



# **BCOnexus: BCOnexus**

## **Platform-Free Editor**

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**August 2024**

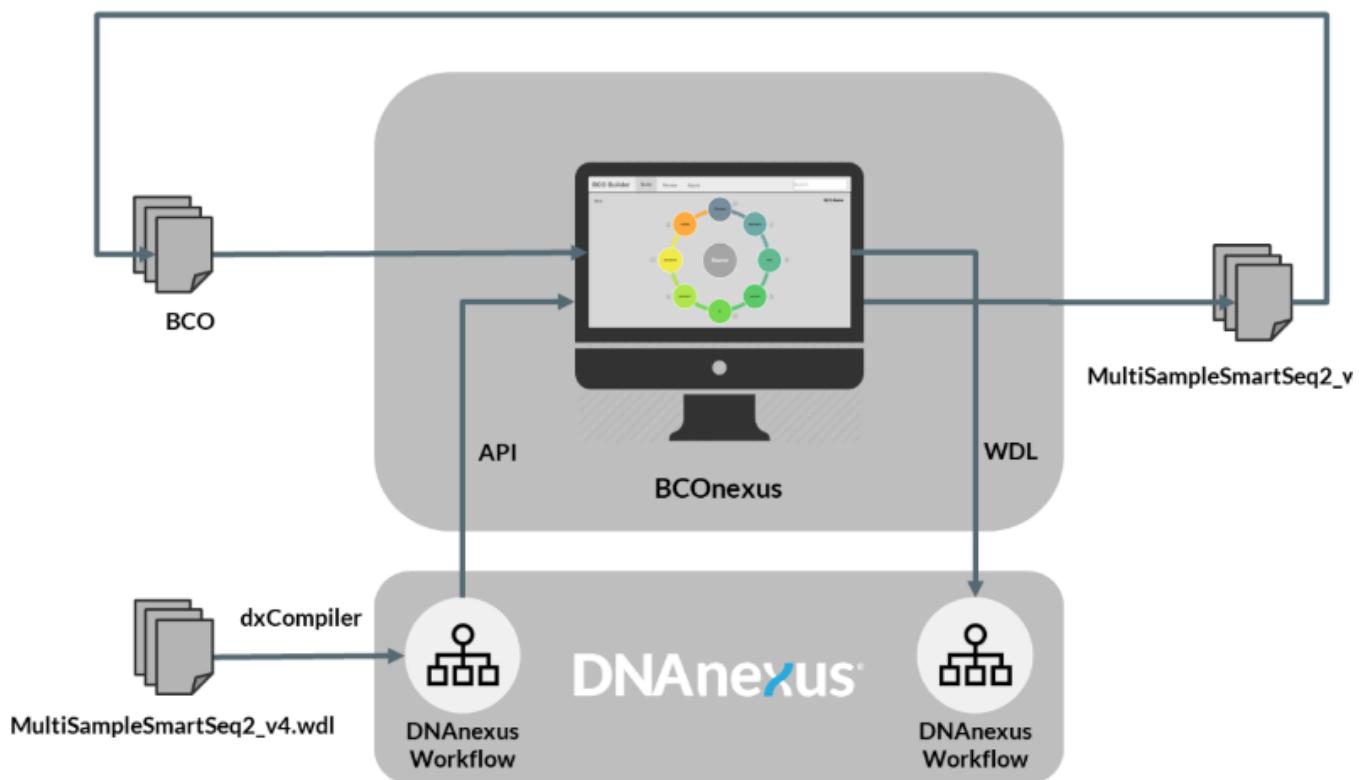
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# What is BCOnexus?

A platform-free application, “BCOnexus”, delivered as a Docker image and open-source code, presents a web-based interactive service for importing, editing, and exporting BCOs. BCOnexus can be launched locally on any platform supporting execution of Docker images, and can be accessed from any web browser using a non-standard port.

BCOnexus will interact with the local file system, supports the uploading of WDL, CWL, and BCO files, downloading, and publishing BCO files. BCOnexus can interact with the DNA Nexus platform via its API to ingest native workflow metadata into BCOs and to create native workflows from WDL and CWL scripts.



# How to Setup and Install

1. Install docker on your local machine.

<https://docs.docker.com/desktop/install/linux-install/>

<https://docs.docker.com/desktop/install/mac-install/>

<https://docs.docker.com/desktop/install/windows-install/>

2. Download the BCOnexus docker image (docker\_image\_name: **bconexus\_uat\_v1\_\***) tar file from the shared drive.

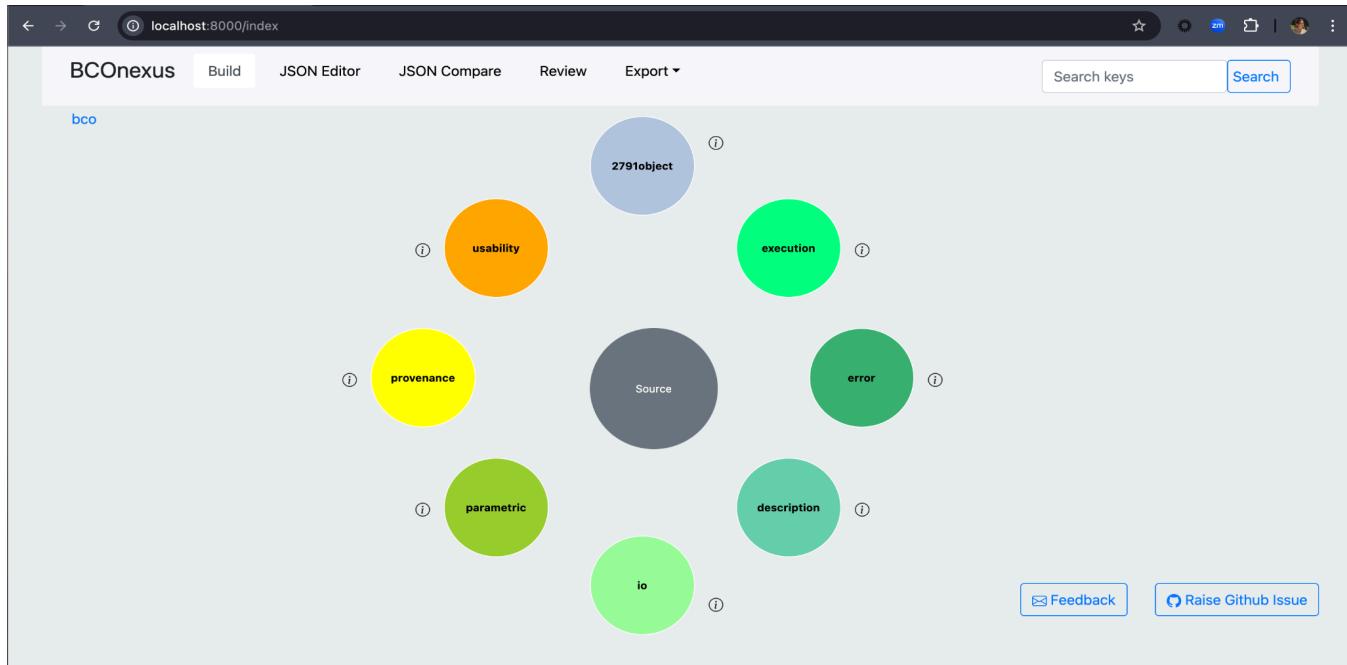
3. Open the terminal or command line application and run the below commands

*docker load --input <path to the downloaded docker image tar file>*

*docker run --publish 8000:8000 <docker image tag name>*

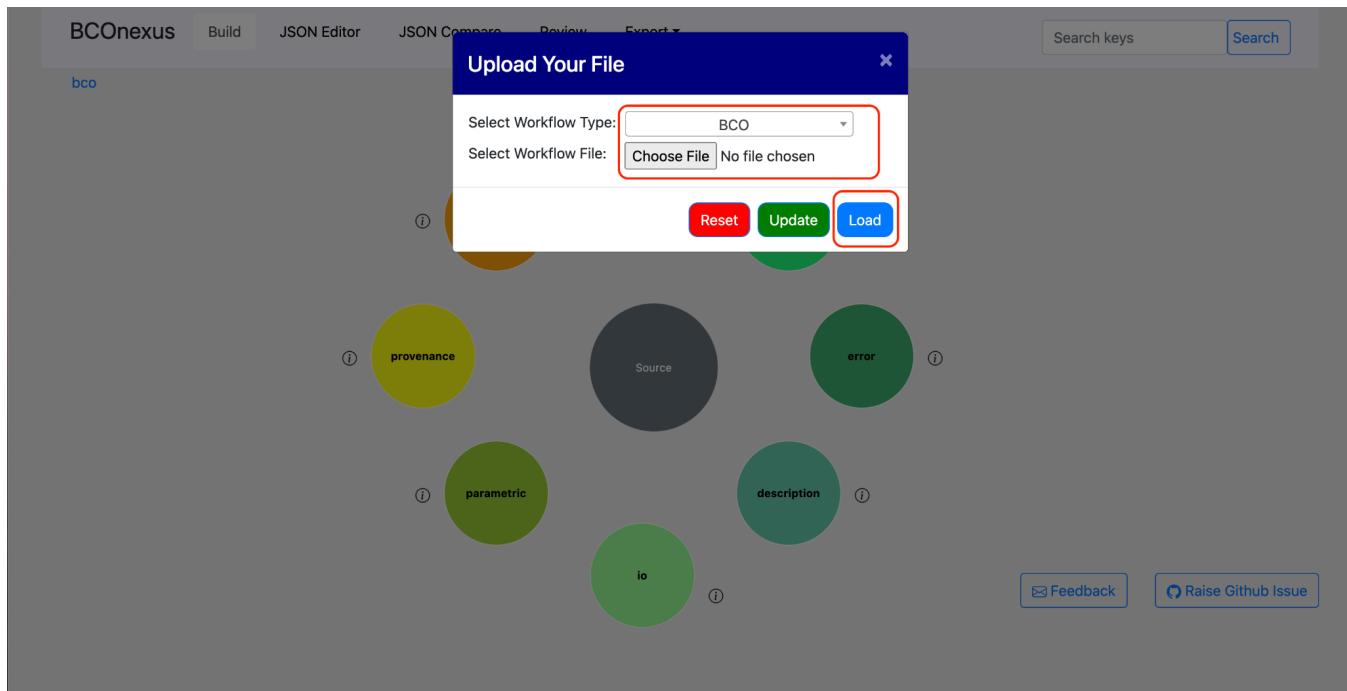
4. Open any browser and enter the URL: <http://127.0.0.1:8000/index> and the below page will be displayed.

## BCOnexus Home page:



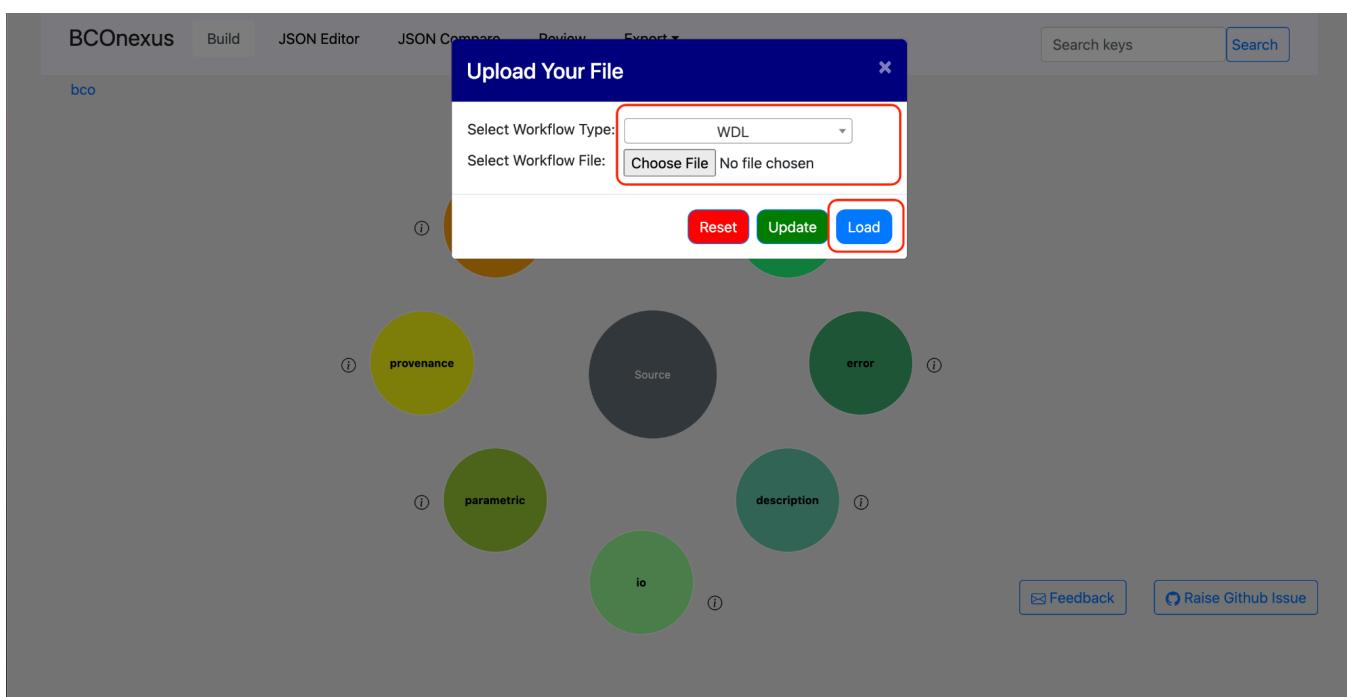
# Loading the BCOnexus Editor with workflow files

