

Document TG-GISAID-01, Version 2

Date: 4/3/2024

PHB v2

Workflow Versions:

#### 1. PURPOSE/SCOPE

To automate the process of uploading SARS-CoV-2 assembly data to GISAID from within the Terra platform using Theiagen's Terra\_2\_GISAID\_PHB workflow. Acceptable data types include FASTA files prepared using the Mercury Prep and Batch 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
- FASTA files in Terra workspace
- Terra\_2\_GISAID\_PHB workflow in Terra, see TG-TER-03 appendix 9.2

# PRIOR STEPS ARE REQUIRED!

- Request client ID from GISAID at clisupport@gisaid.org
- Contact Theiagen to link GISAID user credentials to the Terra workflow at <u>support@theiagen.com</u>
- FASTA output files in Terra workspace
- Mercury Prep N Batch workflow run on FASTA files to be uploaded

## 3. RELATED DOCUMENTS

Document Number	Document Name
TG-TER-03	Uploading Local or SRA NGS Data & Creating a
10-128-03	Results Metadata Table in Terra

#### 4. PROCEDURE

## 4.1RUNNING THE TERRA\_2\_GISAID WORKFLOW

- In Terra, navigate to the workflows tab within the workspace containing SC2 data
- Select the <u>Terra\_2\_GISAID\_PHB</u> workflow (Fig 1)
- Run the latest version of v2 of the workflow
   (Fig 2, a) or the version used for internal validation
- Select the second bullet to *run workflow(s) with inputs defined by data table* (Fig 2, b)

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5. Select the relevant set-level data table under the select root entity type dropdown (Fig 2, c)

Terra_2_GISAID_PHB
Version: v2.0.0 v Contraction 2
Source: github.com/theiagen/public_health_bioinformatics/Terra_2_GISAID_PHB:smw-gisaid-dev
Synopsis:
No documentation provided
O Run workflow with inputs defined by file paths
Run workflow(s) with inputs defined by data table
C_t_t
Figure 2. Ching Content Conten

- 6. Click *select data* (Fig 2, d)
- 7. In the pop-up window, select the *second bullet* to process an existing set of samples (Fig 3)
  - a. NOTE: the Mercury Prep and Batch workflow must be run prior to submitting to GISAID

b.	Select the			٦
	checkbox to	5	elect Data	
	select the		Create a new theiacov_illumina_se_set from selected theiacov_illumina_ses     Choose specific theiacov_illumina_se_sets to process	
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	GISAID (Fig 3)		TheiaCoV_Illumina_SE_2023-06         3000301353, 30003         (5 entities)	
c.	Scroll to the		-	
	bottom and			
	click <i>ok</i>			
In t	the <i>inputs tab</i> ,			
set	the first three			
att	ributes in the		1-lof1 ≪ < 1 → » Items per page: 100 v	
tab	ole to the		Figure 3.	
fol	lowing,			

respectively (Fig 4):

8.

- a. The *client id* will have to be requested from <u>clisupport@gisaid.org</u>
- b. this.gisaid\_fasta
- c. this.gisaid\_metadata

•	ce Data to GISAID using 2 GISAID Workflow
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9. For initial submissions, *contact support@theiagen.com* to set up user credentials for GISAID

de optional inputs	Download jsor	n   Drag or click to upload	json   Clear inputs SEARCH INPUTS
Task name 🖡	Variable	Туре	Attribute
Terra_2_GISAID	client_id	String	" "
Terra_2_GISAID	concatenated_fastas	File	this.gisaid_fasta
Terra_2_GISAID	concatenated_metadata	File	this.gisaid_metadata
gisaid_upload	authentication_file	File	Optional
gisaid_upload	disk_size	Int	Optional {}
gisaid_upload	frameshift_notification	String	Optional {}
gisaid_upload	gisaid_credentials	File	"gs://gisaid- credentials/gisaid_credent lals_eas.txt"
Figure 4.	timezone	String	Optional {}

