

Progenesis LC-MS : Quantitative label free workflow for the differential analysis of complex samples

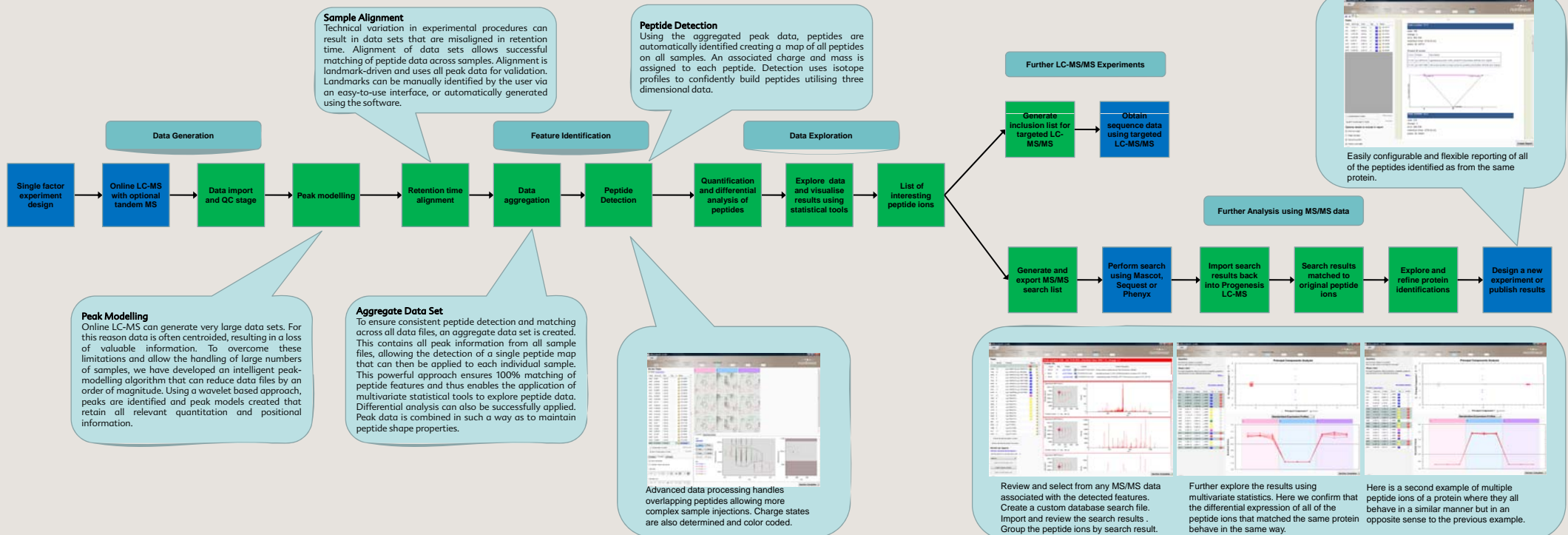
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MS based quantitative differential proteomics issues:

- **Per sample run times can be prohibitively long** — a 40 fraction offline / 3 hour online separation strategy can require as many as 5 days data capture per sample
- **Researchers forced to make experiment design compromises** — at 5 days a sample there can be real time pressures on collecting the amount of data that the researcher desires
- **Greater exposure to technical variation** — with data capture spread across many weeks the chances of a significant change in the properties of the chromatography system are greatly increased.
- **Quantitation strategies rely heavily on protein identification** — with the data spread across so many runs, protein identifications are usually required to reassemble the complete data set. This means that the quality of data is highly dependent on the success of identifying the proteins. Studies have shown that successful identification in MUDPIT runs is proportional to abundance. [e.g. Liu et al, Anal Chem 2004, 76, 4193-4201]

Workflow details

Progenesis LC-MS is a workflow-driven software designed to optimise the analysis of label-free comparative data sets. An example workflow is shown in below. The green squares represent functionality provided by Progenesis LC-MS and the blue squares are external operations or functionality.



Progenesis LC-MS:

- Handles complex samples - reducing the need to offline pre-fractionate resulting in huge time savings
- Is designed to handle large numbers of replicates
- Gives the researcher additional options to allow more optimal experiment designs
- Rapid sample acquisition reduces the chances of drift or equipment failure influencing the results
- Protein identification is supported but not necessary for quantitative analysis

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www.nonlinear.com/LC-MS