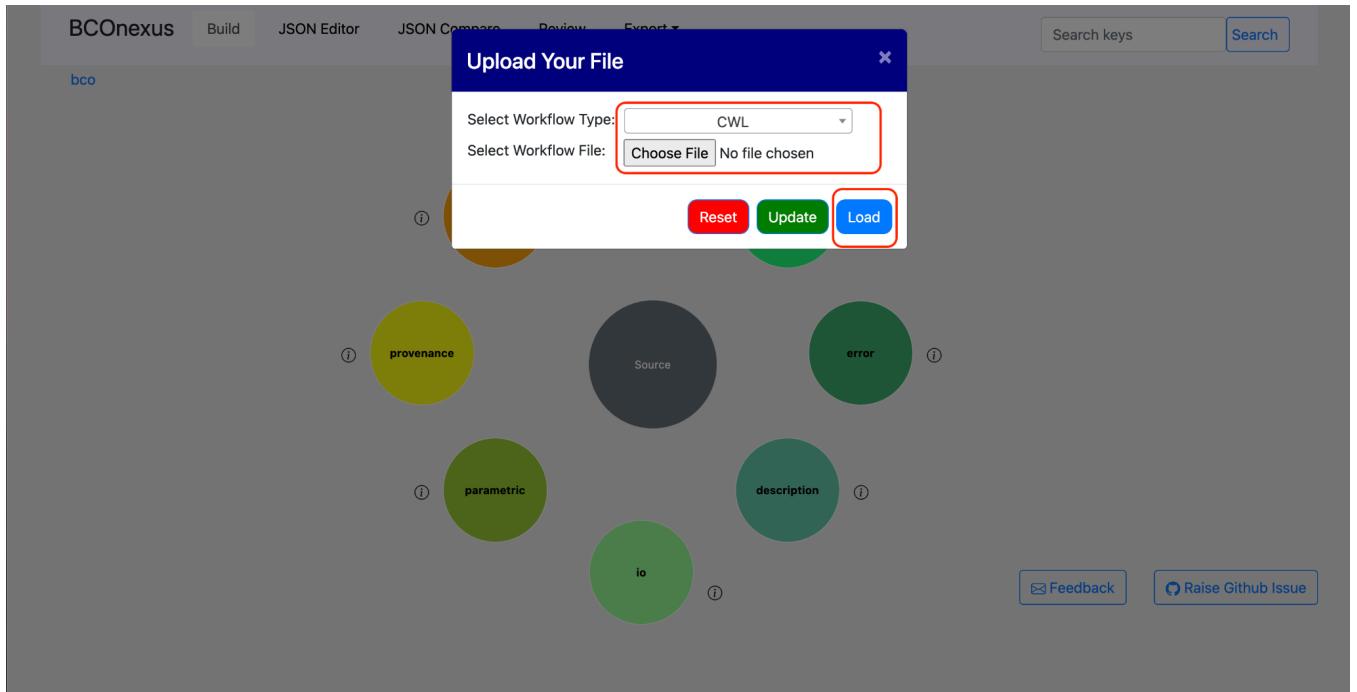
1. Click on Source circle on the home page.
2. Select workflow type as **BCO** and click on the “Choose File” button to select a <bco\_name>.json file.
3. Click on the “Load” button to load the <bco\_name>.json file into the in-memory bco.json file.



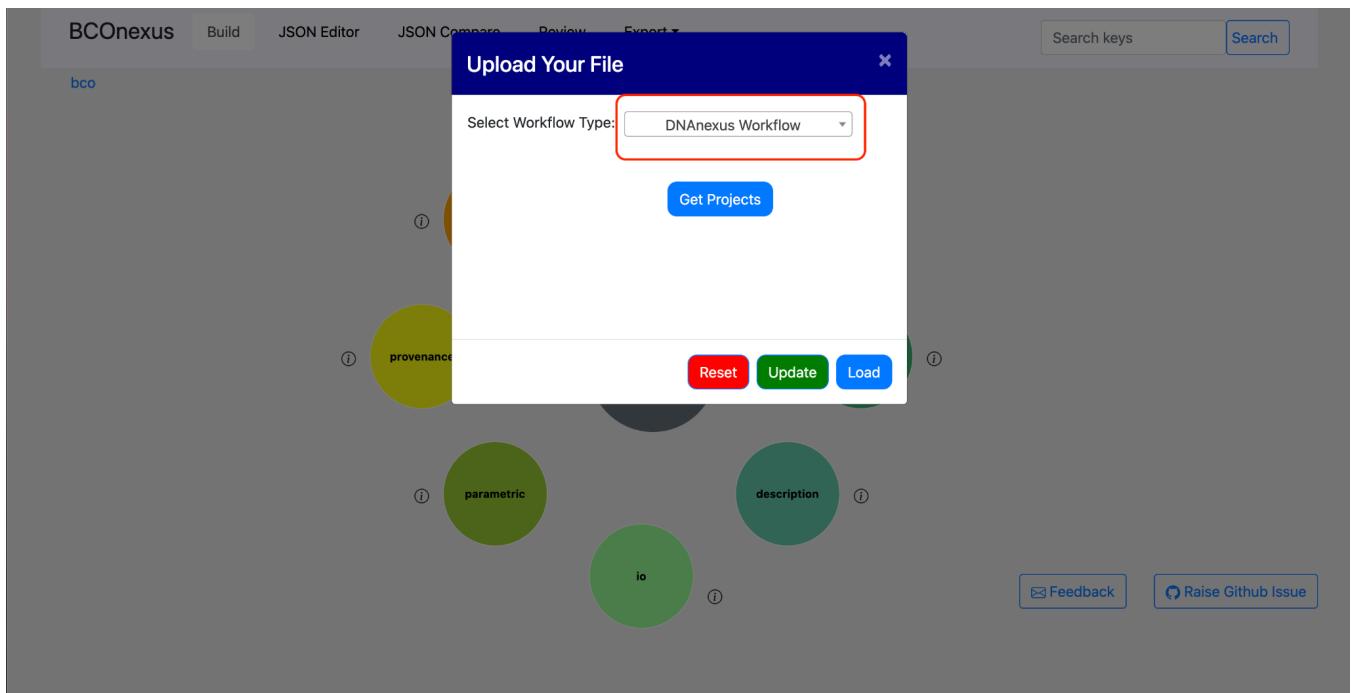
# Updating the BCONexus Editor with workflow files

1. To update the in-memory bco with a WDL/CWL workflow, click on the Source circle on the home page.
2. Select workflow type as WDL/CWL and select the respective .wdl/.cwl file by clicking on the “Choose File”button.
3. Click on the “Update” button to update the in-memory bco.json file with the information from the WDL/CWL workflow.

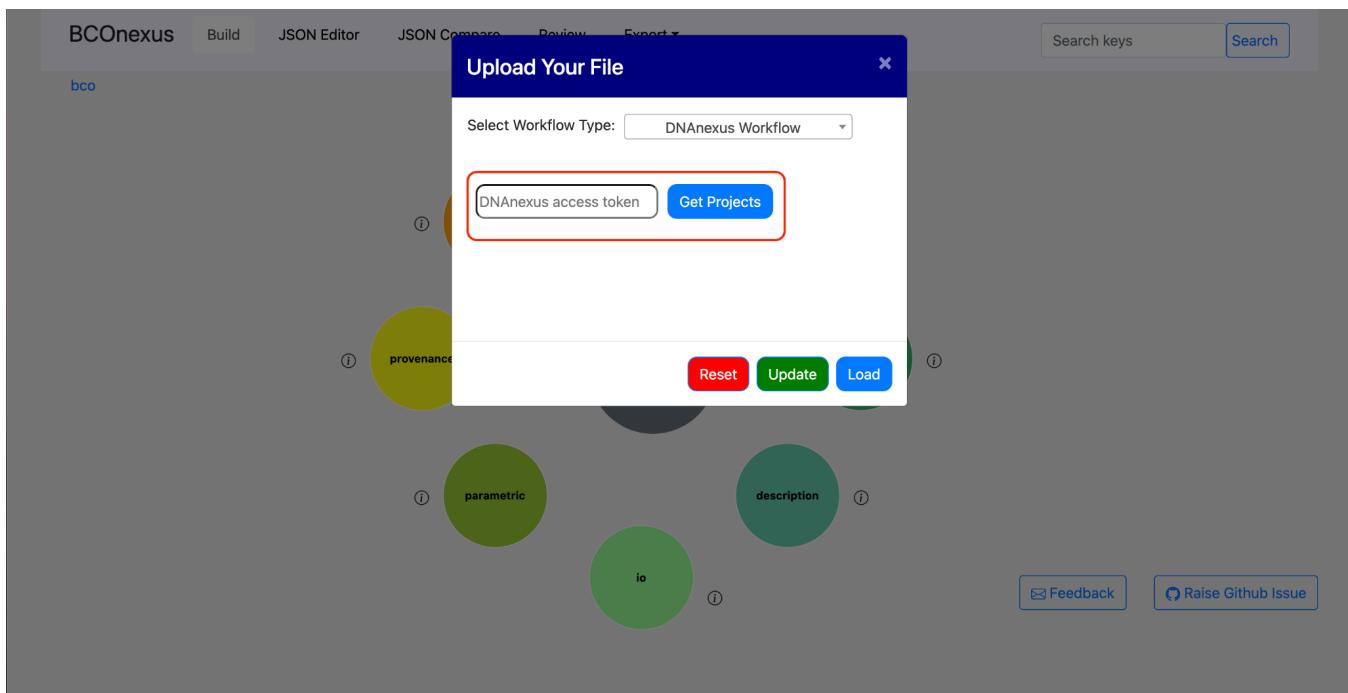
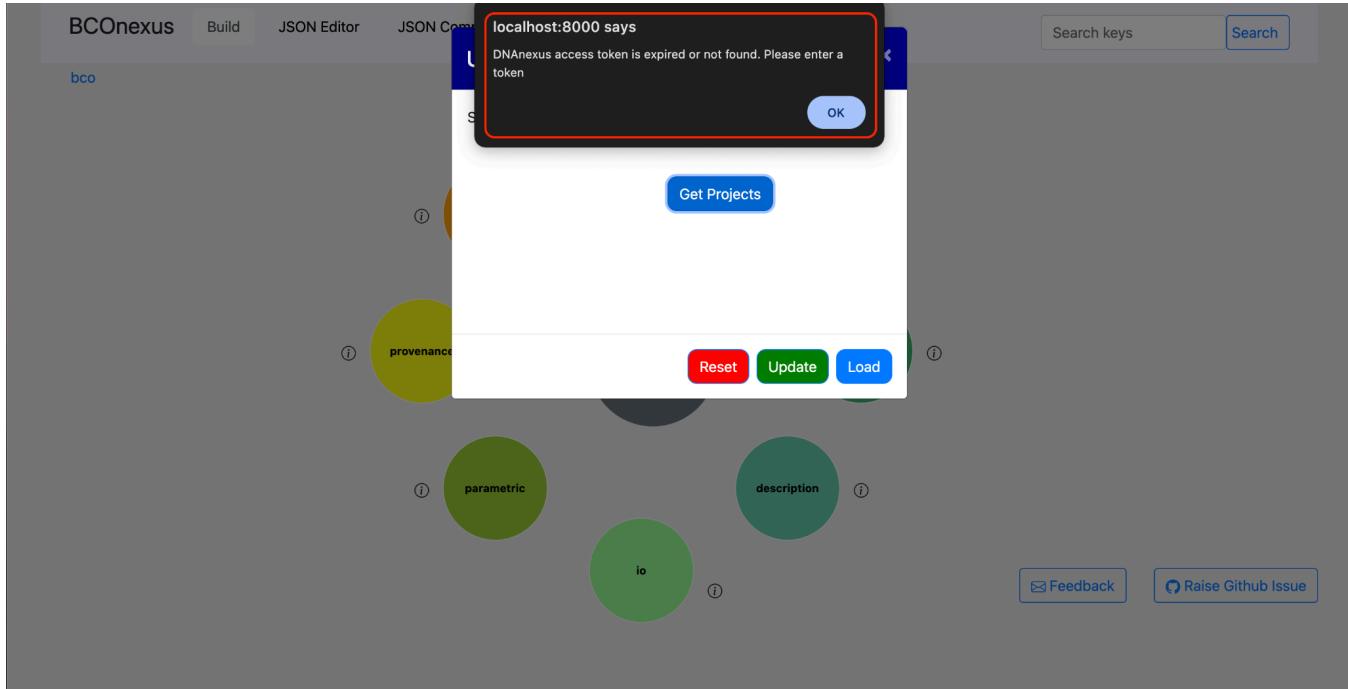




