The i5k Workspace@NAL:
a pan-Arthropoda Genome Database

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USDA-ARS, National Agricultural Library

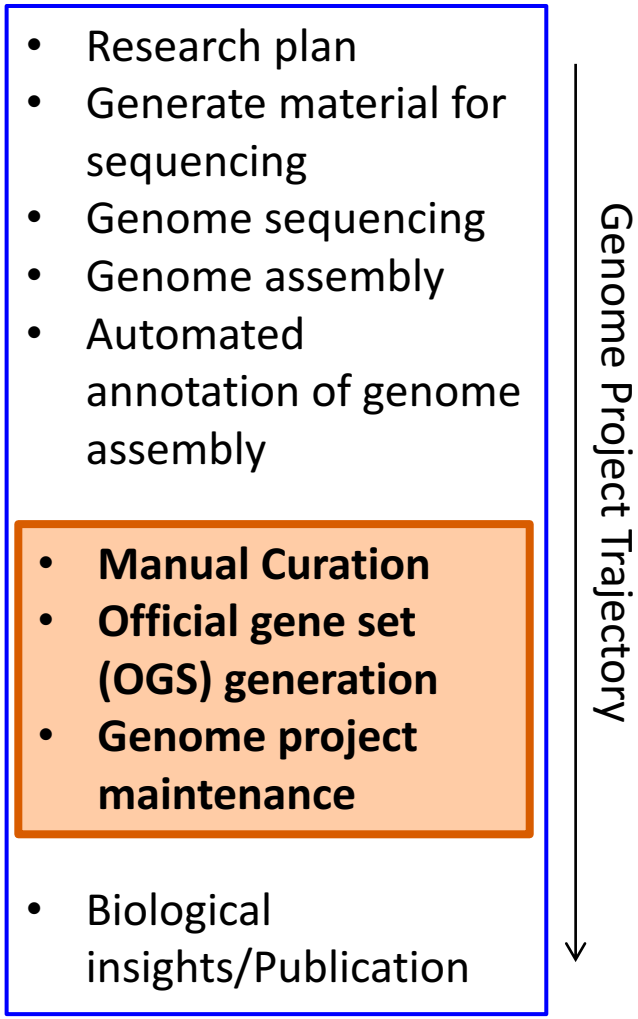
USDA

Outline

- Background and overview
- Why join the i5k Workspace?
- What do we need for a project?
- What we do with your data?
- What don’t we do with your data?
- Our new system for submitting projects and data

Background

- The i5k initiative tasked itself with coordinating the sequencing and assembly of 5000 insect or related arthropod genomes
- International effort to **prioritize** insect genomes for sequencing; provide **guidelines for genome sequencing and curation**; and seek **funding.**
- The i5k Workspace@NAL is available to help any i5k (arthropod) project with genome hosting needs



Workspace Project Basics

- The i5k Workspace centers around ***projects.***
  - A project is a collection of data based on the genome assembly of an arthropod
  - All data is used in the context of the genome assembly
- Each project has a ***project coordinator.***
  - Serves as the point of contact for questions about the project
  - Main responsibility: approve or reject new Apollo users
- **All** of our data is user-submitted

Why join the i5k Workspace?

- Gain access to a large diverse community
  - A diversity of organisms
    - 58 species and counting
    - 20% of the arthropods with genome assemblies at NCBI
  - Large user community with many different interests
    - People versed in the biology of specific systems
    - Experts in a species or group of species
- A common interface for accessing data, tools and search
- Detailed policies on data and project management
  - Helpful if you have data management requirements
  - Data management
    - https://i5k.nal.usda.gov/data-management-policy
  - Long-term project management
    - https://i5k.nal.usda.gov/long-term-i5k-workspace-project-management

What do we need for a project?

- Your project metadata
  - Information about your organism
  - Metadata for submitted data files (the more the better)
    - What tools or methods were used
    - Software versions and options set
    - When and where the data were generated
    - Other information (location collected, life-stage, etc.)
- Your data files
  - Genome assembly needs to be in GenBank/ENA/DDBJ
  - Data should be open access (no private repositories)
  - Additional datasets need to be mapped to the same assembly

What do we do with your data?

- Create resources
  - Organism and gene pages
  - Data downloads
- Integrate your data with our tools
  - Genome browser
  - BLAST, Clustal, HMMer
  - Apollo for gene curation
- Offer post curation services
  - Annotation QC and Official Gene Set (OGS) Creation
  - Update gene pages, Apollo, BLAST with OGS

‘Frozen’ genome assembly

Automated annotations

Ancillary datafiles (e.g. RNA-Seq alignments)

