The University of Chicago
Department of Statistics

Seminar Series

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Rapid Evolution in the Human Genome

MONDAY, January 14, 2008 at 4:00 PM
133 Eckhart Hall, 5734 S. University Avenue
Refreshments following the seminar in Eckhart 110.

ABSTRACT

Comparative genomics is a powerful approach to investigating the genetic basis for what makes us human. I will describe two different methods we have developed for identifying lineage-specific evolution: a phylogenetic hidden Markov model (phylo-HMM) and a likelihood ratio test (LRT). The phylo-HMM works well for identifying relatively ancient events, while the LRT is much more powerful at the leaves of a phylogeny (e.g. the human lineage). Using this LRT, we identified 202 Human Accelerated Regions (HARs) that were extensively changed in the last 6 million years since divergence from our common ancestor with chimpanzee, but are highly conserved in other species and thus are likely to be functional. The HARs are mostly non-coding sequences, and the set of genes near HARs is enriched for transcription factors, suggesting a role for HARs in the evolution of human gene regulation. I will describe a few of the most intriguing HARs before turning to a curious observation: the most accelerated regions of our genome show a striking bias for AT to GC ("weak-to- strong") nucleotide substitutions. This pattern is used to speculate about the cause of rapid, biased evolution in the primate genome and to date the chromosome fusion that formed human chr2.

Please send email to Mathias Drton (drton@galton.uchicago.edu) for further information. Information about building access for persons with disabilities may be obtained in advance by calling Karen Gonzalez (Department Administrator and Assistant to Chair) at 773.702.8335 or by email (karen@galton.uchicago.edu).