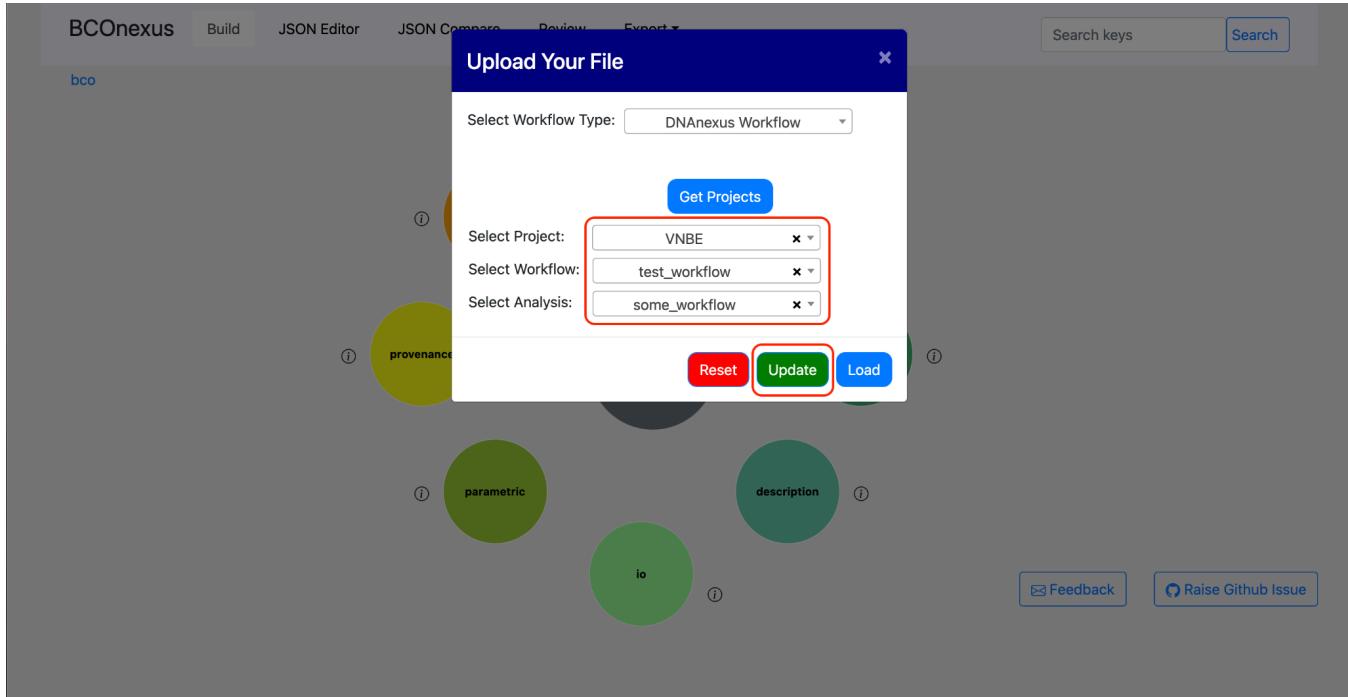
4. To update the in-memory bco with a DNAAnexus workflow (for which you will need a DNAAnexus access\_token; refer to the manual section [How to get a DNAAnexus token?](#)), select workflow type as **DNAAnexus Workflow** and click on “**Get Projects**”.



5. If there is no active DNAAnexus token available, the user will be prompted with an alert to provide a DNAAnexus access token. Paste the access\_token in the field and click on “**Get Projects**”.

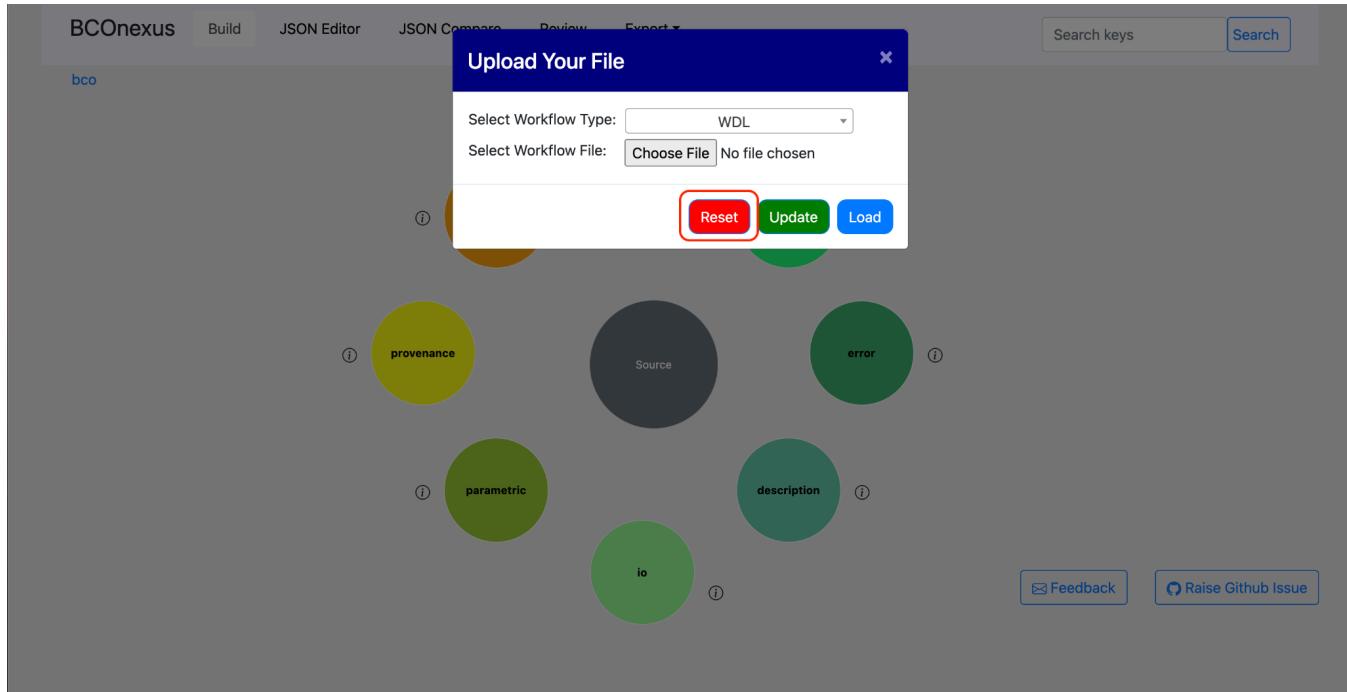


6. Select a DNA Nexus project, workflow and analysis from the drop downs and click on the “Update” button to update the in-memory bco.json file with the DNA Nexus workflow.



# Resetting the BCO

Click on the Source circle on the home page and click on the “Reset” button to clear the in-memory bco.json file.



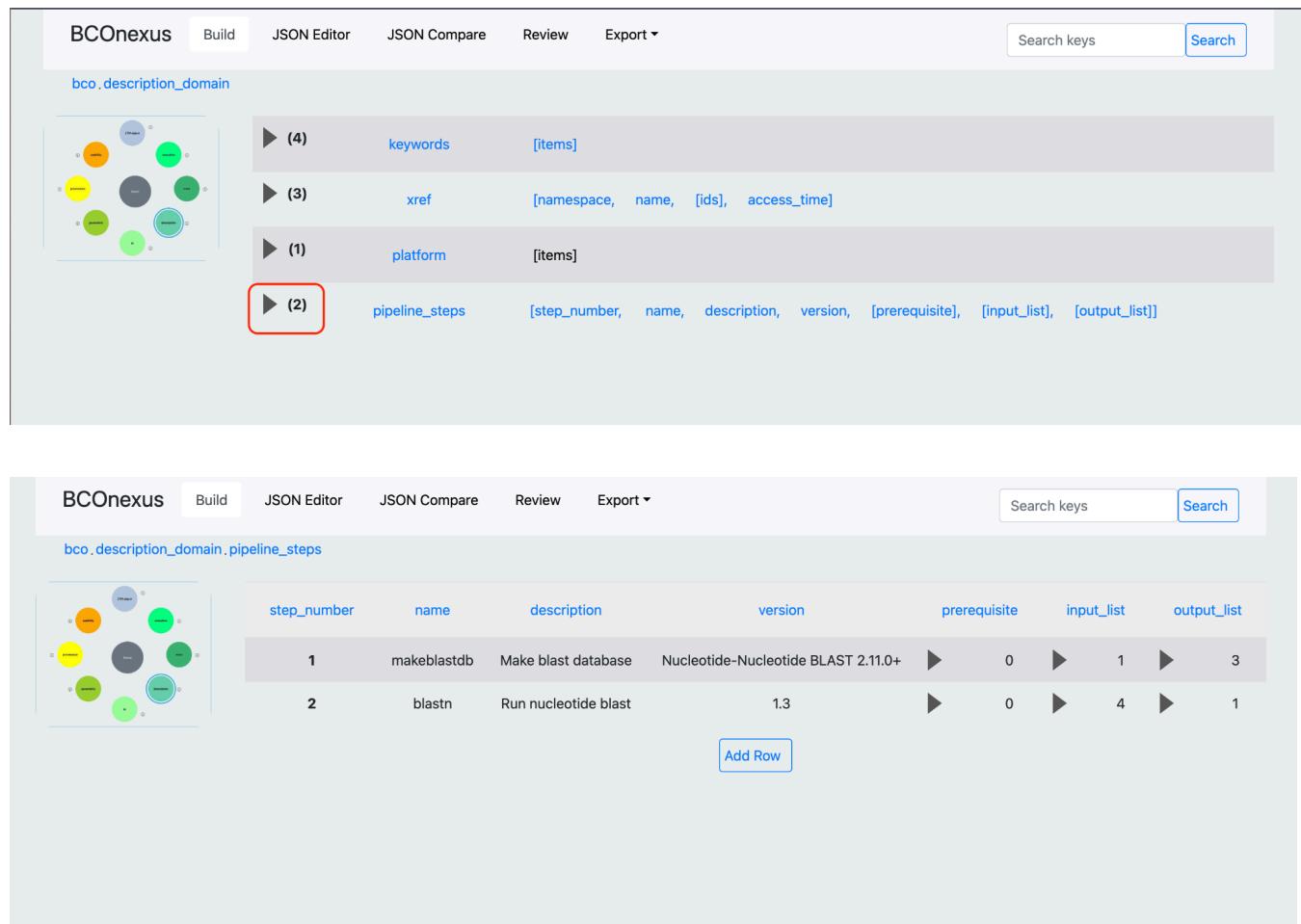
# Editing the open BCO

The in-memory bco.json file can be edited domain-wise by clicking on the respective domain circle on the homescreen.

## Example:

To edit the “**description domain**”, click on the “**description**” circle on the homescreen. The below screen will be displayed.

Click on the  for **pipeline\_steps** to view and edit the description\_domain.pipeline\_steps.



The screenshot shows the BCONexus interface with the "Build" tab selected. The main area displays the "bco.description\_domain" section. On the left, there is a circular navigation menu with several colored nodes (yellow, orange, green, blue, grey) representing different domains. A red box highlights the "pipeline\_steps" node. To the right, a table lists the following entries:

Index	Category	Description
1	platform	[items]
2	pipeline_steps	[step_number, name, description, version, [prerequisite], [input_list], [output_list]]

Below this, another screenshot shows the "bco.description\_domain.pipeline\_steps" table. The table has columns: step\_number, name, description, version, prerequisite, input\_list, and output\_list. It contains two rows:

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1

An "Add Row" button is located at the bottom of the table.

