MSPypeline: a python package for streamlined data analysis of mass spectrometry-based proteomics

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Authors

Simon Heming Pauline Hansen Artyom Vlasov Florian Schwörer Stephen Schaumann Paulina Frolovaitė Wolf-Dieter Lehmann Jens Timmer Marcel Schilling Barbara Helm Ursula Klingmüller

Abstract

Summary

Mass spectrometry-based proteomics is increasingly employed in biology and medicine. To generate reliable information from large datasets and ensure comparability of results, it is crucial to implement and standardize the quality control of the raw data, the data processing steps and the statistical analyses. MSPypeline provides a platform for importing MaxQuant output tables, generating quality control reports, data preprocessing including normalization and performing exploratory analyses by statistical inference plots. These standardized steps assess data quality, provide customizable figures and enable the identification of differentially expressed proteins to reach biologically relevant conclusions.

Availability and implementation

The source code is available under the MIT license at https://github.com/siheming/mspypeline with documentation at https://mspypeline.readthedocs.io. Benchmark mass spectrometry data are available on ProteomeXchange (PXD025792).

Supplementary information

Supplementary data are available at Bioinformatics Advances online.