

KBase

PREDICTIVE BIOLOGY

DOE Systems Biology Knowledgebase

OSTI Workshop

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User Engagement Lead

INTEGRATION and
MODELING *for*
PREDICTIVE BIOLOGY



U.S. DEPARTMENT OF
ENERGY

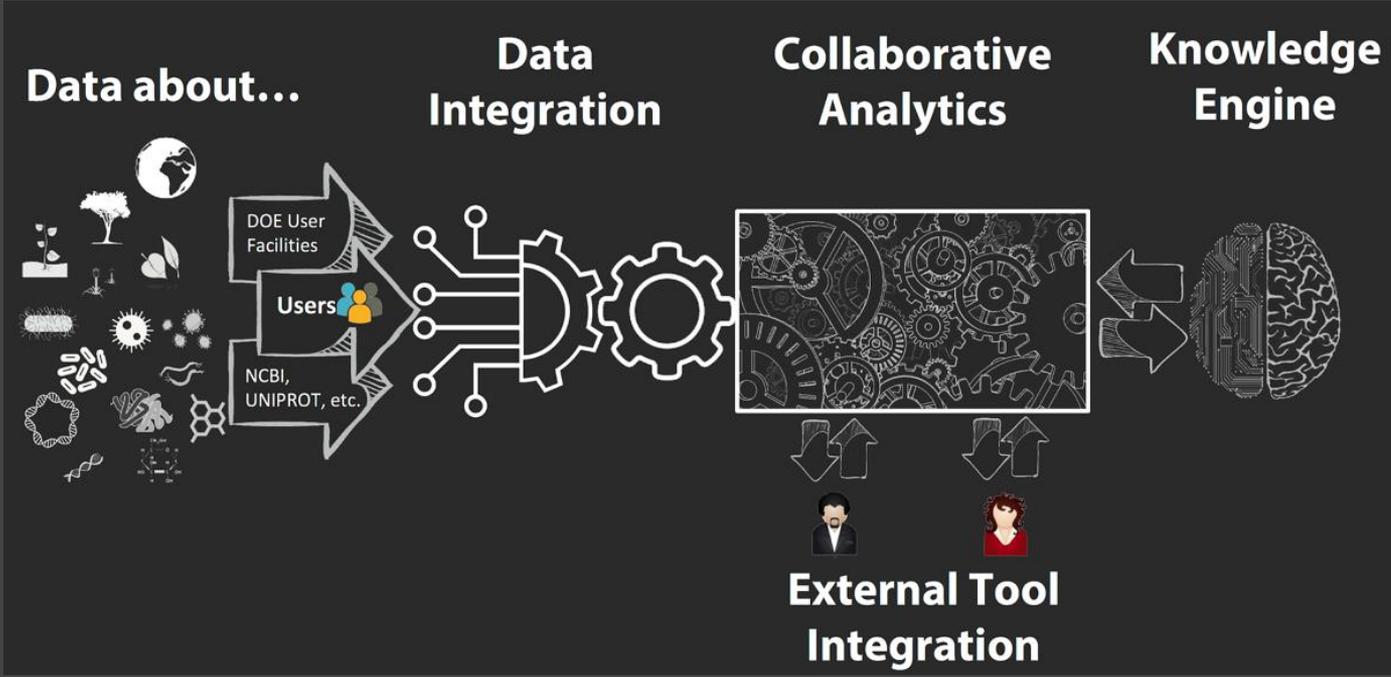
Office of
Science

Office of Biological and Environmental Research

KBase Mission

An open-source analysis platform that enables discovery and knowledge creation to build a stronger, more collaborative research community

FAIR data best practices; scalable data science; transparent, reproducible, and reusable methods



Our DOE Community - JGI, EMSL, ESS-DIVE

- Working towards:
 - Enabling seamless push-pull access to data
 - Co-development of community resources
 - Integration of tools and pipelines
- Future:
 - Support for standard workflow tools to simplify sharing workflows
 - Exploring shared infrastructure (w/ JGI at LBL)
 - *Tracking data from sample to publication*



