

Explore, analyze, and share genomic data using Integrated Genome Browser

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To benefit from high-throughput sequencing techniques, scientists need easy-to-use visual analytics software tools that support all aspects of the scientific process. To meet this need, we added new visualization capabilities to Integrated Genome Browser, a fast, flexible and free Java-based desktop software tool originally developed at Affymetrix. IGB is available from <http://www.bioviz.org> and <https://bitbucket.org/lorainelab/integrated-genome-browser>. IGB supports a wide range of interactions with data, from simple counting by selection to complex filtering operations that can highlight biologically meaningful aspects of data. With collaborators from Genentech, we re-architected IGB to use an OSGi-based framework that enables rapid addition of new visualization components and features via OSGi bundles, called plug-ins. Using this new architecture, we implemented new visual analytics tools, including a tool to quantify and visualize splicing support (FindJunctions), new linkouts to run blast searches at NCBI, a heatmap editor that enables color-coding features by score, and many others. For some new features, such as the heatmap editor and blast searches, we imported code from Cytoscape and Apollo, two other well-established Java-based open source projects. To enable data sharing, IGB implements a simple Web-based system called IGBQuickLoad. A new release of the blueberry genome, annotations, and fruit development RNA-Seq data set highlights the possibilities. IGB also supports ReST-style bookmark URLs that enable integration with sophisticated data sharing and analysis environments, such as Galaxy and GenomeSpace. IGB is released under the Common Public License, v1.0.