

1. Record Nr.	UNINA990008243930403321
Autore	Turchiarulo, Giuseppe
Titolo	Contributi di miglioria per le opere eseguite dallo Stato o con il suo concorso e dagli Enti locali / Giuseppe Turchiarulo
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2. Record Nr.	UNINA9910483148503321
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Altri autori (Persone)	EskinEleazar WorkmanChris
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Predicting Genetic Regulatory Response Using Classification: Yeast Stress Response -- Detecting Functional Modules of Transcription Factor Binding Sites in the Human Genome -- Fishing for Proteins in the Pacific Northwest -- PhyloGibbs: A Gibbs Sampler Incorporating Phylogenetic Information -- Application of Kernel Method to Reveal Subtypes of TF Binding Motifs -- Learning Regulatory Network Models that Represent Regulator States and Roles -- Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs -- Parameter Landscape Analysis for Common Motif Discovery Programs -- Inferring Cis-region Hierarchies from Patterns in Time-Course Gene Expression Data -- Modeling and Analysis of Heterogeneous Regulation in Biological Networks.
Sommario/riassunto	<p>Research in the field of gene regulation is evolving rapidly in an ever-changing scientific environment. Microarray techniques and comparative genomics have enabled more comprehensive studies of regulatory genomics and are proving to be powerful tools of discovery. The application of chromatin immunoprecipitation and microarrays (chIP-on-chip) to directly study the genomic binding locations of transcription factors has enabled more comprehensive modeling of regulatory networks. In addition, complete genome sequences and the comparison of numerous related species has demonstrated that conservation in non-coding DNA sequences often provides evidence for cis-regulatory binding sites. That said, much is still to be learned about the regulatory networks of these sequenced genomes. Systematic methods to decipher the regulatory mechanism are also crucial for corroborating these regulatory networks. The core of these methods are the motif discovery algorithms that can help predict cis-regulatory elements. These DNA-motif discovery programs are becoming more sophisticated and are beginning to leverage evidence from comparative genomics (phylogenetic footprinting) and chIP-on-chip studies. How to use these new sources of evidence is an active area of research.</p>