

# New Web-Based Tools

## Make Systems Pharmacology More Accessible Using Data from the NCI-60

High-throughput biological techniques, like microarrays and drug screens, generate an enormous amount of data that may be critically important for cancer researchers and clinicians. Being able to manipulate the data to extract those pieces of interest, however, can require computational or bioinformatics skills beyond those of the average scientist. One rich source of information is the NCI-60 panel of tumor cell lines. Originally developed to screen anticancer compounds by NCI's Developmental Therapeutics Program, these 60 cell lines have

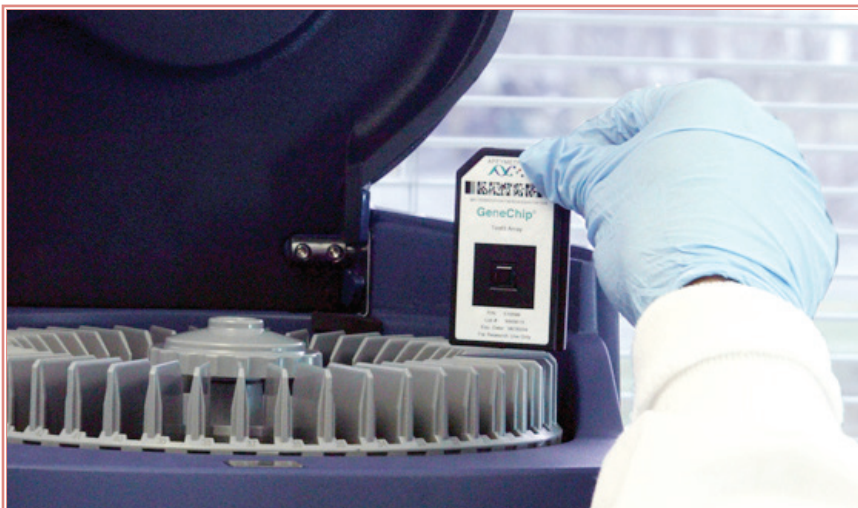
generated a series of online tools, which are freely accessible through their CellMiner web-application.

The tools, described in a recent *Cancer Research* paper, allow users to access expression levels for 26,065 genes and 360 microRNAs as well as the activity of 20,503 compounds, including 98 that are already approved by the Food and Drug Administration. An additional tool that performs pattern comparisons can be used to identify connections between these three parameters or with a user-supplied pattern of interest. The tools perform the complex computational

were returned, two are known to be over-expressed in colon cancer, and a third, which had the highest specificity, is a little-studied gene that may make an excellent colon cancer biomarker. Several drugs were also highly active in colon cancer cell lines. Three of these are currently being tested in clinical trials, while the fourth drug with the strongest colon-specific activity pattern, could be considered for testing. Looking at the activity pattern across all 60 cell lines for one of the drugs under clinical investigation, the researchers also noted strong activity in melanoma cell lines suggesting the drug could be a therapy for that cancer type as well.

The researchers plan to add more tools in the future including two that provide access to DNA copy number variations and whole genome sequences across the NCI-60. Together, these freely available tools can help researchers with little bioinformatics training find novel hypothesis-generating associations from data previously buried in complex databases.

(Photo: Christopher Spielmann)



Gene Chip is one of five microarray platforms used to determine gene expression.

also been analyzed for their gene and microRNA expression levels, DNA mutation status, and DNA copy number variations. Researchers from CCR and the Division of Cancer Treatment and Diagnosis, led by Yves Pommier, M.D., Ph.D., of CCR's Laboratory of Molecular Pharmacology, wanted to make this data more readily available so they

tasks required to normalize the data captured from five distinct microarray platforms and varying numbers of drug experiments and present it in a format that is easier for users to analyze.

To demonstrate the usefulness of their tools, the researchers tested a colon-specific pattern. Of the genes with a highest colon specificity that

*To learn more about Dr. Pommier's research, please visit his CCR Web site at <http://ccr.cancer.gov/staff/staff.asp?name=pommier>.*

*For more information about CellMiner and to access its tools, please visit <http://discover.nci.nih.gov/cellminer>.*