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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Preface -- Introduction -- Phylogenetic Data in R -- Phylogenetic Diversity -- Functional Diversity -- Phylogenetic & Functional Beta Diversity -- Null Models -- Comparative Methods & Phylogenetic Signal -- Partitioning the Phylogenetic, Functional, Environmental and Spatial Components of Community Diversity -- Integrating R with Other Phylogenetic and Functional Trait Analytical Software -- References -- Index.
Sommario/riassunto	Functional and Phylogenetic Ecology in R is designed to teach readers to use R for phylogenetic and functional trait analyses. Over the past decade, a dizzying array of tools and methods were generated to incorporate phylogenetic and functional information into traditional ecological analyses. Increasingly these tools are implemented in R, thus greatly expanding their impact. Researchers getting started in R can use this volume as a step-by-step entryway into phylogenetic and functional analyses for ecology in R. More advanced users will be able to use this volume as a quick reference to understand particular analyses. The volume begins with an introduction to the R environment and handling relevant data in R. Chapters then cover phylogenetic and functional metrics of biodiversity; null modeling and randomizations

for phylogenetic and functional trait analyses; integrating phylogenetic and functional trait information; and interfacing the R environment with a popular C-based program. This book presents a unique approach through its focus on ecological analyses and not macroevolutionary analyses. The author provides his own code, so that the reader is guided through the computational steps to calculate the desired metrics. This guided approach simplifies the work of determining which package to use for any given analysis. Example datasets are shared to help readers practice, and readers can then quickly turn to their own datasets.