

# Nextstrain, Nextclade



WHO Collaborating Centre  
for Reference and  
Research on Influenza  
**VIDRL**



A joint venture between The University of Melbourne and The Royal Melbourne Hospital

# Objectives

- To familiarise online tools, Nextstrain and Nextclade

# What is Nextstrain?

Nextstrain is a project to harness the scientific and public health potential of pathogen genome data. Our goal is to aid epidemiological understanding of pathogen spread and evolution and improve outbreak response.

## Pathogen surveillance

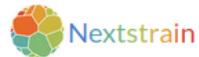
Our website, [nextstrain.org](#), provides real-time snapshots of evolving pathogen populations such as [SARS-CoV-2](#), [influenza](#), and [Ebola](#). We use interactive visualizations to enable exploration of curated datasets and analyses which are continually updated when new genomes are available. This offers a powerful pathogen surveillance tool to virologists, epidemiologists, public health officials, and community scientists. In many cases old snapshots of these analyses are able to be easily accessed, see [viewing previous analyses](#) for more.

## Open-source software

The software we write to power [all parts](#) of Nextstrain—bioinformatics, visualizations, analysis pipelines, data management, and more—is entirely [open-source](#) and [available to the public](#). We aim to empower the wider genomic epidemiology and public health communities to tweak our analyses, create new ones, and communicate scientific insights using the tools we do.

# Links

- <https://nextstrain.org> - Surveillance
- <http://nextclade.org/> - Clade/lineage calling
- Documentation at: <https://docs.nextstrain.org>
- Code: <https://github.com/nextstrain/>
- Workflows at eg: <https://github.com/nextstrain/seasonal-flu>



# Nextstrain

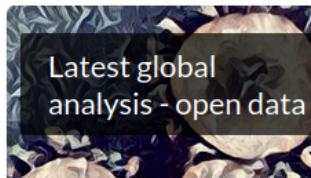
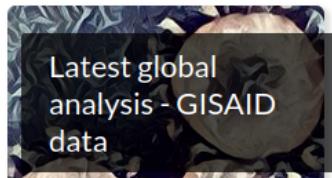
## Real-time tracking of pathogen evolution

Nextstrain is an open-source project to harness the scientific and public health potential of pathogen genome data. We provide a continually-updated view of publicly available data alongside powerful analytic and visualization tools for use by the community. Our goal is to aid epidemiological understanding and improve outbreak response. If you have any questions, or simply want to say hi, please give us a shout at [hello@nextstrain.org](mailto:hello@nextstrain.org).

[READ MORE](#)

## SARS-CoV-2 (COVID-19)

We are incorporating SARS-CoV-2 genomes as soon as they are shared and providing analyses and situation reports. In addition we have developed a number of resources and tools, and are facilitating independent groups to run their own analyses.



## Nextstrain Groups

We want to enable research labs, public health entities and others to share their datasets and narratives through Nextstrain with complete control of their data and audience.

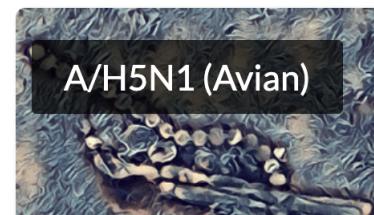
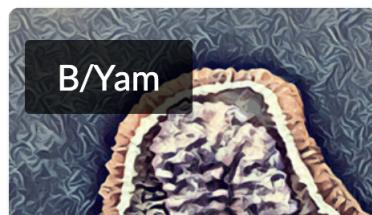
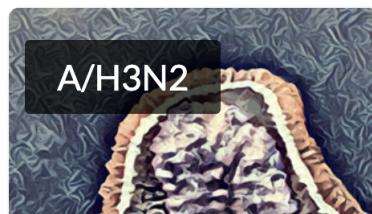
neherlab

spheres



# Influenza resources

The Nextstrain team maintains datasets and other tools for analyzing a variety of influenza viruses. We track the evolution of seasonal influenza viruses (A/H3N2, A/H1N1pdm, B/Victoria, and B/Yamagata) and use these analyses to inform recommendations for the World Health Organization's influenza vaccine composition meetings. We also maintain datasets for a subset of avian influenza viruses that have caused recurrent outbreaks in humans and domestic birds, including novel reassortant H5 viruses.





## Real-time tracking of influenza A/H3N2 evolution

Built with nextstrain/seasonal-flu. Maintained by Jover Lee, Richard Neher and Trevor Bedford. Enabled by data from **GISAID**.

Showing 1949 of 1949 genomes sampled between Sep 2015 and May 2023.

## Dataset

flu

seasonal

h3n2

ha

2y

## Date Range

2013-11-11 2023-05-12

PLAY RESET

## Color By

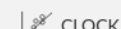
Clade

## Filter Data

Type filter query here...

