KBase Reference
kbase.us

KBase Data Types and Identifiers

Genomes (kb|g.*nnn*)

Genes (kb|g.*nnn*.locus.*nnn*)

Networks (kb|g.*nnn*.nds.*nnn*)

Transcripts (kb|g.*nnn*.mrna.*nnn*)

Proteins (kb|g.*nnn*.cds.*nnn*)

Plant-Specific Services

Central Store

Manages data related to genome annotation, expression, biochemistry, models, alignments, subsystems, genotype/phenotype relations, and experiment-related entities.

ID Server

Provides a centralized mechanism to generate KBase IDs for all entities in the KBase stores.

Expression

Handles queries for tissue- and condition-specific expression samples and differentially expressed genes and provides functionality for constructing coexpression networks.

Functional Ortholog Prediction

Predicts the best functional ortholog, given a well-studied gene in organism A and several orthologs in organism B, based on gene co-expression networks.

Interlog Projection

Provides methods to project an interlog network of species A from the query network of species B based on ortholog information. The ortholog information is precomputed by the Inparanoid algorithm.

Annotation

Provides a set of services for genome annotations, functional roles, subsystems, and metabolic reconstructions.

FBA Modeling

Supports the reconstruction, optimization, and analysis of genome-scale metabolic models.

Ontology

Enables retrieval of ontology term distribution for a given set of genes and also identifies statistically overrepresented GO terms within given gene sets.

Networks

Allows KBase users or services to access data for protein-protein interaction, regulatory, metabolic, and functional association networks in microbes and plants.

IRIS Shell-like Commands:

- grep (searches for a pattern in file)
- cat (displays the contents of a file)
- tail (displays last 10 lines of a file)
- uniq (report or omit repeated lines)
- sort (sort lines of files)
- wc (word count)

Central Store Data Retrieval:

Entities:
(these commands retrieve *every* single entity and take time):
all_entities_Genome
all_entities_Feature

Relationships:
(these commands link entities, they're listed in italics and are preceded with 'get_relationship_'):
Source *Submitted* Genome
Genome *WasSubmittedBy* Source
Genome *IsOwnerOf* Feature
Feature *IsOwnedBy* Genome
Feature *Encompasses* Feature (retrieve transcripts and proteins)
Feature *IsEncompassedBy* Feature (retrieve transcripts and genes)

Specialized Commands:
(these commands perform work on retrieved data before passing to output)
fids_to_dna_sequences
fids_to_protein_sequences

Network Service:
net_get_all_datasets
net_taxon_to_datasets
net_entity_to_datasets
net_get_all_network_types

Ontology Service:
get_goidlist
get_go_enrichment

Expression Service:
get_all_eo
get_all_po
get_eo_sampleidlist
get_po_sampleidlist
get_experiments_by_sampleid_geneid

* All commands below take the *--help* option and print out the usage information