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| 1. Record Nr.           | UNINA9910495701303321   |
| Autore                  | Amabiamina Flora  |
| Titolo                  | Ahmadou Kourouma : mémoire vivante de la géopolitique en Afrique /<br>/ Jean-Fernand Bédia, Jean-Francis Ekoungoun  |
| Pubbl/distr/stampa      | Pessac, : Presses Universitaires de Bordeaux, 2020  |
| ISBN                    | 979-1-03-000626-1   |
| Descrizione fisica      | 1 online resource (242 p.)  |
| Collana                 | Eidôlon   |
| Altri autori (Persone)  | BassiouniNahla<br>BédiaJean-Fernand<br>BoumaajouneJaouad<br>CisséIsmaïla<br>EkoungounJean-Francis<br>FriedliLisa<br>GuédallaOumar<br>James-RaoulDanièle<br>Kouamé DagoHonoré<br>LattroTite<br>S. DiopCheikh M<br>SiendouKonaté<br>SissaoAlain Joseph<br>SouBenjamin<br>Taba OdoungaDidier |
| Soggetti                | History<br>roman<br>géopolitique<br>colonialisme<br>postcolonialisme<br>francophonie<br>littérature francophone<br>horizon d'attente<br>langue d'écriture<br>néocolonialisme<br>histoire des idées  |
| Lingua di pubblicazione | Francese  |
| Formato                 | Materiale a stampa  |

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| <b>Livello bibliografico</b>   | Monografia   |
| <b>Sommario/riassunto</b>      | Ce livre, consacré à l'œuvre d'Ahmadou Kourouma, prend pour thème majeur la géopolitique, sorte de téléologie cristallisant la carrière de l'écrivain, dont l'« essentiel », pour lui, semble avoir été éludé au profit d'une approche longtemps fascinée par sa créativité formelle et linguistique. Derrière cet horizon d'attente, se forme un magma d'idées et de paradigmes éculés, comme le rapport du romancier ivoirien à la langue du colonisateur et son aversion pour les régimes dictatoriaux africains. Pareille lecture, au contraire de toutes les gloses élogieuses à l'égard d'Ahmadou Kourouma, fait courir le risque de la marginalisation dans l'histoire des idées à la critique consacrée à l'ensemble de ses romans. Questionner l'œuvre sous le prisme de la géopolitique et de la question postcoloniale permet de la saisir, tout comme son auteur, loin des fantasmes dominants d'une herméneutique qui s'est fossilisée, au fil du temps, dans des grilles de lecture qui ont parfois donné l'impression, même à Kourouma de son vivant, de se trouver devant une impasse. |
| <b>2. Record Nr.</b>           | UNINA9910831040903321  |
| <b>Autore</b>                  | Eidhammer Ingvar   |
| <b>Titolo</b>                  | Computational and statistical methods for protein quantification by mass spectrometry [[electronic resource] /] / Ingvar Eidhammer ... [et al.]  |
| <b>Pubbl/distr/stampa</b>      | Chichester, West Sussex, U.K., : John Wiley & Sons Inc., 2013  |
| <b>ISBN</b>                    | 1-118-49404-0<br>1-299-18826-5<br>1-118-49378-8<br>1-118-49377-X   |
| <b>Descrizione fisica</b>      | 1 online resource (356 p.)   |
| <b>Altri autori (Persone)</b>  | BarsnesHarald<br>EideGeir Egil<br>MartensLennart   |
| <b>Disciplina</b>              | 572.636<br>572/.636  |
| <b>Soggetti</b>                | Proteomics - Statistical methods<br>Mass spectrometry - Data processing  |
| <b>Lingua di pubblicazione</b> | Inglese  |
| <b>Formato</b>                 | Materiale a stampa   |

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| Livello bibliografico | Monografia   |
| Note generali         | Description based upon print version of record.  |
| Nota di bibliografia  | Includes bibliographical references and index.   |
| Nota di contenuto     | <p>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 features 1.6.4 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</p> |
| Sommario/riassunto    | <p>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</p>   |

book covers the full scope of a quantitative experim

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