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Titolo	Natural selection : methods and applications // Mario A. Fares, School of Genetics and Microbiology, Department of Genetics, University of Dublin, Trinity College, Dublin, Ireland
Pubbl/distr/stampa	Boca Raton : , : Taylor & Francis, , [2015] ©2015
ISBN	0-429-09506-6 1-4822-6373-4
Descrizione fisica	1 online resource (274 p.)
Disciplina	547.79
Soggetti	Nucleotides
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	A Science Publishers book.
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Front Cover; Dedication; Preface; Contents; CHAPTER 1: The Role of Natural Selection in Evolution; CHAPTER 2: Identifying Evolution Signatures in Molecules; CHAPTER 3: Modeling Evolution of Molecular Sequences; CHAPTER 4: Identifying Natural Selection with Molecular Data; CHAPTER 5: Inferring Functional Divergence in Protein Sequences; Chapter 6: The Influence of Re combination on the Estimation of Selection from Coding Sequence Alignments; Chapter 7: Why Proteins Evolve at Different Rates: The Determinants of Proteins'Rates of Evolution Chapter 8: The Network Framework of Molecular EvolutionChapter 9: Molecular Coevolution:Methods and Applications; Color Plate Section; Back Cover
Sommario/riassunto	This book summarizes the knowledge in the field of methods to identify signatures of natural selection. A number of mathematical models and methods have been designed to identify the fingerprints of natural selection on genes and genomes. Such methods are provided in a simple and direct way so that students of different disciplines can navigate through molecular fitness landscapes using complex methods with a basic knowledge on bioinformatics. A collection of the main methods to detect selection in protein-coding genes and amino acid

sequences is given at different levels of complexity, from nucleotides to proteins and molecular networks. The importance of identifying natural selection in genes and genomes through the methods described in this book transcends the bioinformatics and computational biology fields, presenting applications for experimental biologists in a straightforward and understandable way--Provided by publisher.
