



GMOD Browser Tools and Exercises Workshop

Part of the Next Generation DNA Sequencing Analysis Satellite Meeting

ABRF 2010

3-4:30pm, 20 March 2010

Sacramento, CA, USA

Workshop

From the morning session

A Note about the GFF from the morning session:

The first column of the GFF indicates the reference sequence for the features in the GFF, and it has to match up with the reference sequences that the browser knows about. Make sure that the first column of your GFF file says NC_003070.9

GMOD Genome Browser Tools

GBrowse

About

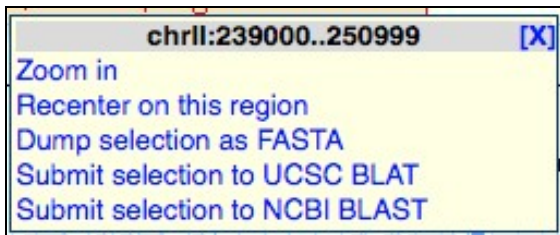
GBrowse is the most widely implemented genome browser in use today, with several hundred servers around the world. For this tutorial, we created a server at <http://gbrowse.gmod.org/gbrowse2>, and specifically, a GBrowse instance of *A. thaliana* Chromosome 1. You might want to open that in another tab now to follow along and try things out during this section. This is another link to a similar site on the same server if the above one is giving you problems: Slower Chromosome 1.

Navigation and Searching

The primary way people "get into" GBrowse is by searching for a gene or other keyword. To search, the user just enters the text (gene name or other identifier, or something in the description) into the "Landmark or Region" box at the top of the display. Since we have arabidopsis data, we could try things like "AT1G01930" or "Chr1:100000..200000". We can also do wild card searches, like "AT1G019*", which will give a list of matches

that we can choose from.

Once looking at the GBrowse display, there are typically two or three graphical sections: the overview, region and details panel. The region panel is optional (and can be configured to be on or off by the administrator) and shows a neighborhood overview that doesn't cover as much area as the overview (which is always the full length of the chromosome or contig being looked at). While GBrowse has left and right pan buttons on the side of the details panel, and similar buttons along with a zoom menu above the overview panel, most people navigate GBrowse by click and drag selection on one of the scale bars for the chromosome at the top of each of panels. By pressing down on the left mouse button and moving the mouse over the region to be navigated to, GBrowse will either automatically go to the region selected, or depending on how GBrowse is configured, will pop up a menu to let the user choose what action to take. For example, in a sample yeast data set that comes with GBrowse, this is the menu that is given when the user selects a region in the details panel:



When GBrowse navigates to a new location, it uses AJAX (Asynchronous Javascript and XML) to reload all of the tracks, so a complete page reload is not necessary, making the browsing experience more continuous (though admittedly not as continuous as the JBrowse experience). This same technology enables a few other niceties of GBrowse:

- When new tracks are selected from the ones available in the list below the details panel, the new track is added without having to reload the page
- Since the tracks are drawn separately, they can also come from different servers, giving GBrowse the ability to work with multiple rendering and database servers to make it faster than it would otherwise be with just one server.
- The tracks can also be moved up or down relative to other tracks just by clicking on the name of the track and dragging it up or down.

Uploading user data

Several file formats are supported for upload to GBrowse:

- BED
- GFF
- GFF3
- Wiggle (WIG) (for dense quantitative data)
- BAM or SAM (for sequence alignment data)

Files that are uploaded in this way are secure, in that they can only be seen by the person who uploaded them (or more specifically, on the computer where they were uploaded), and with people that they have been explicitly shared (see the section below for more on that).

In the morning section of the tutorial, we created GFF (not GFF3), so we'll use that as an example of how to upload data. (This marks the first time the server we are using is being used by a classroom, so let's hope there are no

fireworks!)

To make this work, you need to have the GFF file you created in the morning session on your computer.

[Go Here and find your profile](#), then find the GFF file from this morning and save it on your computer.

