THE UNIVERSITY OF
CHICAGO

Departments of Statistics and Ecology and Evolution

STATISTICS COLLOQUIUM

Special Statistics Consult/Natural History Seminar

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Elucidating Principles of Gene Regulation from Stochastic Models

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ABSTRACT

The complexity of multicellular organisms arises largely from reusing many of the same genes in numerous combinations, rather than by the introduction of novel genes for each new cell-type. Put another way, what makes you human is not so much which genes you have but how you use them. The instructions on how to put these genes together to make a human or a fly, lies in the noncoding, regulatory sequences, which may account for the larger portion of total sequence in the genome. These regulatory sequences affect gene expression by directing the assembly of multifaceted macromolecular complexes, which can interact with transcription machinery. Understanding the link between the type and arrangement of sequences in a regulatory region and the transcriptional properties of its target gene is a major challenge in understanding the genetic basis of life.

Mathematical models can help distill this complexity by providing a framework in which to relate regulatory architecture to transcriptional outcomes. I will argue that finite Markov models provide an attractive approach for deriving transcriptional behaviors from known or hypothesized models of regulatory biochemistry. I introduce a few, recently developed, mathematical results from this approach, and illustrate their utility by exploring the transcriptional consequences of two common, enigmatic features of multicellular gene regulation: binding site multiplicity and promoter proximal paused polymerase.