Click on a field to make the field editable. You may update the value for the field, and then click or use the tab key to move to the next field.

BCOnexus Build JSON Editor JSON Compare Review Export ▾

Search keys Search

bco.description\_domain.pipeline\_steps

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1

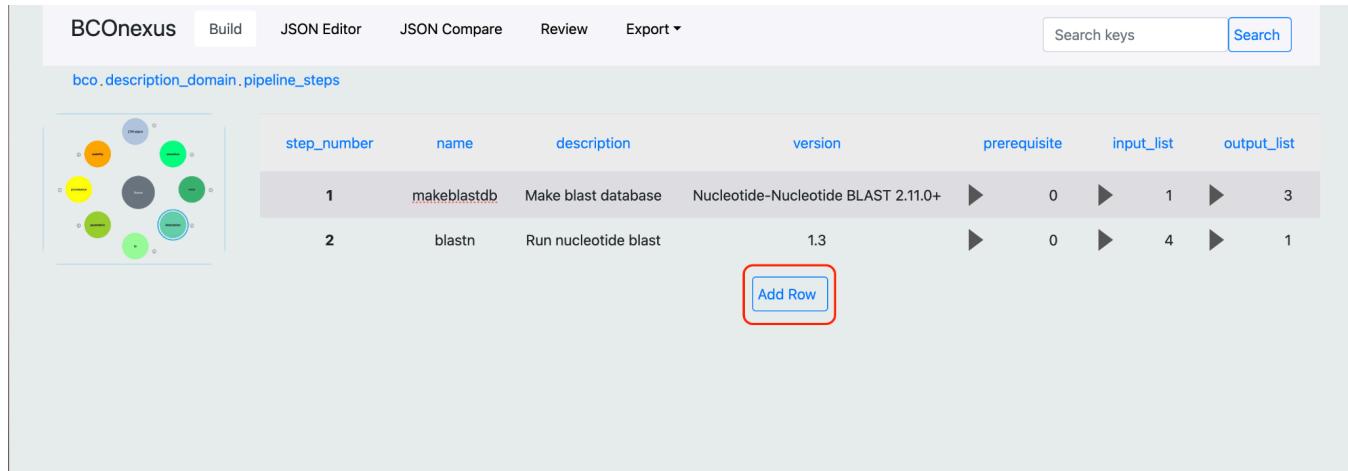
Add Row



# Adding new rows to the BCO

## Example:

To add a new row, click on the “Add Row” button.



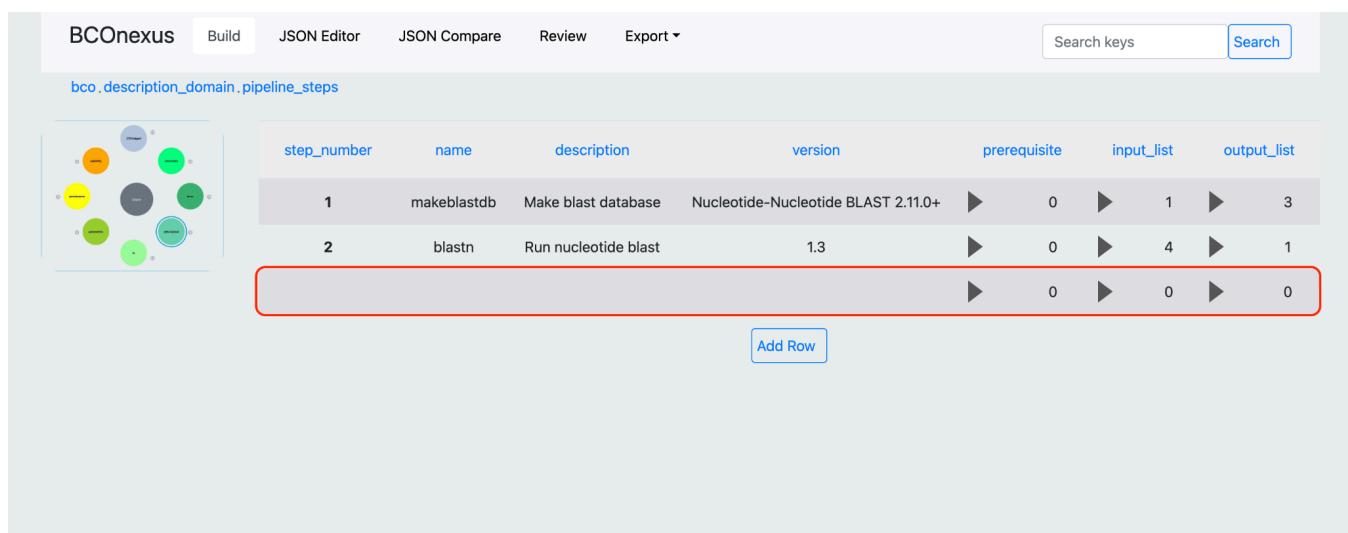
BCOnexus Build JSON Editor JSON Compare Review Export ▾

Search keys Search

bco.description\_domain.pipeline\_steps

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1

Add Row



BCOnexus Build JSON Editor JSON Compare Review Export ▾

Search keys Search

bco.description\_domain.pipeline\_steps

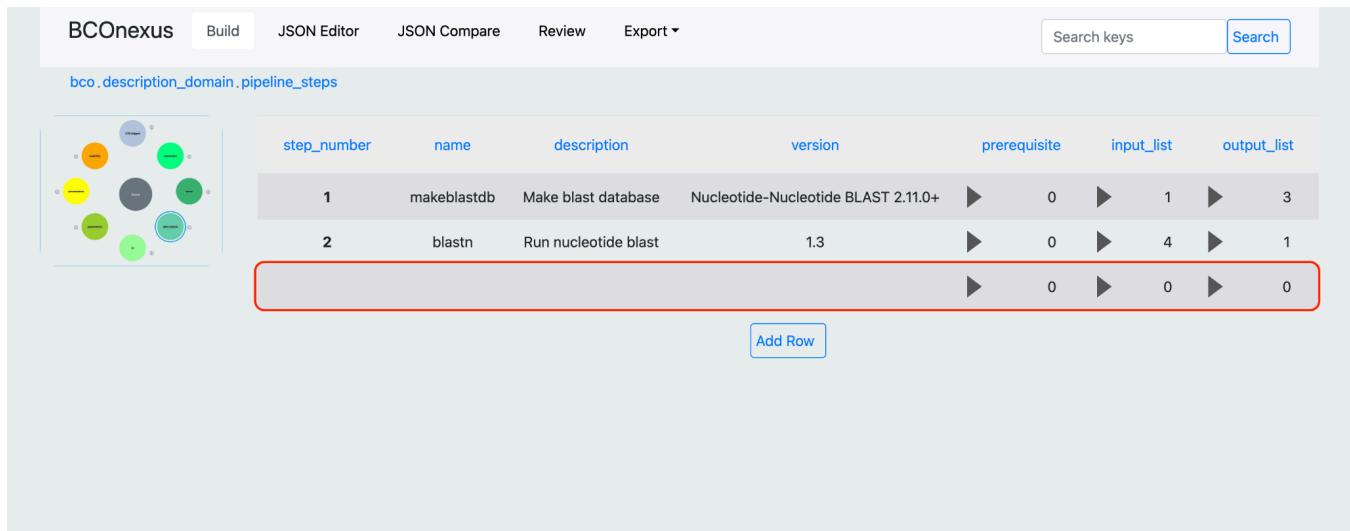
step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1
				▶ 0	▶ 0	▶ 0

Add Row

# Deleting a row from the BCO

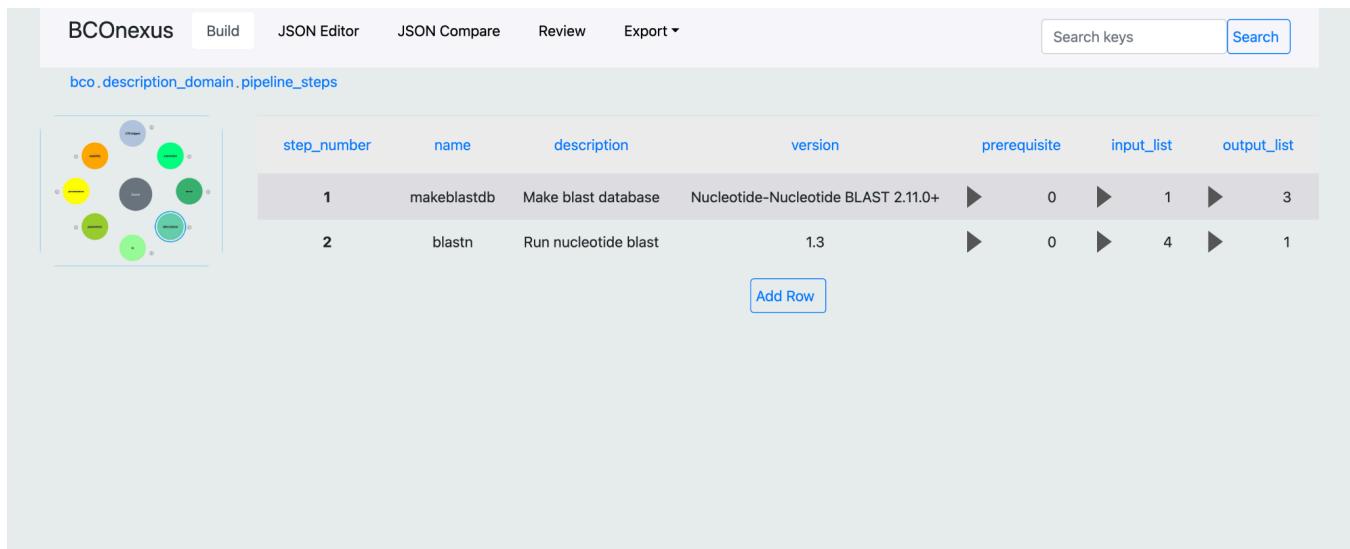
## Example:

To delete a row, make sure all fields in the row are updated with an empty value and go back to the previous screen and come back to the same screen. You may also refresh the screen once all fields are blank/empty.



The screenshot shows a table titled "bco.description\_domain.pipeline\_steps". The table has columns: step\_number, name, description, version, prerequisite, input\_list, and output\_list. There are two rows visible. The first row (makeblastdb) has values: step\_number 1, name makeblastdb, description Make blast database, version Nucleotide-Nucleotide BLAST 2.11.0+, prerequisite 0, input\_list 1, output\_list 3. The second row (blastn) has values: step\_number 2, name blastn, description Run nucleotide blast, version 1.3, prerequisite 0, input\_list 4, output\_list 1. A third row is present but is completely empty (all fields are blank), indicated by a red border around its entire row.

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1
				▶ 0	▶ 0	▶ 0



The screenshot shows the same table after the empty row has been deleted. Now there are only two rows: makeblastdb and blastn, both with their original values.

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1

# How to Search for a key

The search operation in the upper right will look for the key searched in the in-memory bco.json file. It will then display the screen that first matches the key.

The screenshot shows a web browser window for 'BCOnexus' at 'localhost:8000/index?'. The search bar contains 'pipeline\_steps' and the 'Search' button is highlighted with a red box. The results table has columns: step\_number, name, description, version, prerequisite, input\_list, and output\_list. Two rows are shown:

step_number	name	description	version	prerequisite	input_list	output_list
1	makeblastdb	Make blast database	Nucleotide-Nucleotide BLAST 2.11.0+	▶ 0	▶ 1	▶ 3
2	blastn	Run nucleotide blast	1.3	▶ 0	▶ 4	▶ 1

An 'Add Row' button is located at the bottom of the table. To the left of the table is a circular diagram with colored nodes (yellow, green, blue, grey) connected by lines, representing a network or dependency graph.

