1046-15-766   **Orly Alter*** (`orlyal@mail.utexas.edu`), Department of Biomedical Engineering, 1 University Station, A4800, University of Texas at Austin, Austin, TX 78712. *Discovery of Principles of Nature from Mathematical Modeling of DNA Microarray Data: Computational Prediction and Experimental Verification.*

Future discovery and control in biology and medicine will come from the mathematical modeling of DNA microarray data. Such models were recently created using matrix 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. The ability of these models to predict previously unknown biological as well as physical principles was also demonstrated [1]. I will describe the first comparative and integrative models that were created from DNA microarray data using tensor computations [2–4].

Pseudoinverse projection and a higher-order singular value decomposition models uncovered independently a genome-scale correlation between DNA replication and mRNA expression, which might be due to a previously unknown cellular mechanism of regulation. I will describe recent experimental results that verify this computationally predicted mechanism.

1. Alter, PNAS 103, 16063 (2006).
2. Alter & Golub, PNAS 102, 17559 (2005).
3. Omberg, Golub & Alter, PNAS 104, 18371 (2007).
4. Ponnapalli, Saunders, Golub & Alter, submitted. (Received September 13, 2008)