# The i5k Workspace@NAL – A place for arthropod genome communities to curate, visualize and share data

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#### What is the i5k Workspace@NAL?

Assembly Methods NCBI BioProject

- A workspace for genomic data access, dissemination, and curation for arthropods, hosted by the USDA's National Agricultural Library (NAL)<sup>2</sup>.
- We currently host genome project data for 53 arthropod species.
- We provide a central organism page for each project, gene pages for projects with an Official Gene Set, data downloads, BLAST<sup>3</sup>, and the JBrowse<sup>4</sup> genome browser.
- We facilitate community gene curation via Apollo<sup>5</sup>.
- The i5k Workspace is built on a customized version of **Tripal**<sup>6</sup>.

#### Start an i5k Workspace project.

- Any orphaned arthropod genome project in need of manual curation or other genome portal resources can submit their data.
- Our main requirement is that the assembly needs to be accessioned by the INSDC (e.g. in GenBank). If your genome is already hosted in another database, let's discuss.
- Contact i5k@ars.usda.gov to get started.

#### Join an i5k Workspace project.

- 1. Help annotate an existing genome project.
  - Over 400 annotators curating over 30 genome projects
  - Register for an Apollo account:

#### https://i5k.nal.usda.gov/web-apollo-registration

- 2. Add data to an existing genome project.
  - Browse our list of existing projects:

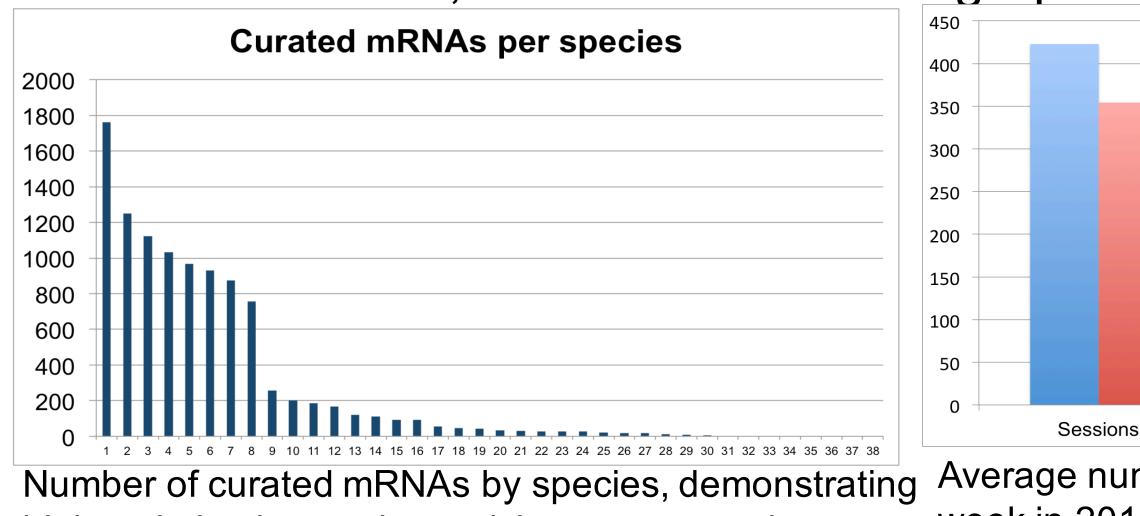
#### https://i5k.nal.usda.gov/species

Register here for a data submission account:

https://i5k.nal.usda.gov/register/project-dataset/account

### How is the i5k Workspace being used?

We have over 400 registered annotators, who have manually curated over 10,000 annotations using Apollo.



high variation in curation activity among species.

2014/2015

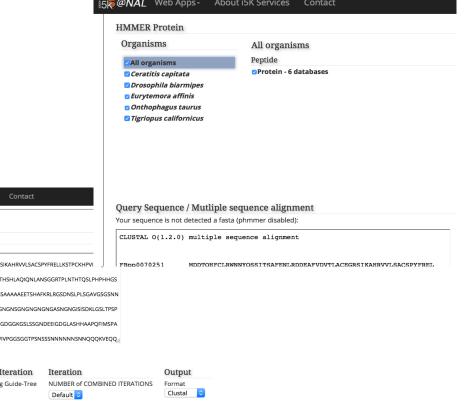
Average number of sessions or users per week in 2014/2015 vs 2015/2016.

Visit us online Web: https:/i5k.nal.usda.gov Email: i5k@ars.usda.gov

## Updates for 2016

#### New web applications

ClustalW<sup>7</sup>, ClustalOmega<sup>8</sup>, and Hmmer<sup>9</sup> web applications provide more sequence search options. Built in the Django framework. Features include: automatic input file format detection; query queuing system; and user accounts for result retrieval.



i5k Workspace@NAL

#### New data submission forms

Our new web-based data submission forms make it easier to start i5k Workspace projects, and to add data to existing projects.

Request a new i5k Workspace Project Thank you for your interest in submitting your genome project to the i5k Workspace! Please answer the following questions to help us decide if the resources at the i5k Workspace are a good fit for your

Sign up for an account:

https://i5k.nal.usda.gov/regisτer/project-αaτasevaccounτ

#### New organisms and datasets

- New species for 2016 include Dufourea novaeangliae, Habropoda laboriosa, Lasioglossum albipes, Megachile rotundata, Melipona quadrifasciata, Microplitis demolitor, Diachasma alloeum, Neodiprion lecontei, Amyelois transitella, and Tribolium castaneum.
- Official Gene Set pipeline developed at the NAL
  - Four are complete
  - Two are in progress
  - https://github.com/NAL-i5K/I5KNAL\_OGS
- We regularly receive new RNA-Seq datasets from our contributors to facilitate manual curation.

## For more information about \$5



- Visit us online: https://i5k.github.io
- Visit us at Booth #320.

Skinner, M.E., *et al.* (2009) JBrowse: A next-generation genome browser. *Genome Res.*, **19**, 1630–1638. Ficklin, S.P., et al. (2011) Tripal: a construction Toolkit for Online Genome Databases. Database: bar044 Larkin, M.A., et al. (2007) "Clustal W and Clustal X version 2.0." Bioinformatics 23.21: 2947-2948. Sievers, F., et al. (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology 7:539 Eddy, S.R. (2009) A new generation of homology search tools based on probabilistic inference. Genome Informatics 23(1):205-11.

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