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Subject: Postgraduate Seminar by Mr Vipin Narang

SCHOOL OF COMPUTING,NUS

POSTGRADUATE SEMINAR BY

MR VIPIN NARANG

Gene Regulatory Element Prediction with Bayesian Networks

Supervisor: A/P Ken Sung

Meeting Room 1 (COM1 03-43)

29 April 2009 (Wednesday) 9am

Abstract:

While computational advances have enabled sequencing of genomes at a rapid rate, annotation of functional elements in genomic sequences is lagging far behind. Of particular importance is the identification of sequences that regulate gene expression. This dissertation contributes to the computational modeling and detection of three very important regulatory elements in eukaryotic genomes, viz. transcription factor binding motifs, gene promoters and cis-regulatory modules (enhancers). Position specificity of transcription factor binding sites is the main insight used to enhance the modeling and detection performance in all three applications.

The first application concerns in-silico discovery of transcription factor binding motifs in a set of regulatory sequences which are bound by the same transcription factor. A novel tool, LocalMotif, is developed for detecting biological motifs that are localized in a regulatory sequence relative to an anchoring point such as the transcription start site or the center of the ChIP sequences.

The second application is the development of a statistical model for promoter sequences. The modeling is based on the positional densities of oligonucleotides in promoter sequences. The model automatically recognizes transcription factor binding sites in the promoter along with their preferred occurrence positions. Based on this model, a continuous naïve Bayes classifier is developed for the detection of human promoters.

The third application concerns computational prediction of cis-regulatory modules or enhancers that control the expression of genes in a particular tissue at a particular development stage. Enhancers are clusters of binding sites for a set of cooperating transcription factors. The cooperating factors constitute a “regulatory code”. So far very few regulatory codes are known which have been determined by wet lab experiments. This research develops the first computational approach to learn regulatory codes de-novo from a repository of enhancers. A probabilistic graphical model is used to derive the regulatory codes and to predict novel enhancers.

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