Apollo is a web-based genomic annotation editor built on top of the JBrowse genome viewer. To accommodate a diverse array of both large and small genome annotation projects, we have undertaken several major efforts:

1) A flexible and informative layout via a side-dock that allows a deeper, alternate view of the data
2) A suite of secure web services used to build the interface make it easy to integrate with other software and create customized interfaces
3) Support multiple organisms per server to minimize server resources and allow for optional public access
4) User and group level permissions for editing and viewing annotations to support larger teams

Support for Multiple Genomes

Multiple organisms may curated from a single server.

Point to an existing JBrowse directory to start annotating organism

Organisms can be allowed to be publicly viewed without a login

Works with existing JBrowse track selectors if needed

Search and export annotated scaffolds as GFF3 or FASTA

Drag and Drop Annotation

ARemovable side-dock provides an alternate view of annotation information.
B) Tabs have search functionality, additional details, and editing capability.
C) Allows detailed view of data.
D) Allows annotator to quickly switch between organisms and sequences.
E) Admin Panel for reporting and configuration.

Future Work

• Arbitrarily align scaffolds and features, hide introns
• Variant annotation and visualization
• Phenotype annotation
• Track-level permissions

Apollo is a real-time, collaborative, web-based tool for manually editing genome workflows.

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