

Protein Identification

Database Searching

- Match spectra to sequence databases
- Multiple search engines available
- Statistical scoring algorithms

Peptide-Spectrum Matching

- Compare experimental vs theoretical
- Fragment ion matching
- Mass accuracy requirements

Score Calculations

- Probability-based scoring
- Expectation values (E-values)
- Confidence metrics

FDR Estimation

- False discovery rate control
- Target-decoy approach
- Typically 1-5% FDR threshold