

About the code base

- [IGB git repo \(main\)](#)
- [Genoviz SDK](#)
- [Maven](#)
- [History](#)

IGB git repo (main)

The main repository address is: <https://bitbucket.org/lorainelab/integrated-genome-browser>.

The IGB project uses git for source code management. We use maven and Bitbucket pipelines to build and release IGB artifacts and user-friendly installers.

Genoviz SDK

IGB depends on the Genoviz Software Development Kit (Genoviz SDK) which is version-controlled in a separate repository at <https://bitbucket.org/lorainelab/genoviz-sdk>. When you build IGB, the compilation tool we use (mvn) will obtain the latest copy of the genoviz compiled code (a "jar" file) and install it locally.

Maven

The IGB project uses maven to build IGB, IGB Apps, and the GenoViz SDK. We provide access to new and old IGB-related jar files using the following maven repositories:

- <https://maven.bioviz.org/repo1>
- <https://maven.bioviz.org/repo2>
- <https://maven.bioviz.org/repo3>
- <https://nexus.bioviz.org/repository/maven-releases/> (browse using <https://nexus.bioviz.org/#browse/browse:maven-releases>)

To include these in your project, see the top-level POM.xml file in the Integrated Genome Browser project code base.

History

The original GenoViz library - called "BioViews" - was first developed by Gregg Helt at UC Berkeley as part of his PhD research in the mid-1990s. Around then, Helt and two colleagues (Martin Reese and Cyrus Harmon) formed a bioinformatics software company called Neomorphic, which licensed the software from the University. With funding and development support from the Bioinformatics Department at Smith Kline Beecham, they continued to improve the library, renaming it the Neomorphic Genome Software Development Kit. Also during this period, Celera Genomics and the Institute for Genomic Research (TIGR) hired Neomorphic to build genome browser and annotation software. Ann Loraine joined the company in 1999 and helped build the Neomorphic Annotation Station for The Institute for Genomic Research.

In October 2000, Affymetrix purchased Neomorphic and re-focused software effort on supporting and developing Affymetrix DNA microarray products. In 2001, Gregg Helt and colleagues began developing Integrated Genome Browser to visualize and analyze data from genome tiling arrays, which contained probes selected from (mostly) regular intervals along the genome. Visualization of probe intensity data alongside gene models was essential to developing algorithms to normalize and analyze the data, and the team at Affymetrix developed some of the first visual analytics algorithms in bioinformatics. Also, they developed some of the first indexed, random access file formats to enable partial loading of data sets that were too large to fit into computer memory. Support from Affymetrix along with federal grants to PIs Tom Gingeras and Gregg Helt funded early IGB development during this period. Affymetrix released IGB as part of their NetAffx Web site in the early 2000s.

In 2004, Affymetrix released IGB and NGSDK as open source software. This first release was done as a "tarball" on their Web site. In Jan. 2005, Affymetrix developers imported the tarball contents into a new CVS repository at Sourceforge and began using that for further development, discarding the internal repository at Affymetrix. In addition, they changed the name of the graphics library from "Neomorphic Genome Software Development Kit" to "Genoviz Software Development Kit". However, many of the graphics library's class names retain the prefix "Neo" - e.g., NeoWidget, NeoMap, etc.

In 2004, Ann Loraine joined the University of Alabama at Birmingham as an Assistant Professor, where she wrote funding proposals requesting further support for IGB and the Genoviz SDK. In 2008, she joined the College of Computing and Informatics at UNC Charlotte. Later that year, NSF awarded her a new grant to develop IGB and its companion data distribution site IGB Quickload. Developers at Affymetrix continued contributing to the code for several years after that. You can see their work by searching for commits from developers "chyeck" (Ed Erwin) and "gregghelt."

After joining UNC Charlotte, Loraine and colleagues migrated the code to a subversion repository, also hosted at Sourceforge. We continued to use this repository for many years. In 2014, we migrated the source code for IGB and the Genoviz SDK to a new git repository hosted at Atlassian's Bitbucket.

Unfortunately, over the years the early development history pre-dating the 2004 open source release has been lost. In addition, early products built using Genoviz SDK are also lost. When the developers at Affymetrix prepared the first open source release, it seemed simpler and less risky to simply migrate the code directly into a new CVS repository and go from there. Now, of course, we are using tools that are more sophisticated than before, and we can easily trace how the code has changed dating from Jan 2005 until the present day. If you have questions about what you see, feel free to get in touch.

Links

- The 13th commit: "License for IGB code, including genoviz (formerly NGSDK) and genomerty" Jan. 31, 2005 - <https://sourceforge.net/p/genoviz/code/13/>
- Press release - Affymetrix Completes Acquisition of Neomorphic - <https://ir.thermofisher.com/investors/news-and-events/news-releases/news-release-details/2000/Affymetrix-Completes-Acquisition-of-Neomorphic/default.aspx>