# Editing a BCO file with the JSON Editor

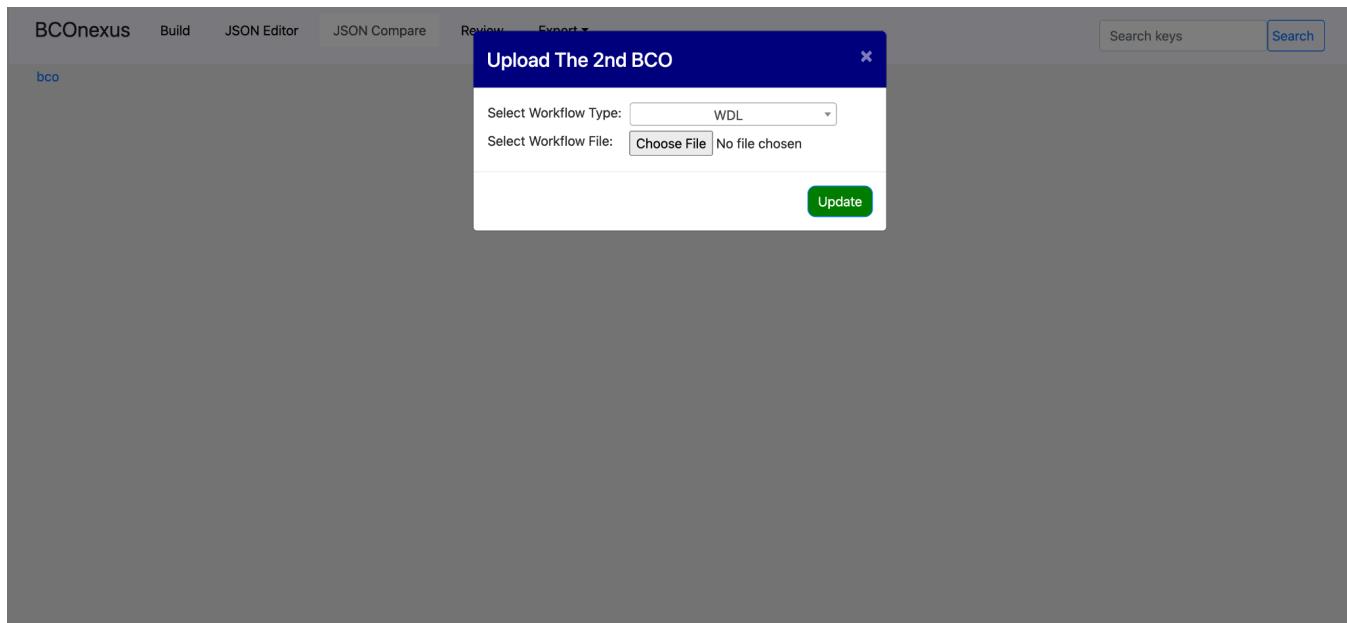
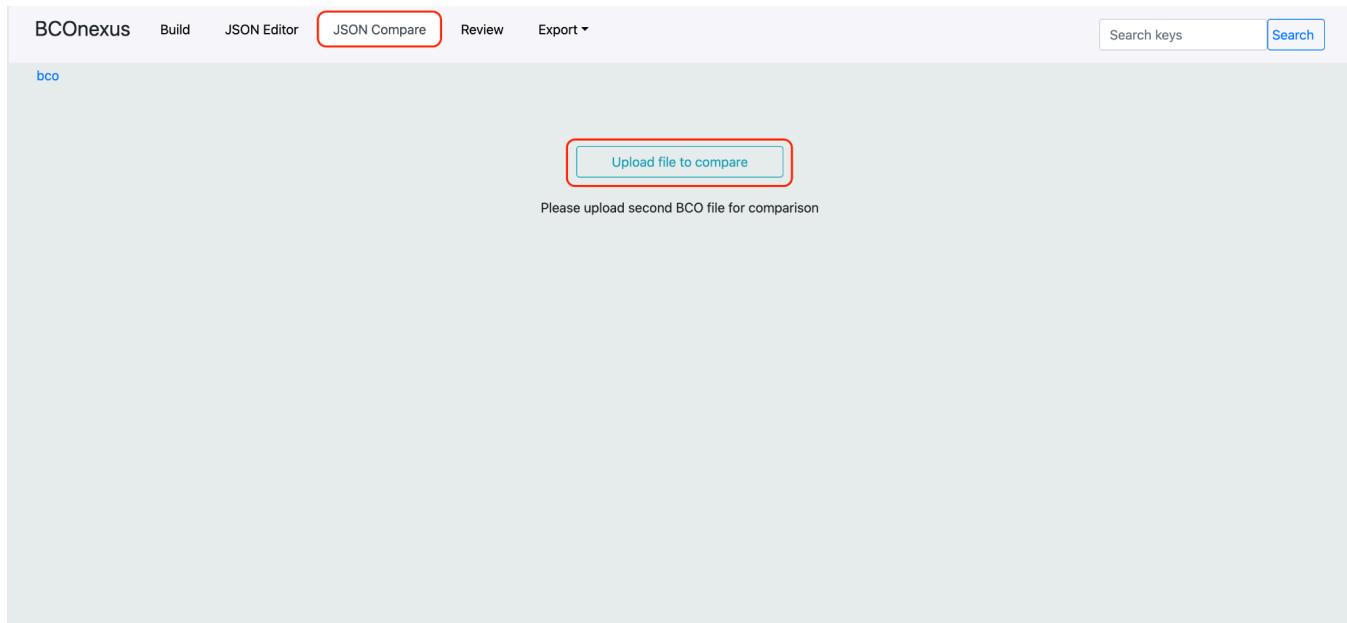
To edit a BCO in JSON format, navigate to the JSON Editor tab.

Click 'Edit' to make changes, use 'Beautify' to format the code, and then click 'Save' to preserve your modifications. After saving, click 'Validate' to check the file's integrity; a green checkmark indicates a valid file, while a red cross signifies errors.

The screenshot shows the BCOnexus web application interface. At the top, there is a navigation bar with tabs: BCOnexus, Build, **JSON Editor**, JSON Compare, Review, and Export. Below the navigation bar, the word "bco" is typed into a search bar. The main content area is titled "JSON Editor". On the left, there is a large text box containing JSON code for a BCO file. On the right, there is a vertical stack of four buttons: "Edit", "Beautify", "Save", and "Validate". The "Edit" button is highlighted with a red border. The "Save" button is green with a white checkmark icon. The "Validate" button is blue.

# Comparing BCOs

To compare BCOs, select the "JSON compare" tab. Click "Upload to compare" to open a modal where you can choose a second BCO (CWL, WDL, JSON, or workflow from DNAlexus) to compare against the currently loaded BCO in memory. The upload process for the comparison file mirrors the BCO file upload steps outlined in the previous section.



Once the second BCO is uploaded, both files will be displayed side-by-side for easy comparison. Any modifications made to the open BCO within the editor tab will be reflected in real-time on the comparison view.

BCOnexus Build JSON Editor JSON Compare Review Export ▾

Search keys Search

bco

Upload file to compare

### JSON Compare

Currently in Editor BCO

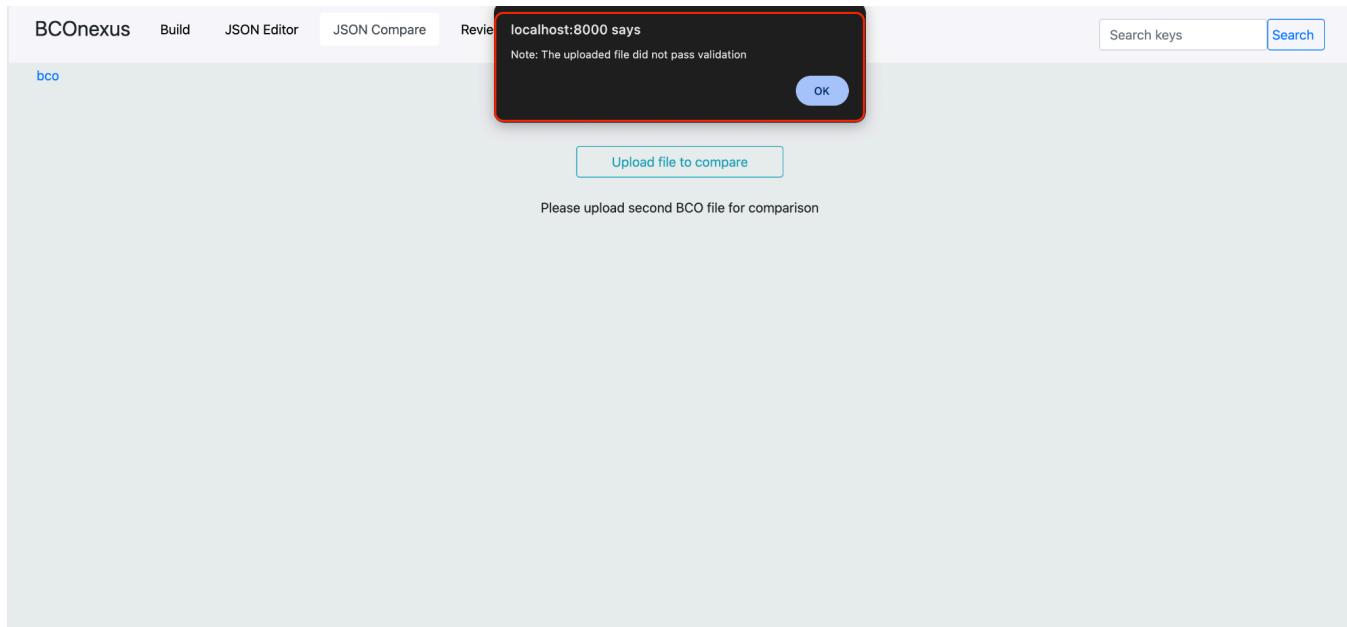
```
@@ -1,424 +1,411 @@
1 {
2   "object_id": "https://raw.githubusercontent.com/HadleyKing/bco-tool/1.1.0/tests/collapse/test_bco.json",
3   "spec_version": "https://w3id.org/ieee/ieee-2791-schema/2791object.json",
4   "etag": "f37a68068e5979b3e1527af258df96a4f116247727f8d1ad8bf2ba6173bece",
5   "provenance_domain": {
6     "name": "HCV1a BLASTN homologue identification, with collapsed secondary files.",
7     "version": "1.0",
8     "review": [
9       {
10         "date": "",
11         "reviewer": {
12           "name": "",
13           "affiliation": "",
14           "email": "",
15           "contribution": [],
16           "orcid": ""
17         },
18         "reviewer_comment": "",
19         "status": ""
20       }
21     ]
22   }
23 }
```

biocompute\_example.json

```
@@ +1,411 @@
1 {
2   "object_id": "object_id",
3   "spec_version": "https://w3id.org/ieee/ieee-2791-schema/",
4   "etag": "5986805969341343E77A95B4023600FC8FEF4887E79F355E5880B40A4F50995",
5   "provenance_domain": {
6     "name": "HCV1a Lepidosaur resistance SNP detection",
7     "version": "2.8",
8     "review": [
9       {
10         "date": "",
11         "reviewer": {
12           "name": "",
13           "affiliation": "",
14           "email": "",
15           "contribution": [],
16           "orcid": ""
17         },
18         "reviewer_comment": "",
19         "status": ""
20       }
21     ]
22   }
23 }
```

To compare with another BCO, simply repeat the file upload process for the second BCO.

Note: The program will also validate the comparison BCO and will notify the user if it is not valid.



# Reviewing the BCO

Clicking on the Review tab will validate the in-memory BCO as per the schema, and produces domain-wise error messages on the right side under validation. Clicking on the message will expand the bco.json tree on the left to the point of error and will highlight the errored field.

