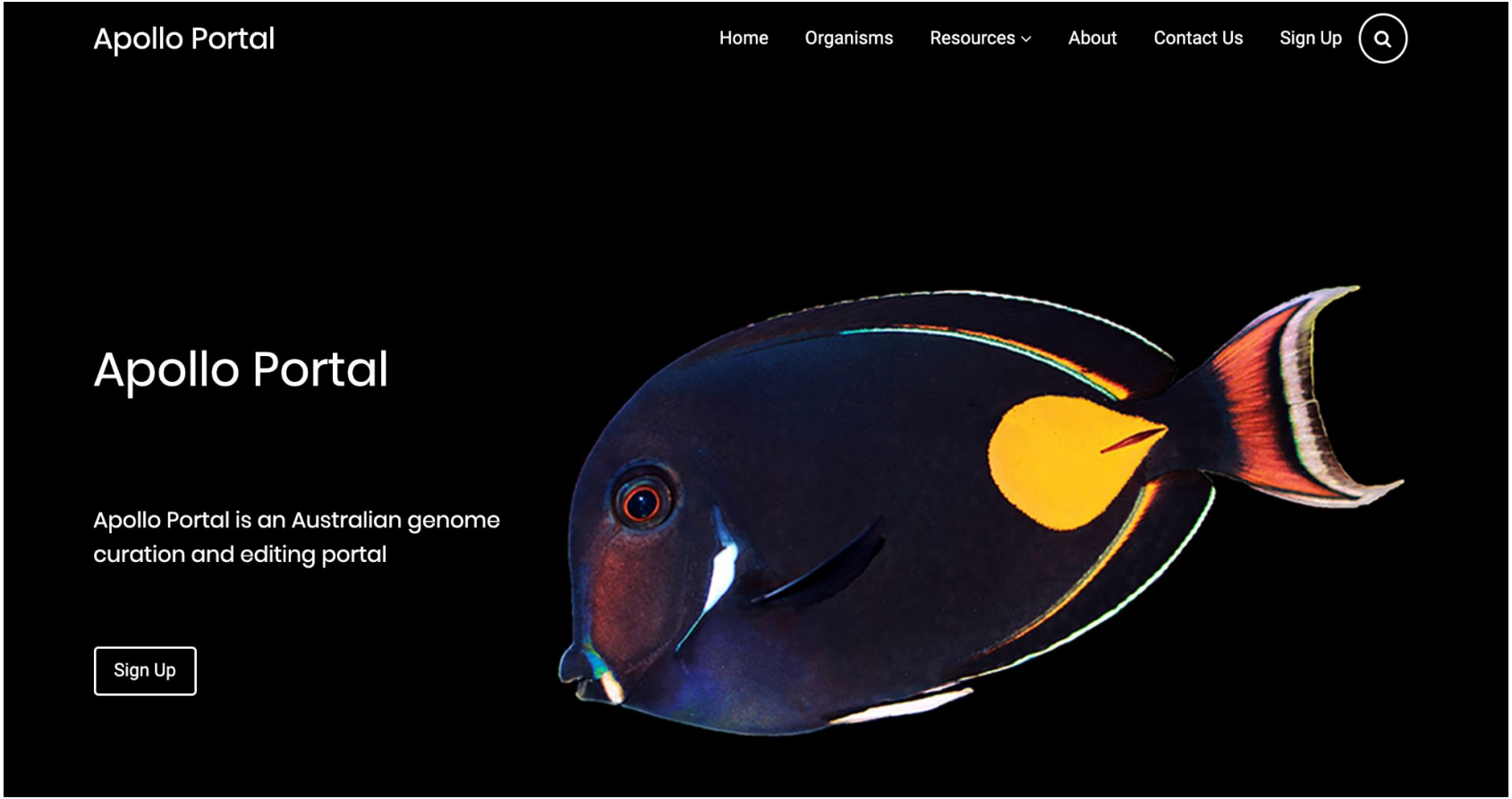
Australian Apollo Service



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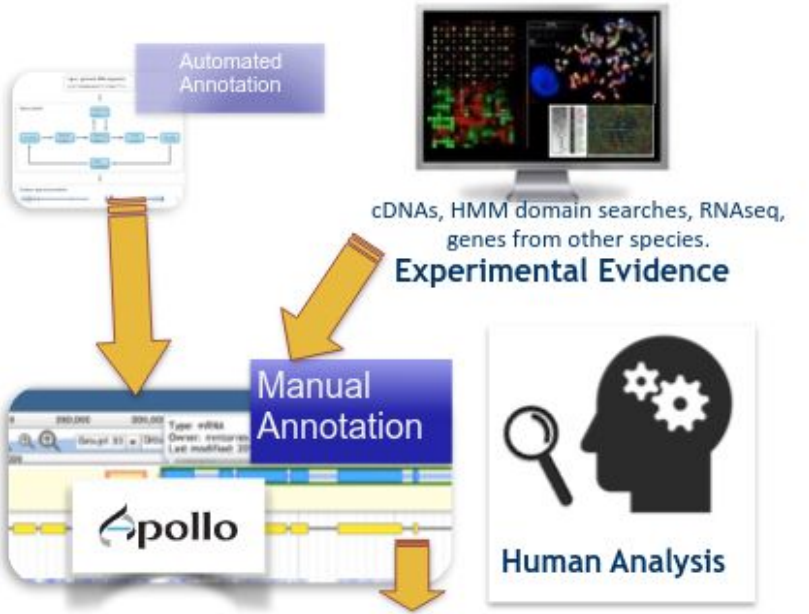
So what is Apollo?



Lewis S, Searle S, Harris N et al. (2002)
Apollo: a sequence annotation editor. Genome Biology 3, research0082.1.
https://doi.org/10.1186/gb-2002-3-12-research0082

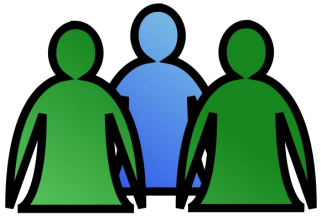
Dunn NA, Unni DR, Diesh C, Munoz-Torres M, Harris NL, et al. (2019)
Apollo: Democratizing genome annotation. PLOS Computational Biology 15(2): e1006790.
https://doi.org/10.1371/journal.pcbi.1006790

Image:
https://training.galaxyproject.org/training-material/topics/genome-annotation/tutorials/apollo/slides-plain.html

High priorities identified in community consultations

I need a hosted system that I can use quickly after registering so that I won't waste time in setting it up myself

I need a genome browser-based system where I can upload and view supporting data alongside the annotations



I need a web-based system to manually correct genome annotations that allows me to share and compare with colleagues

