Researchers develop algebraic model to monitor cellular change

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Researchers at New York University's Courant Institute of Mathematical Sciences have developed a novel algebraic model of DNA "hybridization," a process central to most biotechnology devices that monitor changes in cell's gene expression or characterize a cell's genome. Their work, which is described in the journal *Physical Review E,* provides an additional tool for understanding how biological systems function and could enhance methods and designs of technologies used in cancer and genetics research.

Biology researchers seek to measure cell activity, but the task is a challenging one because of its complexity-a cell has so many facets, all taking place simultaneously, that it is difficult to measure the behavior of its individual parts. Genes that do not necessarily affect each other inside a cell can disturb each others' measurements in a biotechnology device.

To get around these obstacles, the NYU researchers focused on how a cell's most basic components are measured-its DNA and RNA. Specifically, they used a cell's gene expressions as a "tagging system" to monitor cell behavior at its most fundamental level.

For this purpose, they focused on microarray technology in which researchers first gather data on the make-up of RNA molecules in two steps: RNA is first converted into cDNA, or "copy DNA," and then measured by hybridization.

However, the researchers' initial work involved not experiments, but, rather, the creation of mathematical models to predict "DNA-cDNA duplex formation." They developed an algebraic computation that allowed them to model arbitrary DNA-cDNA duplex formation, and, with it, measurements of cellular behavior. Specifically, they assigned to various chemical properties of DNA strands different algebraic values (e.g., "K," "X," "Y"). They then ran a series of computations that resulted in expressing how "matches" or "mismatches" among various strands of DNA can be characterized by the input algebraic variables. These computations could then be used directly to design the most accurate biotechnology for measuring cellular behavior.

To confirm the validity of these algebraic models, the researchers conducted laboratory experiments involving the hybridization of DNA sequences. These results largely confirmed those predicted by the mathematical models-the DNA sequences in the laboratory matched up in most instances in ways the models forecast.

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