Submission

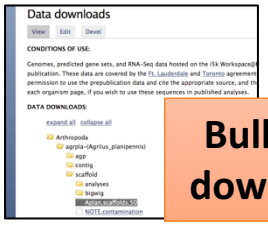
Workspace@NAL

https://i5k.nal.usda.gov/

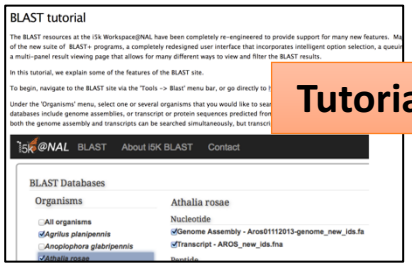
Resources

Organism Information Page

Bulk data downloads

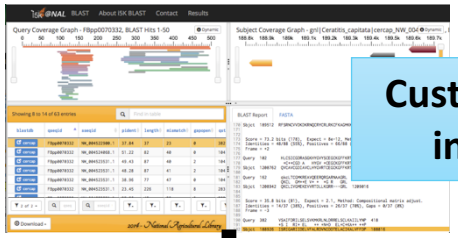


Tutorials

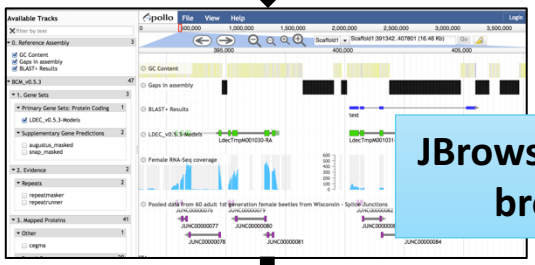


Tools

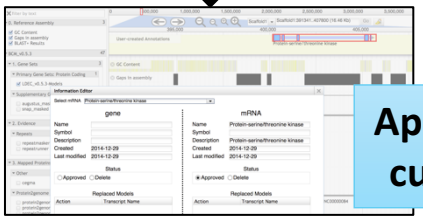
Custom BLAST interface



JBrowse genome browser



Apollo manual curation tool



HMMer

Clustal

Services

Manual annotation quality control

Official gene set generation

Challenges

Non-standard data formatting

Failure to submit all metadata (ex: sample origin; analysis methods)

What don’t we do with your data?

- Computationally intense analyses such as
  - Gene prediction
  - Raw RNAseq mapping
- We are not a long-term archive or repository
  - NCBI
  - Ag Data Commons
  - Dryad Digital Repository
  - CyVerse Data commons
  - Many other options available

Criteria for starting a project

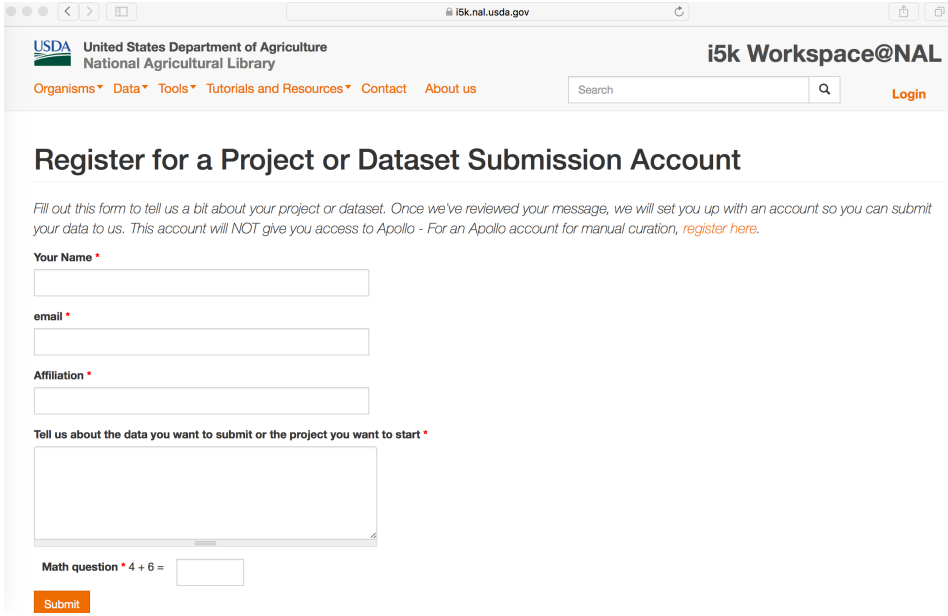
- You need to have an **arthropod** genome assembly, **accessioned by NCBI** (or another INSDC member)
  - Using GenBank's accession numbers avoids confusion about assembly version
  - The GenBank contamination screen improves the assembly quality
  - Using a stable assembly is beneficial for the labor-intensive community annotation process

Other things to consider before submitting

- ***All data submitted to the i5k Workspace is public.***
  - However, we do state whether Ft. Lauderdale/Toronto agreements of data sharing should apply
- Is your genome an 'orphan', or is there another suitable database?
  - We can host genomes that are already hosted elsewhere, and actively communicate with other database providers
  - All manual annotation efforts need to be at one database