## 10. Set up GISAID credentials in Terra

- a. In a new notepad file, type the user's *gisaidusername*, hit *tab*, and type the user *password*; save as a *normal text file (\*.txt)* titled *gisaid\_credentials\_[userinitials]* (Fig 5)
- i. Using the numbers in the left sidebar, ensure the file only contains one line; remove extra lines (Fig 5, red circle)
- b. To upload this file to Terra without security permissions, see appendix 10.1
  i.*Paste* the file link into the gisaid\_credentials attribute field
- c. To secure credential files for viewing only permissible by the credentialed user, see appendix 10.2
- Specify outputs by clicking on the *outputs* tab and *use defaults* (Fig 6)
- 12. Click *save*
- Launch the workflow by clicking run analysis; enter desired comments and click launch

File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ? 🕞 🚔 🖶 🖻 🕞 🎧 🚔 🐇 🐚 🌇 🍃 ⊄ 📾 🏂 🔍 🔍 🏹 🖾 ன 🖓 🖾
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Figure 5. Ers Append extension Save Cancel

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#### 4.2VERIFY SUBMISSIONS WERE SUCCESSFUL

- 1. Navigate to the job history tab within the Terra workspace; successful and failed job submissions will be highlighted green and red, respectively, while jobs in progress are represented in blue
- 2. Sample submission can also be checked by logging into the user's GISAID account and viewing the submission history

#### 5. QUALITY RECORDS

- Sample FASTA files
- Sample metadata files

#### 6. TROUBLESHOOTING

- Consult with internal staff familiar with this procedure or contact <u>support@theiagen.com</u> for troubleshooting inquiries
- For document edit requests, contact <u>support@theiagen.com</u>

#### 7. LIMITATIONS

- Users must have a valid GISAID client ID with credentials linked in Terra workspace
- Terra\_2\_GISAID workflow requires pre-processing of samples using Mercury\_Prep\_N\_Batch workflow



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# 8. **REFERENCES**

None

# 9. **REVISION HISTORY**

Revision	Version	Release Date
Document creation	1	10/2023
Updated some figures; clarification as SET-level workflow; updated appendix 10.3	2	4/2024



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#### **10. APPENDICES**

#### 10.1 UPLOADING LOCAL FILES TO TERRA

- 1. Navigate to the *Terra workspace* where analyses are run
- 2. Open the *Files* tab in the bottom left of the workspace (Fig 7)
  - a. Click upload
  - b. Once the upload is complete, *right click* on the file name and click *copy link*
- 3. Proceed with section 4.1.10.b.i

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No references have been added. Add reference data	nextclade_dataset_tag	2022-07-26112:00:002	Updated on 2022-08-12
OTHER DATA ~	nextclade docker image	nextstrain/nextclade:2.4.0	Updated on 2022-08-12
Workspace Data	pangolin_docker_image	staphb/pangolin:4.1.2-pdata-1.1.3	Updated of 2022-08-12
	vadr docker image	staphb/vadr:1.4.2	22-07-1 ADD VARIABLE +



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#### 10.2 SECURELY UPLOAD CREDENTIAL FILES TO GOOGLE CLOUD BUCKET

- 1. Sign in to Google and navigate to the desired *Google cloud storage bucket* (www.console.cloud.google.com)
- 2. Click upload files (Fig 8), select the relevant file, and click open (Fig 9)
- 3. *Open the file* in the cloud by clicking on the file name (Fig 8) and click *edit access* (Fig 10)

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- 4. Edit access permissions, as desired (Fig 11)
  - a. For credentialed user access only:

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File name: gisaid\_credentials\_eas.txt

SD TheiaProl

Figure 9.

i.If permissions are set for owners, editors, and viewers (Entities 1-3) as in Figure 11, delete them

Authenticated URL

gsutil URI

ii. Click add entry and create similarly to Entity 4 in Figure 11

Date created: 8/18/2023 4:05 PM

Cancel

- 1. Name 4 will be the credentialed user's email
- iii.Click add entry to add the Terra account



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- 1. Set the new entity to *user*
- In Terra, select the hamburger icon and click profile under the user name (Fig 12)
- 3. Copy the proxy group string (Fig 13)
- Paste the proxy group string to the new name # within the Google file permissions window
   Sot the new optity
- 5. Set the new entity access to *owner*

	Storage class	Public access	Protection
States)	Standard	Not public	None
ATION Is <b>[</b> ] D FOLDER	PERMISSION	S PR	Edit access         Object name: gisaid_credentials_eas.txt         If you don't rely on individual object-level access, you can start managing all access         uniformly at the bucket-level. Go to the bucket's Permissions tab to get started. Learn         more [2         Entity 1 *         Project         Name 2         editors-8350702540         Access 2 *         Owner         entity 3 *         Name 3
Fig	gure 11.		Project     viewers-8350702540     Reader       Initity 4 *     Vame 4     Access 4 *       User     emily.smith@thelager     Owner       + ADD ENTRY     CANCEL     SAVE

