



The University of Chicago  
Department of Statistics  
Master's Seminar

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**JAKE BYRNES**

Department of Statistics  
The University of Chicago

**“Using a HMM to Identify Ectopic Gene Conversion Events”**

**WEDNESDAY, November 16, 2005 at 11:30 AM  
110 Eckhart Hall, 5734 S. University Avenue**

**ABSTRACT**

The divergence time between duplicate genes is estimated using sequence divergence which can be greatly affected by the presence of gene conversions. An ectopic gene conversion event causes the sequence of one duplicate to overwrite the other, thereby removing any nucleotide sequence divergence present within the region undergoing the conversion. Thus, gene conversion produces a pattern of blocks of sequence with significantly lower sequence divergence than that of flanking regions. Identification of gene conversions is made difficult by the variation in mutation rates across genomic regions. However, because of the block-like nature of the conversion events, we can employ a Hidden Markov Model to identify these regions of low divergence. Our method is as effective as previous algorithms with the advantages that we only require two sequences, we locate the conversion within the sequences and we obtain estimates for the dates of duplication and gene conversion events.