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Apollo Portal

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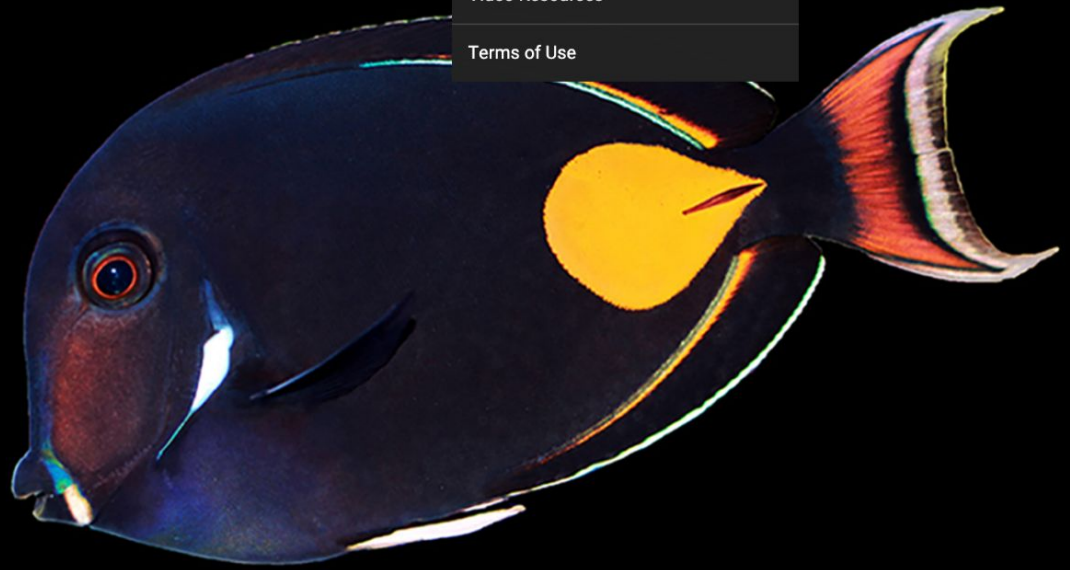
- Getting Started
- User Documentation
- Training, Tutorials & Other Resources
- FAQs
- Video Resources
- Terms of Use

Apollo Portal

Apollo Portal is an Australian genome curation and editing portal

Sign Up



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User Documentation

This document provides guidance and information about:

1. How Do I Sign Up for an Apollo Instance?
2. What Data Files Are Required To Create Genome Tracks In Apollo?
3. How Do I Prepare My Data Prior to Upload?
4. How Do I Generate a Public-Key?
5. How Do I Upload Data and Create a Genome Track via the Command Line?
6. How Do I Upload Data and Create a Genome Track via the Apollo (browser) Interface
7. How Do I Make My Genome Public?
8. How Do I Manually Annotate My Genome In Apollo?

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FAQs

What is the Apollo Service?

The Apollo software package is a web-based tool for visualising genomic contents and manually improving gene p
a reference genome collaboratively. The Apollo Service provides Australian-based researchers with customised, lo
their genome projects.

- How can I get an Apollo Instance?
- Can I trial Apollo before signing up?
- I am a non-Australian-based researcher, can I access the Apollo Service?
- Can Apollo automatically annotate my genome?
- How can I get training to use Apollo?

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Sign Up

Eligibility Criteria

Please note that the Principal Investigator must be affiliated with a recognised Australian academic or research institute. All form elements marked with a * must be filled out. If you have any queries about this form or the questions therein, please contact support at apollo-support@genome.edu.au.

☐ I confirm the Principal Investigator belongs to a recognised Australian institute. *

Research Group/Lab or Consortium name (NB: the names of all Research Labs/Consortia using this service are listed on this page) *

Website link to Research Group/Lab or Consortium

Suggested Apollo Host Name *

Genome Annotation

Genome Annotation Process

- **Genome preparation** (repeat identification and masking),
- **Structural annotation** (identifying the location and structure of genes and other genomic features),
- **Functional annotation** (predicting function of the genomic features),
- **Manual correction** (i.e. curation of automatically-produced genomic features), and
- **Visualisation** (typically using a genome browser displaying multiple data tracks).

