The University of Chicago
Department of Statistics

Seminar Series

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Multilocus Lod Scores in Large Pedigrees: Combination of Exact and Approximate Calculations

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ABSTRACT

To detect the positions of disease loci, lod scores need to be calculated within a (several) pedi- gree(s) for a given set of markers at multiple chromosomal positions. Exact lod score calculations are often impossible when the size of the pedigree and the number of markers are both large. In this case, a Markov Chain Monte Carlo (MCMC) approach provides an approximation. However, to provide accurate results within a reasonable amount of time, the mixing performance is always a key issue in these MCMC methods. In this paper, we propose a new approach, which divides a large pedigree into several parts by conditioning on the haplotypes of some "key" individuals. We perform exact calculations for the descendant parts where more data are often available, and combine this information with sampling of the hidden variables in the ancestral parts. We also improve the ancestral sampling part using a mixture of several conditional Hidden Markov Chains across loci or meioses. Our approach is expected to be useful for a large pedigree with a lot of missing data, in which case most current methods cannot give satisfactory results. We show the improved mixing performance of our new MCMC methods, using simulated data.

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).