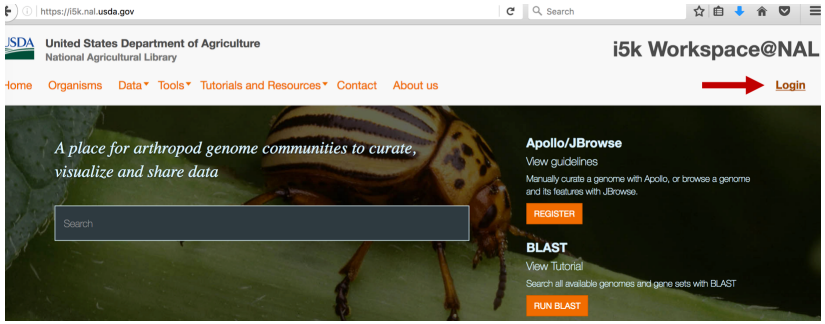
Getting an account

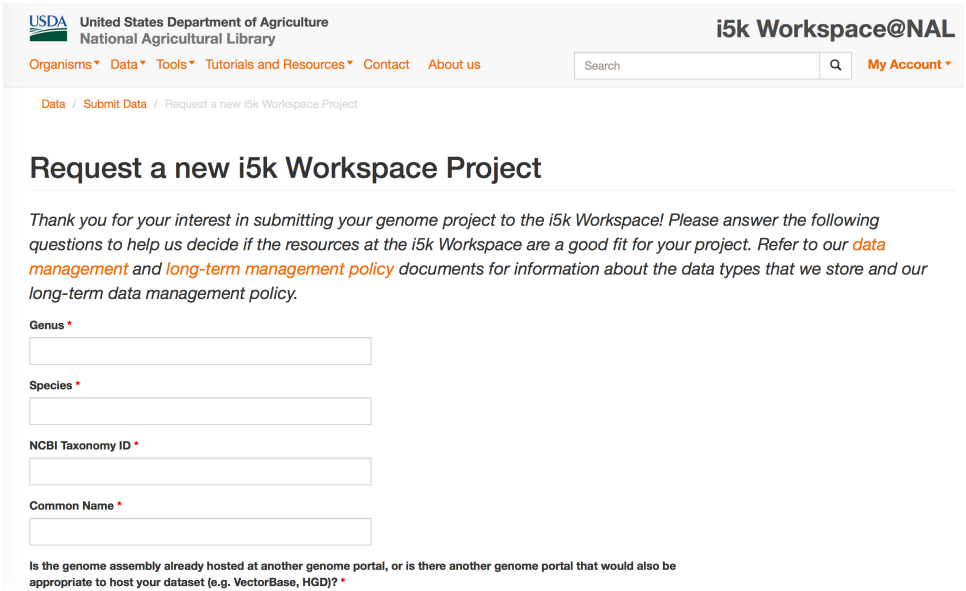
- Apply for a dataset submission account: https://i5k.nal.usda.gov/register/project-dataset/account
- Once your account is approved, you can submit projects, assemblies or other datasets



Start an i5k Workspace Project

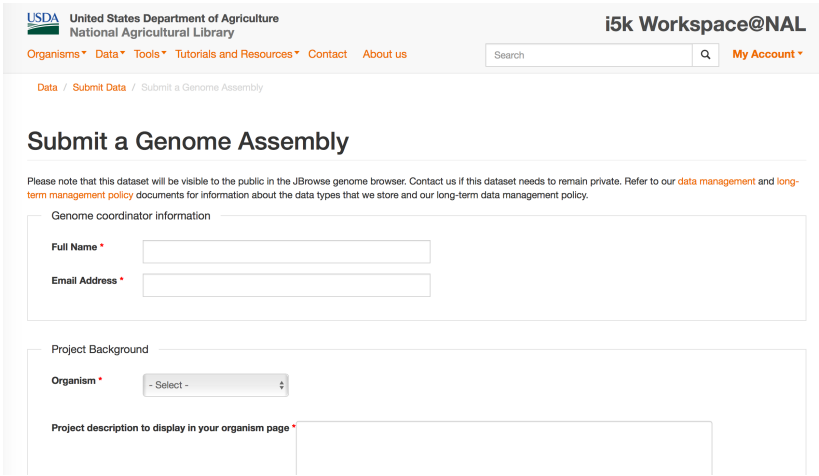
- Log in
  - https://i5k.nal.usda.gov/user
- From menu, select 'Data -> Submit data -> Request a new i5k Workspace Project'
  - https://i5k.nal.usda.gov/datasets/request-project
- We'll review your submission and will get in touch with you





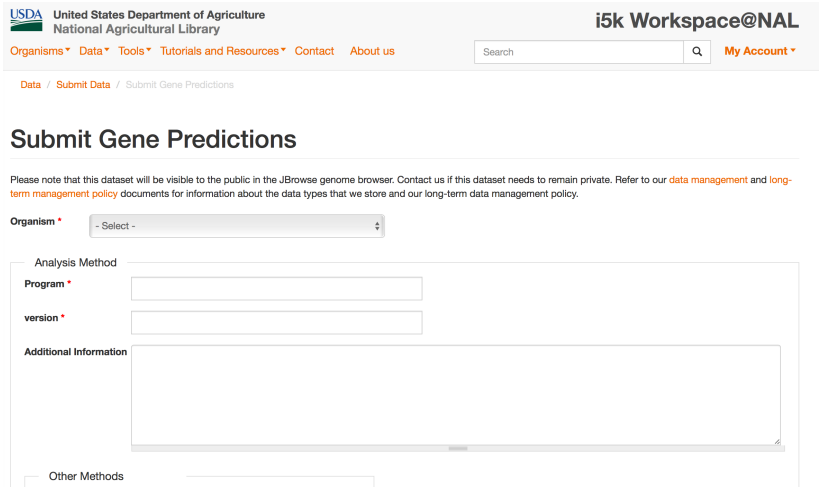
Submit your genome assembly

- *All information submitted through this form will be re-formatted for display at the i5k Workspace (except for email address and file checksum)*
- From menu, select ‘Data -> Submit data -> Submit a genome assembly’
  - https://i5k.nal.usda.gov/datasets/assembly-data



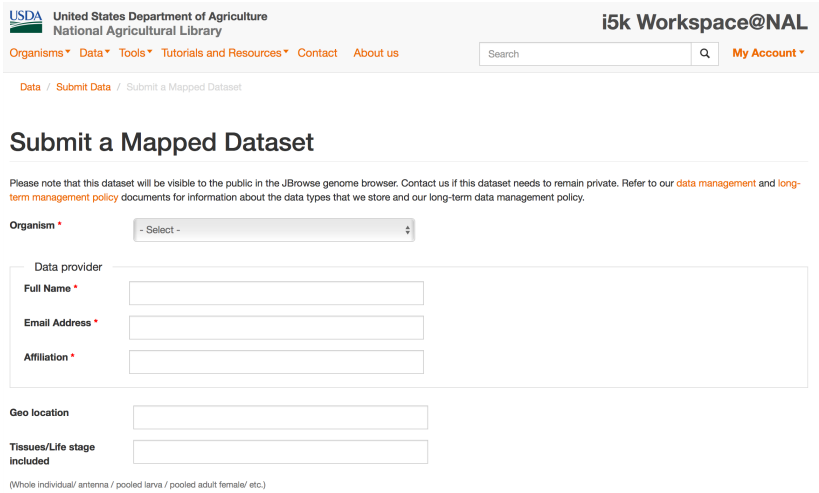
Submit gene predictions

- *All information submitted through this form will be re-formatted for display at the i5k Workspace (except for email address and file checksum)*
- Under menu bar, select ‘Data -> Submit data -> Submit Gene Predictions’
  - https://i5k.nal.usda.gov/datasets/gene-prediction