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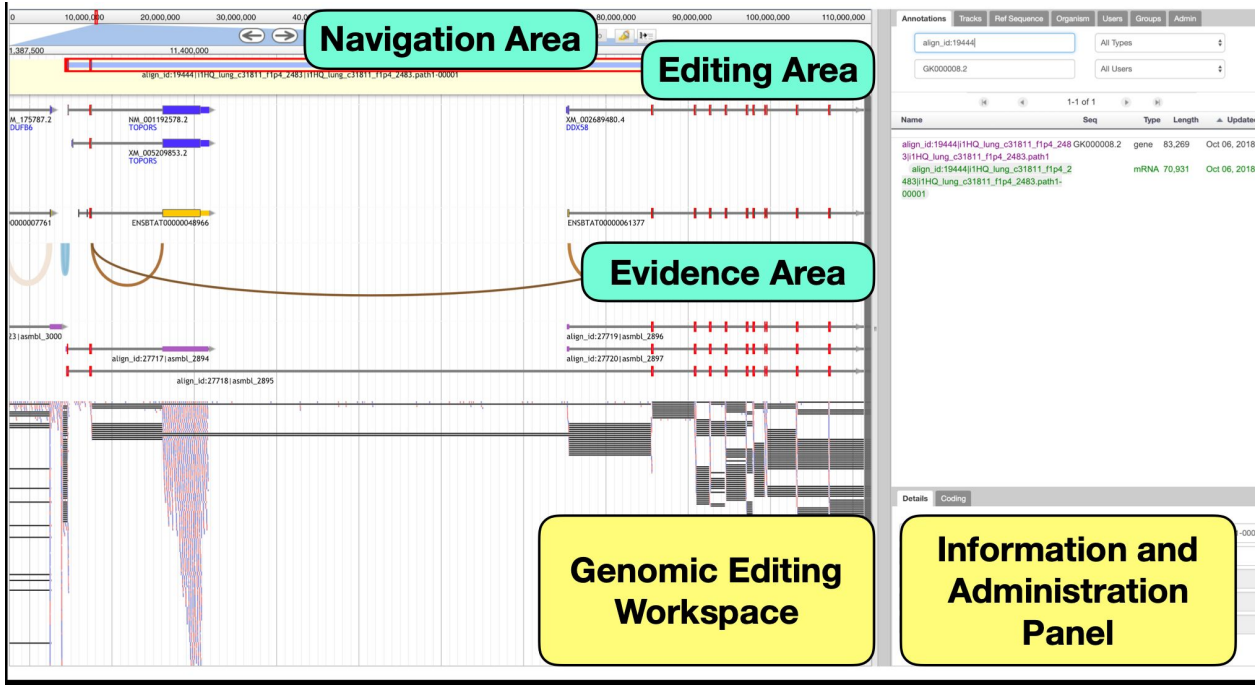
Getting Started in Apollo

The Apollo Software

A

B



The Apollo Software has two main panels: A genome Editing Workspace (A) and a configurable Administration Panel (B).

Ref: https://doi.org/10.1371/journal.pcbi.1006790

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File Types

Table 1. Required Data Files for Genome Track Creation.

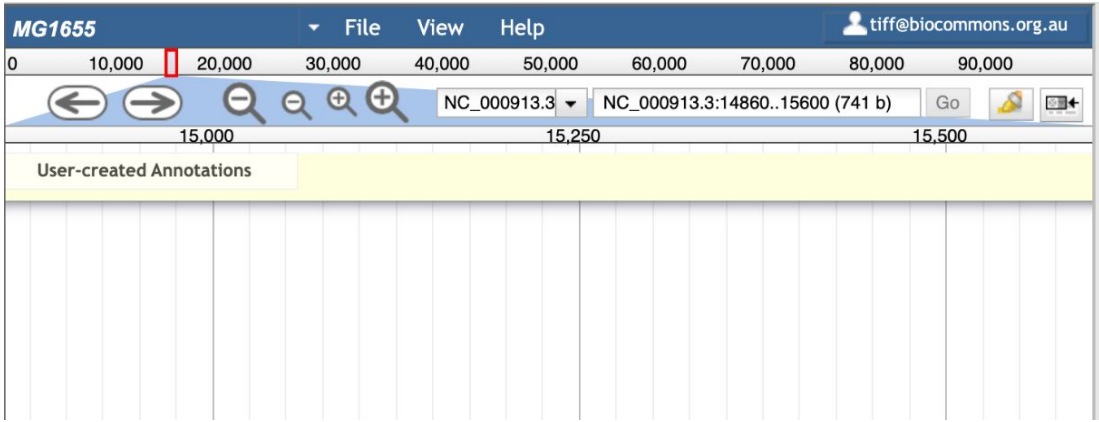
File Format	Description	Requirement
Fasta	Genome Reference File	Mandatory
Fai	Genome Reference Index File	Mandatory
Gff3	Genome Annotation File	Mandatory
Gff3.gz	Genome Annotation Compressed File	Mandatory
2bit	Genomic Sequence in Binary File	Optional
Bam	Alignment File	Optional
Bai	Alignment Index File	Optional
Vcf	Variant Calling File	Optional
Vcf.gz	Variant Calling Index File	Optional
bw	A compressed, indexed, binary format of genome-wide signal data	Optional

