



## Creating a Dashboard Visualization of SARS-CoV-2 Metagenomic Samples in Terra using Theiagen's Freyja Dashboard Workflow

Document TG-FREY-03, Version 2

Date:

4/16/2024

Workflow Versions:

PHB v2

### 1. PURPOSE/SCOPE

To standardize the process of aggregating Freyja sample data to generate an interactive visualization using Theiagen's Freyja Dashboard workflow in Terra. Acceptable data types include Freyja demixed output files generated from the Freyja FASTQ workflow.

### 2. REQUIRED RESOURCES

- Computer
- Internet connection: at least 10 and 5Mbps for download and upload speeds, respectively
- Internet browser
  - Google Chrome, Firefox, or Edge
- Google account
- Terra account, linked to Google account
- Freyja demixed files uploaded to Terra workspace
- Theiagen's Freyja\_Dashboard\_PHB workflow in Terra

#### REQUIRED WORKFLOW INPUTS FILES

- Freyja demixed files (output from Freyja FASTQ)
- Dashboard name
- Collection dates
- Viral load
- *Optional: freyja\_dashboard\_config json file*

### 3. RELATED DOCUMENTS

Document Number	Document Name
TG-TER-03	Uploading Local or SRA NGS Data & Creating a Results Metadata Table in Terra
TG-FREY-01	Running SARS-CoV-2 Metagenomic Samples in Terra using Theiagen's Freyja FASTQ Workflow
TG-FREY-02	Plotting SARS-CoV-2 Metagenomic Sample Data in Terra using Theiagen's Freyja Plot Workflow



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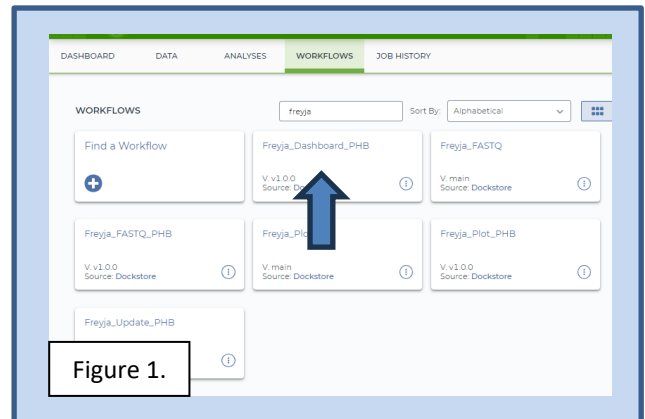
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### 4. PROCEDURE

#### 4.1 RUNNING THE FREYJA DASHBOARD WORKFLOW

1. Open Terra and navigate to the **workflows** tab within the workspace containing metagenomic SARS-CoV-2 data
2. Select the **Freyja\_Dashboard\_PHB** workflow (Fig 1)
3. Choose the latest version of **version 2** in the version dropdown field, or the version used during internal assay validation (Fig 2, a)



#### Freyja\_Dashboard\_PHB

Version: v2.0.0



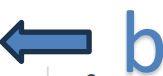
Source: [github.com/theiagen/public\\_health\\_bioinformatics/Freyja\\_Dashboard\\_PHB:v1.0.0](https://github.com/theiagen/public_health_bioinformatics/Freyja_Dashboard_PHB:v1.0.0)

Synopsis:

