

Getting Apollo

- [GMOD/Apollo](https://github.com/GMOD/Apollo)
- AWS Marketplace
- Docker



```
docker run -it -v /jbrowse/directories:/var/lib/postgresql -p 8888:8080 quay.io/gmod/apollo:latest
```

QUESTIONS?

Contacting

- apollo@lbl.gov
- [GMOD/Apollo/issues](https://github.com/GMOD/Apollo/issues)
- <https://gitter.im/GMOD/jbrowse>

Future

- JBrowse2: more modular, synteny support
- “Official” track (last published genome)
- Community need?

Apollo: Democratizing genome annotation

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See the preprint

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Abstract

Genome annotation is the process of identifying the location and function of a genome's encoded features. Improving the biological accuracy of annotation is a complex and iterative process requiring researchers to review and incorporate multiple sources of information such as transcriptome alignments, predictive models based on sequence profiles, and comparisons to features found in related genomes. Despite rapidly increasing costs, there is an ever-growing number of scientists to incorporate sequencing as a routine laboratory technique, there is widespread demand for tools that can assist in the collaborative analytical review of genomic information. To this end, we present Apollo, an open source software package that enables researchers to efficiently inspect and refine the genomic structure and set of genomic features in a graphical browser-based platform. Some of Apollo's novel user interface features include support for real time collaborators, allowing distributed users to simultaneously edit the same encoded features while also instantly seeing the updates made by other researchers on the same region in a manner similar to Google Docs. Its technical architecture enables Apollo to be integrated into multiple existing genomic analysis pipelines and heterogeneous data storage workflow platforms. Finally, we consider the implications that Apollo and related applications may have on how the results of genome research are published and made accessible.

Figures



Extra Slides