

**The University of Chicago**

Department of Statistics

**Seminar**

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**“Measuring Relative Information with Applications to Genetics”**

**Monday, May 6, 2002 at 4:00 PM**  
**133 Eckhart Hall, 5734 S. University Avenue**

**ABSTRACT**

Reliably measuring the relative information in the data at hand is a challenging and interesting statistical problem. Our interest is motivated by problems in genetics: mapping genes for complex diseases and genome assembly using optical mapping. In these studies, missing information can be the result of different sources, such as missing genotypes in gene mapping, or fluorochromes in optical mapping. While the information is in most situations incomplete, at least in theory, the amount of missing information can be made arbitrarily low by increasing the number of observations. Therefore it is important to understand how much of the information is available.

I will discuss both the small and large sample issues in defining meaningful measures of information. The large sample measures are constructed in the context of hypothesis testing. The small sample measures will be treated as distances between two probability measures, and I will discuss the relevance of some of the commonly used distances, e.g. the Kullback-Leibler discrimination measure.