No documentation provided

Run workflow with inputs defined by file paths

Run workflow(s) with inputs defined by data table



⚡

⚡

**SELECT DATA**

**SELECT DATA**

Use call caching

Delete intermediate outputs

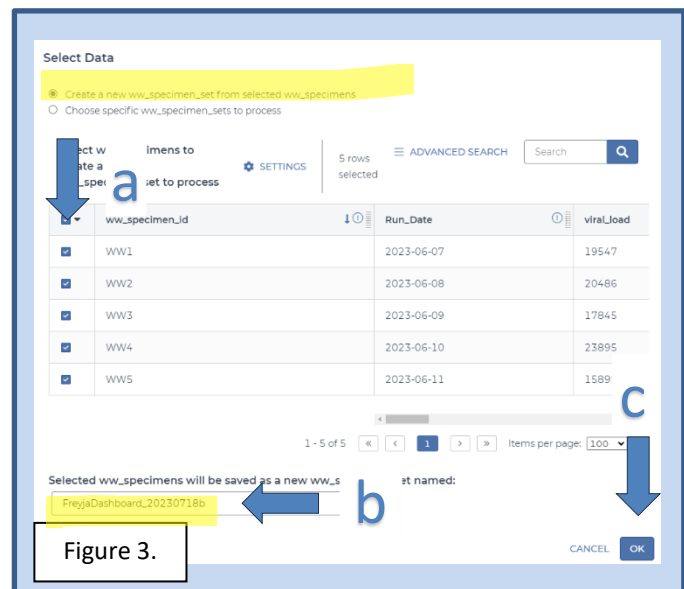
Use reference disks

Retry with more memory

Ignore errors

Figure 2.

4. Select the first bullet to **run workflow with inputs defined by file paths** (Fig 2, b)
5. Select the relevant SET data table name under the select **root entity type** dropdown (Fig 2, c)
6. Click **select data** (Fig 2, d)
7. In the pop-up window select the first bullet to **create a new ww\_specimen\_set from selected ww\_specimens** (Fig 3, highlighted text)
  - a. **Select the checkbox** for each sample to be included in the analysis (Fig 3, a)





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- b. *Optional*: name the output set name to differentiate it from other workflow runs, e.g. `FreyjaDashboard_YYYYMMDDn` (Fig 3, b); this populates a row to the SET data table
- c. Click `ok`

Variable	Type	Attribute
collection_date	Array[String]	this.wv_specimens.Run_Date
freyja_dashboard_title	String	"Default_Dashboard"
freyja_demixed	Array[File]	this.wv_specimens.freyja_demixed
samplename	Array[String]	this.wv_specimens.wv_specimen_id
viral_load	Array[String]	this.wv_specimens.viral_load
dashboard_intro_text	File	Optional
config	File	"gs://theiagen-public-files-rp/terra/freyja-files/freyja_dash_config.json"

Figure 4.

8. In the `inputs` tab, set the first five attributes to the following (Fig 5, yellow highlights):
  - a. `this.wv_specimens.Run_Date`
    - i. Notice an "s" is added to the end of the data table name: `ww_specimen` -> `ww_specimens`
    - ii. "Run\_Date" must match the sample data table column containing collection dates
  - b. `"Default_Dashboard"`; enter the dashboard name you want to display in quotes (Fig 8)
  - c. `this.wv_specimens.freyja_demixed`
  - d. `this.wv_specimens.wv_specimen_id`
  - e. `this.wv_specimens.viral_load`
    - i. "viral\_load" must match the corresponding sample data table column header
9. *Optional*: configure an additional input setting to create lineage groups if there are too many lineages to be visualized together (Fig 4, orange highlight)
  - a. In the config variable, add `"gs://theiagen-public-files-rp/terra/freyja-files/freyja_dash_config.json"` to group lineage according to Figure 5; otherwise, create a customized json file specifying how to define lineage groups
10. Specify outputs by clicking on the `outputs` tab and `use defaults` (Fig 6)
11. Click `save`, `run analysis`, `add comments` if desired, and click `launch`



