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Altri autori (Persone)	BarsnesHarald EideGeir Egil MartensLennart
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Nota di contenuto	Computational and Statistical Methods for Protein Quantification by Mass Spectrometry; Contents; Preface; Terminology; Acknowledgements; 1 Introduction; 1.1 The composition of an organism; 1.1.1 A simple model of an organism; 1.1.2 Composition of cells; 1.2 Homeostasis, physiology, and pathology; 1.3 Protein synthesis; 1.4 Site, sample, state, and environment; 1.5 Abundance and expression - protein and proteome profiles; 1.5.1 The protein dynamic range; 1.6 The importance of exact specification of sites and states; 1.6.1 Biological features; 1.6.2 Physiological and pathological features 1.6.3 Input features1.6.4 External features; 1.6.5 Activity features; 1.6.6 The cell cycle; 1.7 Relative and absolute quantification; 1.7.1 Relative quantification; 1.7.2 Absolute quantification; 1.8 In vivo and in vitro experiments; 1.9 Goals for quantitative protein experiments; 1.10 Exercises; 2 Correlations of mRNA and protein abundances; 2.1 Investigating the correlation; 2.2 Codon bias; 2.3 Main results from

experiments; 2.4 The ideal case for mRNA-protein comparison; 2.5 Exploring correlation across genes; 2.6 Exploring correlation within one gene; 2.7 Correlation across subsets  
2.8 Comparing mRNA and protein abundances across genes from two situations  
2.9 Exercises; 2.10 Bibliographic notes; 3 Protein level quantification; 3.1 Two-dimensional gels; 3.1.1 Comparing results from different experiments - DIGE; 3.2 Protein arrays; 3.2.1 Forward arrays; 3.2.2 Reverse arrays; 3.2.3 Detection of binding molecules; 3.2.4 Analysis of protein array readouts; 3.3 Western blotting; 3.4 ELISA - Enzyme-Linked Immunosorbent Assay; 3.5 Bibliographic notes; 4 Mass spectrometry and protein identification; 4.1 Mass spectrometry; 4.1.1 Peptide mass fingerprinting (PMF)  
4.1.2 MS/MS - tandem MS  
4.1.3 Mass spectrometers; 4.2 Isotope composition of peptides; 4.2.1 Predicting the isotope intensity distribution; 4.2.2 Estimating the charge; 4.2.3 Revealing isotope patterns; 4.3 Presenting the intensities - the spectra; 4.4 Peak intensity calculation; 4.5 Peptide identification by MS/MS spectra; 4.5.1 Spectral comparison; 4.5.2 Sequential comparison; 4.5.3 Scoring; 4.5.4 Statistical significance; 4.6 The protein inference problem; 4.6.1 Determining maximal explanatory sets; 4.6.2 Determining minimal explanatory sets; 4.7 False discovery rate for the identifications  
4.7.1 Constructing the decoy database  
4.7.2 Separate or composite search; 4.8 Exercises; 4.9 Bibliographic notes; 5 Protein quantification by mass spectrometry; 5.1 Situations, protein, and peptide variants; 5.1.1 Situation; 5.1.2 Protein variants - peptide variants; 5.2 Replicates; 5.3 Run - experiment - project; 5.3.1 LC-MS/MS run; 5.3.2 Quantification run; 5.3.3 Quantification experiment; 5.3.4 Quantification project; 5.3.5 Planning quantification experiments; 5.4 Comparing quantification approaches/methods; 5.4.1 Accuracy; 5.4.2 Precision; 5.4.3 Repeatability and reproducibility  
5.4.4 Dynamic range and linear dynamic range

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## Sommario/riassunto

The definitive introduction to data analysis in quantitative proteomics  
This book provides all the necessary knowledge about mass spectrometry based proteomics methods and computational and statistical approaches to pursue the planning, design and analysis of quantitative proteomics experiments. The author's carefully constructed approach allows readers to easily make the transition into the field of quantitative proteomics. Through detailed descriptions of wet-lab methods, computational approaches and statistical tools, this book covers the full scope of a quantitative experim

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