- b. Click save
- 5. Copy the gsutil URI by clicking the *copy to clipboard* button (Fig 10, blue arrow)
- 6. Proceed with section 4.1.10.b.i



OFILE	
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Date:	Workflow Versions:
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# 10.3 IMPORTING THE TERRA\_2\_GISAID WORKFLOW FROM DOCKSTORE

ASHBOARD DATA ANA	ALYSES WORKFLOWS JOB HISTORY	haplotypecaller-gvcf-gatk4	mutect2-gatk4
		Runs HaplotypeCaller from GATK4 in GVCF mode on a single sample	Implements GATK4 Mutect 2 on a single tumor- normal pair
WORKFLOWS		processing-for-variant-discovery-gatk4	validate-bam
Find a Workflow	Augur_PHB	implements data pre-processing according to the GATK Best Practices	This WDL performs format validation on SAM/BAM files in a list.
0	V. main Source: Dockstore		
Freyja_Dashboard_PHB	Freyja_FASTQ	paired-fastq-to-unmapped-bam	generate-sample-map
		Find Additional Workflows	

- 1. In the *Terra workspace* of interest, open the *workflows* tab and click *find a workflow* (Fig 14)
- 2. In the pop-up window, click *dockstore* (Fig 15)
- 3. To find the Theiagen Terra\_2\_GISAID workflow, type *Terra\_2\_GISAID* in the search bar (Fig 16)

Dockstore Q Search	👬 Organizations 🗼 About	📄 Docs 📃 Forum		Login Register
Q Explore Workflows				
	🎲 Work	flows 🚭 Tools		
Expand All Collapse All	L <sup>®</sup> Copy search link Searc	h: contains one of <b>"Terra_2_GISAID"</b> AND the	Language is WDL	
Search Enter search term Terra_2_GISAID	A Workflow can use multiple outlined by one or more des	e containers and executes multiple actions or criptors		pular Keywords +
Language ^	Name and Description	Verified Author	Format	Links Stars 🌡
WDL 1 Language Versions	theiagen/public_health_bioin s <mark>/Terra_2_GISAID_PHB</mark> Bioinformatics workflows for ger characterization, submission pre-	n/a	WDL	0

- 4. In the left hand sidebar, scroll down to Organization and select "theiagen" (Fig 17)
- 5. Find the workflow by looking at the file path suffix; click the name to open the workflow (Fig 16)
- 6. Click *Terra* to launch the workflow in Terra (Fig 18)
- 7. Choose the *destination workspace* in the dropdown and click import or create a new workspace (Fig 19)



Document TG-GISAID-01, Version 2

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PHB v2

Organization	^
Search for organization	
1≩ ↓;	
✓ theiagen	125
broadinstitute	758
human-pangenomics	100
talkowski-lab	100
🗌 shengqh	79
fabio-cunjal	36
Figure 17	<b>≫</b> 213 more

Q Expl	lore Workflows / gith	ub.com/theiagen/public_hea	lth_bioinformatics/Terra_2_	GISAID_PHB			
ast upda	ithub.com/thei te to this workflow ve te to source reposito	ersion: 27 days ago	n_bioinformatics/T	erra_2_GISAID_P	HB:smw-reorganize	e-dev	☆
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TRS:		m/theiagen/public_health_		ISAID_PHB	idensicles: of	*eLwazi	

TETTA IMPORT WORKFLOW		
Importing from Dockstore	Workflow Name	
github.com/theiagen/public_health_bioinformatics/Terra_2_GISAI D_PHB v.smw-reorganize-dev	Terra_2_GISAID_PHB	
Please note: Dockstore cannot guarantee that the WDL and Docker image referenced by this Workflow will not change. We advise you to review the WDL before future runs.	Destination Workspace	
<pre>1 version 1.0 2  port "//tasks/task_versioning.wdl" as versioning port "//tasks/utilities/submission/task gisaid cli.wdl" as gisai</pre>	IMPORT Or create a new workspace	