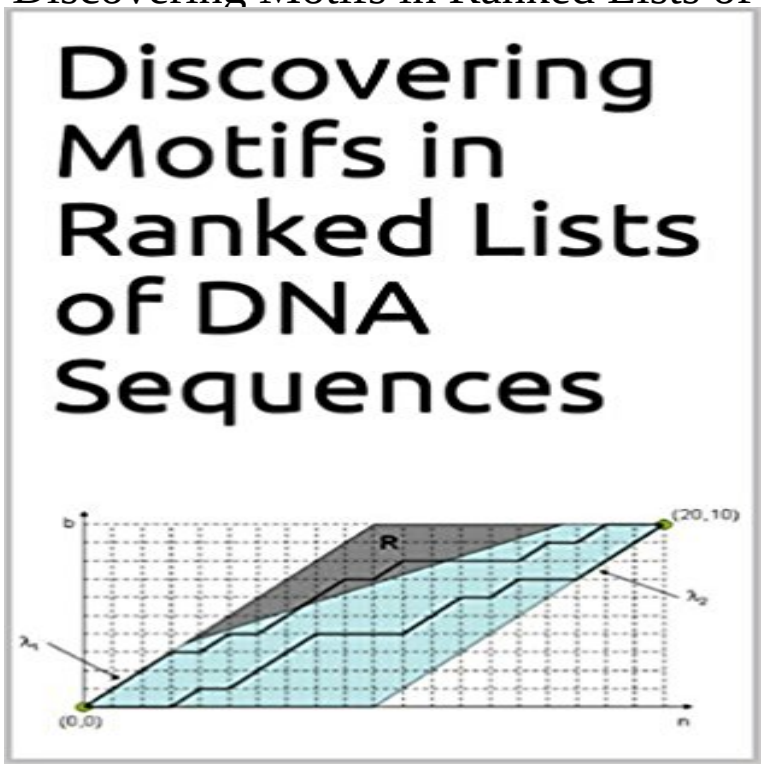
Discovering Motifs in Ranked Lists of DNA Sequences



Computational methods for discovery of sequence elements that are enriched in a target set compared with a background set are fundamental in molecular biology research. One example is the discovery of transcription factor binding motifs that are inferred from ChIPchip (chromatin immuno-precipitation on a microarray) measurements. Several major challenges in sequence motif discovery still require consideration: (i) the need for a principled approach to partitioning the data into target and background sets; (ii) the lack of rigorous models and of an exact p-value for measuring motif enrichment; (iii) the need for an appropriate framework for accounting for motif multiplicity; (iv) the tendency, in many of the existing methods, to report presumably significant motifs even when applied to randomly generated data. In this paper we present a statistical framework for discovering enriched sequence elements in ranked lists that resolves these four issues. We demonstrate the implementation of this framework in a software application, termed DRIM (discovery of rank imbalanced motifs), which identifies sequence motifs in lists of ranked DNA sequences. We applied DRIM to ChIPchip and CpG methylation data and obtained the following results. (i) Identification of 50 novel putative transcription factor (TF) binding sites in yeast ChIPchip data. The biological function of some of them was further investigated to gain new insights on transcription regulation networks in yeast. For example, our discoveries enable the elucidation of the network of the TF ARO80. Another finding concerns a systematic TF binding enhancement to sequences containing CA repeats. (ii) Discovery of novel motifs in human cancer CpG methylation data. Remarkably, most of these motifs are similar to DNA sequence elements bound by the Polycomb complex that promotes histone

methylation. Our findings thus support a model in which histone methylation and CpG methylation are mechanistically linked. Overall, we demonstrate that the statistical framework embodied in the DRIM software tool is highly effective for identifying regulatory sequence elements in a variety of applications ranging from expression and ChIPchip to CpG methylation data. DRIM is publicly available at http://bioinfo.cs.technion.ac.il/drim.

