

Learning to Use KBase to Accelerate Your Research

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<http://kbase.us>

Project Goals: The DOE Systems Biology Knowledgebase (KBase) is a free, open-source software and data platform that enables researchers to collaboratively generate, test, compare, and share hypotheses about biological functions; analyze their own data along with public and collaborator data; and combine experimental evidence and conclusions to model plant and microbial physiology and community dynamics. KBase’s analytical capabilities currently include (meta)genome assembly, annotation, comparative genomics, transcriptomics, and metabolic modeling. Its web-based user interface supports building, sharing, and publishing reproducible, annotated analysis workflows with integrated data. Additionally, KBase has a software development kit that enables the community to add functionality to the system.

KBase’s integration of data and tools and the ease of creating and running large-scale analysis workflows have the potential to empower scientists in a broad range of application areas for systems biology, including environmental analysis and biosystems design. KBase’s sharing capabilities amplify this potential by enabling scientists with differing expertise to work together and leverage each other’s work. Science done within KBase has been published in over 30 peer-reviewed publications (see <http://kbase.us/publications>), including (1) [reconstruction of >8000 models of core metabolism across the microbial tree of life](#); (2) [reconstruction of semi-curated metabolic models for 773 gut microbes](#); (3) [predicting trophic interactions within a microbial community](#); and (4) [reconstruction of regulons from expression data](#). The Narratives associated with many of these publications can be found in our [Narrative Library](#).

If you’ve never used KBase before, we suggest you start with the “[New to KBase?](#)” page (Fig. 1). The [Narrative Interface guide](#) and the [Data Search guide](#) will teach you about those key KBase interfaces. A printable four-page [KBase brochure](#) is also available. Video tutorials, such as “[KBase Quickstart](#)”, are available on our [YouTube channel](#). [Narrative tutorials](#), such as the one about [Assembly and Annotation of Prokaryotic Genomes](#), are step-by-step walkthroughs that demonstrate how to use KBase to perform bioinformatics analysis workflows. Not only can you see an example of how to assemble and annotate data in KBase; you can make your own copy of the Narrative tutorial and run the steps yourself, even changing the parameters or uploading your own datasets to analyze.

New to KBase?

The Department of Energy Systems Biology Knowledgebase (KBase) is a collaborative, open environment for computational systems biology analysis of plants, microbes and their communities. KBase integrates a range of tools and data into one unified, scalable environment and makes your research reproducible, accessible and reusable. [More information...](#)

KBase's User Interface

KBase's main user interface, the **Narrative Interface**, lets you create and execute workflows called **Narratives**. Narratives include your analysis steps, commentary, visualizations, and custom scripts. You can share Narratives to enable other researchers to reproduce your computational experiments and even alter parameters or input data to obtain different results.

The video tutorial at right gives a quick introduction to the Narrative Interface.

Tutorials

These tutorials in the form of Narratives demonstrate how to use KBase tools and data to perform specific analysis workflows. You can copy these Narratives and rerun the steps or try them on your own data.



Assemble and Annotate Microbial Genomes

Learn how to assemble **NGS reads** into **contigs** and then perform structural and functional annotation of the assembled contigs.



Predict and Model Plant Metabolic Functions

Starting with plant coding or protein sequences, discover how to predict function and build a **metabolic model** of plant primary metabolism.



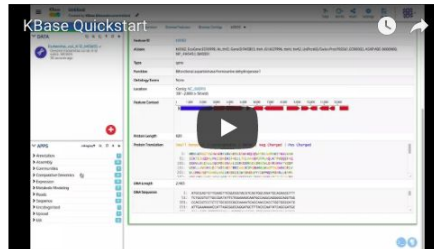
Build Microbial Metabolic Models

Use KBase tools to reconstruct and analyze genome-scale metabolic models for microbes, starting with **genome sequence**.

Visit the [Narrative Library](#) for more tutorials as well as research Narratives that show computational experiments performed in KBase.

Sign up for an account

You will need a KBase user account to use our tools. [Signing up](#) is easy and free!



Analyze data

KBase has a growing collection of more than 70 **analysis apps** that include:

- Assembly and annotation
- Sequence alignment and search
- Metabolic modeling
- RNA-seq and expression data analysis
- Comparative and phylogenetic analysis

You can explore KBase's public reference data or upload your own data to analyze.

Figure 1: The [“New to KBase” web page](#) has pointers to videos, Narrative tutorials and other training materials that will help you learn how to use KBase to accelerate your research.

The KBase team presents at various conferences and conducts workshops to train users and developers. If you would like to host a KBase workshop at your organization, please [contact us](#). We also offer webinars to reach a wider audience.

If you have questions about KBase, or you want to report a bug or request a new feature, you can join the [KBase Help Board](#). In the Help Board, you'll be able to:

- Submit bug reports, questions and suggestions without revealing your email address.
- Engage in a two-way dialog with KBase staff as they track down and resolve your issue.
- Search the issues submitted by other users. If someone else has already reported your problem or suggested the same new feature, you can add a “Me too!” comment.
- Increase your productivity in KBase by seeing other users' suggestions and workarounds.

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