Expressing Yourself

The state-of-the-art technology used by researchers to identify active (expressed) genes in cells is the *microarray*: a "gene chip" imprinted, not with circuits, but with DNA. Active genes of fluorescently tagged cell samples placed on the chip reveal themselves when they bind with their DNA complements on the chip. The amount of data generated by this microscopic activity is enormous: just one row in an array can have 15,000 points. Pattern recognition and image analysis are two fields which use mathematics to help extract important genetic information about several diseases, including Alzheimer's and Parkinson's, from microarray data. In the future, microarrays may enable an individualized approach to medicine, in which your doctor could use these chips to diagnose disease and determine the best treatment for your unique genetic profile.

In one particular area of medicine, cancer research, the points in each column of an array can be thought of as genetic coordinates of samples from tumors. Yet there are so many coordinates that it is difficult to determine which tumors are similar. Algorithms employ statistics and different measures of distance in higher dimensions to group genetically similar tumors into "clusters" so that experiments can be done on treatments corresponding to the clusters. In one case, microarray technology not only distinguished between two different types of leukemia (verifying in the time it took to hit "Return" what had taken 35 years to discover) but also found different clusters within tumors that had been thought to be similar— resulting in clinical trials to confirm the distinction.

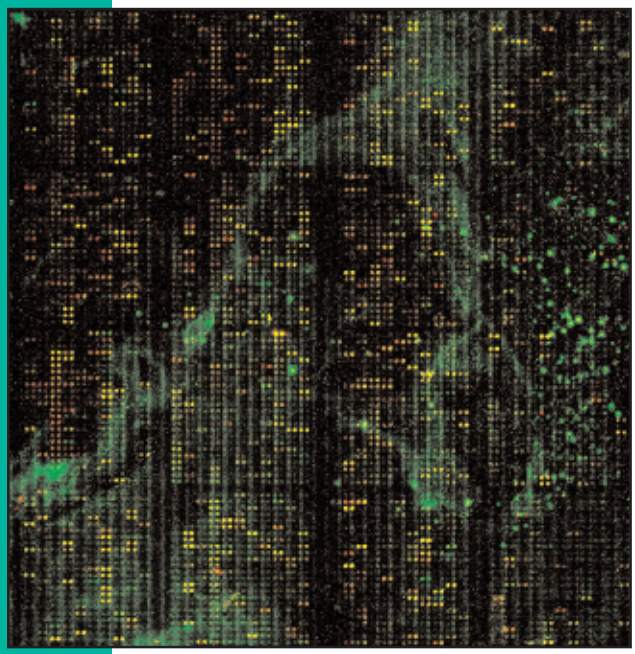

Image courtesy of Professor Rodney J. Scott and the Clive and Vera Ramciotti Functional Genome Array Centre.

For More Information: "Gene Chips and Functional Genomics," Hisham Hamadeh and Cynthia A. Afshari, *American Scientist*, November–December 2000.

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