Three’s a Crowd-Source
The Collaborative Nature of Genome Annotation

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Unlike the more highly polished genomes of earlier projects, recent projects usually have lower coverage that confront researchers with more frequent assembly errors and annotation of genes across multiple scaffolds. Automated genome annotations must be curated to resolve discrepancies, providing clarity and validation.

Web Apollo enables collaboration in real-time, assisting to distill valuable knowledge from genome analysis. Collaborations encourage second opinions and insights from colleagues with diverse domain and gene family expertise.

Continued improvement of genomic annotation and curation will involve increasing the researchers’ efficiency by providing a suite of integrated curation tools, and increasing the effective population of researchers by providing universally accessible tools.

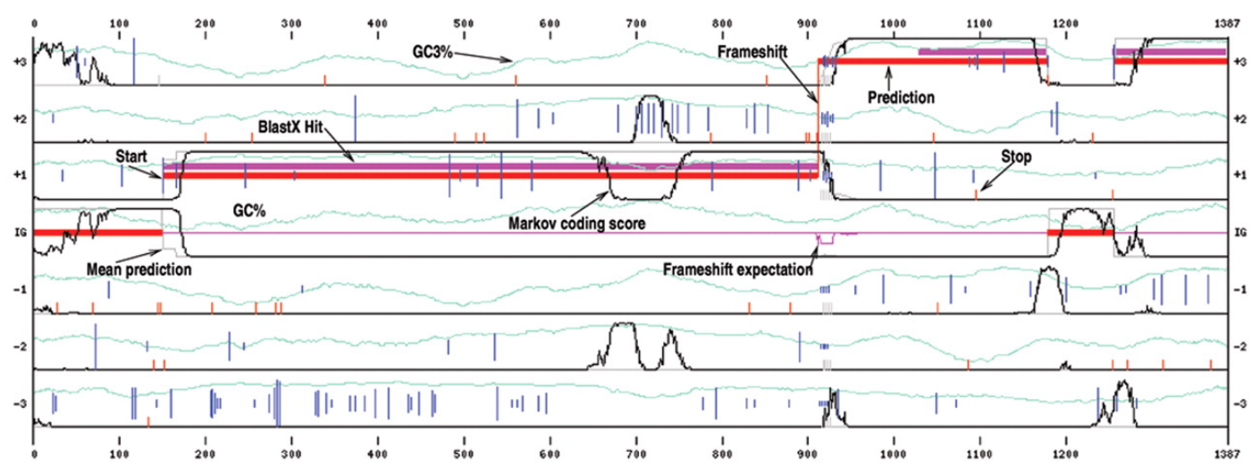
Our goals are: 1) to create a federated environment combining structural, functional, transcriptomic, proteomic, and phenotypic data; and 2) to train the next generation of researchers in making the most effective use of these tools.

MANUAL GENOME ANNOTATION EDITING

To curate automated genome annotations researchers gather and evaluate all available evidence using quality-control metrics to corroborate or modify gene predictions. This resolves discrepancies, providing clarity and validation to the gene model hypothesis.

Manual genome annotation allows us to:

- Identify elements that best represent the underlying biology.
- Eliminate elements that reflect the systemic errors of automated genome analyses.
- Determine functional roles through comparative analysis of well studied, phylogenetically similar genome elements using literature, databases, and the researcher’s experience.