Plant Omics: Trends and Applications - Google Books Result This includes a parameter tuning tool, a support to pattern ranking and typical D., Yogev, S., Yakhini, Z.: Discovering motifs in ranked lists of DNA sequences. **Diskovering motifs in ranked list of DNA sequences** PLoS Comput Biol. 2007 Mar 233(3):e39. Discovering motifs in ranked lists of DNA sequences. Eden E(1), Lipson D, Yogev S, Yakhini Z. Author information: **Discovering Motifs in Ranked Lists of DNA Sequences - PLoS ONE** Mar 23, 2007 We describe a statistical framework for discovering motifs in a list of genomic sequences that are ranked according to a biological parameter or **PLOS Computational Biology: Discovering Motifs in Ranked Lists of** Title: Discovering Motifs in Ranked Lists of DNA Sequences. Language: English Authors: Eden, Eran1 eraneden@. Lipson, Doron1. Yogev **Discovering Motifs in Ranked Lists of DNA Sequences** Mar 23, 2007 Citation: Eden E, Lipson D, Yogev S, Yakhini Z (2007) Discovering Motifs in Ranked Lists of DNA Sequences. PLoS Comput Biol 3(3): e39. **Thesis - Laboratory of Computational Biology** May 21, 2007 In particular, a relevant software called DRIM (discovery of rank imbalanced motifs)- which identifies sequence motifs in lists of ranked DNA **Discovering Motifs in Ranked Lists of DNA Sequences - DRIMust** Mar 22, 2007 Discovering Motifs in Ranked Lists of DNA Sequences. Mar 23, 2007 Citation: Eden E, Lipson D, Yogev S, Yakhini Z (2007) Discovering motifs in ranked lists of DNA sequences. PLoS Comput Biol 3(3): e39. **Authors - PLOS** May 17, 2013 DRIMust takes as input ranked lists of sequences in FASTA format and returns motifs .. Discovering motifs in ranked lists of DNA sequences. **Discovering Motifs in Ranked Lists of DNA Sequences - CS Technion** Ding Q, Zeng J, He XQ (2014) Deep sequencing on a genome-wide scale reveals Yakhini Z (2007) Discovering motifs in ranked lists of DNA sequences. **Related Content - PLOS** In this paper we present a statistical framework for discovering enriched sequence elements in ranked lists that resolves these four issues. We demonstrate the **Discovering Motifs in Ranked Lists of DNA Sequences - NCBI** May 14, 2007 Source. Eden, E., Lipson, D., Yogev, S., Yakhini, Z. 2007. Discovering motifs in ranked lists of DNA sequences. Plos Comput. Biol. Vol. 3, No. **Discovering Motifs in Ranked Lists of DNA Sequences. - ebsco** Discovering Motifs in Ranked Lists of DNA Sequences. Research Thesis. Submitted in partial fulfillment of the requirements for the degree of Master of Science **Discovering Motifs in Ranked Lists of DNA Sequences Digital** Jan 1, 2017 - 20 sec - Uploaded by araujoDNA Computing and Molecular Programming 15th International Meeting on DNA Computing **Systems Biology: Applications in Cancer-related Research - Google Books Result Discovering Motifs in Ranked Lists of DNA Sequences - Figshare** Mar 23, 2007 Author SummaryA computational problem with many **Discovering Motifs in Ranked Lists of DNA Sequences - YouTube** Subject, Discovering Motifs in Ranked Lists of DNA Sequences Remarkably, most of these motifs are similar to DNA sequence elements bound by the **Springer Handbook of Bio-/Neuro-Informatics - Google Books Result** 33. 34. 35. 36. van Helden J, Rios AF, Collado-Vides J. (2000) Discovering regulatory elements in (2007) Discovering motifs in ranked lists of DNA sequences. **Discovering motifs in ranked lists of DNA sequences. - NCBI** Author Summary A computational applications in molecular biology is to **Discovering Motifs in Ranked Lists of DNA Sequences - YouTube** Mar 23, 2007 Author SummaryA computational problem with many **Comments - PLOS** Title: Discovering Motifs in Ranked Lists of DNA Sequences. Authors: Eden, Eran Lipson, Doron Yogev, Sivan Yakhini, Zohar. Publication: **Full Text - Nucleic Acids Research - Oxford Academic** Mar 23, 2007 Citation: Eden E, Lipson D, Yogev S, Yakhini Z (2007) Discovering motifs in ranked lists of DNA sequences. PLoS Comput Biol 3(3): e39. **Discovering Motifs in Ranked Lists of DNA Sequences Eran Eden** Discovering Motifs in Ranked Lists of DNA Sequences. Research Thesis. 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