A Novel Approach to LC-MS Expression Analysis using the Progenesis LC-MS Workflow

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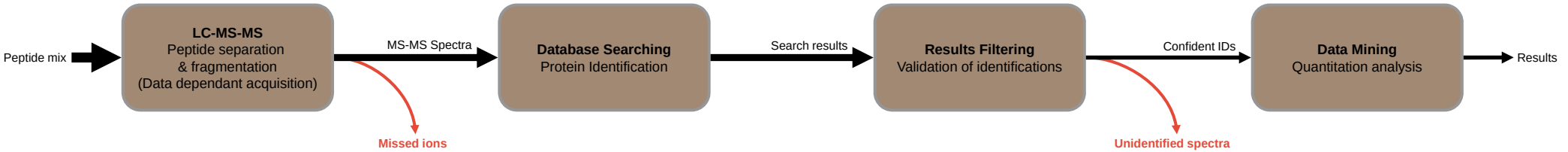
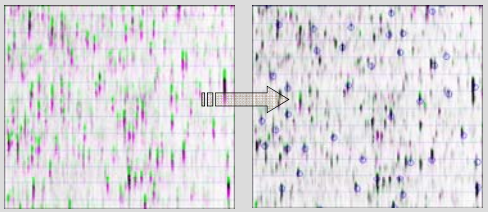
Traditional LC-MS-MS Workflow

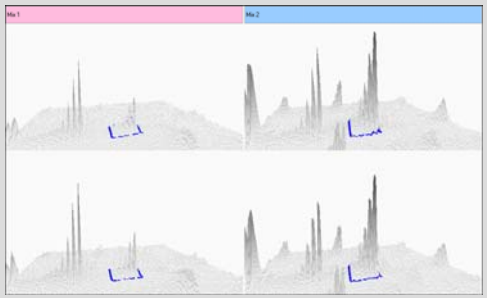


Progenesis LC-MS Workflow



To enable differential expression analysis of LC-MS data it needs to be aligned to compensate for the positional bias introduced by the LC separation technique.

This is achieved using automated LC-MS alignment algorithms coupled with the software's advanced visualisation tools.



In traditional LC-MS-MS analysis, information is discarded where data-dependent acquisition is not quick enough to probe every ion. This can result in significant protein behaviour being overlooked.

In Progenesis LC-MS, data is analysed at the LC-MS level to locate peaks exhibiting significant expression change between experiment groups.

The software ranks peptides in order of p-value and fold change between groups, with the most significant at the top. Using 2- and 3-D montage views and expression profile data, peptides of interest can be selected for further analysis.

The software outputs an inclusion list enabling targeted MS-MS analysis of the selected peptides. Thus, even if a confident protein identification does not follow for a peptide of interest, you are still aware of the significant expression change and can investigate further.

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