<p>Peptides are short chains of amino acids linked by peptide bonds. We can precisely determine the mass of a series of amino acids using mass spectroscopy. After MS1, we know what amino acids are in a peptide and how often each amino acid occurs. However, we do not know the order. By fragmenting the peptide in MS2, we can know the masses sub-peptides from length 2 (dipeptides) to the length of the peptide. Knowing this, we can use an algorithm to reassemble the peptide.

<p>The standard industryapproach compares the masses to those in a known protein database. Instead, this algorithm can be run locally and would not need outside information. This algorithm takes the series of sub-peptide masses as arrays and iterates through them. The smallest mass is a dipeptide and either b(2) or y2(). Iterating through the masses, if the next mass equals b(n) or y(n) + a known amino acid in the peptide, we know the amino acid is next in the order. Since we cannot determine the order of the dipeptides, we use the last added amino acid for y to determine the start of b and vice versa.

<p>The next version of this algorithm will account for missing masses.