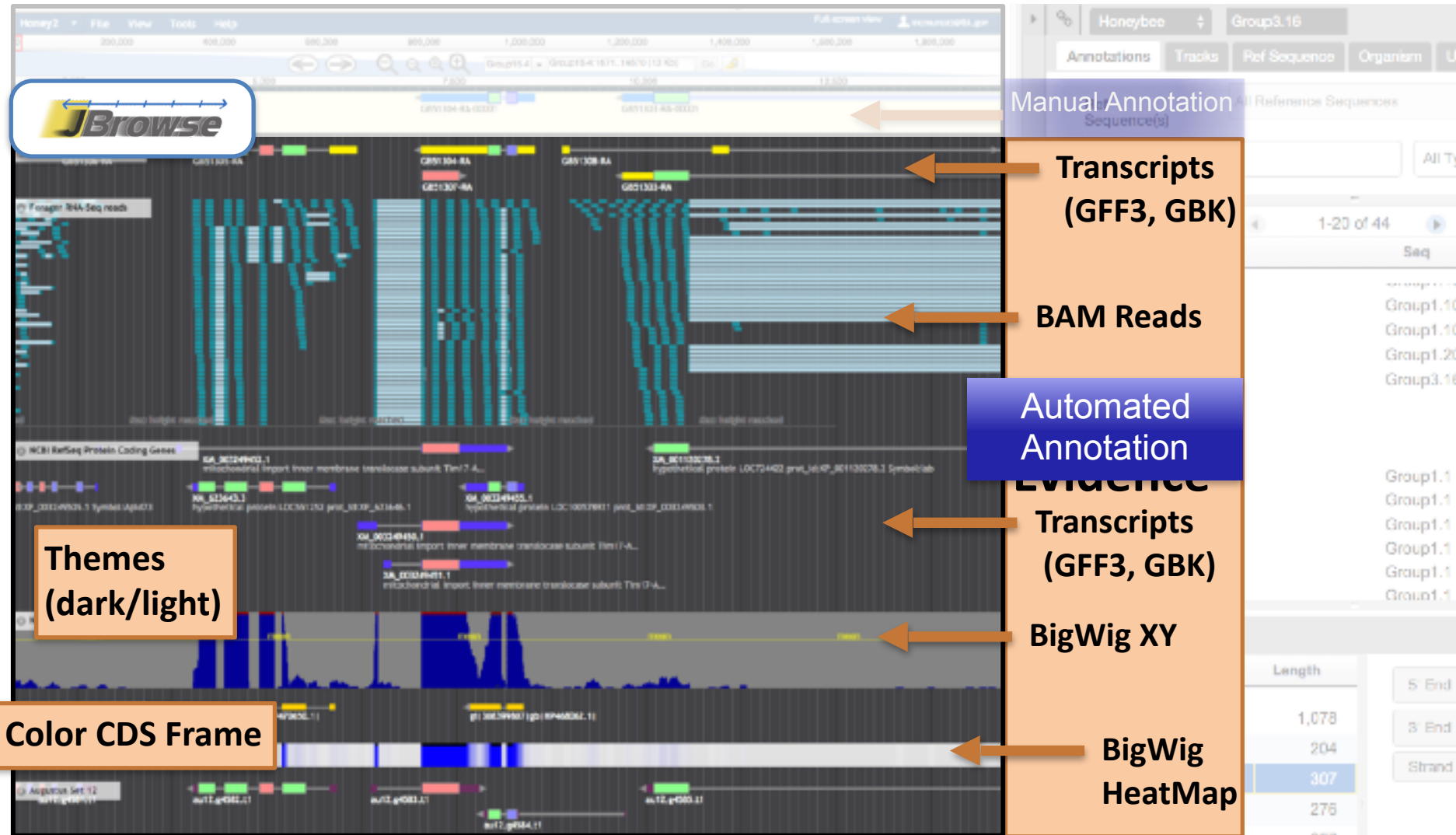# Evidence Area (Genome Browser)

Quick and Easy Genome Annotation Editing with Apollo

Precise descriptions of annotated genomes are vital for modeling the biological function of genomic elements. The ability of a researcher to visually identify and review diverse sets of information such as genomic and transcriptome alignments, predictive models based on sequence profiles, and predicted regulatory elements and repeat regions are essential for the iterative improvement of the modeling of genomic elements. During analysis, researchers also do functional enrichment analysis (such as GO), and need to update functional annotations. Furthermore, as projects increasingly include annotations of a growing number of organisms as well as geographically dispersed researchers, the ability to quickly integrate multiple genomes, sources of evidence, annotations and researchers is essential. The Apollo genome annotation editor fills these needs by providing a graphical platform for researchers to collaboratively review and revise the predicted features on a genome in real-time, similar to Google Docs. Refinement of genome annotations is made efficient through several features including drag-and-drop editing, a large suite of automated structural edit operations, the ability to pre-define curator comments and annotation status to maintain consistency, attribution of annotation authors, and a visual history of revertible edits.

Here, we describe recent improvements that increase the efficient refinement of genome annotations. The first is the automated processing of genomic evidence for annotation, reducing the need for command-line processing of genome annotation evidence. Creating annotation projects can be done by simply uploading the genome's FASTA file. Similarly, genomic annotation evidence can be provided in most cases by uploading GFF3, VCF, BigWig, and BAM files directly in most cases. The second is the ability to associate GO annotations to genome annotations and export in formats such as GPAD or GPI. The third is the ability to predict the effect of individual variants to aid in the annotation of variants. Finally, we demonstrate numerous UI improvements to make annotation editing faster and easier as well as the simplicity of launching Apollo from a simple Docker command or via preconfigured Community AMI on Amazon cloud instances.

In addition to the simplified installation process, Apollo provides extensive web-services that allow it to be integrated with other web-based environments. Apollo and its associated libraries allow numerous customizations, both within Apollo itself and via JBrowse, the genomic browser Apollo is built upon (http://jbrowse.org), which has a large library of plugins (https://gmod.github.io/jbrowse-registry/).

Apollo is used in hundreds of genome annotation projects around the world, ranging from the annotation of a single species to lineage-specific efforts supporting the annotation of dozens of genomes.

Source: https://github.com/GMOD/Apollo/

Documentation: http://genomearchitect.readthedocs.io/en/latest/

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