

# KBase

PREDICTIVE BIOLOGY

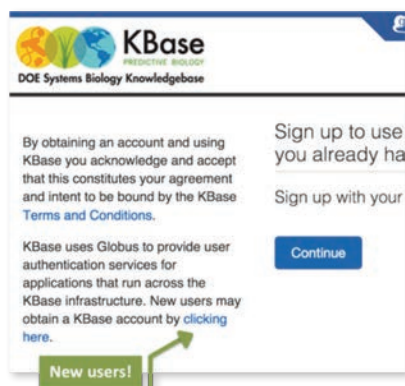


DOE Systems Biology Knowledgebase

## Quick Start Guide

The Department of Energy Systems Biology Knowledgebase (KBase) is a software and data platform designed to meet the grand challenge of systems biology: predicting and designing biological function. KBase's Narrative Interface lets you design and carry out collaborative computational experiments while creating Narratives: interactive, shareable, and reproducible records of your data, computational steps, and thought processes. This Quick Start provides an overview of several key features of the Narrative Interface.

### 1 Create a KBase user account



To sign up for an account, go to:

[kbase.us/signup](https://kbase.us/signup)

*(If you already have a user account, proceed to Step 2.)*

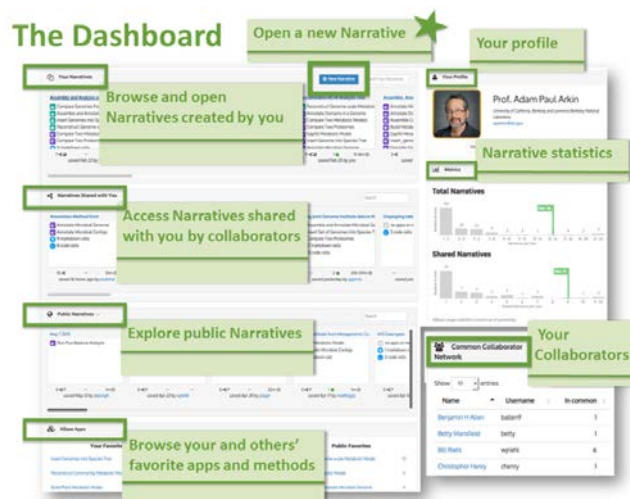
Globus provides the secure platform used to manage

user access to KBase tools and resources. If new to KBase, be sure to select the bottom link (and not the "Continue" button) to access the correct sign-up form.

Once you fill in the required information and click "Create ID," check your email for a message from Globus containing a verification code.

Follow the instructions in the message to use the code to confirm your account. Upon confirmation, you will be asked to join the KBase users group. Once you join, you are ready to log in to KBase.

### 2 Sign in to the Narrative Interface



Access the Narrative Interface at [narrative.kbase.us](https://narrative.kbase.us). After you sign in, you will be taken to your Dashboard.

From the Dashboard, you can open your existing Narratives, access others that have been shared with you, and create new Narratives.

*(If you are a new user, your Dashboard will be empty. Please complete your profile and check your account settings.)*