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```
Lineages:  
grp_1:  
  name: "grp_1"  
  members:  
    - "BA.4*"  
    - "BA.5*"  
  color: "orange"  
grp_2:  
  name: "grp_2"  
  members:  
    - "B.1.617.2*"  
  color: "green"  
grp_3:  
  name: "grp_3"  
  members:  
    - "BA.2*"  
  color: "blue"
```

Figure 5.

Figure 6.

Figure 7.



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## 4.2 ANALYZING DASHBOARDS

1. Navigate to the **data** tab of the workspace containing metagenomic data and open the pertinent **SET data table**

2. Open the **file** located in the **freyja\_dashboard** column for the relevant data set (Fig 7, red oval)

a. *If the sample set name was specified (section 4.1, step 6b) the data set name will be indicated in the **ww\_specimen\_set\_id** column (Fig 7, highlight)*

3. *Different dashboard visualizations are available by clicking on different blue boxes above the graph (Fig 8)*

4. The variants visualization

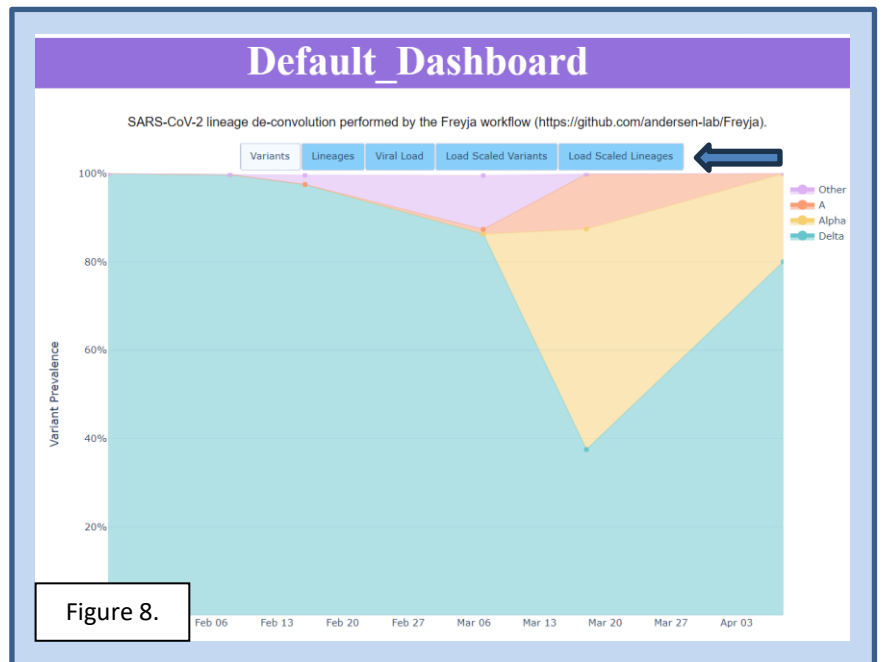
(Fig 8) displays the variant prevalence (y-axis) by collection date (x-axis)

5. In the **lineages** view (Fig 9), the lineage group prevalence by collection date is shown

a. *Lineage groups are displayed according to the group definitions provided by the config variable in section 4.1, step 8; modify groups by changing definitions in the json file and re-running the dashboard workflow*

