

1. Record Nr.	UNINA9910787545103321
Autore	Goosman Stuart L. <1953-2017.>
Titolo	Group harmony [[electronic resource] ] : the black urban roots of rhythm & blues // Stuart L. Goosman
Pubbl/distr/stampa	Philadelphia, : University of Pennsylvania Press, 2005
ISBN	0-8122-0204-X
Descrizione fisica	1 online resource (305 p.)
Disciplina	781.64309
Soggetti	Rhythm and blues music - History and criticism African Americans - Social conditions
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Front matter -- Contents -- Preface -- 1. Antecedents -- 2. Time and Place -- 3. Entrepreneurship -- 4. Mediators -- 5 Patterns -- Epilogue -- Appendix -- Bibliography -- Index -- Acknowledgments
Sommario/riassunto	In 1948, the Orioles, a Baltimore-based vocal group, recorded "It's Too Soon to Know." Combining the sound of Tin Pan Alley with gospel and blues sensibilities, the Orioles saw their first hit reach #13 on the pop charts, thus introducing the nation to vocal rhythm & blues and paving the way for the most successful groups of the 1950s. In the first scholarly treatment of this influential musical genre, Stuart Goosman chronicles the Orioles' story and that of myriad other black vocal groups in the postwar period. A few, like the Orioles, Cardinals, and Swallows from Baltimore and the Clovers from Washington, D.C., established the popularity of vocal rhythm & blues nationally. Dozens of other well-known groups (and hundreds of unknown ones) across the country cut records and performed until about 1960. Record companies initially marketed this music as rhythm & blues; today, group harmony continues to resonate for some as "doo-wop." Focusing in particular on Baltimore and Washington and drawing significantly from oral histories, Group Harmony details the emergence of vocal rhythm & blues groups from black urban neighborhoods. Group harmony was a source of empowerment for young singers, for it provided them with a means of expression and some aspect of control over their lives where there were limited alternatives. Through group

harmony, young black males celebrated and musically confounded, when they could not overcome, complex issues of race, separatism, and assimilation during the postwar period. Group harmony also became a significant resource for the popular music industry. Goosman interviews dozens of performers, deejays, and industry professionals to examine the entrepreneurial promise of midcentury popular music and chronicle the convergence of music, place, and business, including the business of records, radio, promotion, and song writing. Featured in the book's account of the black urban roots of rhythm & blues are the recollections of singers from groups such as the Cardinals, Clovers, Dunbar Four, Four Bars of Rhythm, Five Blue Notes, Hi Fi's, Plants, Swallows, and many others, including Jimmy McPhail, a well-known Washington vocalist; Deborah Chessler, the manager and songwriter for the original Orioles; Jesse Stone, the writer and arranger from Atlantic Records; Washington radio personality Jackson Lowe; and seminal black deejays Al ("Big Boy") Jefferson, Maurice ("Hot Rod") Hulbert, and Tex Gathings.

2. Record Nr.	UNINA9910483148503321
Titolo	Regulatory Genomics : RECOMB 2004 International Workshop, RRG 2004, San Diego, CA, USA, March 26-27, 2004, Revised Selected Papers // edited by Eleazar Eskin, Chris Workman
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2005
Edizione	[1st ed. 2005.]
Descrizione fisica	1 online resource (VIII, 116 p.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 3318
Altri autori (Persone)	EskinEleazar WorkmanChris
Disciplina	572
Soggetti	Biochemistry Algorithms Computer science - Mathematics Discrete mathematics Artificial intelligence - Data processing Database management Bioinformatics Discrete Mathematics in Computer Science Data Science Database Management

Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
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>