#### Watch an introduction to KBase's Narrative Interface

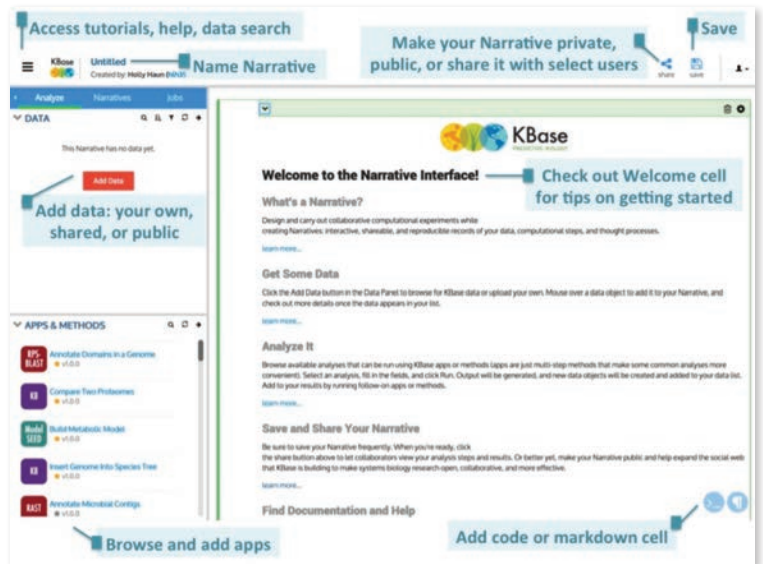
A 12-minute video demonstrating the Narrative Interface is available at [kbase.us/narrative-quick-start/](https://kbase.us/narrative-quick-start/). In it, you'll see how to create a Narrative, find data, use apps to analyze the data, and share Narratives with other KBase users.

## 3 Create a new Narrative

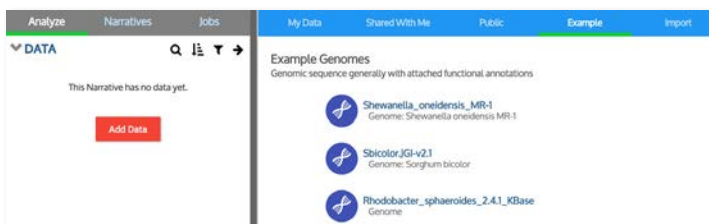
Click the **+ New Narrative** button in the Dashboard to open a new untitled Narrative.

Note the **Welcome to the Narrative Interface** box that offers useful suggestions for adding content to your Narrative. To collapse this box, click the “v” icon at the top left; use the trash icon at right to delete it.

## Tour of the Narrative Interface



## 4 Find data to analyze



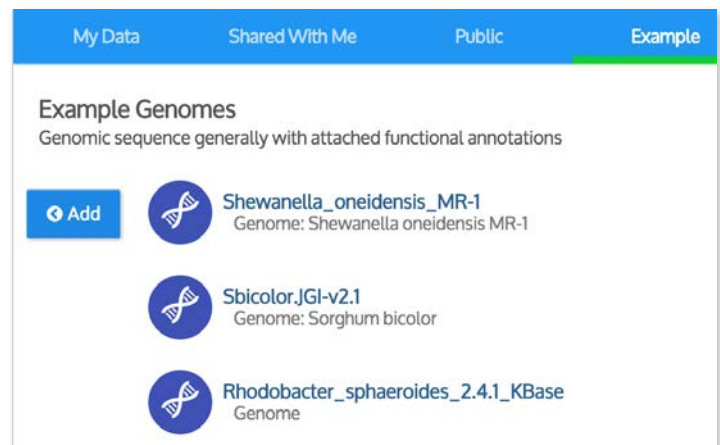
To load data to your Narrative, click the **Add Data** button, which can be found under the *Analyze* tab near the top left of the Narrative. The Data Browser ([kbase.us/narrative-guide/explore-data/](http://kbase.us/narrative-guide/explore-data/)) will slide out with tabs that show several data sources.

- **My Data** — Data you have already loaded or analyzed in other Narratives.
- **Shared With Me** — Data in Narratives shared with you by collaborators.
- **Public** — Data in public Narratives.
- **Example** — Example datasets from KBase’s reference data collection that can be used as inputs to apps (see screenshot above).
- **Import** — Tool allowing you to import your own data. KBase currently supports upload of contigs, expression matrices, flux balance analysis models, genomes, media, phenotype sets, short reads, and transcripts (cDNA or protein).