6. Viral load by collection date may be viewed by selecting the **viral load** tab of the graph (Fig 10)

7. **Scaled variants** (Fig 11) and **scaled lineages** (Fig 12) tabs depict the variant or lineage abundance viral loads by collection date





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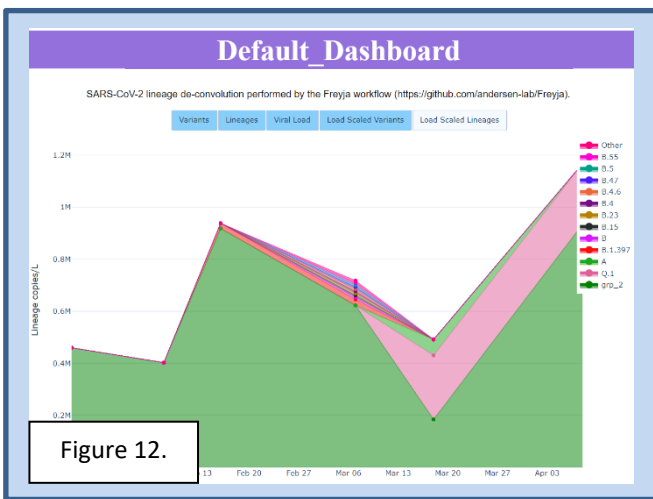
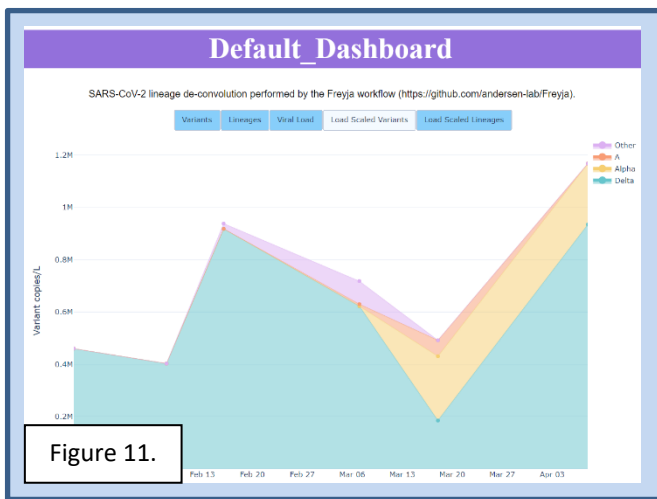
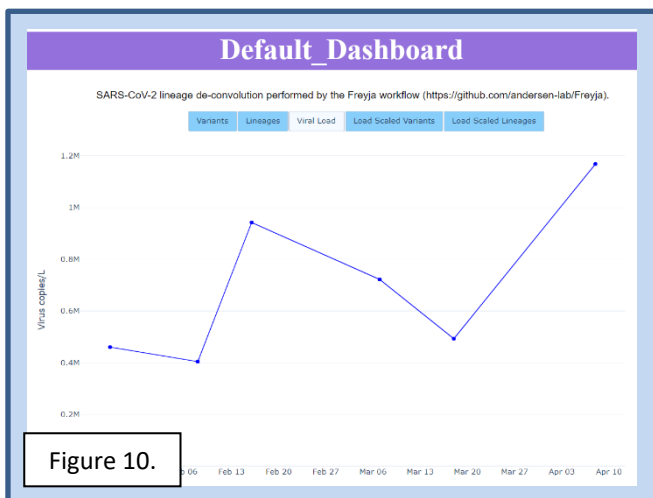
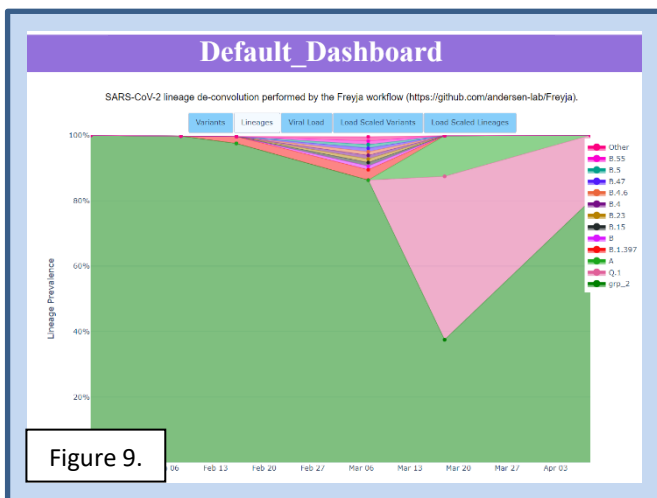
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### 5. QUALITY RECORDS

- freyja\_demixed files
- Dashboard visualizations



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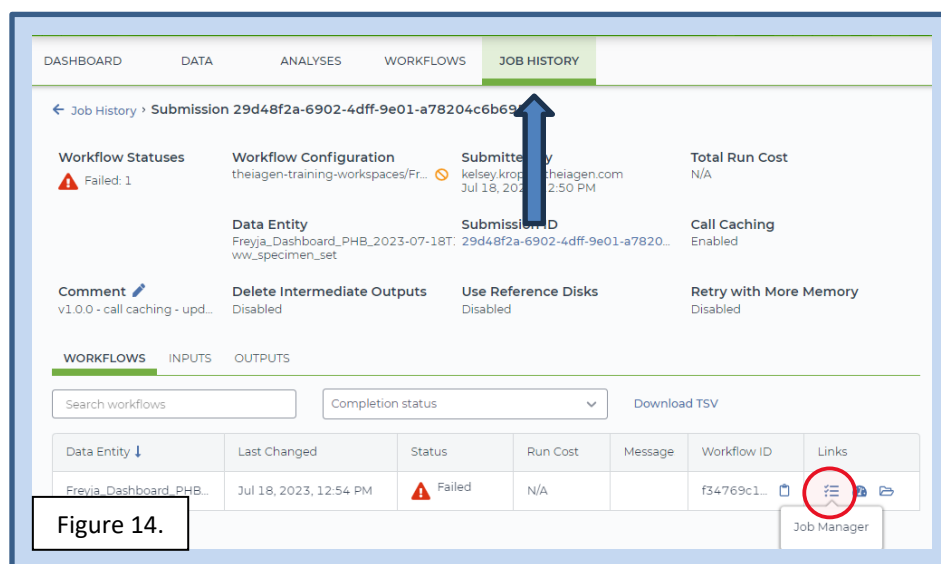
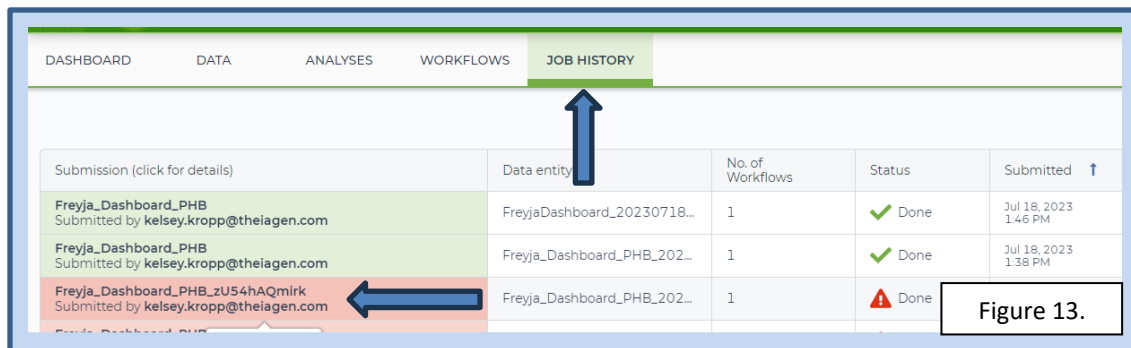
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### 6. TROUBLESHOOTING

1. Identify if failed run is due to "too many lineages to show" error
  - a. In **job history**, click on the **failed run** for freyja dashboard (Fig 13)
  - b. Open **job manager** in the links column within the table by clicking on the three lines (Fig 14)
  - c. Click **sign in** to authenticate sign in; open the **log files** indicated by the cloud on paper (Fig 15)
  - d. Within the code, use the search function (**Ctrl+F** or **Cmd+M**) for "**lineage;**" if the error code indicates "**too many lineages to show,**" **re-run the workflow** with a configuration file included in the workflow input settings to simplify the number of lineage groups to display in the visualization
