Incorporating Digestion Efficiency Analysis to Improve Shotgun Proteomics Analytical Pipelines

Michael R. Hoopmann, Vidur Kailash, Luis Mendoza, and Robert L. Moritz
Institute for Systems Biology, Seattle WA

Overview

- SPACEPro (Shotgun Proteomic Analysis of Cleavage Efficiency of Proteins) is a software tool for evaluating digestion efficiency.
- SPACEPro is seamlessly integrated into the Trans-Proteomic Pipeline.
- SPACEPro identifies digestion deficiencies to optimize sample preparation conditions.

Introduction

Shotgun proteomics relies on efficient and predictable cleavage of proteins in a complex mixture for analysis by liquid chromatography mass spectrometry (LC-MS). Most shotgun proteomics analyses are performed following digestion with proteolytic enzymes, such as trypsin, that have been well characterized for their specificity and efficiency. Protein digestion efficiency is rarely evaluated or reported in proteomics data analyses, perhaps because ubiquitous use of digestion enzymes has led to the assumption that the digestion consistently runs to completion. However, poor protein cleavage can have adverse effects on protein identification and protein quantification, and therefore should be monitored in every experiment. Here, we show how digestion efficiency can be integrated into a shotgun proteomics pipeline to improve proteomics analyses.

Features

Seamless Integration into the Trans-Proteomic Pipeline Shotgun Proteomics Workflows

Clear Summaries of Analysis at PSM, Peptide, and Protein Level

Output

Digestion Optimization

Exploring Peptides with Missed Cleavage: Sequence Analysis and Efficiency Recalculation

Support & Information

Support provided by:
- ROI GM087221
- NIA U19AG023122

http://tppms.org