Submit mapped datasets

- *All information submitted through this form will be re-formatted for display at the i5k Workspace (except for email address and file checksum)*
- Under menu bar, select ‘Data -> Submit data -> Submit a Mapped Dataset’
  - https://i5k.nal.usda.gov/datasets/mapped

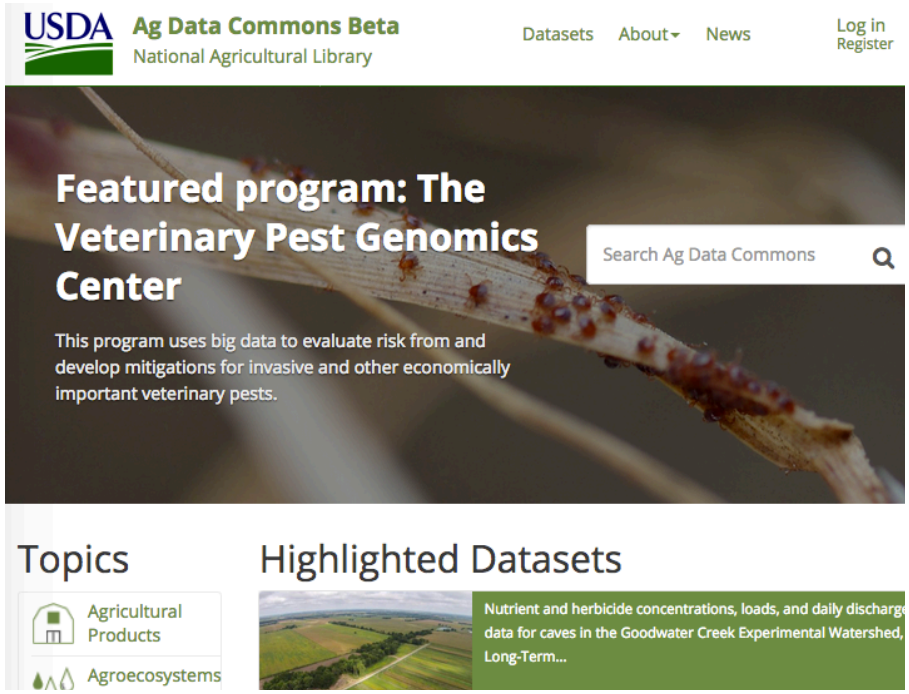


Send us your files

- There are currently **five** ways to share files with us:
  1. Use our data submission forms
  2. Transmit the file via **ftp** (only for files < 2 Gb)
  3. Email it to us (for files < 25 Mb only)
  4. Provide us with a **URL**, if available
  5. Upload the file to **CyVerse** and share with our organization, “NAL Bioinformatics”
- We prefer that you share your files with us via our data submission forms.
- For more information, see https://i5k.nal.usda.gov/content/sharing-files-us

Other resources at the NAL: the Ag Data Commons

- Hosts any dataset funded by the USDA
- Landing page
- Citable DOI
- https://data.nal.usda.gov/
- 9 i5k datasets already available



Need more information?

i5k Workspace@NAL:

- https://i5k.nal.usda.gov/
- https://github.com/NAL-i5K/

The i5k initiative:

- New website: http://i5k.github.io/

Official Gene Set creation at the i5k Workspace

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Official Gene Set creation at the i5k Workspace

- Official Gene Set definition
- Our OGS generation process
  - Manual and community annotation
  - Quality control
  - Merge
  - Release
- Examples and future directions of the OGS generation process

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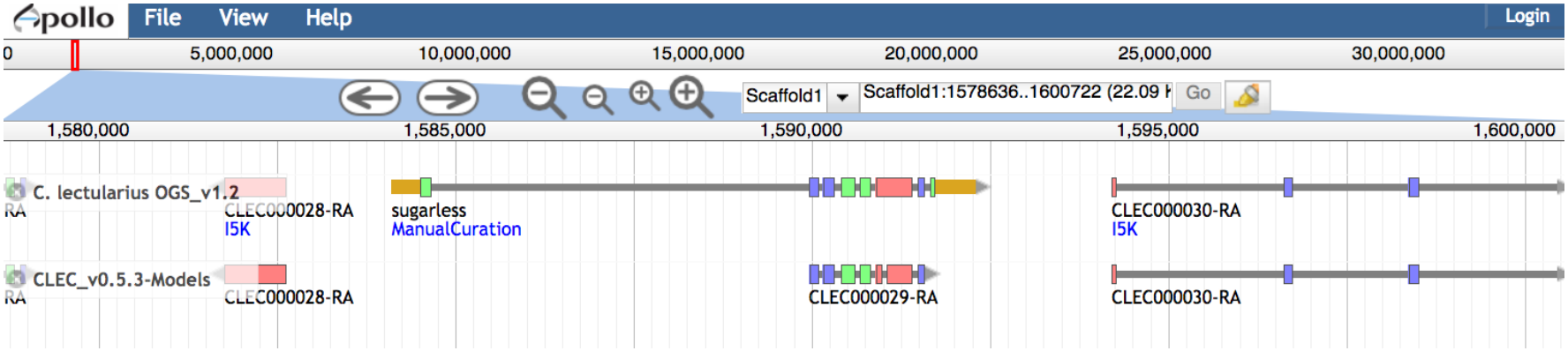
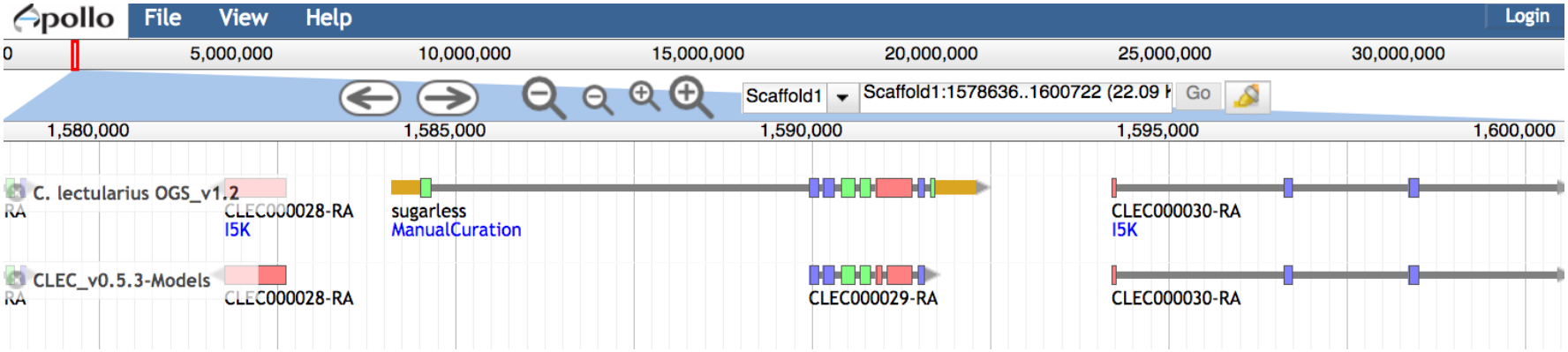
The Official Gene Set – what is it?