    - i. See section 4.1 step 8 for details.
2. Consult with internal staff familiar with this procedure or contact [support@theiagen.com](mailto:support@theiagen.com) for other troubleshooting inquiries
3. For document edit requests, contact [support@theiagen.com](mailto:support@theiagen.com)





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frejya\_dashboard

ID: f34769c1-5161-4a49-a33c-88b2581bd3e3 workspace-id: 774455a0-292b-490f-9766-7b83bacbee59 submission-id: 29d48f2a-6902-4dff-9e01-a78204c6b695

Status: Failed

Tasks: 1 succeeded, 1 failed, 0 currently being processed

Submitted: Today, 12:50 PM  
Started: Today, 12:50 PM  
Ended: Today, 12:54 PM (0h 3m)

Errors (1 total)

Task Name	Shard	Failure Message
frejya_dashboard_task		Task frejya_dashboard.frejya_dashboard_taskNA1 failed. Job exit code 1. Check gs://fc-774455a0-292b-490f-9766-7b83bacbee59/submissions/29d48f2a-6902-4dff-9e01-a78204c6b695/frejya_dashboard/f34769c1-5161-4a49-a33c-88b2581bd3e3/call-frejya_dashboard_task/stderr for more information. PAPI error code 9. Please check the log file for more details: gs://fc-774455a0-292b-490f-9766-7b83bacbee59/submissions/29d48f2a-6902-4dff-9e01-a78204c6b695/frejya_dashboard/f34769c1-5161-4a49-a33c-88b2581bd3e3/call-frejya_dashboard_task/frejya_dashboard_task.log

Figure 15.