## Tree Options

## Layout



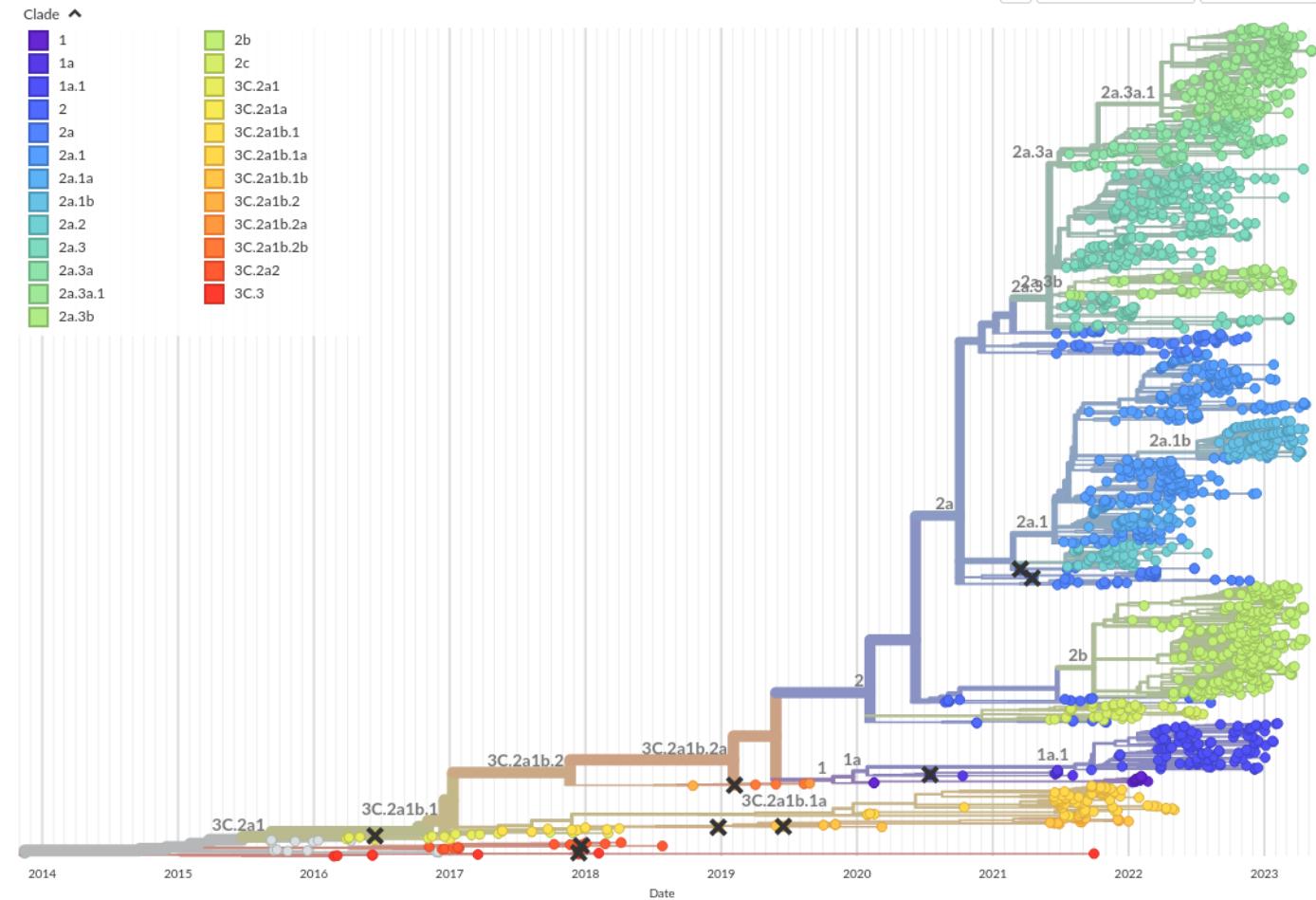
## Branch Length

TIME DIVERGENCE

## Phylogeny

## Clade ▲

1	2b
1a	2c
1a.1	3C.2a1
2	3C.2a1a
2a	3C.2a1b.1
2a.1	3C.2a1b.1a
2a.1a	3C.2a1b.1b
2a.1b	3C.2a1b.2
2a.2	3C.2a1b.2a
2a.3	3C.2a1b.2b
2a.3a	3C.2a2
2a.3a.1	3C.2a2
2a.3b	3C.3

 ZOOM TO SELECTED  RESET LAYOUT



DOCS HELP LOGIN <

RESET ZOOM

Clade ▾

## Dataset

- flu
- seasonal
- h3n2
- ha
- 2y

## Date Range

2013-11-11 2023-05-12

▶ PLAY ⏪ RESET

## Color By

- Clade

## Filter Data

Type filter query here...