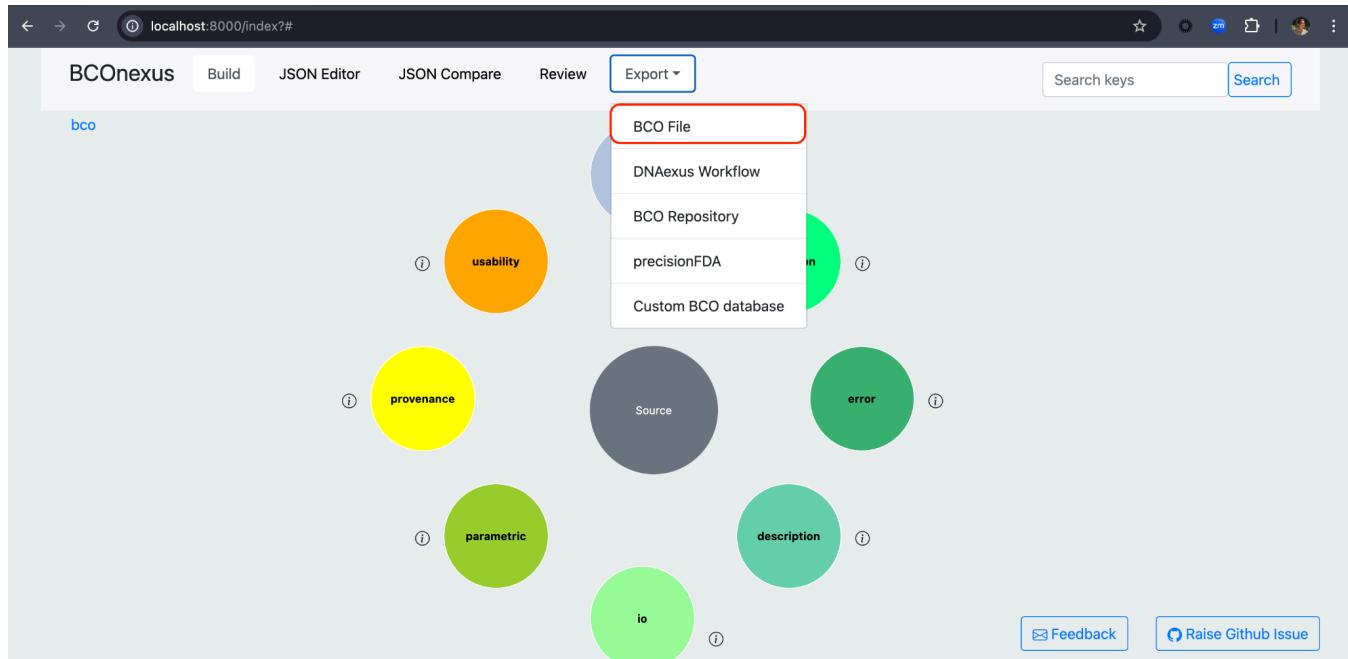
The screenshot shows the BCOnexus web application at localhost:8000/index?. The top navigation bar includes links for BCOnexus, Build, JSON Editor, JSON Compare, Review (which is highlighted with a red box), and Export. A search bar with a 'Search' button is also present. The main content area has a sidebar labeled 'bco' containing a tree view of domains: usability domain +, parametric domain +, io domain +, error domain +, execution domain +, description domain +, and provenance domain +. To the right, under 'Object Information', there is an 'Object Information' section for '2791 Object -' with fields for 'object\_id', 'spec\_version', and 'etag', all of which are highlighted with red boxes. Below this is a 'Validation' section for '2791 Object' which lists several validation errors: 'Fail' for 'object\_id is empty', 'spec\_version is empty', and 'etag is empty'; 'Usability domain' is listed under 'Error domain'; 'Fail' for 'usability\_domain is empty'; 'Error domain' is listed under 'Error domain'; 'Fail' for 'error\_domain is empty', 'empirical\_error is empty', and 'algorithms\_error is empty'; 'Parametric domain' is listed under 'Parametric domain'; 'Fail' for 'parametric\_domain is empty'; and 'IO domain' is listed under 'IO domain'.

# Exporting the BCO

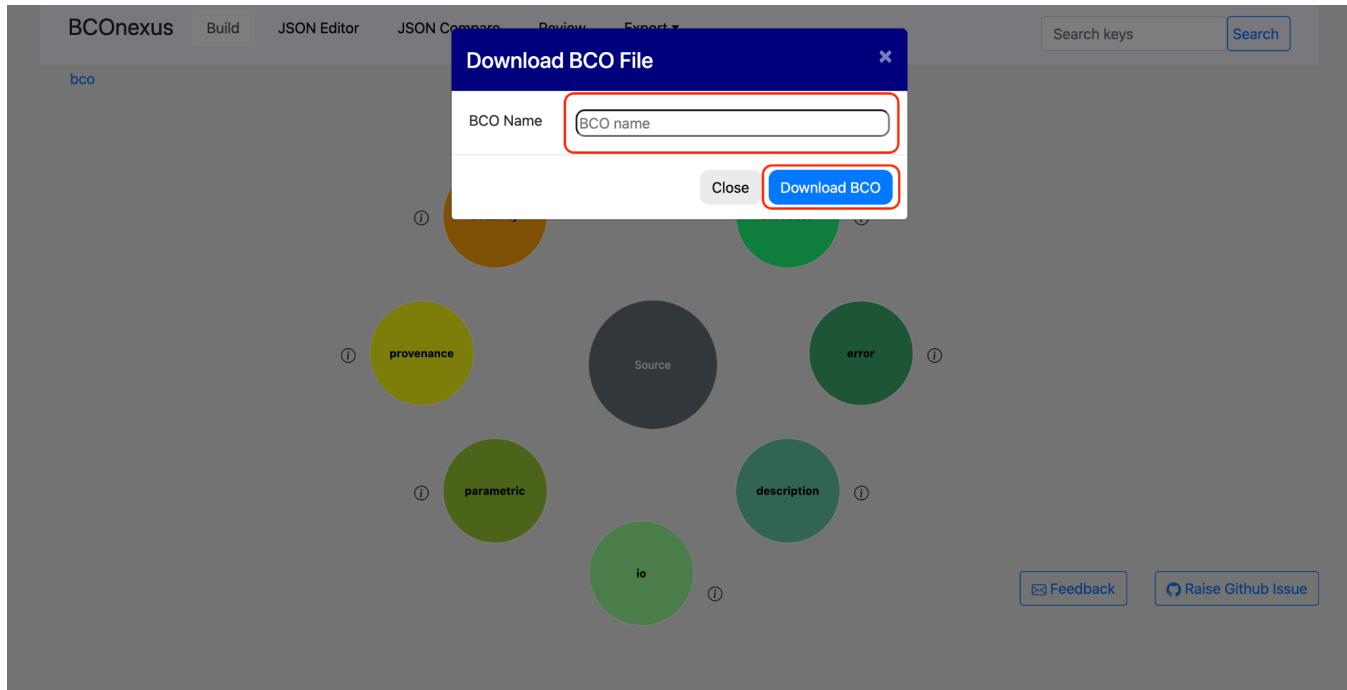
BCOnexus provides many ways to export the current BCO loaded in working memory, either to a local system or to an external repository.

## 1. Downloading the BCO:

Click on the export and select “BCO File” option to download the in-memory BCO.



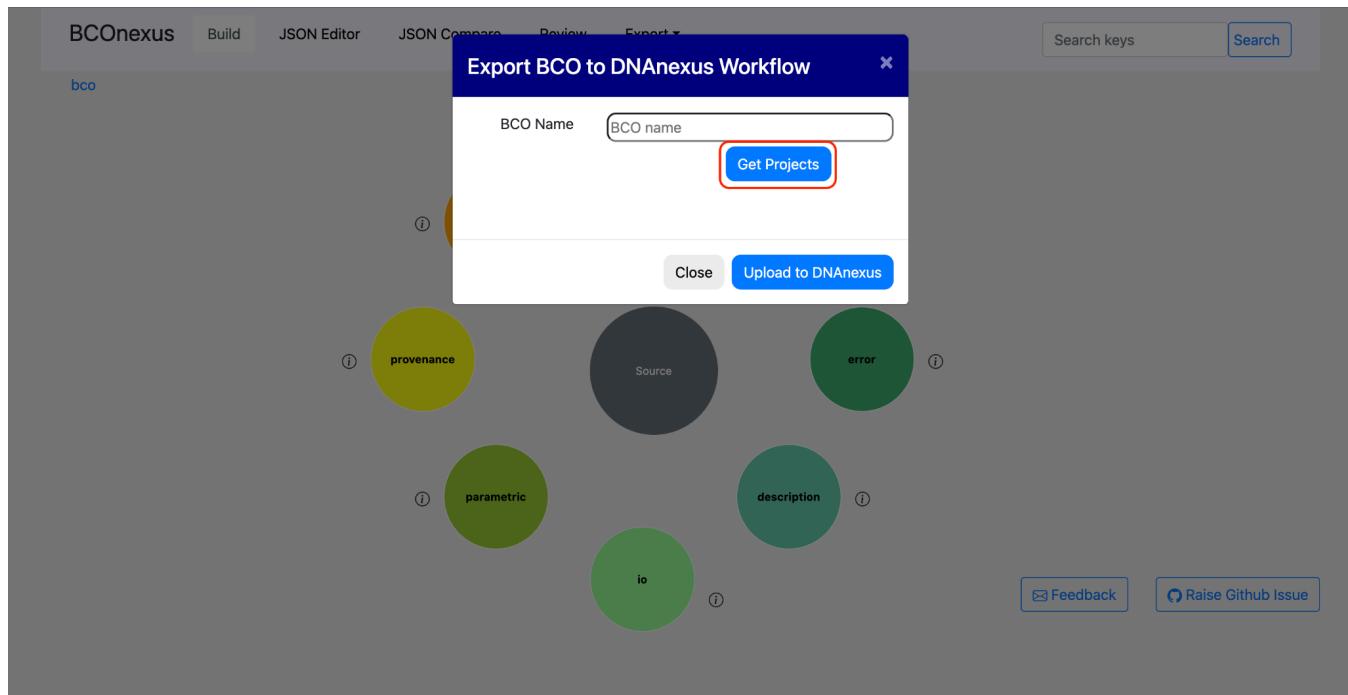
Provide a name for the file in the prompt and click on the “Download BCO” button to download the file.