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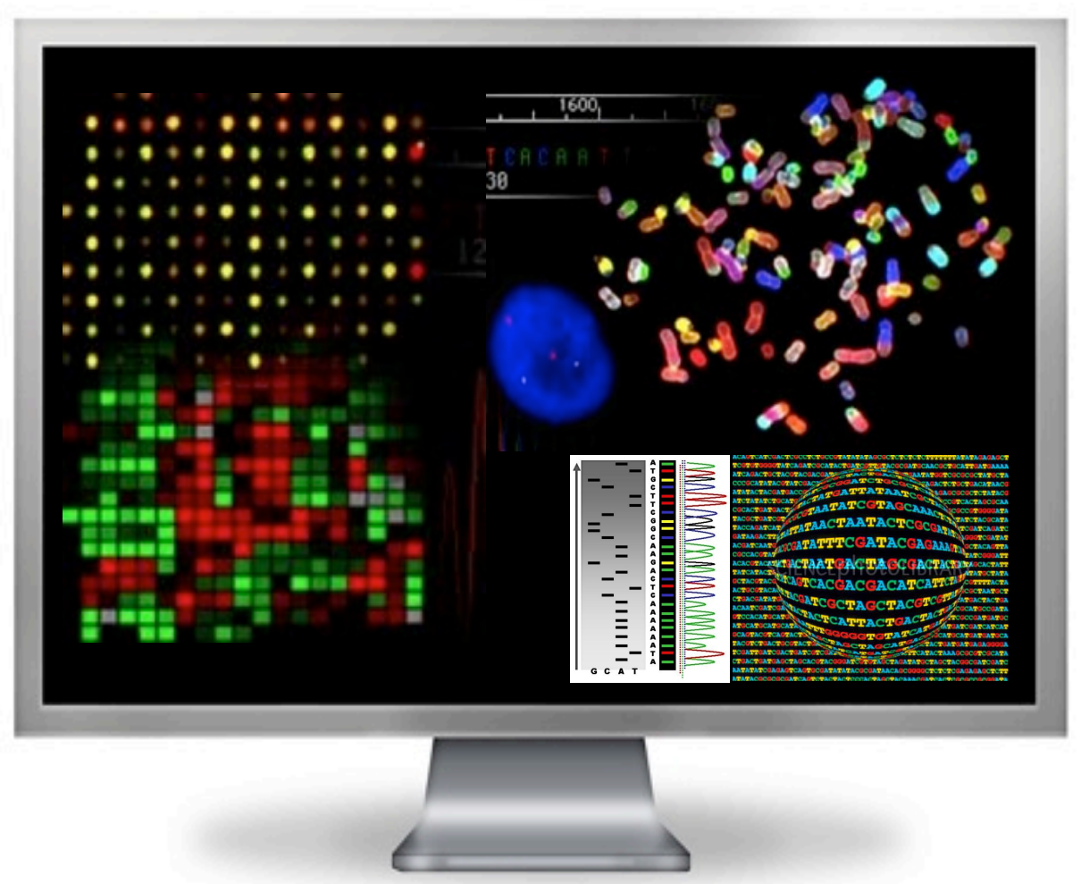
Automated Predictions

+



Experimental Evidence

Manually Curated Consensus Gene Structures

CROWD-SOURCING GENOME CURATION

Unlike earlier genome projects, recent sequencing projects are riddled by a number of factors that confront researchers with additional work to correct for more frequent assembly errors and annotate genes split across multiple contigs.

It is **impossible** for a single individual to fully curate a genome with precise biological fidelity. Beyond the problem of scale, curators need second opinions and insights from colleagues with domain and gene family expertise, an inherently collaborative task.

Crowd-sourcing Exemplars: *Apis mellifera*

Working together, researchers are able to:

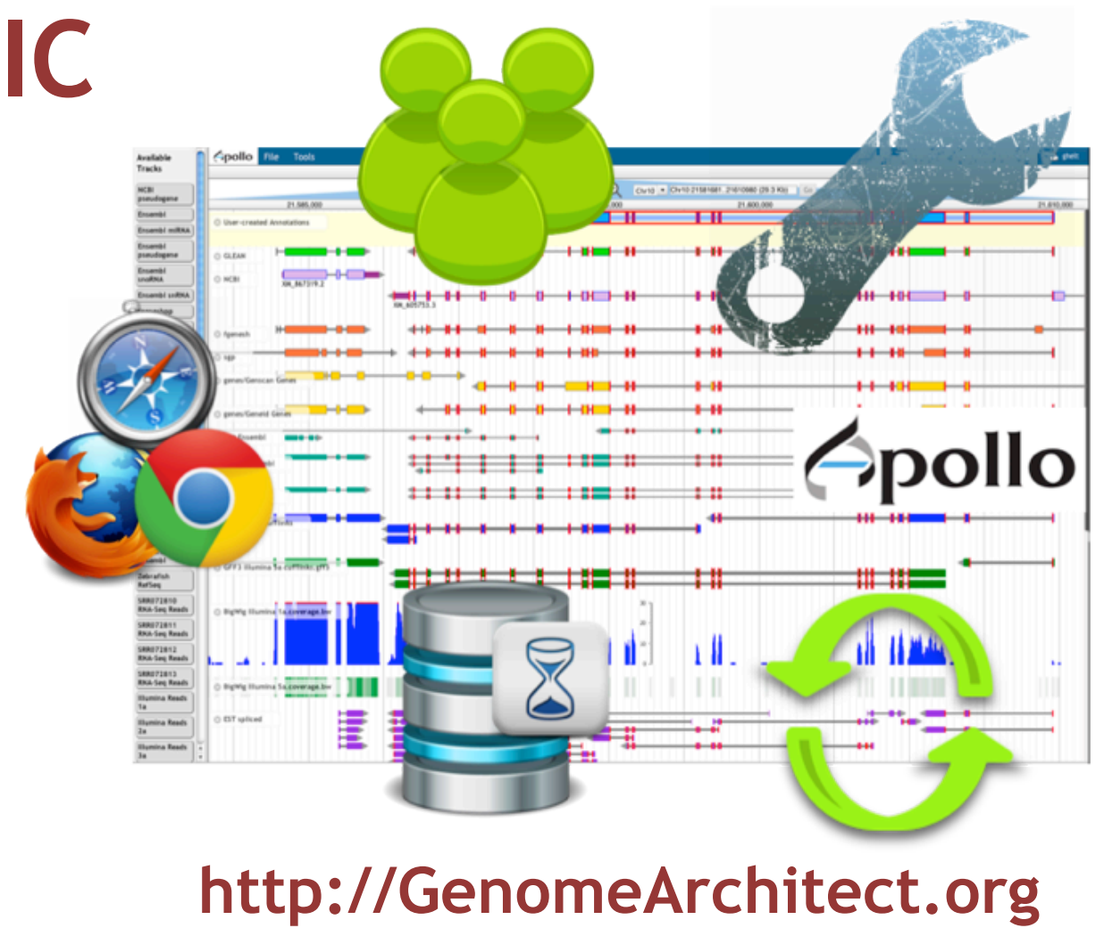
- Distribute problem solving
- Mine collective intelligence
- Access improved quality data
- Process work in parallel

> … *“the research community will need to be involved in the annotation effort to scale up to the rate of data generation. This transition will require, annotation tools, standardized methods, training, and feedback.”*
> -- Howe et al. 2008
> *Nature* **455**, 47-50

Web Apollo: COLLABORATIVE GENOMIC ANNOTATION EDITING PLATFORM

Apollo is now a browser-based annotation tool integrated with the JBrowse genome browser to allow distributed research communities to collaborate performing manual gene annotations. Web Apollo allows users to create and modify transcript and exon structures via intuitive gestures while flagging potential problems.

Web Apollo also provides dynamic access to genomic analysis results from both UCSC and Chado databases as well as database storage of user-created annotations. All user-created sequence annotations are automatically uploaded to a server, ensuring reliability. The server provides synchronized updates over multiple browser instances, so annotation edits are immediately visible to all users who are working on the same region.



http://GenomeArchitect.org

Chado
UCSC (MySQL)
Ensembl (DAS)

BAM
BED
BigWig
GFF3
MAKER output

Atta cephalotes (above) and *Harpegnathos saltator*.
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We continuously train and support hundreds of geographically dispersed scientists to perform biologically supported manual annotations using Web Apollo.

