Visual Refinement of Genome Annotations with Apollo in a Community Environment

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The Galaxy platform provides a powerful environment for annotating genomes with a large selection of tools and workflows for assembling, filtering, and generating annotations as demonstrated by the Galaxy Genome Annotation (GGA) project [http://bit.ly/galaxy-genome-annotation](http://bit.ly/galaxy-genome-annotation). Because visual inspection and editing of genome annotations is an important step in making sure that generated elements are valid, many other projects utilizing Galaxy also include the web-based genome annotation editor Apollo [https://github.com/GMOD/Apollo/](https://github.com/GMOD/Apollo/)[1]. World-wide, 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.

The reason for Apollo’s popularity is that it provides important modern annotation features such as drag-and-drop editing, a visual and revertible history, real-time collaboration akin to Google Docs, and the ability to host a wide range of genomes and researchers with fine-grained permissions. Once installed (Docker build [https://github.com/GMOD/docker-apollo](https://github.com/GMOD/docker-apollo) and pre-built Amazon EC2 instances are provided), it can also be integrated into workflows via a rich suite of web services and a wrapping Python library [https://pypi.org/project/apollo/](https://pypi.org/project/apollo/).

![Figure 1](image_url) **Figure 1**: Apollo UI overview. Genome evidence (lower left) can be dragged by the user up to the refinement area highlighted in yellow to add it to the annotation. Sequences are shown on the right side of the display.

To meet the wider need of our community, several new major enhancements are underway to further increase the utility of Apollo. First, is the ability to annotate variants, including the ability to visualize the effect of individual variants on genome features. Annotated variants can be exported as VCF files. Second, is the ability to import and export genomes and evidence tracks directly from the user-interface, simplifying administration and making it easy to import additional evidence. The third enhancement underway is the ability to add structured Gene Ontology (GO) functional annotations to genome features. More info on its usage and a demo site can be found at: [http://genomearchitect.](http://genomearchitect.org/) (BSD-3 License)

1 - Examples of Galaxy workflows utilizing Apollo: [https://bipaa.genouest.org/is/](https://bipaa.genouest.org/is/)