Once you done that, go to <http://gbrowse.gmod.org/fgb2/gbrowse/arabidopsis>. Near the top of the page, there is a link for a tab called "Upload and Share Tracks." Click on that and there is a simple interface for uploading supported files. Clicking on "From a file" will give a normal "browse" button to find the file on your computer. When you select the file and click the upload button it will, it will show a spinner while it uploads, and then give you a status report (the size of the file uploaded, and links to edit the uploaded file and the created configuration). It will also automatically load the track into GBrowse, and clicking on the Browser link will take you back to the browser display. If you see the track, but no features in it, be sure to navigate to where in the genome the features are. Try this link if you don't know where to look:

http://gbrowse.gmod.org/fgb2/gbrowse/arabidopsis/?start=950000;stop=1050000;ref=NC_003070.9

Going back to the upload tab, you can click the "edit" link for the configuration and see some of the adjustable parameters to make it look different, by changing things like the fill color (bgcolor) or the picture used for the features (glyph). For a list of commonly used parameters, take a look at:

http://gbrowse.gmod.org/gbrowse2/annotation_help.html#customize

If you run into problems and want to start over, you can use this link:

<http://gbrowse.gmod.org/fgb2/gbrowse/arabidopsis/?reset=1>

which will throw away the uploaded file and restore the default settings.

A few comments about the GFF produced this morning

The GFF produced this morning looks like this:

NC_003070.9	cashx_gff	ABRF_Test	1455221	1455257	.	-	.	ABRF_Test;Note	Mismatch=0
NC_003070.9	cashx_gff	ABRF_Test	1200379	1200415	.	-	.	ABRF_Test;Note	Mismatch=0
NC_003070.9	cashx_gff	ABRF_Test	1170111	1170147	.	-	.	ABRF_Test;Note	Mismatch=0
NC_003070.9	cashx_gff	ABRF_Test	1017175	1017211	.	-	.	ABRF_Test;Note	Mismatch=0

This is a "flavor" of GFF2 that GBrowse will accept, but doesn't really care for (yes, you may have hurt it's feelings :-)

The problem is that the first entry in the ninth column is identical ("ABRF_Test") and this tells GBrowse that these things should all be grouped together (in fact, that is called the group column in GFF versions before GFF3). As a result, GBrowse draws lines connecting all of these features as though they were all HSPs and part of one big hit in a BLAST result, and this is probably not what is intended. Two ways to improve upon this is to produce slightly different GFF2 or produce GFF3 (which has a better, more clearly defined specification).

GFF2:

NC_003070.9	cashx_gff	ABRF_Test	1455221	1455257	.	-	.	ABRF_Test read1;Note	Misma
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```
NC_003070.9  cashx_gff  ABRF_Test  1200379 1200415 . - . ABRF_Test read2;Note Misma
NC_003070.9  cashx_gff  ABRF_Test  1170111 1170147 . - . ABRF_Test read3;Note Misma
NC_003070.9  cashx_gff  ABRF_Test  1017175 1017211 . - . ABRF_Test read4;Note Misma
```

Changes:

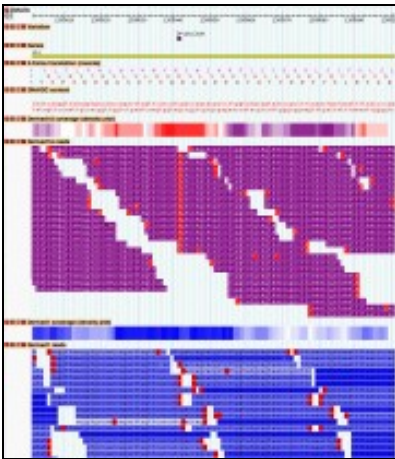
- Added an unique identifier after the "class" (the first word in column nine).

GFF3:

```
NC_003070.9  cashx_gff  match  1455221 1455257 . - . ID=read1;Note=Mismatch%3D0
NC_003070.9  cashx_gff  match  1200379 1200415 . - . ID=read2;Note=Mismatch%3D0
NC_003070.9  cashx_gff  match  1170111 1170147 . - . ID=read3;Note=Mismatch%3D0
NC_003070.9  cashx_gff  match  1017175 1017211 . - . ID=read4;Note=Mismatch%3D0
```

Changes:

- Third column (type) changed to match, which is a Sequence Ontology term.
- Ninth column reformatted to fit GFF3 specification, including:
 - ◆ URL escaping the equals sign in the Note ("%3D" is the code for equals sign).
 - ◆ Used unique IDs for each of the reads.



Two BAM files displayed in GBrowse

Finally, the best way to represent this data would be to create a BAM file, which would result in faster rendering, and the ability to show mismatches, like in this screen shot from an *E. coli* resequencing project. BAM is a binary file format for storing alignment data in a very compact, fast to read way, as part of the SAMtools project.

In addition to showing the individual reads with mismatches highlighted, it will also show coverage plots as density plots (shown in this screen shot) or as xy plots, and will show read pairs, highlighting unpaired reads.

Sharing tracks with other users (customers)

Any track (one that is "part of" the server or uploaded by a user) can be shared with other users, in two different ways. One is to get a URL that can be mailed to a user to click on it and be taken to the same view that the sharer sees, and the other is to "export" the track so that it can be viewed in a GBrowse instance on another server.

their data as well. This is functionally equivalent to the Apache-style per track security, but perhaps a little easier on the GBrowse administrator by pushing some of the work off to the users.

Advanced topics

Installing and configuring GBrowse

Installing GBrowse is relatively simple on Linux or Mac OS X servers. It is a little more challenging on Windows servers, but it can still be done. Typically, a computer science undergrad can do it in half a day, or a computer savvy biology graduate student can do it in a little longer, perhaps a day. There are a few hang ups that people run into typically relating to getting a few of the prerequisites installed.