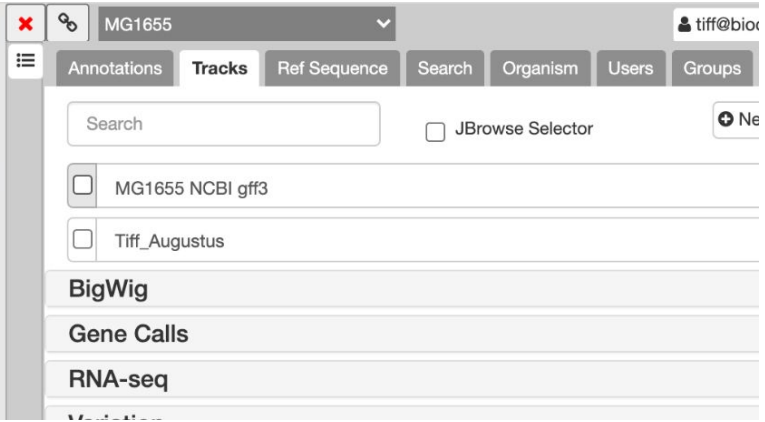
E. coli Test Data

- *Escherichia coli*, MG1655, K-12 wild-type strain
- Publicly available data
- Subset of complete genome (100KB)

Logging into the Apollo Training Instance

https://training.genome.edu.au/apollo/





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Getting Data Into Apollo

tinyurl.com/2021ApolloData

Getting Data Into Apollo.

File 1: Augustus.gff3

tinyurl.com/2021ApolloData

- Under ‘Tracks’ tab
- Select ‘+New Track’
- Select ‘GFF3’
- ‘Enter Track Name’ - Augustus
- ‘Choose File’ - augustus.gff3
- Select ‘Upload’

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

- Under ‘Tracks’ tab
- Select ‘+New Track’
- Select ‘GFF3’
- ‘Enter Track Name’ - Blastp_vs_swissprot
- Under ‘Top Type’ - protein_match
- Under ‘Category’ - ‘MyCategory’

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

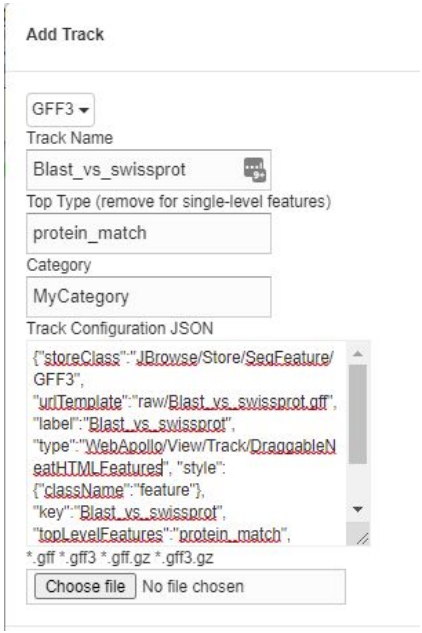
tinyurl.com/2021ApolloData

- Under ‘Tracks’ tab / Select ‘+New Track’ / Select ‘GFF3’
- ‘Enter Track Name’ - Blastp_vs_swissprot
- Under ‘Top Type’ - protein_match
- Under ‘Category’ - ‘MyCategory’
- Under ‘Track Configuration JSON’
- Under “type”
- Replace “JBrowse/View/Track/HTMLFeatures” to - “WebApollo/View/Track/DraggableNeatHTMLFeatures”

