Abstract Submitted
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Detecting cooperative sequences in the binding of RNA Polymerase-II KIMBERLY GLASS, University of Maryland, JULIAN ROZENBERG, National Cancer Institute (NIH), MICHELLE GIRVAN, WOLFGANG LOSERT, ED OTT, University of Maryland, CHARLES VINSON, National Cancer Institute (NIH), UMD/NIH SYSTEMS BIOLOGY COLLABORATION COLLABORATION — Regulation of the expression level of genes is a key biological process controlled largely by the 1000 base pair (bp) sequence preceding each gene (the promoter region). Within that region transcription factor binding sites (TFBS), 5-10 bp long sequences, act individually or cooperate together in the recruitment of, and therefore subsequent gene transcription by, RNA Polymerase-II (RNAP). We have measured the binding of RNAP to promoters on a genome-wide basis using Chromatin Immunoprecipitation (ChIP-on-Chip) microarray assays. Using all 8-base pair long sequences as a test set, we have identified the DNA sequences that are enriched in promoters with high RNAP binding values. We are able to demonstrate that virtually all sequences enriched in such promoters contain a CpG dinucleotide, indicating that TFBS that contain the CpG dinucleotide are involved in RNAP binding to promoters. Further analysis shows that the presence of pairs of CpG containing sequences cooperate to enhance the binding of RNAP to the promoter.

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