Building user communities with Orgs

Build *Organizations* for shared research, projects, and institutions

Share data and Narratives among colleagues

Notifications for updates in your organizations and Narratives

	Joint Genome Institute <i>Functional genomics of microbes, plants and fungi, and communities of organisms. Synthetic biology. Secondary metabolites. Metabolomics.</i> owner Nigel Mouncey created Feb 16, 2019	 4   47 minutes ago
	Wetland Hydrobiogeochemistry SFA <i>Hydrobiogeochemical controls of water quality within wetlands</i> owner Ken Kemner created Feb 8, 2019	 3   5 days ago
	Joint BioEnergy Institute <i>Biofuels, bioproducts, biomass, plant biology, pretreatment, metabolic engineering, synthetic biology</i> owner Jay Keasling created Feb 15, 2019	 1   2 days ago
	Ecosystems and Networks Integrated with Genes and Molecular Assemblies SFA <i>Microbial Ecology, Metagenomics, Systems Biology, Microbiology, OMICS, genetics, modeling</i> owner Adam Paul Arkin created Jan 7, 2019	 7   19 days ago

Building User Working Groups

30 active/near future engagements

- 10 DOE science focus areas
- JGI MAG compendia
- Microbiome and viral genomic tools
- Protein-ligand integration tools

Featured Organizations on KBase

- ORNL KBase Protein Structure
- LLNL Bioenergy SFA
- ENIGMA SFA
- The JGI
- Trent Northen (Web of Microbes)



KBase Narrative Interface

Narrative title and author

Share button

The screenshot displays the KBase Narrative Interface. At the top, the narrative title 'Arabidopsis RNA-seq Analysis Tutorial' and author 'Created by: Sunita Kumari (sunita)' are shown. A 'Share' button is visible on the right. The main content area is divided into several panels:

- Data panel:** A red-bordered box highlights a list of data items:
 - Ath_dge_deseq2_hy5-WT_down_0.0...v1 (FeatureSet, Feb 21, 2019)
 - Ath_dge_deseq2_hy5-WT_up_0.05q...v1 (FeatureSet, Feb 21, 2019)
 - hy5-WT_0.05q_2FC_filteredExp.v1 (ExpressionMatrix, Feb 21, 2019)
 - Ath_dge_deseq2.v1 (DifferentialExpressionMatrixSet, Feb 21, 2019)
- Apps panel:** A blue-bordered box highlights a list of application categories:
 - Comparative Genomics (31)
 - Expression (33)
 - Genome Annotation (12)
 - Genome Assembly (22)
 - Metabolic Modeling (17)
 - Microbial Communities (14)
 - Read Processing (19)
 - Sequence Analysis (15)
 - Uncategorized (4)
- Main panel for work:** A yellow-bordered box contains the narrative's main text and a diagram. The text describes the study on RNA sequencing to examine HY5 mediated gene expression changes between wild-type and hy5 mutant plants. The diagram (e) illustrates the mechanism of light signaling in Arabidopsis, showing COPI and SPA1 proteins in the cytoplasm and nucleus, and the HY5 protein in the nucleus. A photograph shows Arabidopsis seedlings under 'Light' and 'Dark' conditions, with labels for 'Cotyledon', 'Hypocotyl', and 'Root'.

Data panel

Apps panel

Main panel for work

Markdown cell button

Code cell button

KBase Narrative Interface

 **QUAST - Quality Assessment Tool for Genome Assemblies** 
Run QUAST on a set of assemblies to assess quality.

This app is completed [View Configure](#) [Result](#)

Input Objects

Assemblies	['43666/2/8']
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 **Annotate Assembly and ReAnnotate Genomes with Prokka v1.12** 
Annotate Assembly with Prokka annotation pipeline.

This app is completed [View Configure](#) [Result](#)

Objects

Created Object Name	Type	Description
some_genome	Genome	Annotated genome

KBase Narrative Interface



Output from Annotate Assembly and ReAnnotate Genomes with Prokka v1.12

The viewer for the output created by this App is available at the original Narrative here: <https://ci.kbase.us/narrative/43666>



some_genome

v1 - KBaseGenomes.Genome-15.1



The viewer for the data in this Cell is available at the original Narrative here: <https://ci.kbase.us/narrative/43666>

KBase Narrative Interface

Narrative: collection of data, tools, data products

Provenance: owner, **workspace ID**

<https://narrative.kbase.us/narrative/27895>

<https://kbase.us/n/27895>

doi: 10.kbase#.workspaceID.OSTI#

KBase as the model for:

Open, team science enabled by FAIR data, reproducible methods and results, and an approachable UI streamlined to encouraging credit, transparency, and responsibility.

