

STANFORD PROBABILITY SEMINAR

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Monday, 31 January 2005

4:15pm (Refreshments at 4pm in the 1st Floor Lounge)

Sequoia Hall, Room 200

Statistical properties of admixture mapping

Abstract. Recently admixed populations have been proposed as a resource for complex traits mapping in a case-control design. Differences between the two founding populations in the frequencies of alleles, both in markers and in the functional polymorphism, is the vehicle that enables detection. The Hidden-Markov Model (HMM) is used for the computation of the scanning statistic, which can be applied for the detection of the functional polymorphism from the markers' genotypic information.

In this talk we will discuss some of the statistical properties of the scanning statistic when a dense collection of markers is used. Approximations to the covariance structure of the scanning process will be proposed. Similarities between the problem at hand and the problem of change-point detection will be highlighted.