

## Abstract

Integrated Genome Browser (IGB) is a fast, flexible and free Java-based desktop software tool that enables interactive exploration of genomic data sets. To accommodate large data sets, IGB featured a simple ReST-style interface that triggers incremental loading of data from local files or URLs. We used this ReST-style interface and the Galaxy viewers API to enable IGB visualization for Galaxy users. When Galaxy users create compatible data files, they now see a link labeled "View in IGB" upon clicking data file links in their Galaxy History. Clicking this link triggers delivery of data to IGB for display. This is a simple interaction from the user's perspective, but from an engineering point of view, it highlights a key extension point for Galaxy that enables integration with IGB or other visualization tools. By enabling access to data sets in a user-friendly, web-based interface, Galaxy offers many possibilities to enhance user interactions for data analysis and sharing.

## Benefits

- Galaxy makes it easy for biologists to process, analyze, store and share data.
- They can store & curate data sets using **Histories**.
- Users can share Histories and data sets with collaborators or the public.
- IGB links in Galaxy Histories make it easy for users to directly import data from Galaxy into IGB.
- IGB is a powerful desktop visualization tool with many features.

## How it works from user's point of view

**1. Click data set title in History**

**2. Click "display in IGB" link**

**display in IGB View**

New Browser tab opens at BioViz.org

## BioViz.org

This new page at BioViz.org contains Javascript code that looks for IGB, asking...

**Is IGB running?**

No Yes

**3a. Start IGB or download from Bioviz.org**

**3b. After starting IGB, go back to BioViz page and click Refresh**

**4. Load data and explore, using IGB visual analytics functions.**

## Integrated Genome Browser

**Find Junctions** shows read support for splice junctions. In this case, cold increases inclusion of an alternative exon.

**Classic depth** graphs show number of reads that cover each position.

**Start only depth** graphs show the reads that start at a position.

**Filters** hide or show reads based on their properties. Here, only reads with gaps (spliced reads) are shown.

**Gene model** tracks load automatically. Right-click a gene to search google, run BLAST, or view sequence in a new window.

Click-drag to **select sequence** and right-click to copy to external tools, like blast search or primer design.

This image shows cold-induced alternative splicing of Arabidopsis **LHY**, a circadian clock regulator. In plants, many genes that regulate the circadian clock are highly alternatively spliced and their pattern of splicing changes in response to temperature.

**How it works from a programmer's point of view:** IGB leverages the External Viewers API. Within Galaxy, external viewer XML files define URLs that link to the BioViz Web site, which brokers interactions between Galaxy and IGB.

Thanks to...