- Loose definition: The best known representation of gene models for a genome assembly
- When the i5k Workspace generates an OGS, this is a merge between one gene set (usually computationally predicted), and a set of manually validated annotations (usually from the Apollo software)



Why generate an Official Gene Set?

- This depends on your genome community's needs.
- If several groups want to perform downstream analyses, it helps to have an authoritative 'reference gene set' for your community, rather than multiple competing gene sets



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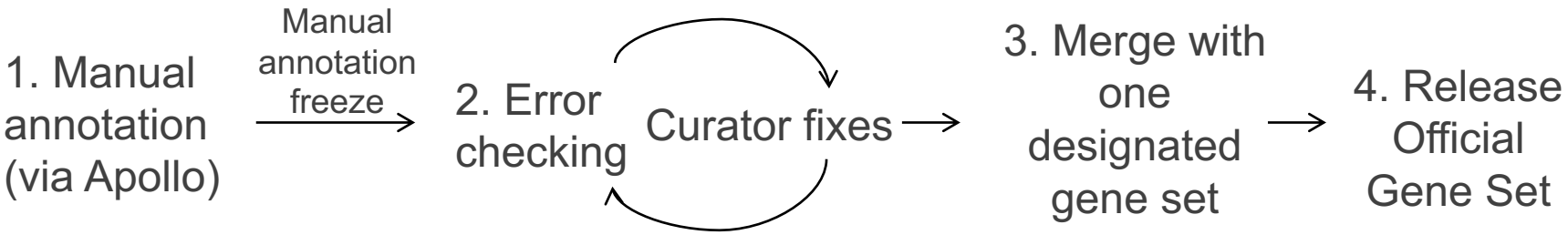
Our OGS generation process

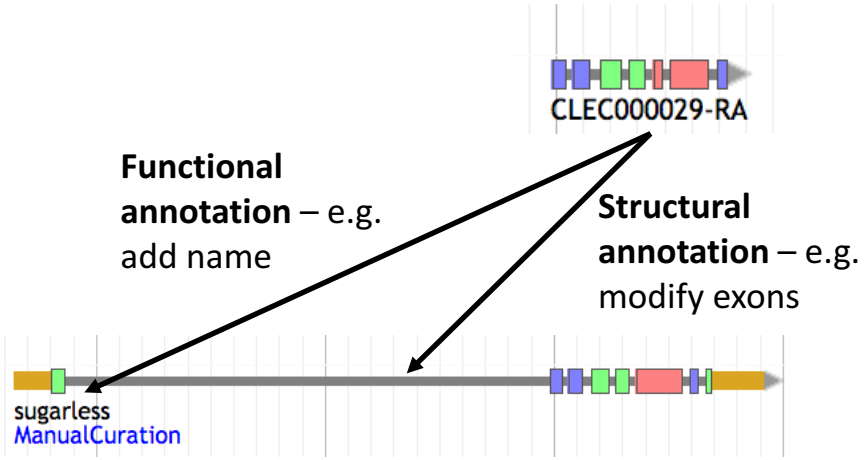


- New public version of program is available: https://github.com/NAL-i5K/GFF3toolkit (Mei-Ju Chen, Li-Mei Chiang)
- The full process is time-consuming, but we are generally available to perform OGS generation for i5k Workspace projects

1. Manual and community annotation

What is manual annotation?

- Manual review and improvement of an existing gene prediction
- Often, but not always: drawing on external evidence (e.g. RNA-Seq, cDNA, genes from other species) to improve a computationally predicted gene model



1. Manual and community annotation

Why manually annotate?