Getting it completely configured can be quick or take a long time depending on the level of complexity desired. Typically, people take an iterative approach, getting simple things done quickly and then working on more complex things as time allows. There are a few good resources for people new to installing and configuring GBrowse:

- The [GMOD wiki](#)
- The [GBrowse mailing list](#)
- A few courses where GBrowse is covered:
 - ◆ The [Programming for Biology](#) course at Cold Spring Harbor Laboratory
 - ◆ Courses put on by NESCent (previously referred to as summer schools, but since this year, one is in May, and another will probably be in the fall, we have to come up with a new name). The next course, [this May](#), is already sold out. There will likely be one next October in Japan in conjunction with the [International Society of Biocuration](#) meeting.

JBrowse

[Demo with next-gen reads](#)

[main fly demo](#)

[HG19 \(subset\) demo](#)

Differences

GBrowse	JBrowse
Older	Newer
More functionality	Faster, smoother UI
Does work on server	Moves work to web browser

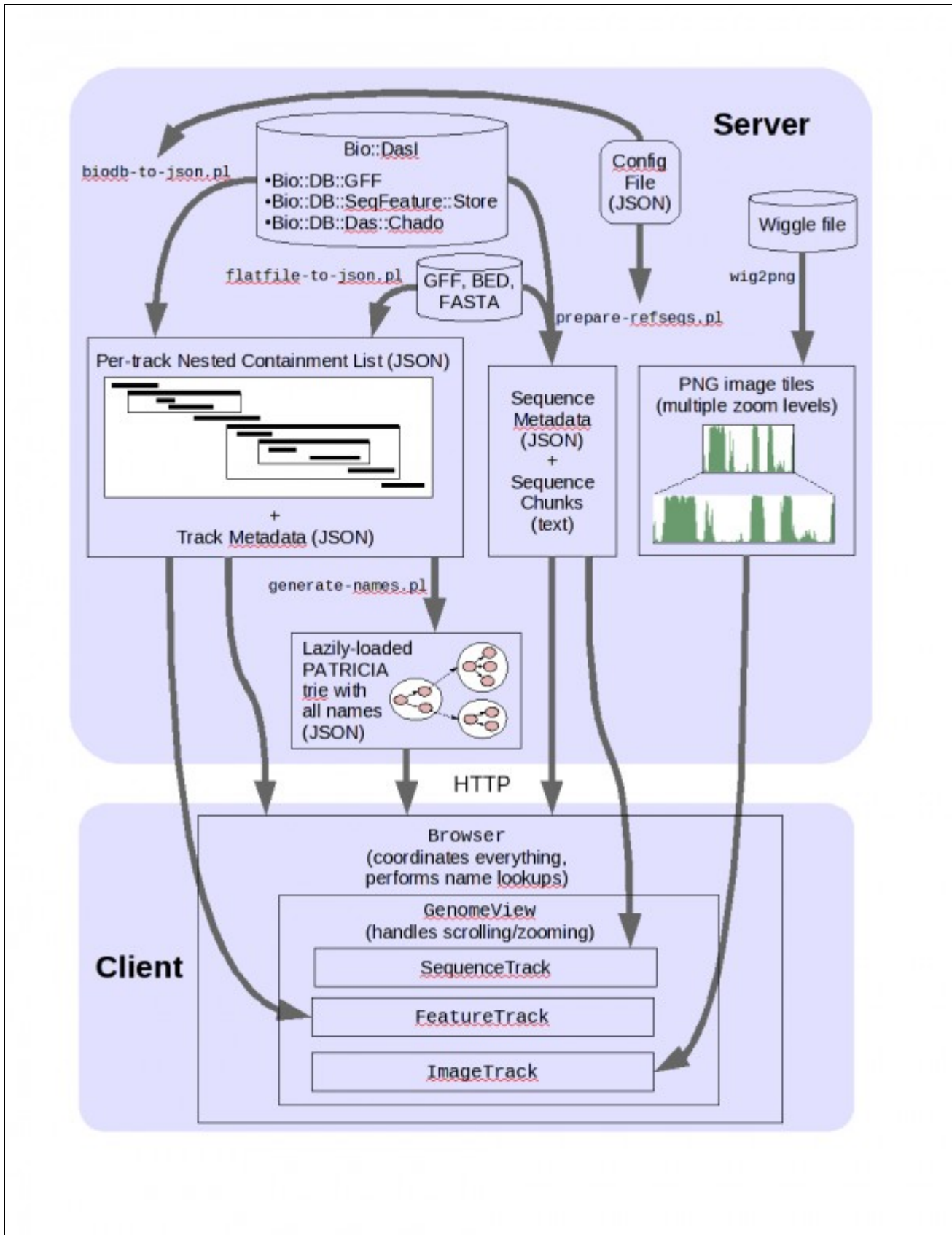
Similarities

Same underlying Perl machinery

Use GBrowse user accounts

Same data sources

The moving parts in JBrowse:



You have your own JBrowse instance on the server:

<http://abrf2010.jbrowse.org/~profilename/>

SSH into the ABRF jbrowse machine: abrf2010.jbrowse.org

User: your profile name from the morning session

Password: abrf_HTS

```
ssh profilename@abrf2010.jbrowse.org
```

Copy your GFF file from this morning to this machine:

```
wget --http-user=abrf_workshop --http-password=abrf_HTS http://abrf.cgrb.oregonstate.edu/UserData
```

OR

```
cp ~mitch/finaloutput-cashx.gff ~/
```

Go into your JBrowse installation:

```
cd public_html
```

Add the GFF file to your JBrowse instance:

```
bin/flatfile-to-json.pl --gff2 ~mitch/finaloutput-cashx.gff --tracklabel "ABRF_Test" --key "ABRF"
```

Conference Talk

Seeing the Forest and the Trees: Visualizing Next Generation Sequence Data, by [Mitch Skinner](#)

*Part of the Session **Tools to Facilitate Management, Analysis and Visualization of 2nd Generation Sequencing Data***

3:45pm - 5:00pm, Monday, March 22