The University of Chicago

Department of Statistics

Seminar

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"Frequentist Estimation of Coalescence Times"

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Thursday, February 7, 2002 at 11:00 am
110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

We propose a method of estimating the time to the most recent common ancestor (TM-RCA) of a sample of DNA sequences, whose variation is characterized by single nucleotide polymorphisms (SNPs). Neither the proposed point estimate nor its confidence interval depends on the demographic history of the population, such as population size, growth, or migration pattern. Simulations show that the estimate is unbiased, and that the confidence interval has correct coverage probability in most situations. Performance of this estimator is compared with existing methods based on coalescence. This new method is applied to SNPs on world-wide samples of human Y chromosome and mitochondrial DNA (mtDNA). The coalescence time for the extant Y chromosome population is estimated as 91,000 years; the corresponding time for the mtDNA population is much older at 240,000 years.

1/29/02