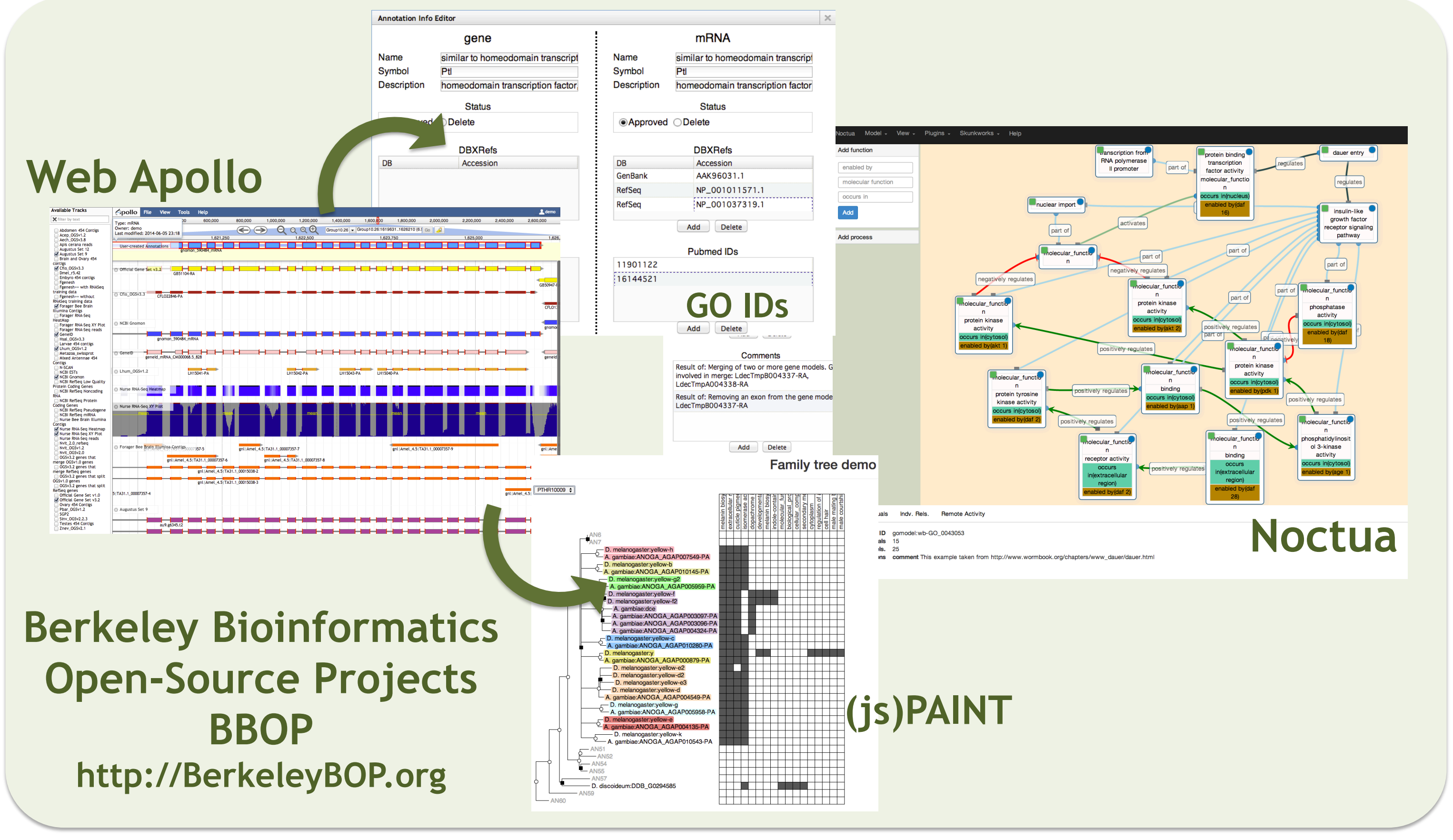
These scientific community efforts bring together domain-specific and natural history expertise that would otherwise remain disconnected.

Breaking down large amounts of data into manageable portions and mobilizing groups of researchers to extract the most accurate representation of the biology from all available data distills invaluable knowledge from genome analysis.

EXAMPLE: Understanding the evolution of sociality. Comparing seven ant genomes provided a better understanding of evolution and organization of insect societies at the molecular level. Insights were drawn mainly from six core aspects of ant biology: Alternative morphological castes, Division of labor, Chemical Communication, Alternative social organization, Social immunity, and Mutualism.
Libbrecht et al. 2013. *Genome Biology*, 14:212

IMPROVING GENOMIC ANNOTATION AND CURATION

Continuing to improve genomic annotation and curation will involve increasing the researchers’ efficiency by providing a suite of integrated curation tools, and increasing the effective population of researchers by providing universally accessible tools. To this end we are in the process of modeling a federated environment that combines gene structural and functional data, transcriptomic, proteomic, and phenotypic data.



