

The University of Chicago

Department of Statistics

Seminar Series

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“Statistical Methods for Genome Comparison”

WEDNESDAY February 2, 2005 at 4:00 PM
110 Eckhart Hall, 5734 S. University Avenue

There will be an informal reception before his talk in Eckhart 110 at 3:00 pm.

ABSTRACT

One goal of computational biology is to find stretches of DNA sequence that are mutating at unusually slow rates. Such conserved elements often turn out to have important functional roles in the cell. Comparing sequence data in specific regions across different organisms has been effective in detecting conserved elements. I will describe the “phylogenetic shadowing” approach to genome comparison, which uses close evolutionary relatives like humans and some primate species. I will present results on detecting regulatory elements such as transcription-factor binding motifs. Then I will discuss a different problem, the identification of conserved genes, using a hidden Markov model which incorporates phylogeny. Power analysis can be used to suggest species that are worth sequencing, in order to identify conserved regions. I will talk about the underlying assumptions and the empirical results.