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Autore	Bacak Miroslav
Titolo	Convex analysis and optimization in Hadamard spaces / / Miroslav Bacak
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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	Front matter -- Preface -- Contents -- 1 Geometry of Nonpositive Curvature -- 2 Convex sets and convex functions -- 3 Weak convergence in Hadamard spaces -- 4 Nonexpansive mappings -- 5 Gradient flow of a convex functional -- 6 Convex optimization algorithms -- 7 Probabilistic tools in Hadamard spaces -- 8 Tree space and its applications -- References -- Index -- Back matter
Sommario/riassunto	In the past two decades, convex analysis and optimization have been developed in Hadamard spaces. This book represents a first attempt to give a systematic account on the subject. Hadamard spaces are complete geodesic spaces of nonpositive curvature. They include Hilbert spaces, Hadamard manifolds, Euclidean buildings and many other important spaces. While the role of Hadamard spaces in geometry and geometric group theory has been studied for a long time, first analytical results appeared as late as in the 1990's. Remarkably, it turns out that Hadamard spaces are appropriate for the theory of convex sets and convex functions outside of linear spaces. Since convexity underpins a large number of results in the geometry of Hadamard spaces, we believe that its systematic study is of substantial interest.

Optimization methods then address various computational issues and provide us with approximation algorithms which may be useful in sciences and engineering. We present a detailed description of such an application to computational phylogenetics. The book is primarily aimed at both graduate students and researchers in analysis and optimization, but it is accessible to advanced undergraduate students as well.

2. Record Nr.	UNINA9910557545803321
Autore	Jiang Hui
Titolo	Statistical Methods for the Analysis of Genomic Data
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Descrizione fisica	1 online resource (136 p.)
Soggetti	Mathematics and Science Research and information: general
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	In recent years, technological breakthroughs have greatly enhanced our ability to understand the complex world of molecular biology. Rapid developments in genomic profiling techniques, such as high-throughput sequencing, have brought new opportunities and challenges to the fields of computational biology and bioinformatics. Furthermore, by combining genomic profiling techniques with other experimental techniques, many powerful approaches (e.g., RNA-Seq, Chips-Seq, single-cell assays, and Hi-C) have been developed in order to help explore complex biological systems. As a result of the increasing availability of genomic datasets, in terms of both volume and variety, the analysis of such data has become a critical challenge as well as a topic of great interest. Therefore, statistical methods that address the problems associated with these newly developed

techniques are in high demand. This book includes a number of studies that highlight the state-of-the-art statistical methods for the analysis of genomic data and explore future directions for improvement.
