



KBbase

PREDICTIVE BIOLOGY

DOE Systems Biology Knowledgebase

INTEGRATION
AND MODELING
for PREDICTIVE
BIOLOGY

Software Carpentry Workshop

July 17-18

Portland, OR

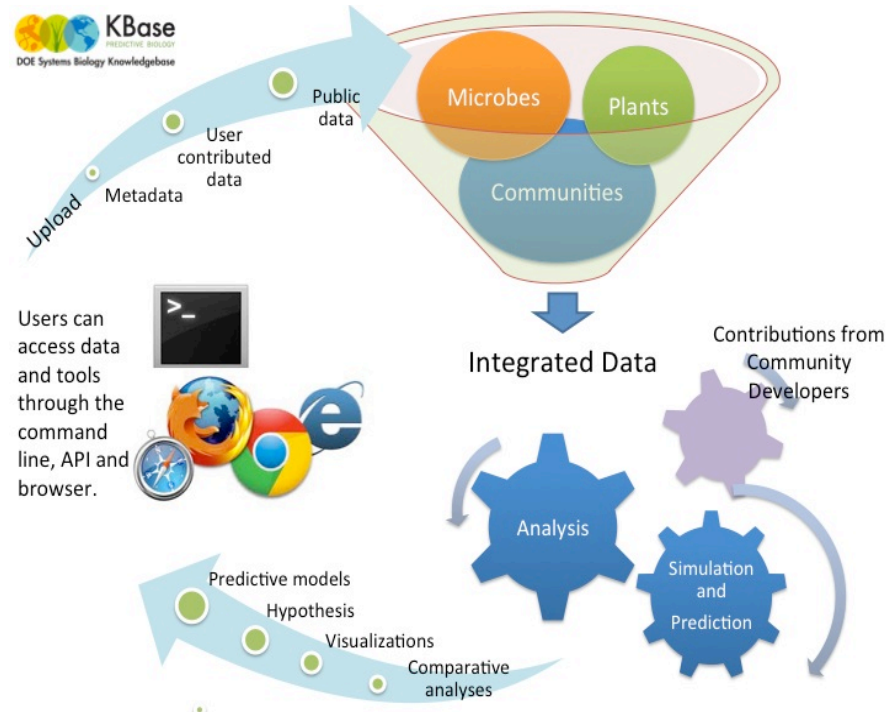
A KBase Primer

KBase is a software and data environment for predictive systems biology.

KBase will serve as a catalyst for biological research, accelerating discovery for DOE missions and providing insights and benefits that can ultimately serve numerous application areas.

How can KBase impact your research?

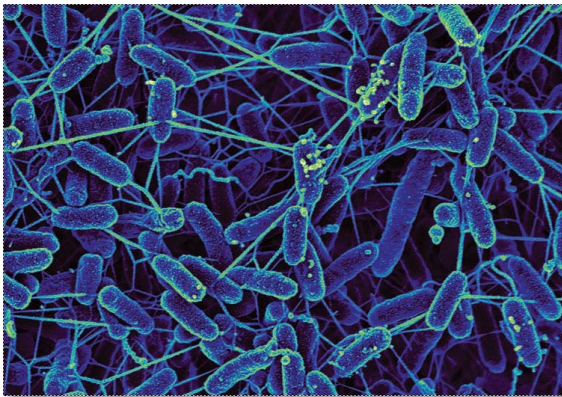
- Integrates diverse data, enabling science and comparisons that were never before possible.
- Connects data with a diverse set of powerful computational tools, to enable prediction of biological behavior, to test and generate hypotheses, and to propose new experiments.
- Improves the knowledge of gene function and protein behavior in microbes, plants, communities
- Permits incorporation of your own data and tools in an open-source, open-architecture framework with access to DOE computing and network
- Promotes research collaborations and cooperation on a scale not previously possible.



KBase Overview

Knowledgebase enabling ***predictive*** systems biology.

- Powerful modeling framework.
- **Community-driven**, extensible and scalable **open-source** software and application system.
- Infrastructure for integration and reconciliation of algorithms and data sources.
- Framework for standardization, search, and association of data.
- Resource to enable **experimental design** and **interpretation** of results.



Microbes



Communities



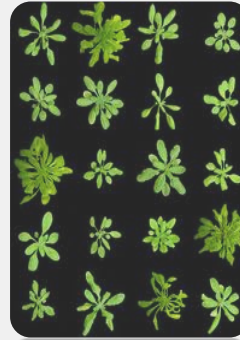
Plants

KBase-Plants: Targeted genomes

Poplar



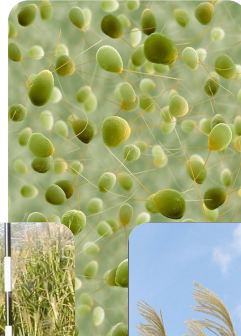
Arabidopsis



Sorghum



Chlamydomonas



Brachypodium



Miscanthus



Switchgrass


KBase-Plants Services:

Providing Plant-specific data and methods:

- **Central Store**
- ID Server
- **Expression**
- Functional Ortholog Prediction
- Interlog Projection
- Annotation
- *FBA Modeling*
- **Ontology**
- **Networks**

IRIS

<http://iris.kbase.us>

 IRIS

Command list

▼ Plant Expression

coex_cluster
coex_cluster2
coex_filter
coex_net
coex_pipeline
get_all_eo
get_all_po
get_eo_descriptions
get_eo_sampleidlist
get_experiments_by_sampleid
get_experiments_by_sampleid_geneid
get_experiments_by_seriesid
get_po_descriptions
get_po_sampleidlist
get_replicates_by_sampleid

Running processes

No processes running

File Browser

Arabidopsis_CDS.txt
Arabidopsis_Features.txt
Arabidopsis_locus.txt
Gramene
history
output
Sitalica.fa
Sitalica.go
tmp2

IRIS Terminal

Welcome to the interactive KBase terminal!
Please click the 'Sign in' button in the upper right to get started.
Type **commands** for a list of commands.
For usage information about a specific command, type the command name with -h or --help after it.
Please visit <http://www.kbase.us/for-users/get-started#iris> or type **tutorial** for an IRIS tutorial.
To find out what's new, type **whatsnew** (v0.0.7 - 02/06/2014)

Authenticated as Sam Seaver

>/ **ws-workspace**
Current workspace set to:
Arabidopsis_Models

Id	Name	Owner	Last_Modified	Size	Permission	GlobalAccess
1571	Arabidopsis_Models	seaver	2014-07-15T07:13:46+0000	8	a	r

Command Completed

>/ **ws-createws Sorghum**
Workspace created with name: Sorghum and id: 1779
Command Completed

