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Mathematical Modeling of DNA Microarray Data: Discovery of Biological Mechanisms with Tensor Decompositions, and Definitions of Novel Tensor Decompositions from Biological Applications

Future discovery and control in biology and medicine will come from the mathematical modeling of DNA microarray data. I will describe models that were recently created using matrix and tensor computations, where the mathematical variables, patterns uncovered in the data, correlate with activities of cellular elements. The operations, such as data reconstruction in subspaces of selected patterns, simulate experimental observation of the correlations and possibly also causal coordination of these activities. I will demonstrate the ability of these models to predict previously unknown biological as well as physical principles, and will show recent experimental results that verify one such computationally predicted cellular mechanism [1].

Future algorithms for integration and comparison of different large-scale data will come from the mathematical modeling of DNA microarray data. I will define a novel tensor decomposition and show that this decomposition extends to higher order most of the mathematical properties of the generalized singular value decomposition (GSVD) [2]. The GSVD enabled comparative modeling of DNA microarray data from yeast and human, the first comparative modeling of data from two different organisms and the only one to date that is not limited to two datasets with a one-to-one mapping between their rows, i.e., their genes. I will describe preliminary results where this novel higher-order GSVD enables comparative modeling of data from complete genomes of more than two organisms.

[1] Omberg, Meyerson, Kobayashi, Drury, Diffley & Alter, submitted.

[2] Ponnappalli, Saunders, Golub & Alter, submitted.