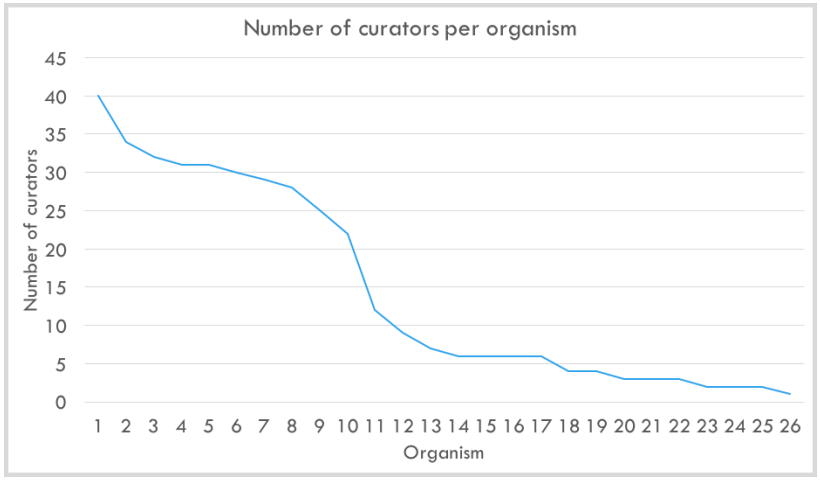
- "Incorrect annotations poison every experiment that makes use of them … Worse still, the poison spreads because incorrect annotations from one organism are often unknowingly used by other projects to help annotate their own genomes."
  - Yandell and Ence 2012, doi:10.1038/nrg3174
- Link gene models to existing literature and ontologies, providing richer data
- One current 'model' of the genome paper often draws heavily from insights confirmed by manual annotation

1. Manual and community annotation

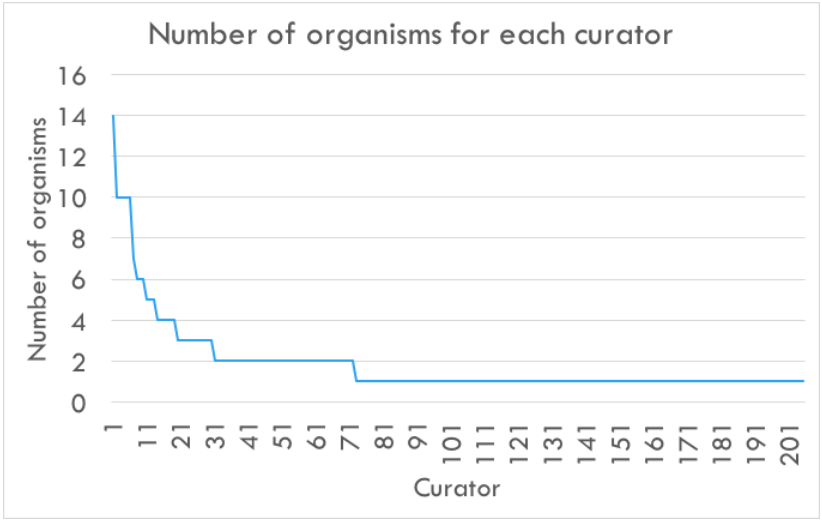
- What is community annotation?
  - Scientists collectively examine and improve gene models (usually computationally predicted)
- Community annotation at the i5k Workspace:
  - Access to a large community of curators
  - Tutorials, guidelines, webinars
  - Registration mechanism for new annotators
  - One-on-one support
  - Over 400 registered annotators have curated over 10,000 gene models using the Apollo software

1. Manual and community annotation – i5k pilot example

Number of curators per organism. Community size varies among organisms.



Number of organisms per curator. 35% of curators worked on more than one organism



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1. Manual and community annotation – i5k pilot example

organism	Total number of manually annotated models	Proportion of manually annotated models with structural changes
Anoplophora glabripennis[6]	1144	0.75
Cimex lectularius[7]	1354	0.76
Oncopeltus fasciatus	1518	0.76

- Three organisms that completed the manual annotation process had to perform similar amounts of structural annotations to computationally predicted gene annotations
  - Computationally predicted genes often have inaccurate gene structures
  - Community annotation can effectively improve gene sets

2. OGS generation – Quality Control

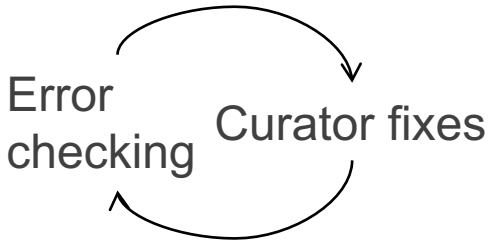
- Manual curation can introduce many errors, even using standard software packages (e.g. Apollo)
- QC program identifies common *formatting* errors from the manual curation process
  - Github repo: https://github.com/NAL-i5K/GFF3toolkit
- Identifies over 50 error types
- Another in-house pipeline corrects many of these errors

2. OGS generation – Quality Control

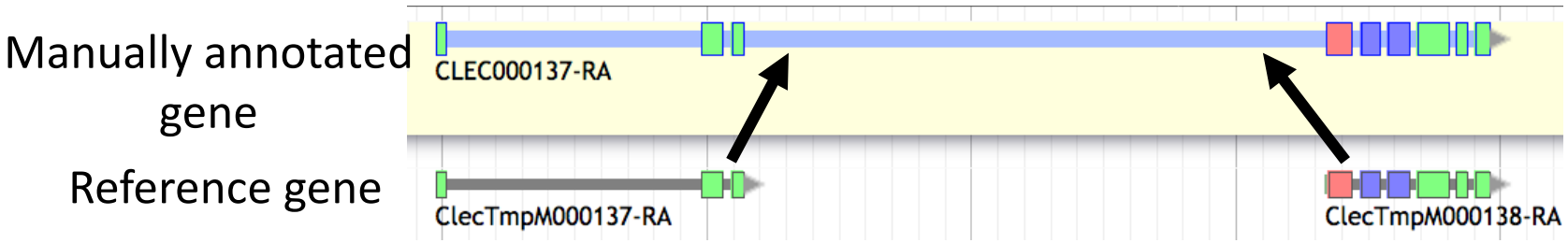
- Requires some manual review – can't be completely automated
  - e.g. did you name your gene model 'test' or 'Contig277'?
- Note that i5k Workspace staff aren't 'curators' in the traditional sense – we ***do not*** review the biological validity of any of the community-annotated models.
- The degree of manual review of community annotations is higher if Official Gene Sets are to be submitted to NCBI