```
return _process_result(sub_ctx.command.invol...
File "/opt/conda/envs/freyja-env/lib/python...
return ctx.invoke(self.callback, **ctx.par...
File "/opt/conda/envs/freyja-env/lib/python...
return __callback(*args, **kwargs)
File "/opt/conda/envs/freyja-env/lib/python3.10/site-packages/freyja/cli.py", line 387, in dash
make_dashboard(agg_df, meta_df, thresh, titleText, introText,
File "/opt/conda/envs/freyja-env/lib/python3.10/site-packages/freyja/utils.py", line 434, in make_dashboard
color_lin = get_color_scheme(df_ab_lin,
File "/opt/conda/envs/freyja-env/lib/python3.10/site-packages/freyja/utils.py", line 72, in get_color_scheme
raise Exception('Too many lineages to show. Use --config to group.')
Exception: Too many lineages to show. Use --config to group.
2023/07/18 18:53:10 Starting delocalization.
2023/07/18 18:53:11 Delocalization script execution started...
```

Figure 16.

## 7. LIMITATIONS

1. When creating visualizations from aggregated sample data over time, ensure all samples have been run with Freyja FASTQ using the same curated\_lineages and usher\_barcodes files
2. Freyja can only be used to analyze SC2 data from Illumina PE sequencing files





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**8. REFERENCES**

None

**9. REVISION HISTORY**

Revision	Version	Release Date
Document creation	1	8/2023
Minor document revisions for PHB v2.0.0 release; added appendix	2	4/2024



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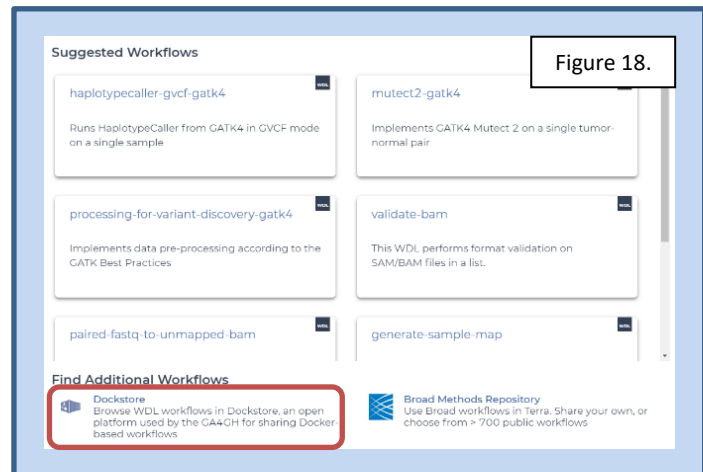
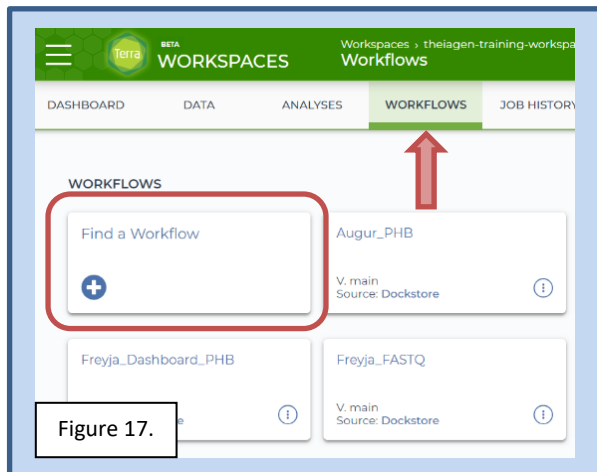
