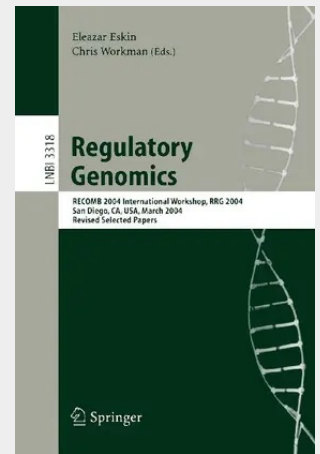


Regulatory Genomics

RECOMB 2004 International Workshop, RRG 2004, San Diego, CA, USA, March 26-27, 2004, Revised Selected Papers

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.

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53,49 €

49,99 € (zzgl. MwSt.)

Lieferfrist: bis zu 10 Tage

Artikelnummer: 9783540244561
Medium: Buch
ISBN: 978-3-540-24456-1
Verlag: Springer
Erscheinungstermin: 16.02.2005
Sprache(n): Englisch
Auflage: 1. Auflage 2005
Serie: Lecture Notes in Computer Science
Produktform: Kartoniert
Gewicht: 204 g
Seiten: 116
Format (B x H): 155 x 235 mm