2. OGS generation – Quality Control

- *Diaphorina citri* example (Database, doi: 10.1093/database/bax032)
  - First round of corrections for community curation:
    - 513 errors in 587 manually annotated models
    - 397 of these errors needed curator feedback
  - Second round of corrections :
    - 15 errors needed annotator feedback



3. OGS generation – Merge



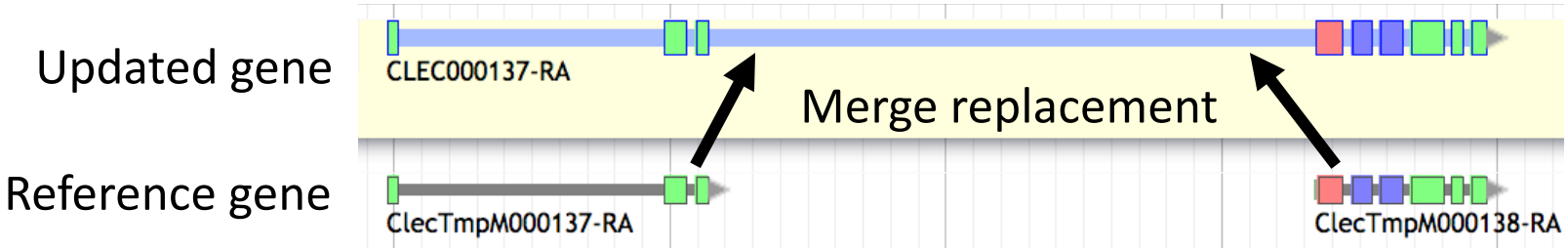
The GFF3toolkit Merge program can identify which gene models in the ‘reference’ gene set should be replaced by gene models in a second gene set (i.e. the manually annotated models) via ‘auto-assignment’)

3. OGS generation – Merge

- Auto-assignment uses both sequence similarity and coordinate overlap
  - Extract CDS and pre-mRNA sequences from mRNA features from both gene sets.
  - Use blastn to determine which sequences from the modified and reference gene set align to each other **in their coding sequence**.
    - These parameters are used: -evalue 1e-10 -penalty -15 -ungapped
  - If two models pass the alignment step, check that matched models also have coordinate overlap
  - Add a ’Replace Tag' with the ID of each overlapping model to the modified gene set.
  - If no reference model overlaps with a new model, then the program will add 'replace=NA'.

3. OGS generation – Merge

- The program determines merge actions based on the Replace Tags:
  1. deletion
  2. simple replacement
  3. new addition
  4. split replacement
  5. merge replacement
- Models from modified manual annotations replace models from reference annotations based on merge actions in step 2.



3. OGS generation – Merge

- *Diaphorina citri* example (Database, doi: 10.1093/database/bax032)
    1. # genes deleted: 1
    2. # genes with simple replacement: 437
    3. # genes added: 72
    4. # genes split: 38
    5. # genes merged: 31
    6. Total number of genes in OGS: 20,217

3. OGS generation – Merge

- Other software tools can be used to merge gene sets
  - Combiner tools that use ‘weights’ for different input annotations, e.g.
    - EVidenceModeler (EVM, https://evidencemodeler.github.io/)
    - Glean (https://sourceforge.net/projects/glean-gene/)
  - Other overlap-based replacement tools, e.g Bedtools intersect (http://bedtools.readthedocs.io/en/latest/)

4. OGS generation – Release OGS

- Generate new or maintain old gene model IDs
- Establish release date with genome coordinator
- Generate fasta files
- Add to i5k Workspace@NAL database
- *Submit to NCBI if requested by genome coordinator*

Completed OGS projects using i5k Workspace's pipeline

- *Diaphorina citri* OGSv1.0
- *Frankliniella occidentalis* OGSv1.0
- *Hyalella azteca* OGSv1.0
- *Oncopeltus fasciatus* OGSv1.2
- *Athalia rosae* OGSv1.0
- *Orussus abietinus* OGSv1.0
- *Leptinotarsa decemlineata* OGSv1.0

Future updates

- Current improvments:
  - GFF3toolkit support for QC and merge of non-coding transcripts (Li-Mei Chiang)
- Future work:
  - Improve methods for merging multi-isoform models
  - Improve QC process – how to improve communications about errors with annotators

Questions?

i5k Workspace@NAL:

- https://i5k.nal.usda.gov/
- https://github.com/NAL-i5K/
- GFF3toolkit issue tracker: https://github.com/NAL-i5K/GFF3toolkit/issues
- Email: i5k@ars.usda.gov

Thank you!

The NAL Team

- Yu-yu Lin
- Chaitanya Gutta
- Li-Mei Chiang
- Yi Hsiao
- Gary Moore
- Susan McCarthy

I5k Workspace alumni

- Chien-Yueh Lee
- Han Lin
- Jun-Wei Lin
- Vijaya Tsavatapalli
- Mei-Ju Chen
- Chao-I Tuan

i5k Workspace@NAL advisory committee

- i5k Coordinating Committee
- i5k Pilot Project
- Apollo & JBrowse Development Teams
- GMOD/Tripal community
- All of our users and contributors!