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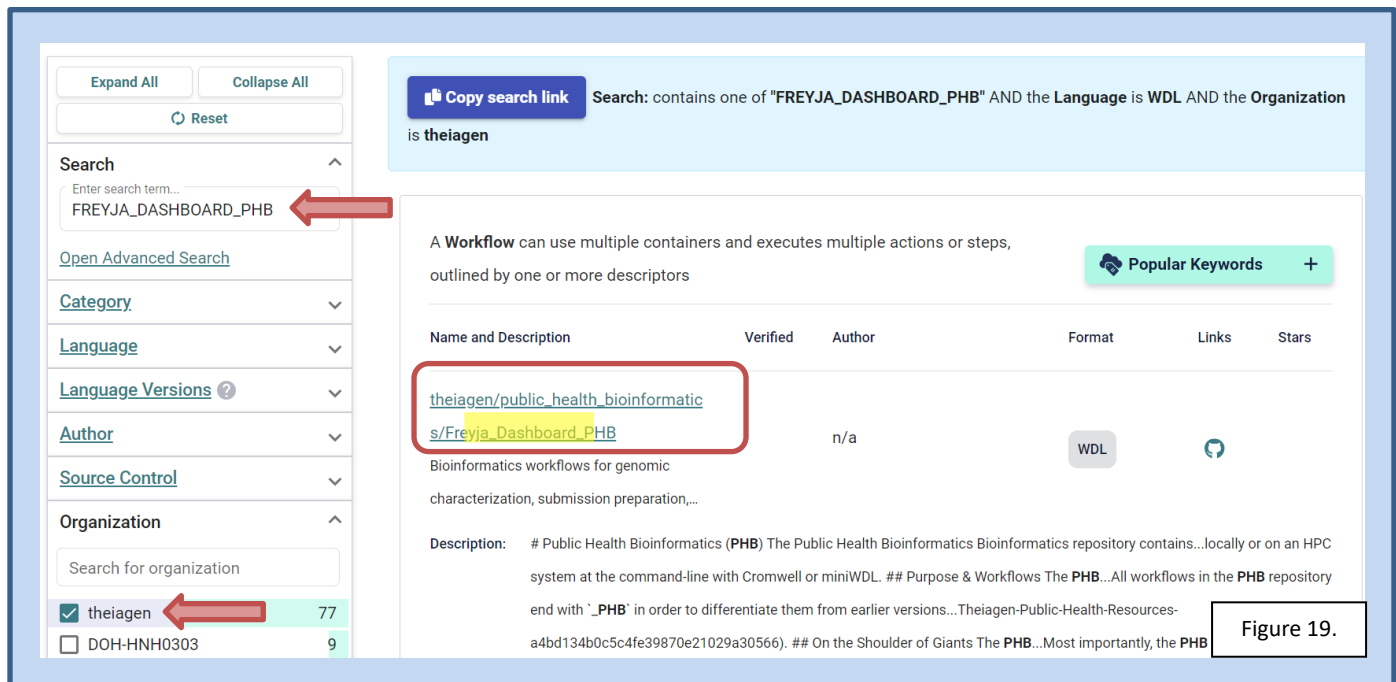
### 10. APPENDICES

#### 10.1 IMPORTING FREYJA WORKFLOWS FROM DOCKSTORE

1. In the **Terra workspace** of interest, open the **workflows** tab and click **find a workflow** (Fig 17)
2. In the pop-up window, click **dockstore** (Fig 18)



3. Type **"Freyja\_Dashboard\_PHB"** in the search bar (Fig 19)
4. In the left hand sidebar, scroll down to Organization and select **"theiagen"** (Fig 19)
5. Find the workflow by looking at the file path suffix; click the name to **open the workflow** (Fig 19)





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6. Click **Terra** to launch the workflow in Terra (Fig 20)
7. Choose the **destination workspace** in the dropdown and click **import** or create a new workspace (Fig 21)

The screenshot shows the Dockstore interface for the workflow 'Freyja\_Dashboard\_PHB'. The page includes a navigation bar with 'Login' and 'Register' buttons. The main content area displays the workflow's source code repository, last update times, and a 'Launch with' section. The 'Terra' option is highlighted with a red box, indicating it is the selected platform for launching the workflow.

Figure 20

The screenshot shows the Terra 'IMPORT WORKFLOW' page. The 'Importing from Dockstore' section displays the workflow's source code repository and a warning message. The 'Destination Workspace' dropdown is set to 'Training\_demo', and the 'IMPORT' button is highlighted with a red box, indicating it is the selected action for importing the workflow.

Figure 21