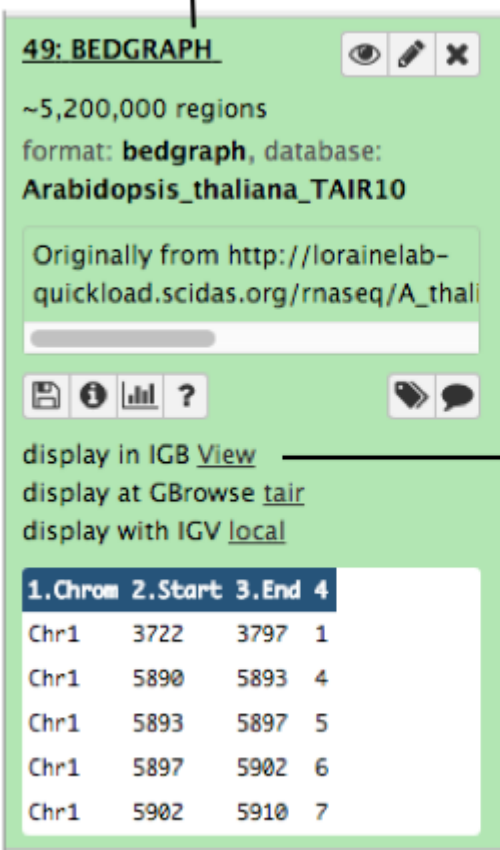


# View Galaxy files in IGB

To view a Galaxy file in IGB

- start IGB
- click a file title to open the file in your Galaxy history
- click the View link to open the Galaxy bridge page at BioViz.org



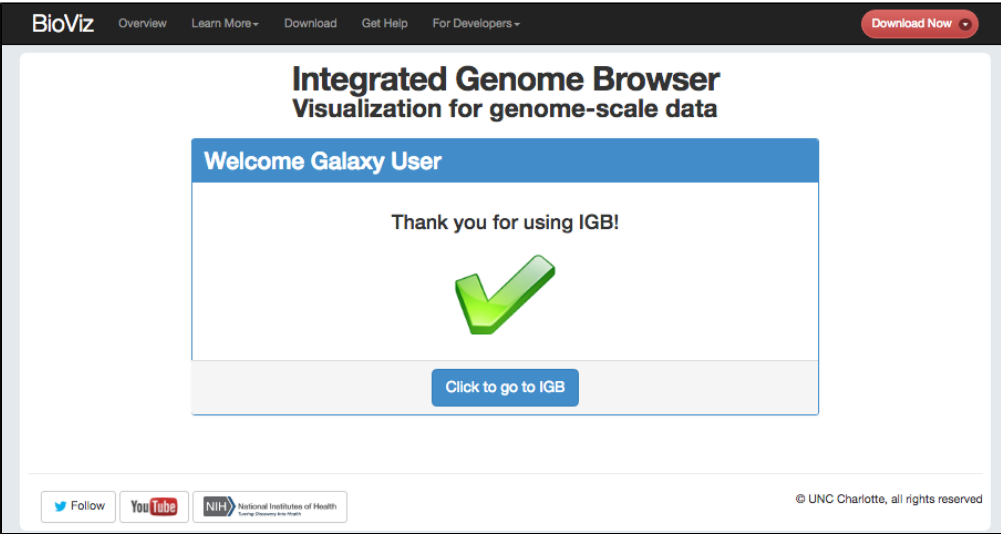
The screenshot shows a Galaxy file interface for a BEDGRAPH file. The file name is "49: BEDGRAPH" and it contains approximately 5,200,000 regions. The format is bedgraph and the database is Arabidopsis\_thaliana\_TAIR10. The original source is cited as http://lorainelab-quickload.scidas.org/rnaseq/A\_thali. Below the file information, there are icons for file operations and a "View" link. A table below the file information shows genomic coordinates for Chr1.

1. click to open file

2. click to open Galaxy bridge page at BioViz.org

1. Chrom	2. Start	3. End	4
Chr1	3722	3797	1
Chr1	5890	5893	4
Chr1	5893	5897	5
Chr1	5897	5902	6
Chr1	5902	5910	7

Clicking **View** opens a new Web browser page at BioViz. This is the BioViz-to-Galaxy bridge page. It page contains JavaScript code that helps IGB make a new track from your Galaxy file. Once the new track appears in IGB, you will see a message like this:



The screenshot shows the BioViz Integrated Genome Browser interface. The page title is "Integrated Genome Browser Visualization for genome-scale data". A blue banner says "Welcome Galaxy User" and a message says "Thank you for using IGB!". A green checkmark icon is displayed, and a button says "Click to go to IGB". The footer includes social media links for Twitter, YouTube, and NIH, and a copyright notice for UNC Charlotte.

Go back to IGB to view your data. You will see a new entries in the Available Data Sets section of the Data Access tab showing your new track.

**Note:** IGB may show a message asking you to accept a certificate from the Galaxy site. Click Accept to continue loading data.

