Researchers introduce next generation tool for visualizing genomic data

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Researchers are collecting vast amounts of diverse genomic data with ever-increasing speed, but effective ways to visualize these data in an integrated manner have lagged behind the ability to generate them. To address this growing need, researchers at the Broad Institute have developed the Integrative Genomics Viewer (IGV), a novel and freely available visualization tool that helps users simultaneously integrate and analyze different types of genomic data, and gives them the flexibility to zoom in on a specific genomic region of interest or to pan out for a broad, whole genome view.

"This new tool offers a Google Maps-like view of integrative genomic data," said Jill Mesirov, Chief Informatics Officer and Director of Computational Biology and Bioinformatics at the Broad Institute. "It brings together different kinds of genomic data into a single, holistic view. I'm incredibly proud of our computational scientists for responding so rapidly and effectively to the critical needs of the growing genomics research community."

With IGV, researchers can still choose a Google Maps-like "street view" of the As, Cs, Ts, and Gs that make up the genome, but they can also simultaneously visualize additional layers of complex information about gene expression as well as sequence alterations, or mutations, in the genetic code. Other genomic details, such as copy number variation, chromatin immunoprecipation data, and epigenetic modifications, can also be viewed in IGV. Moreover, all these data types can be overlaid or superimposed to determine how changes at one level will affect another.

Users can choose from a variety of display options, viewing their data as a heat map, histogram, scatter plot, or other formats of their choice. This new visualization tool is free and publicly available to researchers via the web.

"Other tools offer detailed, localized views of genomic data, and a few tools are equipped to provide a whole genome view," said Senior Software Engineer Jim Robinson, one of the program's creators. "IGV was designed to integrate both and to provide smooth zooming and panning across all resolution scales. "

"Most visualization tools are limited in their ability to handle multiple types of genomic data and are typically 'retrofitted' to accommodate new data types as they have arisen," said Michael Reich, Director of Cancer Informatics Development at the Broad Institute. "IGV was designed from the ground up to integrate all of these data, and to provide a strong platform for future growth and refinement."

Broad Associate Member John Rinn, an assistant professor at Harvard University and Beth Israel Deaconess Medical Center, has used a variety of visualization tools to sift through different types of genomic data. "Before I was introduced to IGV, I had to use three different programs to visually integrate my data," Rinn said. "But now this one, universal browser allows me to rapidly scan the entire genome and identify promising regions, which has revolutionized my work."

IGV promises to increase the flow of discovery in many areas of biomedical research. "This tool is designed to enable researchers to view many types of genomic data, especially those relevant to human disease," said Reich. "We're particularly excited about its already groundbreaking use in ongoing studies of the cancer genome."

IGV is made publicly available to researchers worldwide and can be

accessed at: www.broad.mit.edu/igv

Source: Broad Institute of MIT and Harvard