GBrowse version 2.13 has been released. 2.13 is a maintenance update to 2.12. GBrowse 2.13 and 2.12 include these changes:

New features & enhancements

- The DAS server and client are now functional. You will need Bio::Das version 1.17 and Bio::Graphics version 2.11 for best results.
- The "import track" function now allows you to specify the URL of either a BAM or a BigWig file. The track will be displayed without physically copying the file onto the GBrowse server. You will need Bio::DB::Sam and Bio::DB::BigWig for these features to work.
- Uploading a Wig file now generates a BigWig database for improved performance and scalability. This requires Bio::DB::BigWig to be installed.
- There is now a **Get chromosome sizes** entry in the File menu.
- Calling GBrowse with the CGI argument `action=scan` will generate a quick summary of track contents.
- Improved performance when working with truly huge (>1000 track definition) configuration files.
- Fasta, GFF3, SAM and wiggle dumps now include the genome build ID if that information is provided in the data source "metadata" configuration variable.

Bug fixes

- When MySQL is used as the back end for user uploads, it will no longer fail on long filenames.
- Fixed the "eurl" CGI parameter for importing data sets by their URLs.
- Fasta and GFF3 dumps are now working when invoked from the File menu.
- Fixed SAM file processing so as not to die when presented with a SAM @SQ header. This requires Bio::DB::Sam 1.20 to work properly.
- Fixed upload listing table so as not to duplicate track labels.
- Fixed track importation via the eurl parameter so that it works when the user's uploadid is empty (due to clearing cache of cookies).
- Fixed DAS server handling of the link option.

Please use the GMOD bug tracking system to report bugs or feature requests.

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