I5k Workspace updates: What’s new with Apollo2

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Updates at the i5k Workspace

• Introduction
• Apollo2.1.1 vs Apollo2.6.5
  • New look
  • New interfaces
• Apollo1.0.4 Vs Apollo2.6.5
  • LOTS of changes
• An example annotation workflow
This has been a long time coming...

- Updating Apollo to this version has taken a lot longer than anticipated
- A large number of updates on the back-end
- Reworking the track styling system
- Manually checking each evidence track for issues
- Creating a new feature type for showing BLAST hits

- If you see any issues, please let us know
- i5k@usda.gov
What is Apollo?

• Apollo is a web-based visual gene curation tool
• Apollo is an extension for the JBrowse genome browser
Apollo Basics

• Many of the functions are located in the panel on the right
• Your account can have access to multiple organisms
• Tabs allow quick access to the tools
• Annotations – show annotations created by users
• Tracks – shows the groups of tracks, can be turned on/off by group
• Ref Sequences – view and navigate to any scaffold
• Search – BLAT sequence search
Example Gene annotation workflow

- Obtain sequence of interest / map to assembly using BLAST
- Use link in BLAST results to see the matches in JBRowse
- Turn on other evidence tracks (gene predictions, Transcriptome, etc)
- Login to Apollo -> create and refine the gene model
1. Find sequence/search the assembly
3. Use BLAST linkouts to see hits in the assembly
View in Jbrowse, turn on evidence tracks
Login to Apollo

Upon Login You Agree to the Following Information

- You are accessing a U.S. Government information system, which includes (1) this computer, (2) this computer network, (3) all computers connected to this network, and (4) all devices and storage media attached to this network or to a computer on this network. This information system is provided for U.S. Government authorized use only.
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Username (small)

Password

Login

Remember me
Start curating

- Annotations may be created by
- Click-dragging a model to the User created Annotations panel
- Right-clicking a model then clicking through the “Create new annotation” menu
A few Apollo tips

• The Color by CDS feature is useful for fast comparisons
• The CDS is auto-calculated whenever a change is made
• Special symbols show if exons don’t end with canonical splice sites
• Edge matching – select a model and other models that have the same splice sites become highlighted in red (next slide)
Right-click menu for many options
Updates in Apollo 2.6.5

• Many under-the-hood updates
  • Bug fixes, improved responsiveness
  • Supports newer versions of Jbrowse

• User interface changes
  • Better
  • Faster
  • More stable
  • Updated styles
Updated styles

“NeatFeatures” – draw introns to show the direction a model goes
New built-in support for color by feature type (previously was a plugin)
Apollo updates in the latest release

• More functions are moved into the right side panel
• Updated Search features
  • New results
  • Hits can be used to create annotations
Annotation Editor updates

• More functions moved to the right side panel
• Gene is the default level
• GO Annotations, name, etc
• Many more validation steps
Built in BLAT search

• Moved to the right-side panel
• Updated Search features
  • New results
  • Hits can be used to create annotations
Special instructions for *E. affinis*

- This is a community that transitioned from Apollo1 to the newest Apollo during their annotation window.
  - Special considerations
  - The previously created annotations were migrated as a new data track
    - Only visible to logged in users
    - Will have to be harmonized with newly created annotations for generation of the new OGS/submission to NCBI
  - Annotation editor window now defaults to Gene level.
  - Annotation information may still need to be entered into the transcript section
Training session for *E. affinis*

- [https://i5k.nal.usda.gov/training/webapp/blast](https://i5k.nal.usda.gov/training/webapp/blast)
Thanks!

If you have questions or comments reach out to us at

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