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New Tool Makes Cancer Analysis More Accessible

By RAGHU DHARA, CONTRIBUTING WRITER   October 14, 2014

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A team of Harvard researchers and their colleagues have developed a new software platform that makes it easier for scientists to understand and analyze the many forms of cancer.

Called StratomeX, the software can be used to visualize patterns in cancer-related bioinformatics data in a more lucid and less technical manner.

The field of bioinformatics has been churning out data at a much faster pace than can be analyzed and interpreted, according to a Harvard Medical School release. Databases like the Cancer Genome Atlas are mined by sophisticated computer algorithms, which then provide a researcher with data that indicates how many cancer variants exist and which genes are associated with that type of cancer.

The output of those computer programs can be cryptic and inaccessible to researchers who lack mathematical background, according to Alexander Lex, a postdoctoral researcher and member of the team that created StratomeX.

But StratomeX—developed by researchers from the Medical School, the School of Engineering and Applied Sciences, and two Austrian institutions, the Johannes Kepler University of Linz and the Graz University of Technology—makes that output more comprehensible.

"StratomeX is the first tool that can actually give the everyday bench scientist the power to readily perform cancer subtype analysis," he said.

Nils Gehlenborg, a research associate in biomedical informatics at the Medical School, explained how StratomeX complements existing statistical analysis tools.

"[StratomeX] is an interface that allows users to import results precomputed by algorithms that analyze the raw data [from cancer genomics studies]," he said. "It then presents visuals to the researchers that help guide investigators through the data."

Lex also noted that the software allows investigators to make specific queries about the data and then presents the results in a user-friendly format.

Another feature of StratomeX is a built-in adaptor that connects it directly to data from The Cancer Genome Atlas. This data analysis pipeline lets researchers easily import datasets and saves them time, Gehlenborg said.

According to Lex, current efforts in regards to StratomeX are dedicated to analyzing gene variants, assessing the data at the DNA sequence level in addition to the gene level, and improving the overall user-friendliness.

"It's a work in progress," he said.

In the future, the StratomeX team is planning to offer a version that can be run in a web browser without any prior installation.

StratomeX is available for download on the public repository, GitHub, where developers can add extensions and modifications.

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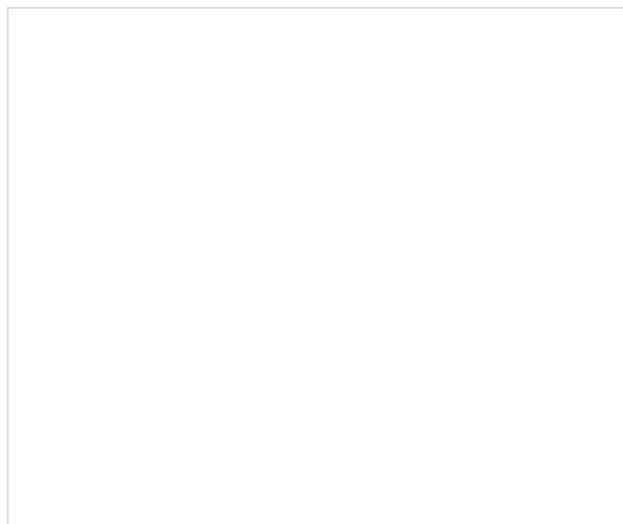
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