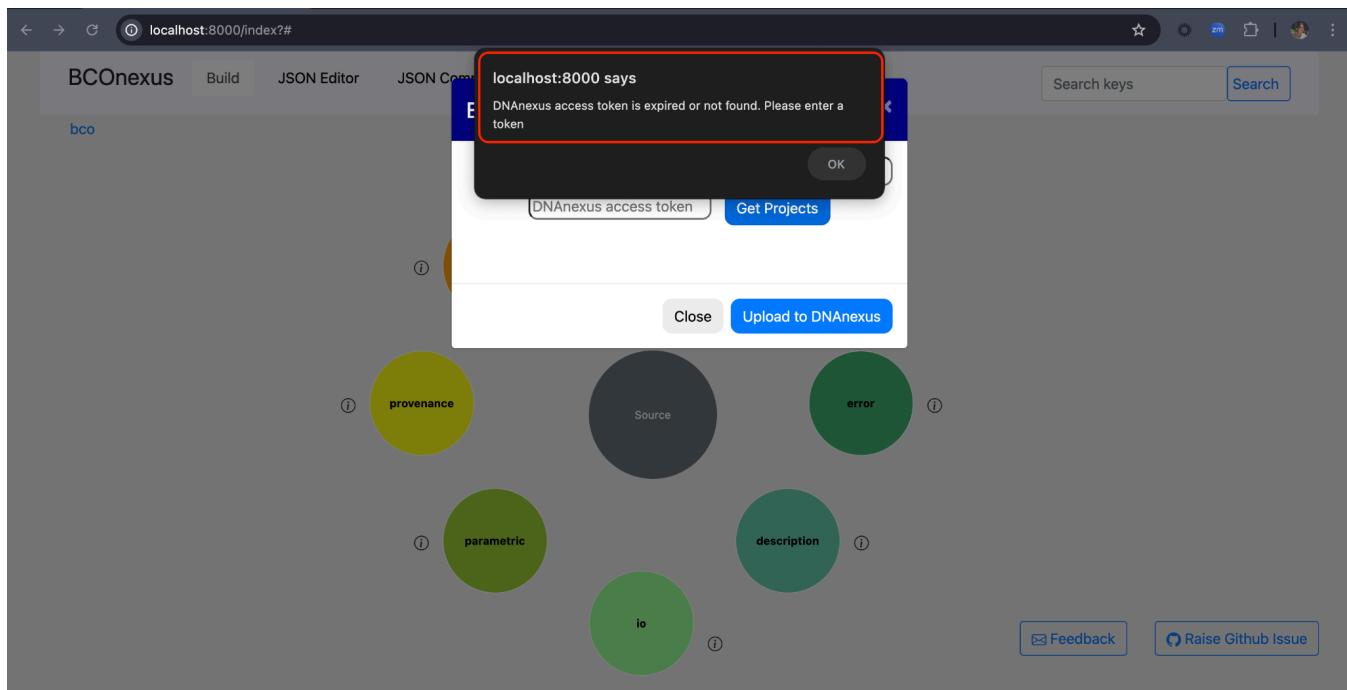


## 2. How to export the BCO file to a DNAAnexus project:

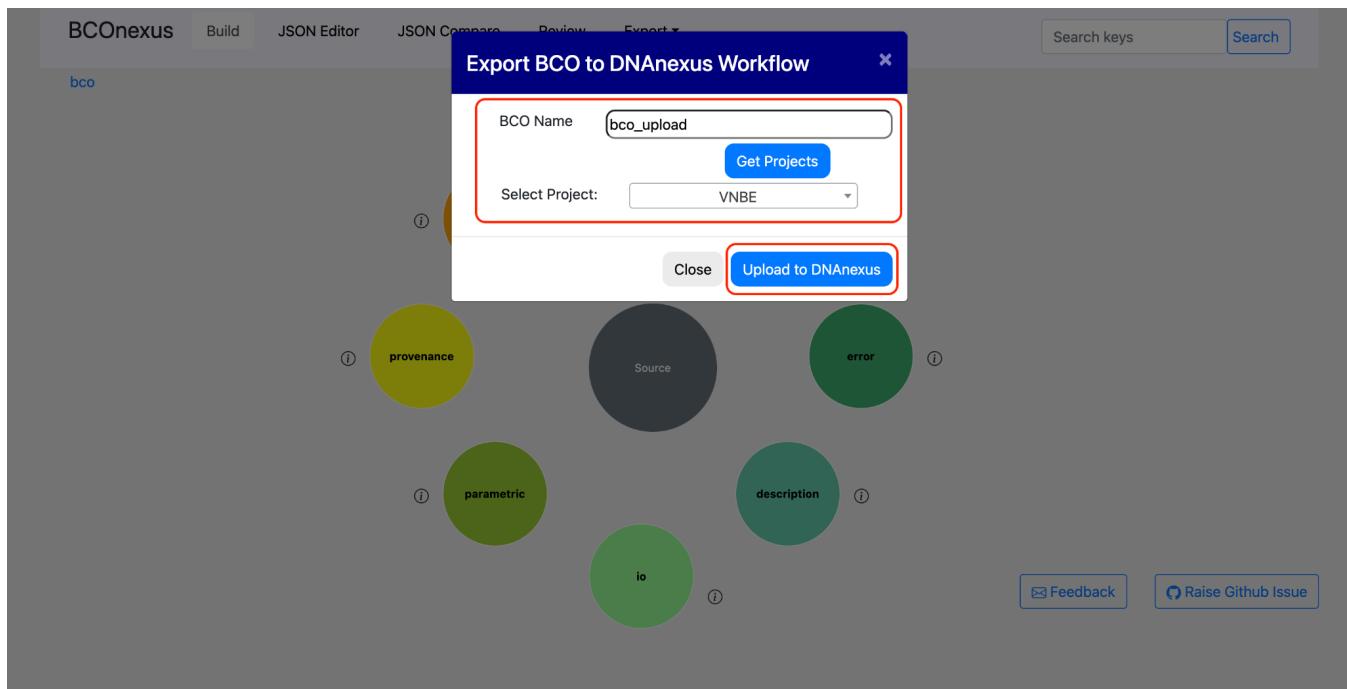
Click on the Export menu button and select the “DNAAnexus Workflow” option to export the in-memory BCO file to a DNAAnexus project.

Provide a name for the file in the prompt and click on the “Get Projects” button to fetch all the projects. If there is no active token, you will be prompted with an alert to provide a token, obtainable on the DNAAnexus Platform. (If you do not have a DNAAnexus token, see later section, “How to get a DNAAnexus token” in this guide.)





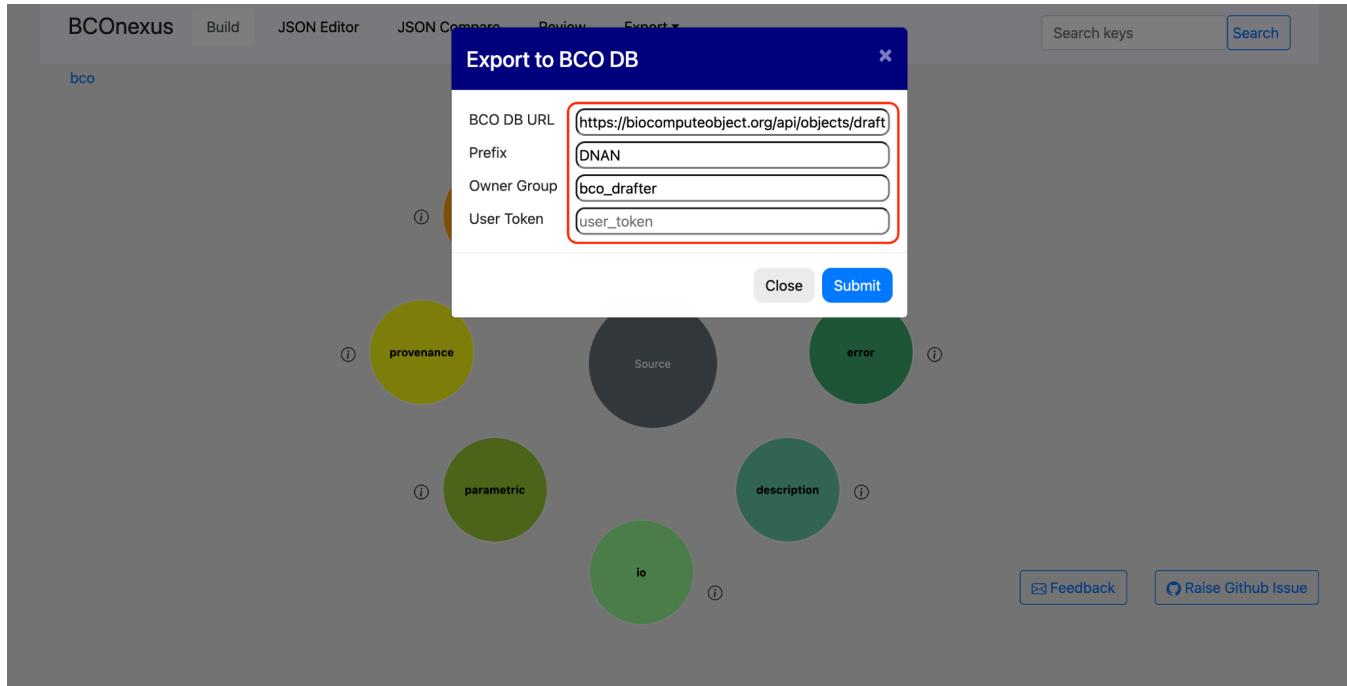
Provide a valid token to fetch the projects from DNAexus to which you may upload the in-memory bco.json file. Select a project from the available list of projects and click on the “Upload to DNAexus” button to upload.



### 3. How to export the BCO file to the BCO Repository:

Click on the Export button in the top menu and select the “BCO Repository” option to export the in-memory BCO file to a BCO Repository.

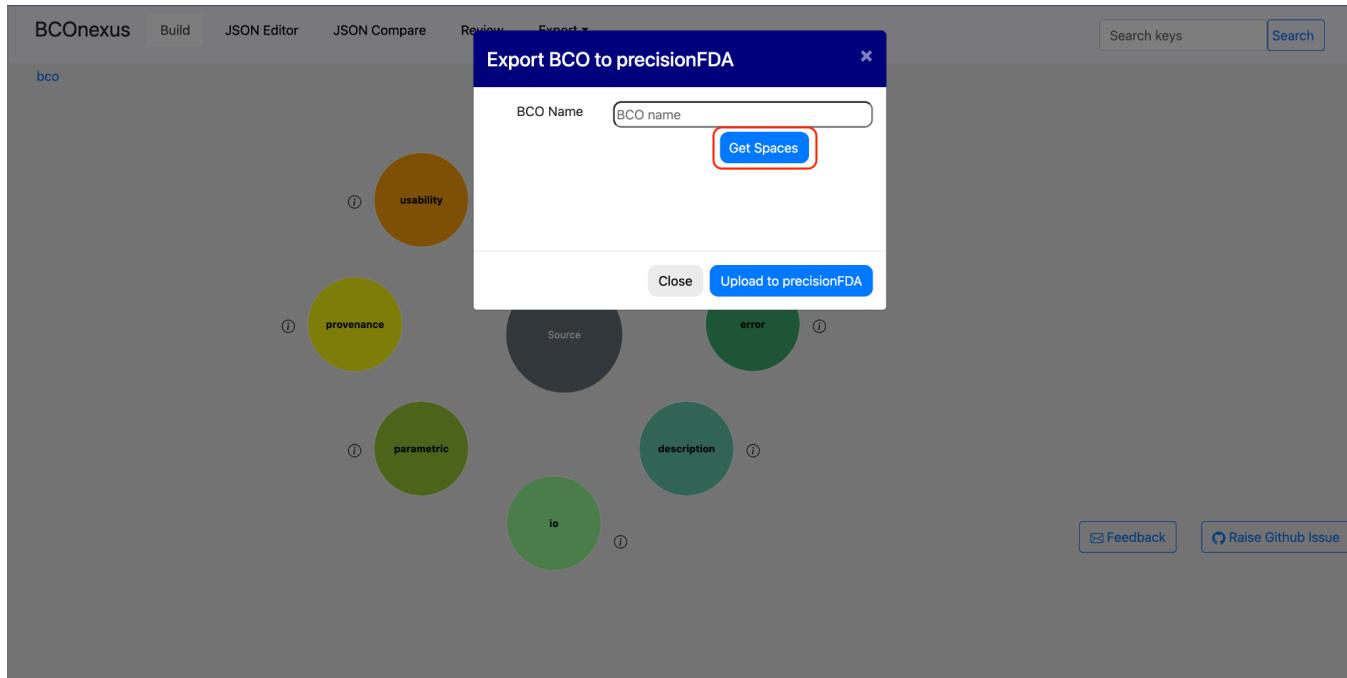
Provide the BCO DB URL, Prefix, Owner Group, and User token, and then click on “Submit” to upload the object to the BCO Repository.

