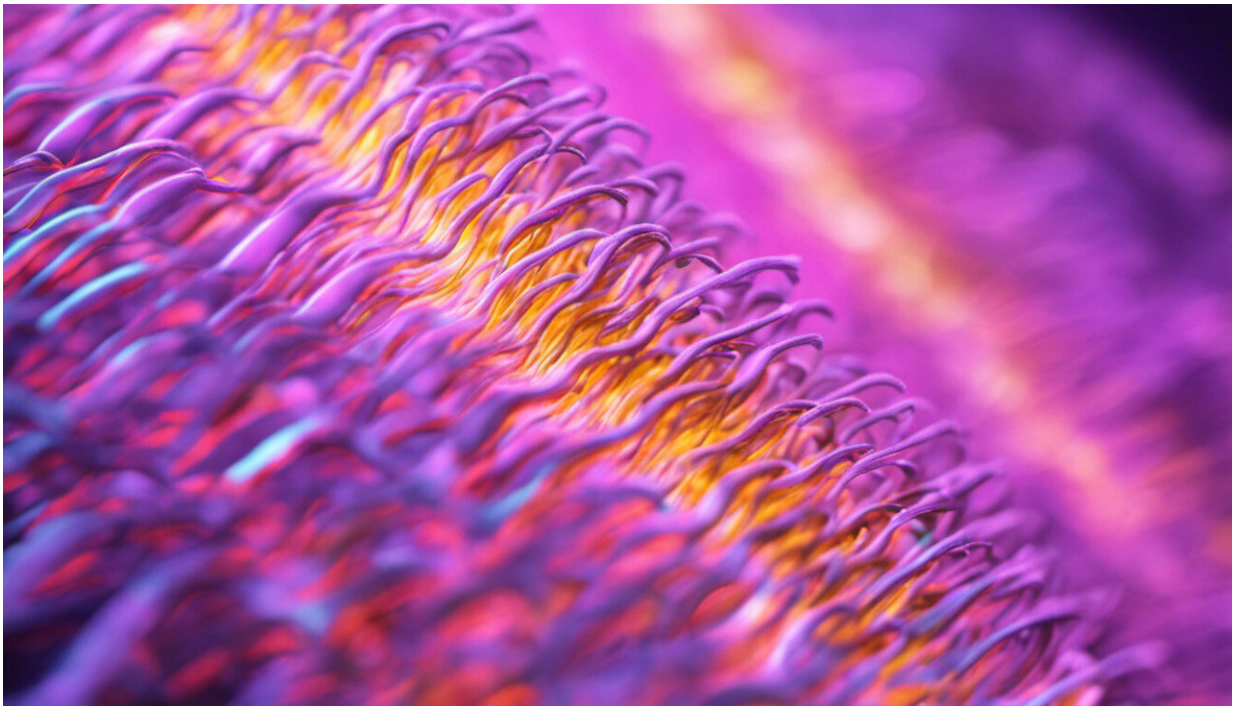
Researchers devise a faster, less expensive way to analyze gene activity

March 3 2015, by Vicky Agnew



Credit: AI-generated image (disclaimer)

A team of Yale researchers has developed a simple method that could significantly reduce the time and cost of probing gene expression on a large scale. The findings were published March 2 in the journal *Nature Methods*.

The team, led by Dr. Abhijit Patel, assistant professor of therapeutic radiology at the Yale School of Medicine, created a tool that takes advantage of new high-throughput DNA sequencing technologies to make it easier to simultaneously measure gene activity in large numbers of cells or tissues. While DNA is considered the blueprint of life, knowledge of which genes are activated or de-activated under different conditions is fundamental to our understanding of biology and disease.

Gene expression profiling is commonly used in clinical tests. For example, in patients with breast cancer, gene expression is often measured within tumor specimens to predict the likelihood of recurrence and to determine whether chemotherapy would be beneficial. With additional validation, Patel said, this high-throughput approach could be used to measure gene expression from many patients' tumors simultaneously. Ultimately, the method could reduce the cost of such tests, making them more broadly accessible.

"To make meaningful conclusions about complex gene expression patterns, it is usually necessary to perform statistical analysis on large numbers of clinical or experimental samples. We believe that this new technology will facilitate such work," said Patel, senior author on the paper. "We are excited because this method makes large-scale RNA profiling studies more practical and accessible to most researchers and clinical labs."

More information: "High-throughput RNA profiling via up-front sample parallelization." *Nature Methods* (2015) DOI: 10.1038/nmeth.3311

Provided by Yale University