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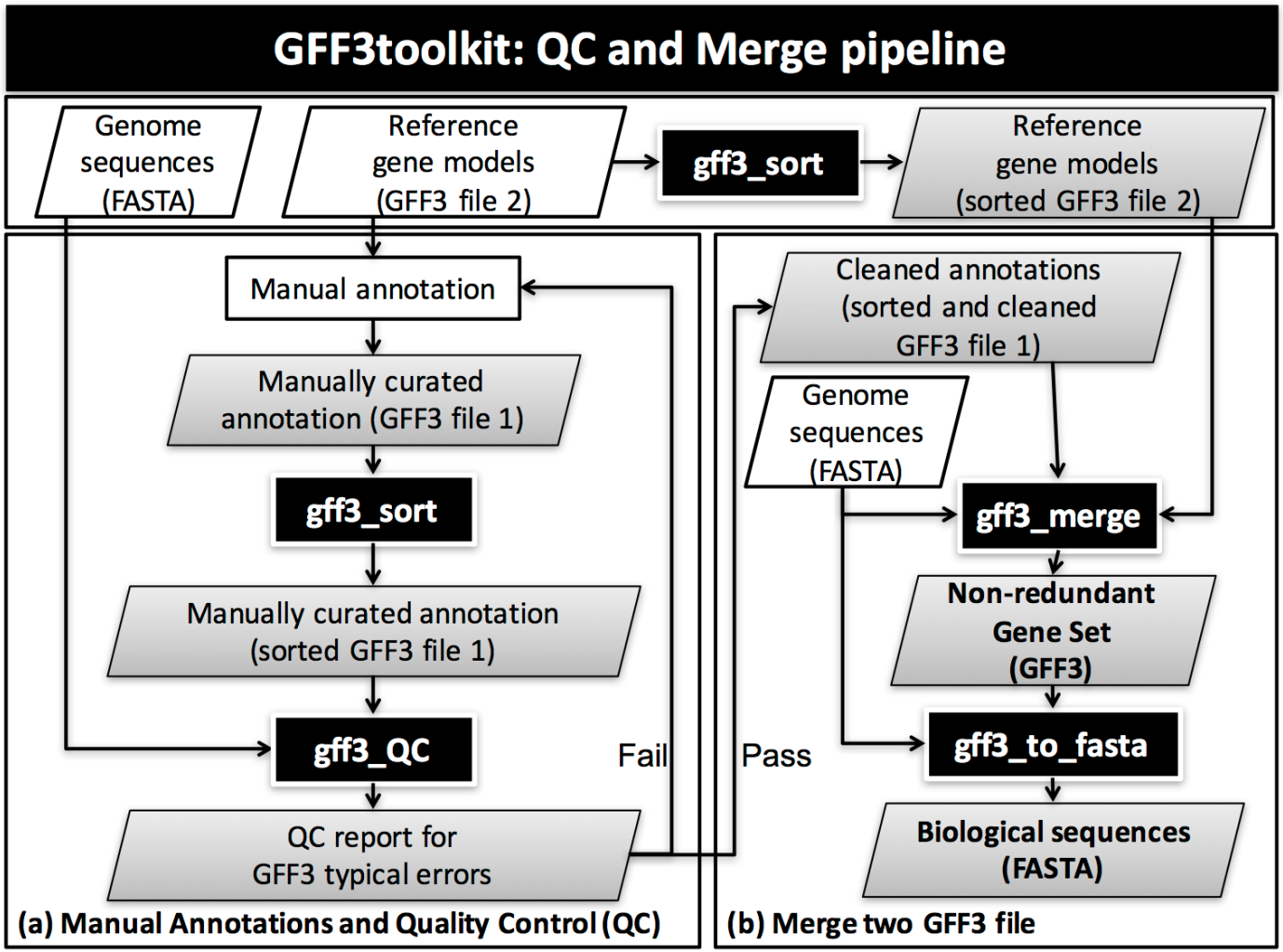
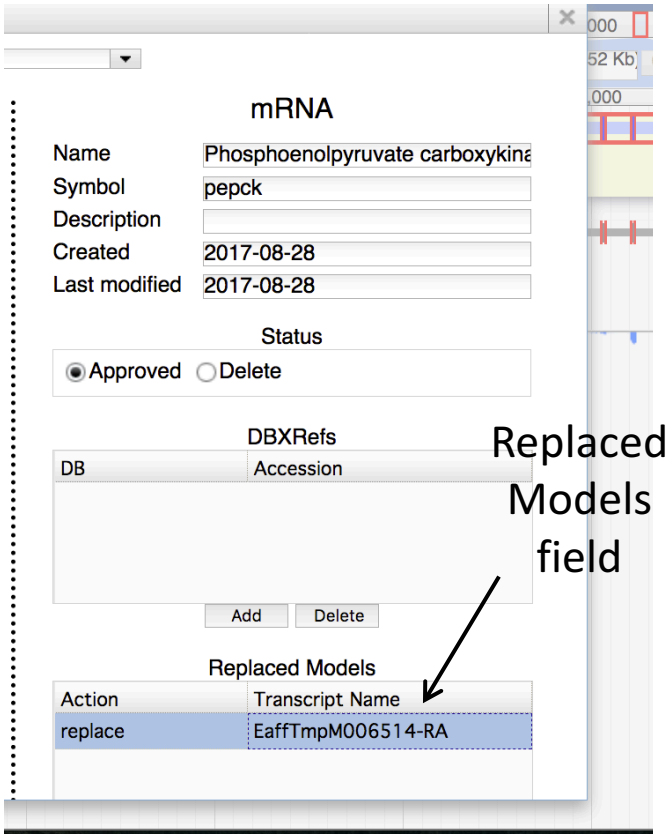
OGS generation – the GFF3toolkit



The Replaced Models field

- We use the information in this field to generate a merged, non-redundant gene set from the manually curated models and the official or primary gene set
- Your official or primary gene set is listed in the category field of the track selector
- If you don't know what your project's gene set is, contact us!



https://i5k.nal.usda.gov/apollo-replaced-models-field-explanations-and-examples

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Community annotation life cycle (end goal: OGS)