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Epiviz: A tool to analyze human genomic data

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Researchers at the University of Maryland (UMD) report the development of a new, web-based tool that enables researchers to quickly and easily visualize and compare large amounts of genomic information resulting from high-throughout sequencing experiments. The free tool, called Epiviz, was described in a paper (Epiviz: interactive visual analytics for functional genomics data) published online in Nature Methods.

"Epiviz seamlessly integrates with the open-source Bioconductor analysis software widely used by genomic scientists, through its Epivizr Bioconductor package," said Mr HÃ©ctor Corrada-Bravo, PhD assistant professor in computer science at UMD.

"Epiviz, a web-based genome browser, and the Epivizr Bioconductor package allows interactive, extensible, and reproducible visualization within a state-of-the-art data-analysis platform," explained the investigators.

"Prior tools limited visualization to presentation and dissemination, rather than a hybrid tool integrating interactive visualization with algorithmic analysis," explained Mr Corrada-Bravo.

It supports many popular next-generation sequencing techniques, such as ChIP-seq, which is used to analyze protein interactions with DNA; RNA-seq, which reveals a comprehensive snapshot of the abundance of RNAs in cells; and DNA methylation analyses.

Epiviz links data across different visualizations giving users visual insights of the spatial relationships of multiple datasets. The tool is designed to allow biomedical scientists to easily incorporate their own visualizations.

"Epiviz helps biomedical scientists meet the challenge of visualizing large genomic datasets while supporting creative data analysis in a collaborative environment," he pointed out.