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData



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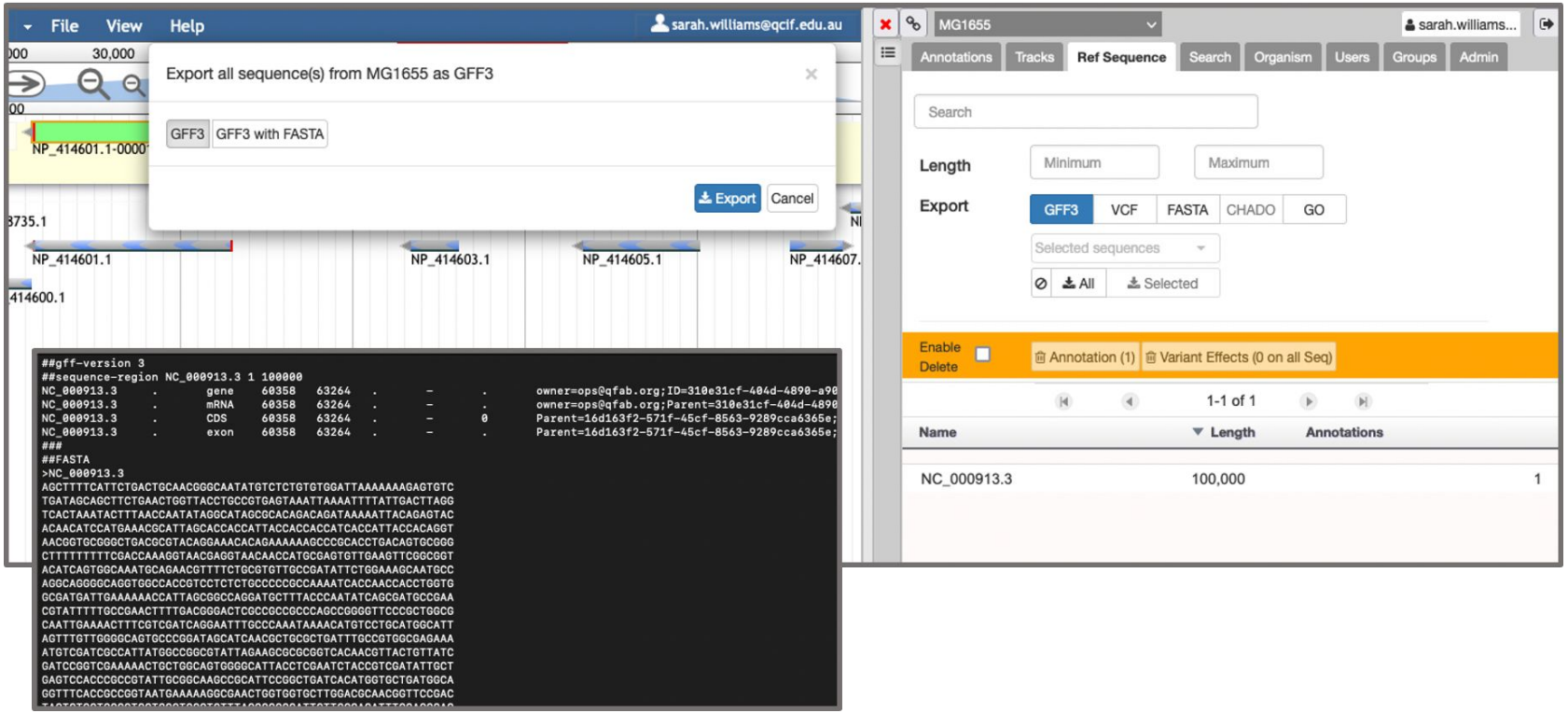
Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