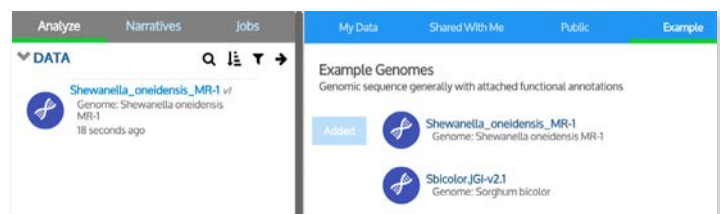
*Note that any data you upload to KBase is private unless you choose to share it.*

## 5 Add data to your Narrative

When you hover over a data object in the Data Browser, an **Add** button will appear to its left. Click this button to add the data to your Narrative.



Notice that the data object now appears in the left Data Panel (see below). Once you finish adding data, exit the Data Browser by clicking either the **Close** button at the bottom left of the browser window or the arrow at the top right of the Data Panel.



## Remember to save your work!

Don't forget to periodically save your Narrative by clicking the **Save** button at the top right of the Narrative Interface.



## 6 Choose an app to analyze your data

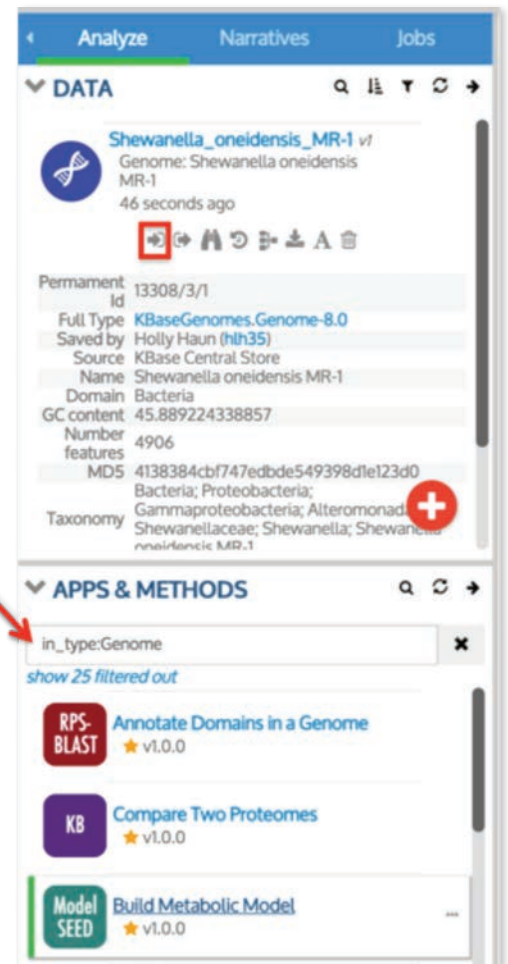
Once data is added to your Narrative, you can analyze it using one or more of the KBase apps ([kbase.us/apps/](https://kbase.us/apps/)) listed below your data.

You can quickly filter this list to display only the apps that work with a particular data object in your Narrative. To do this, click the data object to see its expanded view. The first icon in this view will show only the apps that can use your data as input; the second will display those that generate your selected data type as output.

In the example at right, the list has been filtered to show only apps that take genomes as input.

KBase's new App Catalog provides even more options for browsing apps; designating them as favorites; and filtering them based on analysis type, popularity, and more. Access this catalog by clicking the arrow at the top right of the panel.

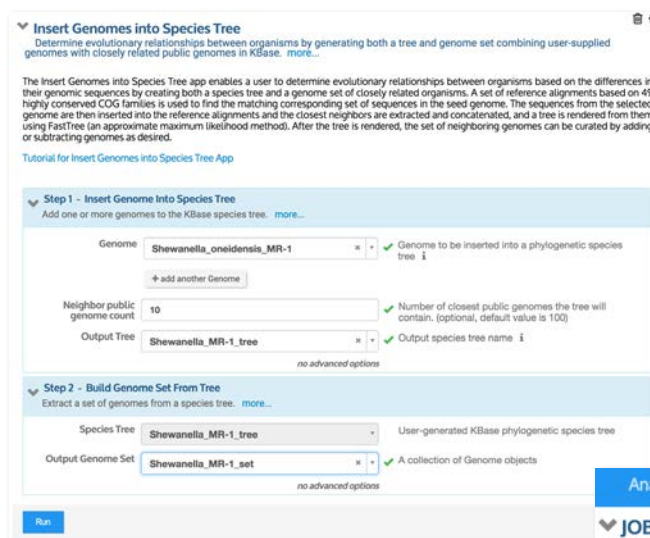
To add an app to your Narrative, click on its name in the panel or App Catalog.



