

Apollo Genome Annotation Editor: Latest Updates, Including New Galaxy Integration

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Project Website: <http://genomearchitect.org/>

Source Code: <https://github.com/GMOD/Apollo>

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Manual curation is crucial to improving the quality of the annotations for a genome sequencing project. During this portion of the genome sequencing workflow, curators use a variety of experimental evidence to improve on automated predictions to more accurately represent the underlying biology.

Apollo is a web-based genome annotation editor that allows curators to manually revise and edit genomic elements. It provides a reporting structure for annotated genomic elements and an ‘*Annotator Panel*’ that allows users to quickly browse the genome and all available annotations. Users can manually edit the structure of a genomic element as well as add metadata, including references to other databases, adding functional assignments to genes and gene products with specific lookup support for Gene Ontology (GO) terms, as well as including references to published literature in support of these annotations.

Apollo is currently used in more than one hundred genome annotation projects around the world, ranging from the annotation of a single species to lineage-specific efforts supporting annotation for dozens of organisms at a time. Apollo enables collaborative, real-time curation (akin to Google Docs); researchers may restrict access to certain annotations depending on the role of users and groups within the community, as well as share tracks of evidence data with the public. Users are able to export their manual annotations via FASTA and GFF3 files, the Chado database schema, and web services. The news hot of the presses is that Apollo is now available for integration with Galaxy via Docker! This allows users to run analyses on their genome of interest, including a step of manual curation, all from the comfort of their installation of the versatile Galaxy platform.