

Algorithm developed to detect cancer genes

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New York scientists say they have developed an algorithm that enhances the ability to detect cancer genes.

The researchers at New York University's Courant Institute of Mathematical Sciences say they have applied their algorithm to map the set of tumor-suppressor genes involved in lung cancer.

The algorithm uses data from Affymetrix's gene-chips that can scan hundreds of patients' genomes to find gains and losses in gene-copies.

Previous research had found certain gene-chips -- a technology that allows the genome-wide screening for mutations in genes or changes in gene expressions all at once -- shed light on genes and mechanisms involved in the onset and spread of cancer.

Specifically, chromosomal segments, when deleted in a single or both copies of genomes of a group of cancer patients, point to locations of tumor suppressor genes implicated in the cancer. The NYU study focused on automatic methods for reliable detection of such genes, their locations and their boundaries.

The findings will appear in the July issue of the American Journal of Human Genetics.

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