



The University of Chicago
Department of Statistics

Master's Seminar

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**Detection of Allelic Deletion via Inference of Loss
of Heterozygosity in Acute Lymphoblastic Leukemia
by use of a Hidden Markov Model**

**Wednesday, August 2, 2006 at 10:00 AM
110 Eckhart Hall, 5734 S. University Avenue**

ABSTRACT

I develop a hidden Markov model to infer loss of heterozygosity in genome-wide single nucleotide polymorphism data. This is done with the goal of determining the location of tumor suppressant genes, which, when deleted, may be of aetiological importance in the development of leukemia. The model formulates transition probabilities based on intermarker distances and estimates of the linkage disequilibrium between markers.

I study five pediatric acute lymphoblastic leukemia cases using a 250k SNP array. Using the state probabilities of the HMM as well as the most likely state sequence, I identify several regions with loss of heterozygosity, the most extensive being chromosome 9p. Other regions with significant, though less extreme loss of heterozygosity, include 1p31, 1p35, 2q14, 3p21, 8q11, 10q22, 10q25, 11q14, 12q24 and 16q23.