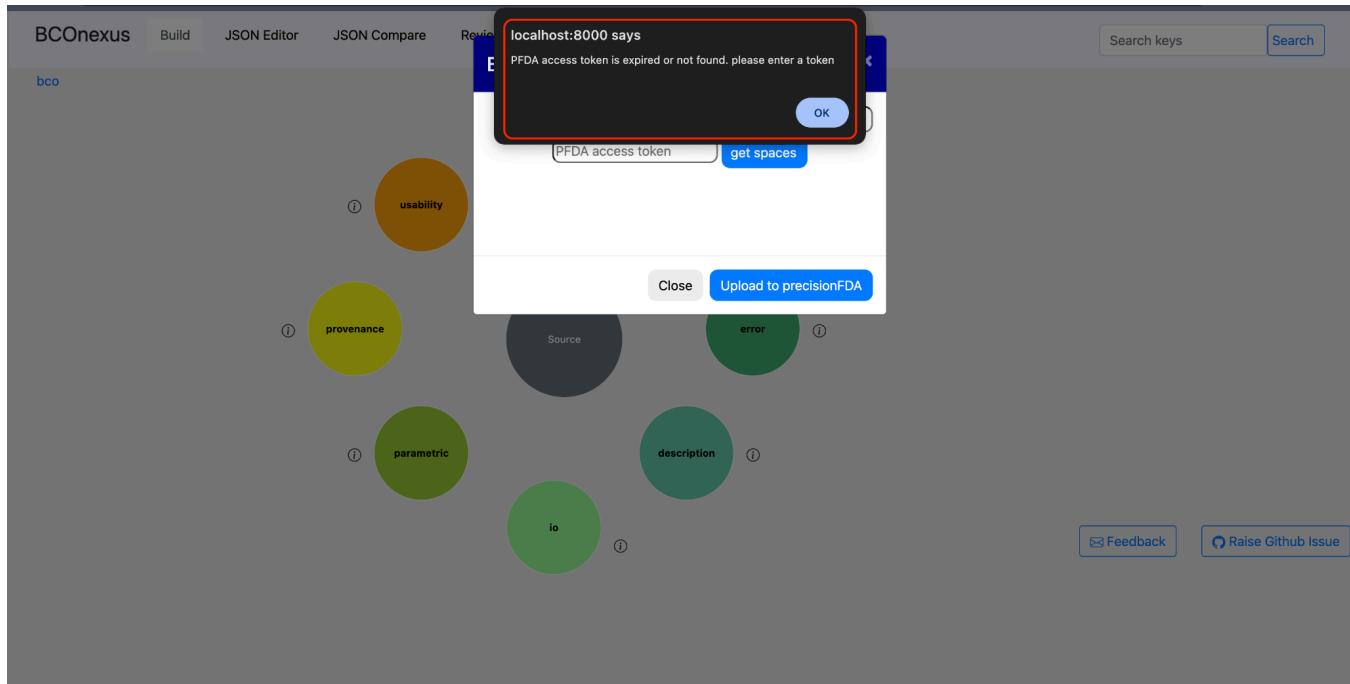


#### 4. How to export the BCO file to a precisionFDA platform:

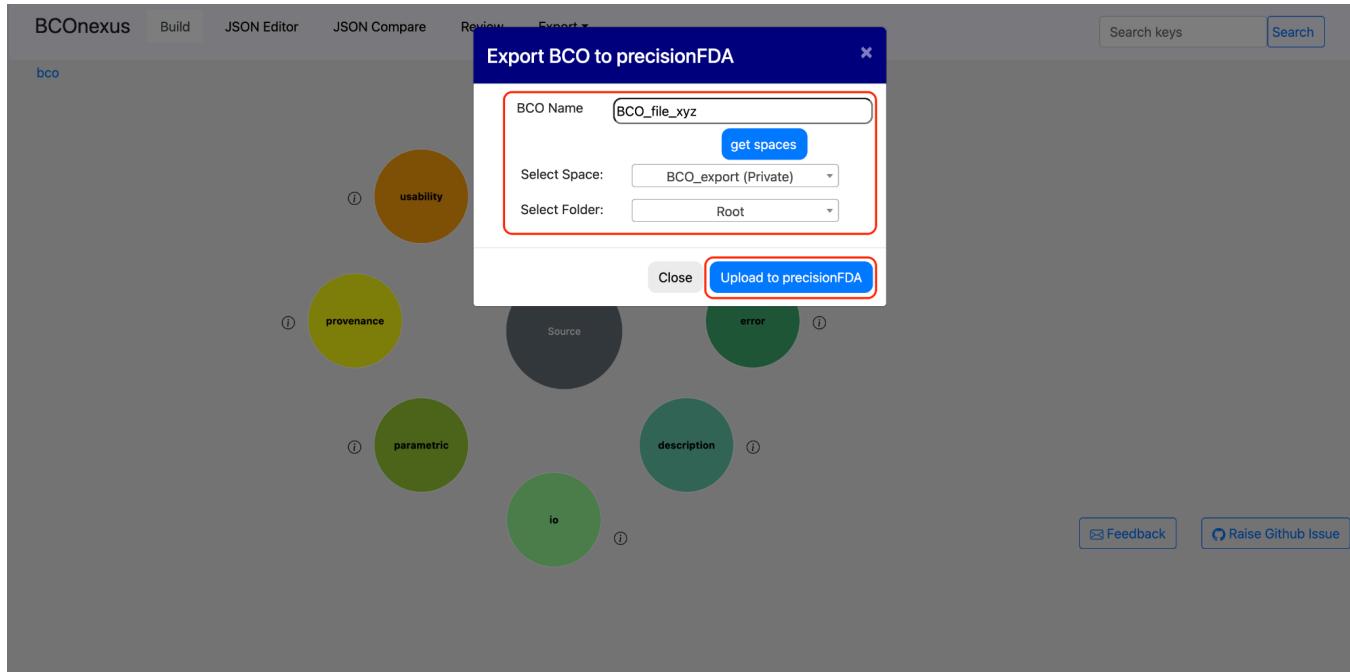
Click on the Export menu button and select the “precisionFDA” option to export the in-memory BCO file to a precisionFDA platform.

Provide a name for the file in the prompt and click on the “Get Spaces” button to fetch all the spaces. If there is no active token, you will be prompted with an alert to provide a token, obtainable on the precisionFDA Platform.





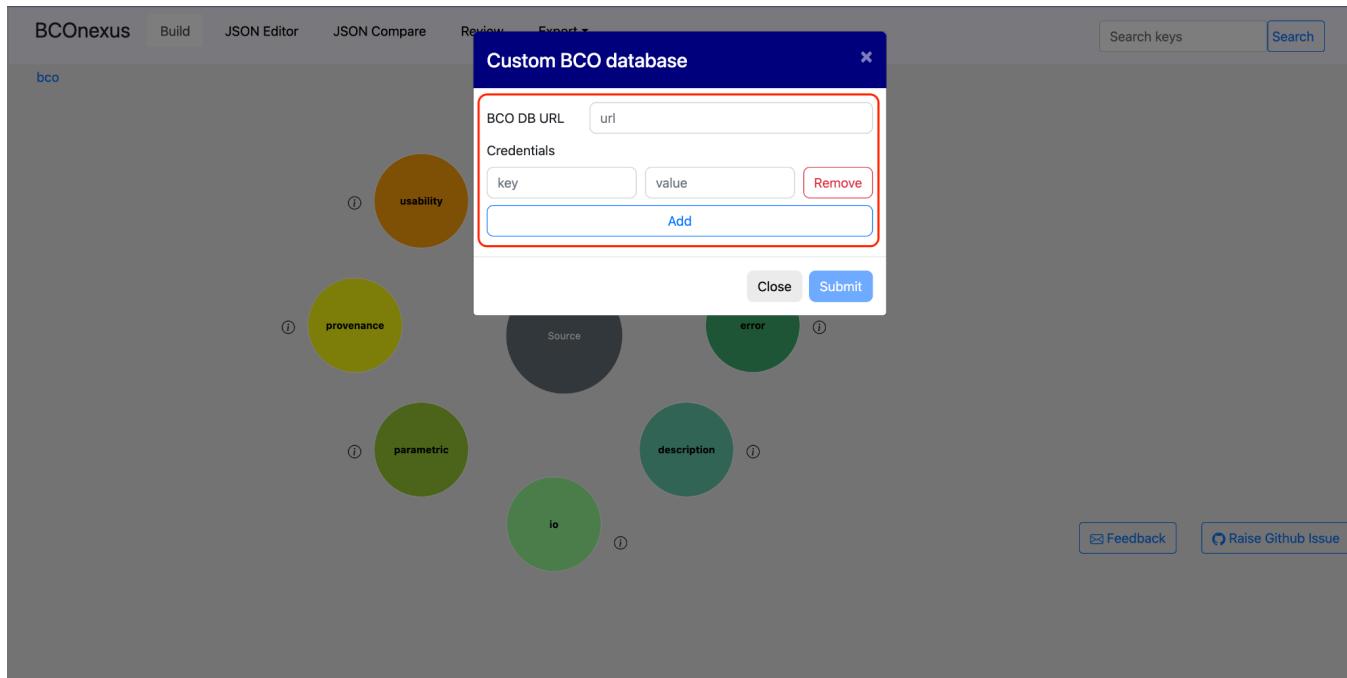
Provide a valid token to fetch the spaces and folders from the precisionFDA to upload the in-memory bco.json file. Select a project and a folder in the project from the available list of projects and click on the “Upload to precisionFDA” button to upload.



## 5. How to export the BCO file to the Custom BCO Database:

Click on the Export button in the top menu and select the “Custom BCO Database” option to export the in-memory BCO file to a Custom BCO Database.

Provide the BCO DB URL, add Credentials key and value, and then click on “Submit” to upload the object to the Custom BCO Database.



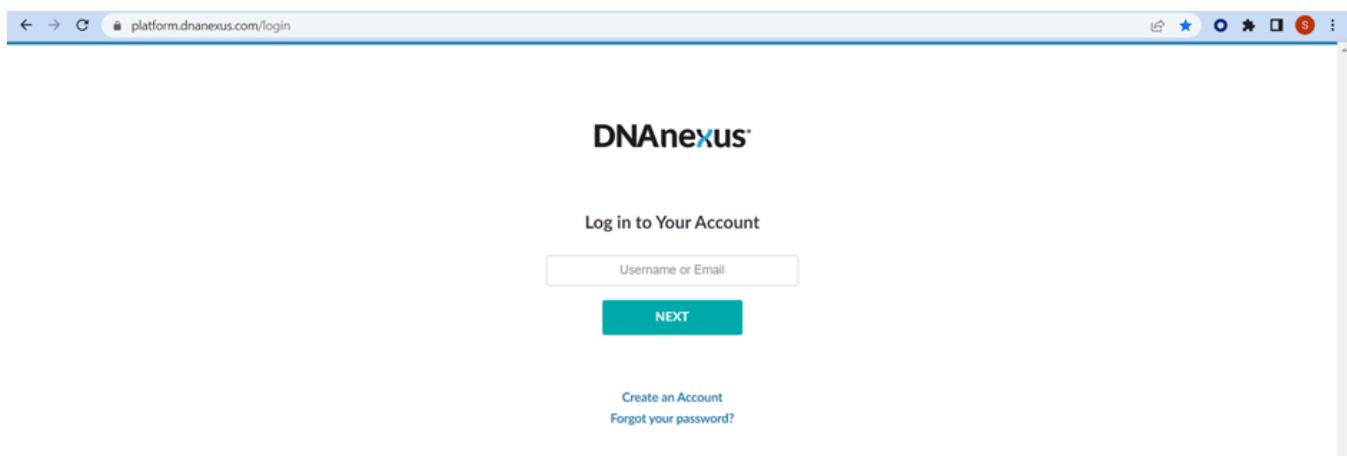
# How to get a DNAexus token

## Prerequisite:

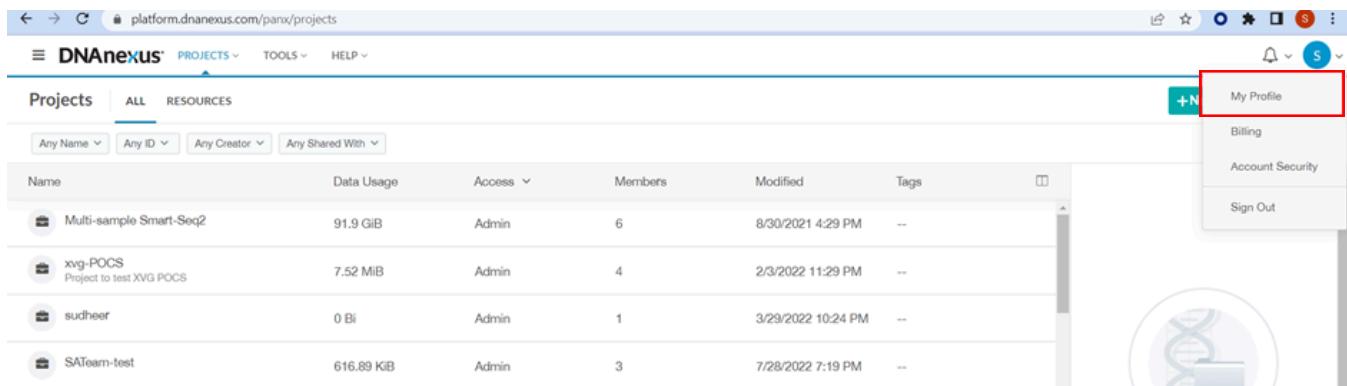
1. You will need to have a DNAexus Platform account on <https://platform.dnanexus.com/>.

## Steps to generate a DNAexus access token:

1. Log in to the DNAexus platform.



2. Click on the user icon on the right and select “My Profile” from the options.



3. Click on API TOKENS.

The screenshot shows the DNA Nexus platform interface. At the top, there's a navigation bar with links for 'PROJECTS', 'TOOLS', and 'HELP'. Below the navigation bar, the user profile 'Sudheer Naidu Sirasapalli' is displayed. A red box highlights the 'API TOKENS' tab, which is currently active. Under the 'API TOKENS' tab, there's a section titled 'ACCOUNT INFO' containing fields for 'EMAIL' (sudheer), 'PASSWORD', and 'PLATFORM PREFERENCES' (First Name: Sudheer). To the right, there's a 'Account Info' section with the same information.

4. Click on New Token, if you do not have an existing one.

The screenshot shows the 'tokens' page under the 'User Account' section. A red box highlights the green '+ New Token' button. The page includes tabs for 'User Account', 'Billing Account', and 'API Tokens'. Below the tabs, there are filters for 'Token Label', 'Expiration Date', and 'Project Permissions'.

5. Enter a token Label, select the Token Scope, set the Expiration Date, and then enter your DNA Nexus account Password. Click on “Generate Token”. Once generated, you should save the token.

The screenshot shows a modal dialog box titled 'NEW TOKEN'. It has a note that '\* Fields are required'. The 'LABEL' field contains 'Label for your token, e.g. "My Sequencer"'. The 'TOKEN SCOPE' section has a radio button selected for 'All projects'. The 'EXPIRATION DATE' section shows a date input field with 'dd-mm-yyyy' placeholder and a note that tokens will expire in one month if no date is given. A password input field below the date field contains the placeholder 'Please enter your password to generate a token'. A 'Generate Token' button is at the bottom right of the dialog.

## Questions

If you have any questions, please feel free to contact us at [support@dnanexus.com](mailto:support@dnanexus.com). Please make sure to communicate that you have questions about the BConexus Platform-Free Editor.