

Abstract Submitted
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On geometric measures of regulatory complexity ILYA NEMENMAN, Columbia University, CHRIS WIGGINS, Columbia University — Transcriptional regulation of a gene in a network can be characterized by a vector that counts the numbers of binding sites in the gene's promoter region where a protein product of every other gene can bind. We analyze the distribution of such vectors in the full *S. cerevisiae* genome and notice that they form an interesting low dimensional structure. This is significant for analyses that attempt to integrate expression and sequence information for the reconstruction of transcriptional networks since, in this case, one should be able to use similarity of promoter regions and expression profiles as effective aids.

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