



The University of Chicago
Department of Statistics

Seminars for Fourth Year Ph.D. Students

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A Geometric Approach for Detecting Cell Cycle Gene Expression

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ABSTRACT

We propose a method for detecting cell-cycle-regulated genes by studying the geometric structure of gene expression data.

Since this method does not require a synchronization step (as has been used to study the cell cycle in yeast), it can in principle be applied to any growing cell population, e.g.: embryonic, stem, epithelial, apical, or tumor cells, from any species.

Starting from a data set containing the expression level for m genes in n individual cells randomly sampled from a growing population, we consider it as a set of n points in m -dimensional Euclidean space. Under reasonable assumptions, these points cluster around a closed curve that represents the ideal evolution of expression levels during the cycle. The core of our method is finding the (parameterized) curve that best fits the points.

In this talk we will present some preliminary theoretical results and examples using simulated as well as existing time-course and single-cell data, as arguments for the potential usefulness of the method.