1. Record Nr. UNINA9910463629603321

Autore	Minoiu Camelia
Titolo	Kernel density estimation based on grouped data : the case of poverty assessment / / Camelia Minoiu and Sanjay G. Reddy
Pubbl/distr/stampa	[Washington, District of Columbia] : , : International Monetary Fund, , 2008 ©2008
ISBN	1-4623-9111-7 1-4527-8641-0 1-4518-7041-8 1-282-84134-3 9786612841347
Descrizione fisica	1 online resource (36 p.)
Collana	IMF working paper ; ; WP/08/183
Altri autori (Persone)	ReddySanjay G
Disciplina	339.46
Soggetti	Poverty - Measurement Income distribution - Econometric models Kernel functions Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Contents; I. Motivation; II. The Data Structure and the Bias of the Estimator; III. The Bandwidth and Kernels Considered; IV. Monte Carlo Study; A. Theoretical Distributions; B. Summary Statistics, Density Estimates and Diagrams; C. Poverty Estimates; V. Country Studies; VI. Global Poverty; VII. Conclusions; References; Appendix; Appendix Figures; 1. Distributions used in Monte Carlo analysis; 2. Bias of KDE-based density (log-normal distribution); Appendix Tables; 1. Summary statistics from KDE-based sample; 3. Bias of estimated density (multimodal distribution) 4. Bias of estimated density (Dagum distribution)2. Bias of poverty measures (Low and High Poverty Lines); 5. Bias in the poverty headcount ratio versus location of poverty line; 3. Bias of poverty measures (Triweight kernel, Poverty line: 0.25 x median); 4. Bias of poverty measures (Hybrid bandwidth, Poverty line: 0.5 x median); 5.

	Bias of poverty measures (Epanechnikov kernel, Silverman bandwidth); 6. Bias of poverty measures (Gaussian kernel, Poverty line: Capability); 6. Survey-based and grouped data KDE-based density estimates; 7. Global poverty rates (% poor) 8. Global poverty counts (millions)
Sommario/riassunto	We analyze the performance of kernel density methods applied to grouped data to estimate poverty (as applied in Sala-i-Martin, 2006, QJE). Using Monte Carlo simulations and household surveys, we find that the technique gives rise to biases in poverty estimates, the sign and magnitude of which vary with the bandwidth, the kernel, the number of datapoints, and across poverty lines. Depending on the chosen bandwidth, the 1/day poverty rate in 2000 varies by a factor of 1.8, while the 2/day headcount in 2000 varies by 287 million people. Our findings challenge the validity and robustness of pove

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Record Nr.	UNINA9910830125203321
Autore	Budisa Nediljko
Titolo	Engineering the genetic code [[electronic resource]] : expanding the amino acid repertoire for the design of novel proteins / / Nediljko Budisa
Pubbl/distr/stampa	Weinheim, : Wiley-VCH, c2006
ISBN	1-280-85417-0 9786610854172 3-527-60718-8 3-527-60709-9
Descrizione fisica	1 online resource (314 p.)
Disciplina	572.65
Soggetti	Protein engineering Amino acids - Synthesis
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Engineering the Genetic Code; Foreword; Contents; Preface; 1 Introduction; 1.1 Classical Approaches to Protein Modification; 1.2

Peptide Synthesis, Semisynthesis and Chemistry of Total Protein Synthesis; 1.3 Chemoselective Ligations Combined with Biochemical Methods; 1.4 Methods and Approaches of Classical Protein Engineering; 1.5 Genetically Encoded Protein Modifications - Reprogramming Protein Translation; 1.6 Basic Definitions and Taxonomy; References; 2 A Brief History of an Expanded Amino Acid Repertoire; 2.1 The ""Golden Years"" of Molecular Biology and Triplet Code Elucidation
2.2 Early Experiments on the Incorporation of Amino Acid Analogs in Proteins2.3 Test Tube (Cell-free) Synthesis of Proteins and Early Incorporation Experiments; 2.4 Noncanonical Amino Acids as Tools for Studying Cell Metabolism, Physiology, Protein Processing and Turnover; 2.5 Problem of Proofs and Formal Criteria for Noncanonical Amino Acid Incorporation; 2.6 Recent Renaissance - Genetic Code Engineering; References; 3 Basic Features of the Cellular Translation Apparatus; 3.1 Natural Laws, Genetic Information and the ""Central Dogma"" of Molecular Biology
3.2 Cellular Investments in Ribosome-mediated Protein Synthesis3.3 Molecular Architecture of AARS; 3.4 Structure and Function of the tRNA Molecule; 3.5 Aminoacylation Reaction; 3.6 AARS:tRNA Interactions - Identity Sets; 3.7 Translational Proofreading; 3.8 Ribosomal Decoding - A Brief Overview; 3.9 Codon Bias and the Fidelity of Protein Synthesis; 3.10 Preprogrammed Context-dependent Recoding: fMet, Sec, Pyl, etc.; 3.11 Beyond Basic Coding - Posttranslational Modifications; References; 4 Amino Acids and Codons - Code Organization and Protein Structure
4.1 Basic Features and Adaptive Nature of the Universal Genetic Code4.2 Metabolism and Intracellular Uptake of Canonical Amino Acids; 4.3 Physicochemical Properties of Canonical Amino Acids; 4.4 Reasons for the Occurrence of Only 20 Amino Acids in the Genetic Code; 4.5 What Properties of Amino Acids are Best Preserved by the Genetic Code?; 4.6 Evolutionary Legacy: Dual Nature of Conserved Code and Finite Number of Protein Folds; 4.7 Natural Variations in Assignment of Codons of the Universal Genetic Code; 4.7.1 Nucleoside Modifications and Codon Reassignments
4.8 Codon Reassignment Concepts Possibly Relevant to Code Engineering4.8.1 Genome Size, Composition, Complexity and Codon Reassignments; 4.8.2 Stop Codon Takeover, Codon Capture and Codon Ambiguity; References; 5 Reprograming the Cellular Translation Machinery; 5.1 Enzyme Specificity of Aminoacyl-tRNA Synthetases (AARS) and Code Interpretation; 5.1.1 Living Cells as Platforms for Amino Acid Repertoire Expansion; 5.1.2 Uptake, Toxicity and Metabolic Fate of Noncanonical Amino Acids; 5.1.2.1 General Considerations; 5.1.2.2 Amino Acid Transport
5.1.2.3 Metabolic Conversions and Toxicity of Analogs and Surrogates

Sommario/riassunto

The ability to introduce non-canonical amino acids in vivo has greatly expanded the repertoire of accessible proteins for basic research and biotechnological application.Here, the different methods and strategies to incorporate new or modified amino acids are explained in detail, including a lot of practical advice for first-time users of this powerful technique.Novel applications in protein biochemistry, genomics, biotechnology and biomedicine made possible by the expansion of the genetic code are discussed and numerous examples are given.Essential reading for all molecular life s

3. Record Nr. UNINA9910854696703321

Titolo	Encyclopaedia of food science, food technology and nutrition / edited by R. Macrae, R.K. Robinson, M.J. Sadler
Pubbl/distr/stampa	London [etc.], : Academic Press, 1993
ISBN	0122268504
Descrizione fisica	8 v. (5365 p. compless.) : ill. ; 29 cm
Disciplina	664.00321
Locazione	FAGBC
Collocazione	A MIC 1624-1 A MIC 1624-2 A MIC 1624-3 A MIC 1624-4 A MIC 1624-5 A MIC 1624-6 A MIC 1624-7 A MIC 1624-8
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia