Analyzing Phylogenetic R using Theiagen's Au	elationships in Terra ugur Workflows
Document TG-AUGUR-01, Version 1	
Date:	Workflow Version:
10/7/2023	
	Analyzing Phylogenetic R using Theiagen's Au Document TG-AUGU Date: 10/7/2023

1. PURPOSE/SCOPE

To standardize the process of preparing viral next generation sequencing (NGS) sample assemblies and metadata using Theiagen's Augur_Prep_PHB workflow for analysis via Theiagen's Augur_PHB workflow in Terra to generate a phylogenetic tree and SNP matrix. Acceptable data types include assembly FASTA files and metadata imported via TSV file format. NOTE: For flu-specific augur procedures, refer to the influenza SOP, TG-FLU-PE, on the Theiagen Public Health Resources website (Theiagen Public Health Resources Notion site).

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
- Sample assembly files uploaded to Terra workspace
- Theiagen's Augur_Prep_PHB, and Augur_PHB workflows in Terra workspace

1. REQUIRED AUGUR PREP INPUTS (5):

- Sample assembly (FASTA) files
- Associated sample metadata fields
 (4) from (TSV) file* or Terra table

2. REQUIRED AUGUR INPUTS (both output from Augur Prep):

- Array file of FASTA files
- Array file of sample metadata

3. RELATED DOCUMENTS

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

NOTE: Text in *gray* indicated throughout this SOP may be customized, while *black* indicates required text. Remember, data table column names can serve as workflow inputs, but must align to do so. E.g. a table containing sample assemblies in a column titled *assemblies* would use *this.assemblies* as the Augur Prep assembly file input attribute (value). *this.* and *workspace*. prefixes are used in workflow input fields to link to data table columns and workspace files/data, respectively.



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4. PROCEDURE

4.1 CREATE A TSV FILE FOR ASSOCIATED SAMPLE METADATA*

*Existing samples in Terra with the required inputs (5) listed below do not need a new TSV file created; proceed with section 4.2

1. In Excel or Google Sheets, create a list containing the following sample information:

Create a copy of THIS template and customize! Don't forget to download in .tsv format.

- a. In cell A1, specify the data table name, e.g. entity:augur_id (Fig 1)
 - List all sample IDs in column 1; do not include spaces in sample names i.
- b. Specify the following required sample metadata fields (5) as columns and fill in the relevant information for each sample:

	A	В	С	D	E	F	
1	entity:augur_id	collection_date	continent	country	state	pango_lineage	assembly_fasta
2	Sample_01	2021-04-12	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resources
3	Sample_02	2021-04-15	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resources
4	Sample_03	2021-04-14	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
5	Sample_04	2021-04-14	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
6	Sample_05	2021-04-14	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
7	Sample_06	2021-04-16	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
8	Sample_07	2021-04-15	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
9	Sample_08	2021-04-15	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
0	Sample 09	2021-04-16	North America	USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
Figur	e 1. Evample M	atadata (TS)		USA	Nevada	B.1.1.7	gs://theiagen-public-files/terra/training_resource
rigui	e 1. Example iv	letauata (15	v) riie.	USA	Washington	B.1.1.7	gs://theiagen-public-files/terra/training resource

- assembly fasta add the cloud file path for each sample assembly file (begin with "gs://") i. 1. If this output exists in the Terra data table from a prior workflow, this can be skipped ii.
 - collection date must use the format YYYY-MM-DD
- continent iii.
- iv. country
- state ٧.
- c. <u>Optional</u>: additional columns may be used to add metadata like run id, lineage, demographic data, etc
- d. Do not include spaces in the column headers
- 2. Save as a txt or tsv file
- Upload to Terra workspace; see TG-TER-03 for details 3.
- Workspaces > theiagen-training-v Workflows WORKSPACES DASHBOARD DATA ANALYSES WORKFLOWS JOB HISTORY WORKFLOWS SEARCH WORKFLOWS Find a Workflow Augur_PHB Augur_Prep_PHB V. main Source: Dockstore V. main Source: Dockstore (() Figure 2.



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4.2 RUNNING THE AUGUR PREP WORKFLOW

- 1. Ensure sample data passes quality control (QC) metrics per internal protocols before proceeding with Augur Prep
 - a. For samples that do not meet QC thresholds, resequence or proceed with Augur Prep at the discretion of the laboratory
- 2. Navigate to the *workflows* tab and open the *Augur_Prep_PHB* workflow (Fig 2)
- 3. Uncheck use call caching (Fig 3, highlight)
- 4. Choose the latest version of <u>v1</u> in the <u>version dropdown field</u> (Fig 3, a) or the workflow version that was used during internal assay validation
- 5. Select the second bullet to run workflow(s) with inputs defined by data table (Fig 3, b)
- 6. Select the relevant data table name under the select root entity type dropdown (Fig 3, c)
- 7. Click *select data* (Fig 3, d)

← Back to list	Figure 3.
Augur_Prep_PHB	
Version: v1.1.0 ~	
Source: github.com/theiagen/public_health_bioinformatics/Augur_Prep_PHB:v1.1.0	
Synopsis:	
No documentation provided	
O Run workflow with inputs defined by file paths	
Run workflow(s) with inputs defined by data table	
Step 2	
27 elected Augurs (reate a new Augur_set named	
SELECT DATA "A port ropt re 2026 -09-07T19-40-36")	
Use call caching 0 Delete intermediate outputs 0 Use reference disks 0 Retry with more memory 0 Ignore em	pty outputs 🟮

- 8. In the pop-up window select the checkbox for each sample to be included in the analysis (Fig 4)
 - a. Do not include any samples that are missing assemblies
 - b. Click the down arrow in the top left of the sample table and select all to process all samples
 - c. Additionally, the search bar may be used to narrow down the sample list to only those matching search criteria (e.g. only "SRR" sample names or just "B.1.1.7" samples, etc)
 - d. <u>Optional</u>: the output of this workflow will populate a row in the <u>SET</u> data table for the Terra table selected in Figure 3c. This SET row (job) must be selected when running the Augur workflow; as such, it may be helpful to name the output file so the user knows which prep output to select, e.g. AugurPrepPHB_YYYYMMDD[initials] or similar (Fig 4, c)
 - e. Scroll to the bottom and click ok

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-	Augur_id 1	assembly_fasta	collection_date	iso_continent ①	iso_country
~	Sample_01	Sample_01.medaka.consensus.f	4/12/2021	North America	USA
~	Sample_02	Sample_02.medaka.consensus.f	4/15/2021	North America	USA
~	Sample_03	Sample_03.medaka.consensus.f	4/14/2021	North America	USA
	<u>/</u>	Sign 04.medaka.consensus.f	4/14/2021	North America	USA
~	Sample_05	Sample_05.medaka.consensus.f	4/14/2021	North America	USA
~	Sample_06	Sample_06.medaka.consensus.f	4/16/2021	North America	USA
~	Sample_07	Sample 07.medaka.consensus.f.	4/15/2021	North America	USA

- 2. Set the first five input attributes in the table to the following, respectively (Fig 5)
 - a. this.assembly_fasta
 - b. this.collection_date
 - c. this.continent
 - d. this.country
 - e. this.state
- 9. <u>Optional</u>: if sample metadata for other inputs already exist in the Terra data table, they may be specified using the optional input attribute fields (Fig 5, e.g. pango_lineage, nextclade_clade, etc)
- 10. SARS-CoV-2 (SC2) is the organism set by default; if samples other than SC2 are being analyzed, enter the organism name in the organism attribute field in quotation marks (Fig 5)
 - a. Optional inputs are "flu", "MPXV", and "WNV"
 - i. Note that for MPXV and WNV, additional inputs will be required for the Augur workflow
- 11. Specify outputs by clicking on the *outputs* tab and *use defaults*; click *save* (Fig 6)
- 12. Launch the workflow by clicking run analysis; enter desired comments and click launch



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Task name ↓	Variable	Туре	Attribute
augur_prep	assembly	File	this.assembly_fasta
augur_prep	collection_date	String	this.collection_date []
augur_prep	continent	String	this.continent []
augur_prep	country	String	this.country {}
augur_prep	state	String	this.state {}
augur_prep	county	String	Optional {}
augur_prep	nextclade_clade	String	Optional {}
augur_prep	pango_lineage	String	this.pango_lineage {}
prep_augur_metadata	disk_size	Int	Optional {}
prep_augur_metadata	organism	String	Optional []
Figure 5.	timezone	String	Optional {]

SCRIPT •• INPUTS ••	OUTPUTS •• RUN ANALYSIS					
Output files will be saved to						
Files / submission unique ID / augur_prep / workflow unique ID						
References to outputs will be written to I Tables / Augur Fill in the attributes below to add or update columns in your data table						
Download json Drag or click to upload json Clear outputs SEARCH OUTPUTS						
Task name J Variable Type Attribute Use defaults						
augur_prep	augur_metadata	File	this.augur_metadata {}			
augur_prep_analysis_date String this.augur_prep_phb_analysis_date						
Figure 6.	augur_prep_phb_version	String	this.augur_prep_phb_ver sion {}			



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4.3 RUNNING THE AUGUR [ANALYSIS] WORKFLOW

- 1. Open the Augur_PHB workflow in the same workspace where Augur_Prep_PHB was run
- 2. Choose latest version of v1 in the version dropdown field, or the version used for assay validation
- 3. Select the second bullet to *run workflow(s) with inputs defined by data table* (Fig 3, b)
- 4. Select the relevant SET data table under the select root entity type dropdown (Fig 3, c)
- 5. Click <u>select data</u> and choose the output file name from the Augur Prep workflow previously ran, e.g. AugurPrepPHB_YYYYMMDD[initials] (Fig 7)

Select D	Data			
O Create	e a new Augur_set from selected Augurs se specific Augur_sets to process			
Select	Augur_sets to process 🌼 SETTINGS	1 row selected		E ADVANCED SEARCH Search Q
▼ ▼	Augur_set_id	Augurs		
~	AugurPrepPHB_20230907kk	Sample_01, Sample	(25 entities)	
				1-lof1 ≪ < 1 > ≫ Items per page: 100 v
Figur	e 7.			CANCEL

- 6. Click on the *inputs* tab and set attributes as follows (Fig 8):
 - a. this.Augurs.assembly_fasta
 - b. this.Augur_set_id
 - c. this.Augurs.augur_metadata
- 7. If running SC2 or flu, set the organism field to *"sars-cov-2"* or *"flu"*, respectively (Fig 8)
 - a. This sets the appropriate default values to mimic NextStrain builds for the following fields:
 i. See appendix 10.1 for default values
 - b. For organisms other than SC2 or flu, users will need to provide the following data:
 - i. <u>min_num_unambig</u>: specify the minimum acceptable number of ambiguous basepairs in the sample consensus assembly; think of this in terms of percentage of the genome size, but input the desired value in basepairs (e.g. 150000)
 - ii. reference_fasta
 - 1. For "MPXV" (monkeypox virus): gs://theiagen-public-files-rp/terra/augur-mpox-references/NC_063383.1.reference.fasta
 - 2. For "WNV" (west nile virus): gs://theiagen-public-files-rp/terra/augur-wnv-references/NC_063383.1.reference.fasta
 - iii. reference_genbank
 - 1. For MPXV: gs://theiagen-public-files-rp/terra/augur-mpox-references/NC_063383.1_reference.gb
 - 2. For WNV: gs://theiagen-public-files-rp/terra/augur-wnv-references/NC_063383.1_reference.gb
- 8. Specify outputs by clicking on the *outputs* tab and *use defaults* (Fig 9); click *save*
- 9. Launch the workflow by clicking run analysis; enter desired comments and click launch

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		CANCEL SAVE
	Download json Drag	g or click to upload json Clear inputs SEARCH INPUTS
Variable	Туре	Attribute
assembly_fastas	Array[File]+	this.Augurs.assembly_fasta {}
build_name	String	"SC2_202104_B.1.1.7s" {}
sample_metadata_tsvs	Array[File]+	this.Augurs.augur_metadata {}
auspice_config	File	Optional 🖻 []
clades_tsv	File	Optional 🖻 []
distance_tree_only	Boolean	Optional {}
flu_segment	String	Optional {}
flu_subtype	String	Optional {}
lat_longs_tsv	File	Optional 🕞 {}
min_num_unambig	Int	Optional {}
organism	String	Optional {}
	Variable assembly_fastas build_name sample_metadata_tsvs auspice_config clades_tsv distance_tree_only flu_segment flu_subtype lat_longs_tsv min_num_unambig organism	Variable Type assembly_fastas Array[File]+ build_name String build_name Array[File]+ clauspice_config File clades_tsv File flu_segment String flu_subtype String idat_longs_tsv File corganism String

Download json Drag or click to upload json Clear outputs SEARCH OUTPUTS										
Task name ↓	Variable	Туре	Attribute Use defaults							
augur	aligned_fastas	File	this.aligned_fastas							
augur	augur_phb_analysis_date	String	this.augur_phb_analysis_date ()							
Figure 9.	augur_phb_version	String	this.augur_phb_version []							

	_						<u></u>
DASHBOARD DATA		ANAL	YSES WORKFLOWS JOB	HISTORY			
IMPORT DATA)	/ EDI	T 🔀 OPEN WITH 🕒 EXPORT		S 0 rows selected		ED SEARCH Search
TABLES	,	•	Augur_set_id	1 Q	auspice_input_json	0	metadata_merged
Search all tables			AugurPrepPHB_20230907kk		Augur_Prep_PHB_2023-	<u>09-09T13-</u>	metadata-merged.tsv
🗏 Augur (25)	D						
🔳 Augur_set (2)							Figure 10.



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4.4 VISUALIZING THE AUGUR TREE IN AUSPICE

- Navigate to the workspace data tab select the SET data table containing phylogenetic data
- 2. Click settings (Fig 10) and none (Fig 11)
- Select the <u>auspice_input_ison</u> and <u>metadata_merged</u> columns (Fig 11)
- Click the auspice_input_json file for the desired Augur Prep sample set (Fig 12)
- In the file details pop-up, *click download* for <\$0.01* (Fig 13); this will open a new window
- 6. *Save* the file (Fig 14)
 - a. In windows, *either right click > save as* or *Ctrl + S*; note the destination folder and click *save*
 - b. Follow relevant commands for macintosh or linux environments
- Return to the workspace and <u>click</u> the metadata_merged file for the relevant Augur Prep sample set (Fig 12)



alphabetical	THIS COLUMN SELECTION
SAVE	THIS COLUMN SELECTION

 NGS
 0 rows selected
 Figure 12.

 Augurs
 i
 auspice_input_json
 i
 metadata_merged

 (25 entities)
 (25 entities)
 (25 entities)
 metadata-merged.tsv

 (25 entities)
 SC2_Augur_auspice.json
 metadata-merged.tsv





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- 8. In the file details pop-up, click download for <\$0.01* (Fig 13); this will open a new window
- 9. Save the file (Fig 14)
- 10. In a new browser window *open https://auspice.us/*; *drag and drop* the auspice input json file onto the webpage
- 11. *Drag and drop* the metadata file onto the webpage
 - a. The sample names in the auspice output json and the metadata file must match; if they don't, open the metadata file and manually edit the names
- 12. In auspice, click the *color by* dropdown and *select the desired metadata attribute* to visually highlight sample groups by color
 - a. Unassigned clades may be older clades that are not currently assigned a clade by nextclade; these are displayed in black in the auspice timetree
- 13. *View the timetree and map* with geographical coordinates of the analyzed strains (Fig 15)
 - a. Guidance on interpreting phylogenetic trees²



- 14. To view phylogeny relationships via SNP differnces, click the snp_matrix hyperlink for the relevant prep sample set and download for <\$0.01
- 15. In excel, highlight all cells with data, click conditional formatting, color scales, and choose the color scale that makes sense to you (Fig 16)
- 16. The same sample set is listed along both axis so the the SNP difference between all sample combinations is visible
- 17. The fewer SNP difference between samples, the more closely related the samples
 - a. Guidance on interpreting SNP matrices³

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snp-dists (Sa	ample_2 Sar	nple_1 Sar	nple_1 Sa	mple_1 Sa	mple_2 MI	N908947Sa	mple_0 Sa	mple_1 Sar	nple_1 Sa	nple_0 Sa	mple_0 Sa	mple_0 Sa	m			nple_2 Sa	mple_2 Sar	nple_2	Sample_0 Sa	mple_1 Sa	ample_1 Sa	mple_1 Sa	mple_0 Sar	nple_1 Sar	nple_0 Sar	nple_
Sample_2	0	9	9	17	17	29	51	57	59	56	59	59	📕 🔛 D	ata Bars	>	60	59	57	58	51	49	52	53	52	54	50
Sample_1	9	0	0	14	14	25	47	53	56	55	56	<u> </u>					6.4	52	53	48	45	49	48	47	49	5
Sample_1	9	0	0	14	14	26	47	55	58	55	_	_/		olor <u>S</u> cales	>			4	55	48	45	49	50	49	51	5
Sample_1	17	14	14	0	10	22	44	52	54	51	54	34						0	51	44	42	45	46	45	47	4
Sample_2	1/	14	14	10	0	22	42	50	54	51	54	54	<u>i</u>	on Sets	>				51	44	40	45	46	45	4/	4
ample 0	29	25	20	22	42	22	33	40	41	39	41	41	EE Neu	. Dula				(38	34	33	30	30	30	30	
Sample_1	57	52	47	52	42	40	17	1/	1/	1/	1/	1/	Hill Idea	v Kule				1 (j	19	19	16	17	17	17	17	- 1
Sample 1	59	56	58	54	54	41	17	4	0	0	0	0	🔯 💭	ar Rules	>			9	19	19	16	17	17	17	17	1
Sample 0	56	55	55	51	51	39	17	4	ő	ő	ő	ő	🖽 Mar	nage <u>R</u> ules		Mor	e Rules		16	19	16	17	17	17	17	1
ample 0	59	56	58	54	54	41	17	4	0	0	0	0	1	18	19	21	21	19	19	19	16	17	17	17	17	1
ample 0	59	56	58	54	54	41	17	4	0	0	0	0	1	18	19	21	21	19	19	19	16	17	17	17	17	1
ample_0	60	57	59	55	55	42	18	5	1	1	1	1	0	19	20	22	22	20	20	20	17	18	18	18	18	1
ample_1	59	54	56	52	52	39	15	18	18	18	18	18	19	0	17	19	19	18	17	17	14	15	15	15	15	1
ample_2	57	52	54	50	50	38	14	18	19	18	19	19	20	17	0	2	2	3	10	14	12	14	14	14	14	1
ample_2	60	55	57	53	53	40	16	19	21	20	21	21	22	19	2	0	2	3	12	17	14	16	16	16	16	1
ample_2	59	54	56	52	52	39	16	19	21	20	21	21	22	19	2	2	0	3	12	16	14	16	16	16	16	1
ample_2	57	52	54	50	50	37	14	17	19	18	19	19	20	18	3	3	3	0	12	16	13	15	15	15	15	1
ample_0	58	53	55	51	51	38	14	18	19	16	19	19	20	17	10	12	12	12	0	15	12	14	14	14	14	1
sample_1	51	48	48	44	44	34	13	19	19	19	19	19	20	17	14	17	16	16	15	0	2	2	1	1	2	
ample_1	49	45	45	42	40	33	11	10	16	10	16	16	17	14	12	14	14	13	12	2	0	0	0	0	0	
ample_1	52	49	49	45	45	35	12	17	17	17	17	17	18	15	14	16	16	15	14	1	0	0	0	0		
ample_0	52	40	49	40	45	35	12	17	17	17	17	17	18	15	14	16	16	15	14	1	0	0	0	0		
ample_r			51	47	47	36	12	17	17	17	17	17	18	15	14	16	16	15	14	2	0	0	0	0	0	
			53	49	49	38	14	19	19	19	19	19	20	17	16	18	18	17	16	4	2	2	2	2	2	

5. QUALITY RECORDS

- Sample assemblies and metadata
- Pango_lineage determinations
- Auspice timetree and map
- SNP matrix

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. INTERFERENCES

N/A

8. REFERENCES

- Wright, S., Doughty, E., and Otieno, J. (August 2023). Augur. Retrieved from <u>https://theiagen.notion.site/Augur-33c1307d9f28427fbed95aeeba254446</u> on September 7, 2023
- 2. "Module 1: Introduction to COVID-19." Centers for Disease Control and Prevention, URL: <u>https://www.cdc.gov/amd/training/covid-toolkit/module1-3.html</u>.
- 3. "NGS Result Report Interpretation Guide" Centers for Disease Control and Prevention (CDC), URL: https://www.cdc.gov/labguality/gms-tools-and-resources.html?textFilter=result.



9. REVISION HISTORY

Revision	Version	Release Date
Document creation	1	10/2023



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10. APPENDICES

10.1 AUGUR DEFAULT VALUES FOR SARS-CoV-2 AND FLU

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Default Values for SARS-CoV-2

- min_num_unambig = 27000
- clades_tsv = defaults/clades.tsv
- lat_long_tsv = defaults/lat_longs.tsv
- reference_fasta = defaults/reference_seq.fasta
- reference_genbank = defaults/reference_seq.gb
- auspice_config = defaults/auspice_config.json
- min_date = 2020.0
- pivot_interval = 1
- pivot_interval_units = "weeks"
- narrow_bandwidth = 0.05
- proportion_wide = 0.0
- Default values and additional information are provided on the Augur workflow page within the Theiagen Public Health Resource Notion Site, <u>https://theiagen.notion.site/Augur-</u> 33c1307d9f28427fbed95aeeba254446
 - a. Check the Notion site for the most up-to-date values and information

Default Values for Flu

- lat_longs_tsv = "gs://theiagen-public-files-rp/terra/flu-references/lat_longs.tsv"
- min_num_unambig = 900
- min_date = 2020.0
- pivot_interval = 1
- narrow_bandwidth = 0.1666667
- proportion_wide = 0.0
- ▼ H1N1
- ▼ HA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_h1n1pdm_ha.gb"
 - clades_tsv = "gs://theiagen-public-files-rp/terra/flureferences/clades_h1n1pdm_ha.tsv"
- ▼ NA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_h1n1pdm_na.gb"

auspice_config = "gs://theiagen-public-files-rp/terra/flureferences/auspice_config_h1n1pdm.json"

- ▼ H3N2
 - ▼ HA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_h3n2_ha.gb"
 - clades_tsv = "gs://theiagen-public-files-rp/terra/flureferences/clades_h3n2_ha.tsv"
 - ▼ NA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_h3n2_na.gb"

auspice_config = "gs://theiagen-public-files-rp/terra/flureferences/auspice_config_h3n2.json"

- Victoria
 - ▼ HA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_vic_ha.gb"
 - clades_tsv = "gs://theiagen-public-files-rp/terra/flureferences/clades_vic_ha.tsv"
 - ▼ NA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_vic_na.gb"

auspice_config = "gs://theiagen-public-files-rp/terra/flureferences/auspice_config_vic.json"

- Yamagata
 - ▼ HA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_yam_ha.gb"
 - clades_tsv = "gs://theiagen-public-files-rp/terra/flureferences/clades_yam_ha.tsv"
 - ▼ NA
 - reference_fasta = "gs://theiagen-public-files-rp/terra/flureferences/reference_yam_na.gb"

auspice_config = "gs://theiagen-public-files-rp/terra/flureferences/auspice_config_yam.json"