein reference standards (troponin) used in clinical chemistry assays, by analysing the effect of storage conditions. The results illustrate a broad applicability of the metric based on shared tandem mass spectra between LC/MS/MS datasets for analysing protein digests in different types of experiments. There is no reason to assume that our instance of this method is optimal in any of these situations, as it makes limited or no use of accurate mass and chromatographic retention time. We propose that with further improvement and refinement, this type of analysis can be applied as a simple but informative first step in many pipelines for bottom-up tandem mass spectrometry data analysis in proteomics and other fields, comparing or analysing large numbers of samples or datasets.

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