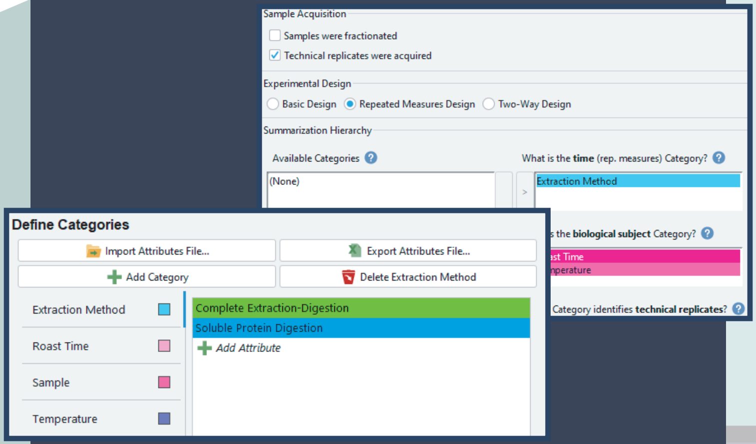
Experiment-driven Labeled and Label-free Quantitative Analysis

Analyze iTRAQ/TMT data from Proteome Discoverer, Mascot, or PEAKS mzIdentML files or label-free/isobaric-labeled samples from Scaffold


Sample Acquisition

☐ Samples were fractionated

☑ Technical replicates were acquired

Experimental Design

○ Basic Design ● Repeated Measures Design ○ Two-Way Design

Summarization Hierarchy

Available Categories: (None)

What is the **time** (rep. measures) Category?: Extraction Method

…s the **biological subject** Category?: …ast Time, …nperature

…Category identifies **technical replicates**?

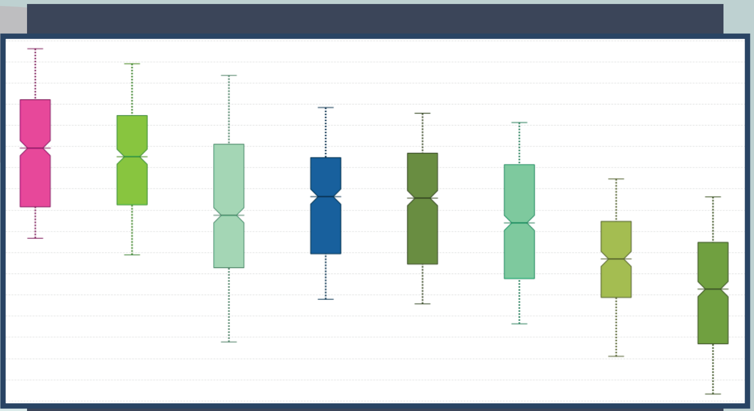
Define Categories

Extraction Method: Complete Extraction-Digestion, Soluble Protein Digestion

Normalize, roll-up, and interpret biological differences and find sources of technical variation at the fraction, technical, and biological replicate level

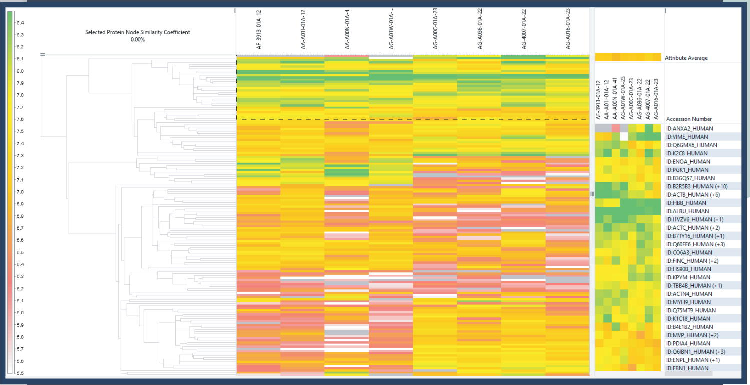
Select the most appropriate experimental design with easy-to-use wizards: basic, repeated measures, or two way

Share data using the free Scaffold Quant Viewer or exportable reports and graphics



Quantify differential expression and test for statistical significance

Assess biological meaning with gene ontology (GO) annotations



Analyze your data using PCA and heatmaps. Scaffold Quant's flexible organization is an ideal environment for exploratory data analysis

Proteome Software
www.proteomesoftware.com

Version 4.1