- Under ‘Tracks’ tab / Select ‘+New Track’ / Select ‘GFF3’
- ‘Enter Track Name’ - Blastp_vs_swissprot / Under ‘Top Type’ - protein_match / Under ‘Category’ - ‘MyCategory’
- Under ‘Track Configuration JSON’ / Under “type”
- Replace “JBrowse/View/Track/HTMLFeatures” to - “WebApollo/View/Track/DraggableNeatHTMLFeatures”
- ‘Choose File’ - Blastp_vs_swissprot.gff3
- Select ‘Upload’

Getting Data Out Of Apollo



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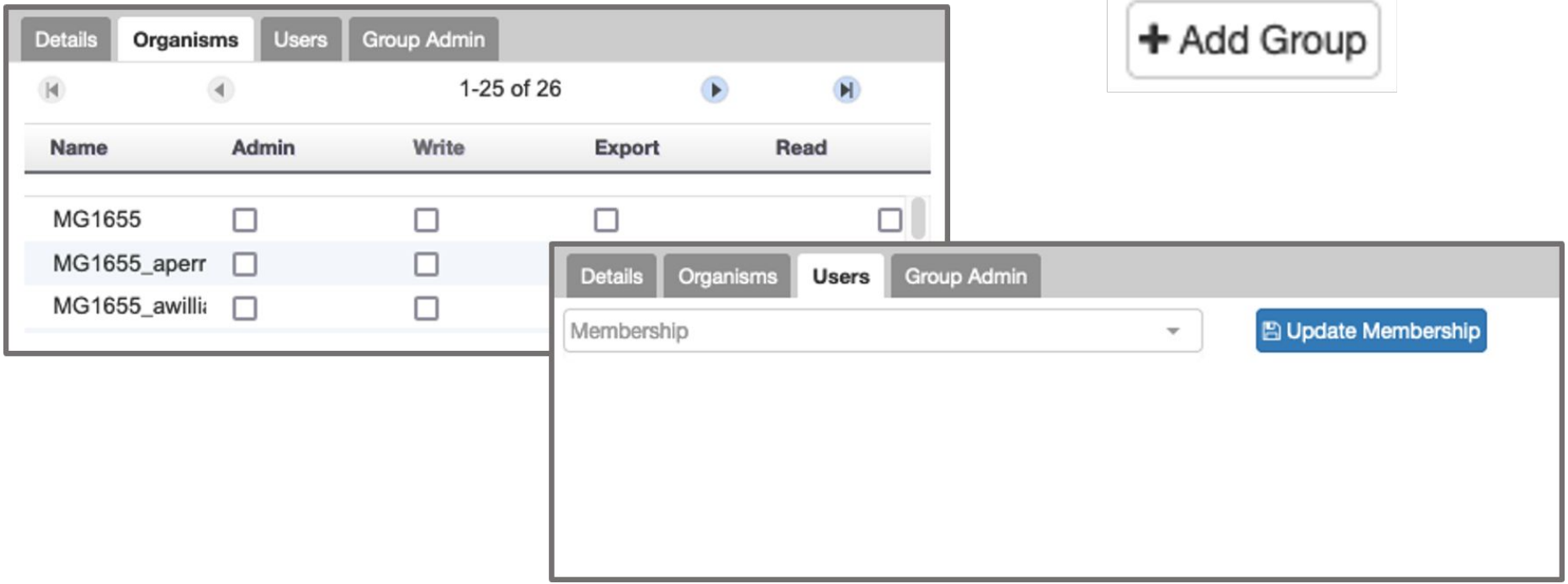
Annotating together



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Next steps...

- Australian Apollo Service, visit:

  https://apollo-portal.genome.edu.au/

- Apollo demo site:

  http://demo.genomearchitect.io/Apollo2/annotator/index

  Username: *demo@demo.com*

  Password: *demo*

- Apollo Official Google Group:

  https://groups.google.com/a/lbl.gov/g/apollo

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