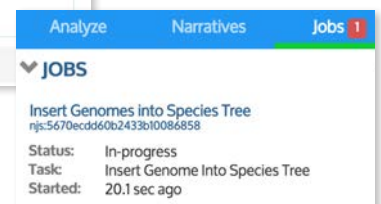
## 7 Run the app

Fill in all the required fields in your app. Note that some fields are "smart" and know which data in your Narrative is valid for that field. These "smart" fields have a pull-down list of all the data objects from your Data Panel that you can choose from as input.

Once all required fields are specified, the red arrows next to those fields will change to green checkmarks, indicating that the app is ready to run. Click **Run** to start the analysis.

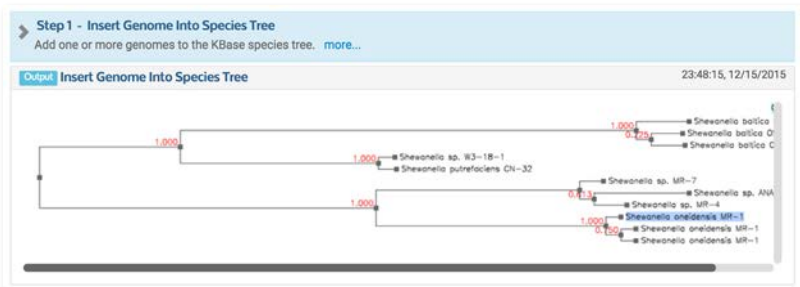


To monitor the progress of your analysis job, click the **Jobs** tab at the top left of your Narrative.



## 8 Review the results

Once the analysis is complete, one or more viewers will appear in your Narrative showing the output. In this example, the *Insert Genomes into Species Tree* app generates a phylogenetic species tree used to distinguish taxonomically distinct organisms. Here, the tree displays the 10 closest relatives of our input genome, *Shewanella oneidensis* MR-1.



A second viewer lists the genomes comprising the species tree. You can curate this genome set, adding or removing genomes using various buttons within the viewer.

In addition to output viewers, KBase analysis jobs may generate new data objects that appear in the Data Panel. In this example, notice the new genomes, genome set, and species tree objects.

## 9 Share your Narrative

All Narratives that you create are private by default. You can make a Narrative public or share it with specific collaborators by clicking the **Share** button at the top right ([kbase.us/narrative-guide/share-narratives/](https://kbase.us/narrative-guide/share-narratives/)).

### Next Steps and Additional Resources

With these basic steps, you now can begin using the Narrative Interface to create Narratives and analyze data. An extensive set of tutorials is available:

- **Narrative Interface User Guide**  
[kbase.us/narrative-guide/](https://kbase.us/narrative-guide/)
- **Data Upload and Download Guide**  
[kbase.us/data-upload-download-guide/](https://kbase.us/data-upload-download-guide/)
- **Transfer JGI Data Guide**  
[kbase.us/transfer-jgi-data/](https://kbase.us/transfer-jgi-data/)
- **App Tutorials**  
[kbase.us/tutorials/](https://kbase.us/tutorials/)

## Contact us

Learn more about using KBase at [kbase.us](https://kbase.us).

To contact us, please go to:  
[kbase.us/contact-us/](https://kbase.us/contact-us/)

We welcome your feedback on what you like or don't like about KBase and what you'd love to see us add in the future. Please share your opinions by taking our questionnaire at [kbase.us/feedback/](https://kbase.us/feedback/).