Annotation Info Editor

gene
Name: similar to homeodomain transcript
Symbol: Ptl
Description: homeodomain transcription factor

mRNA
Name: similar to homeodomain transcript
Symbol: Ptl
Description: homeodomain transcription factor
Status: ● Approved ○ Delete

DBXRefs

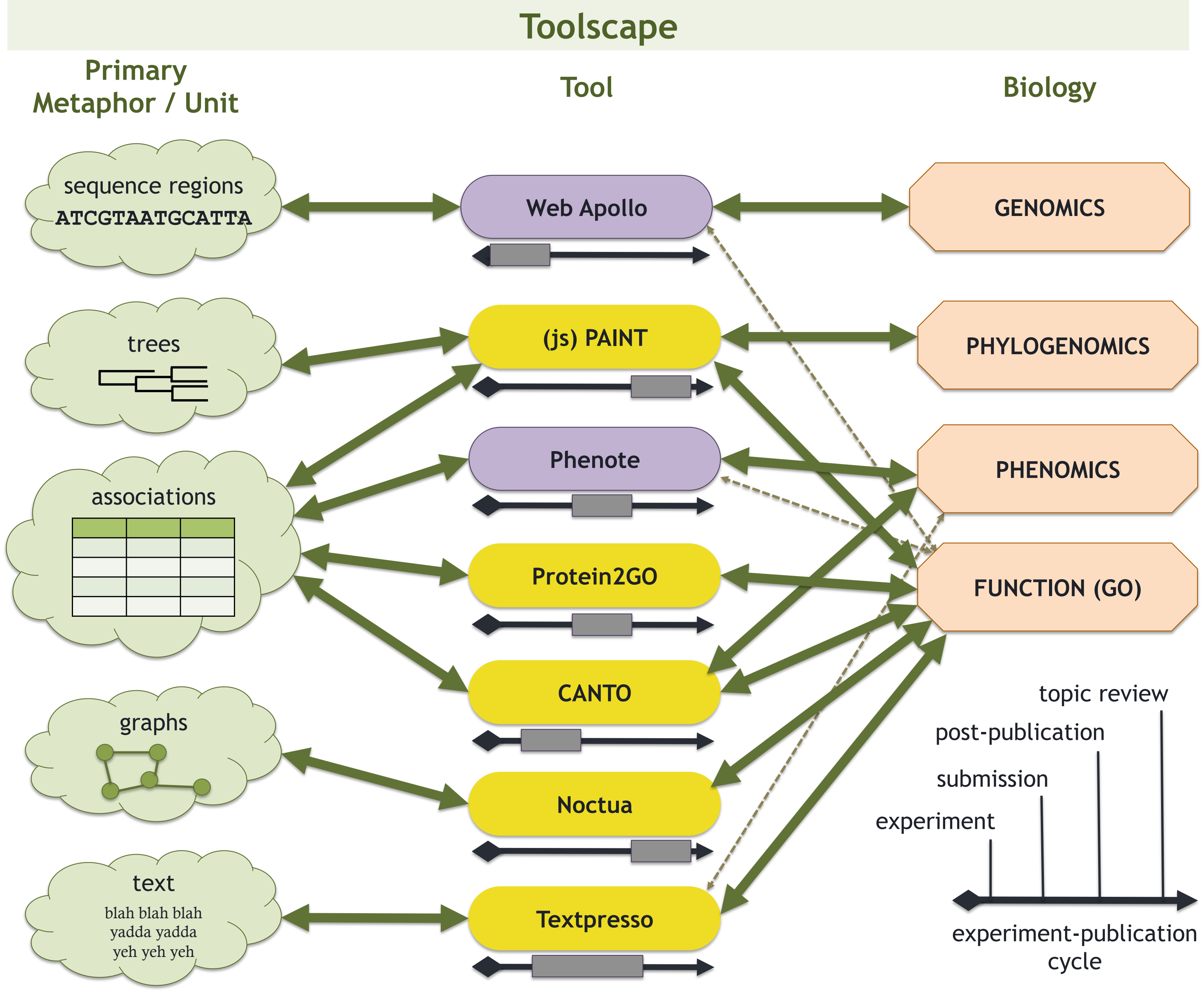
DB	Accession
GenBank	AAK96031.1
RefSeq	NP_001011571.1
RefSeq	NP_001037319.1

Pubmed IDs
11901122
16144521

Comments
Result of: Merging of two or more gene models. Genes involved in merge: LdecTmpB004337-RA, LdecTmpA004338-RA
Result of: Removing an exon from the gene model LdecTmpB004337-RA

Berkeley Bioinformatics
Open-Source Projects
BBOP
http://BerkeleyBOP.org

Toolscape



Learn more about BBOP’s projects and collaborations at

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