## Tree Options

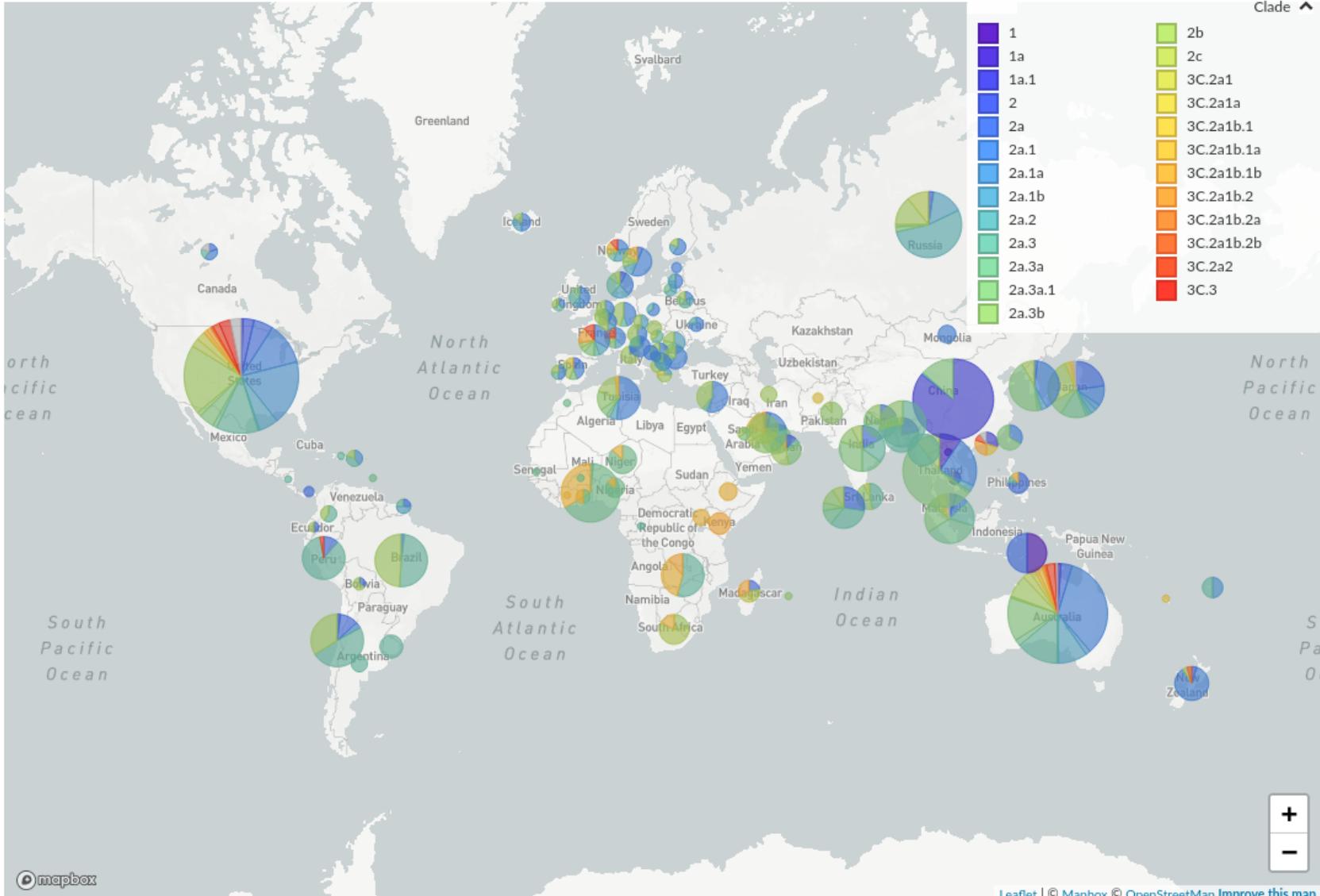
Layout

RECTANGULAR

RADIAL

UNROOTED

## Geography



mapbox

Leaflet | © Mapbox © OpenStreetMap Improve this map

[DOCS](#) [HELP](#) [LOGIN](#) [◀](#)[ENTROPY](#) [EVENTS](#) [AA](#) [NT](#)**Dataset**

flu

seasonal

h3n2

ha

2y

**Date Range**

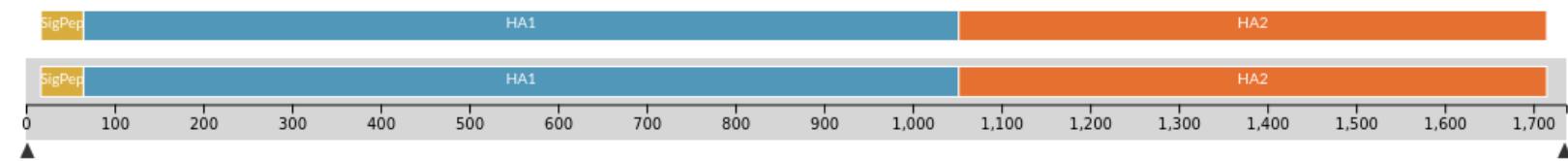
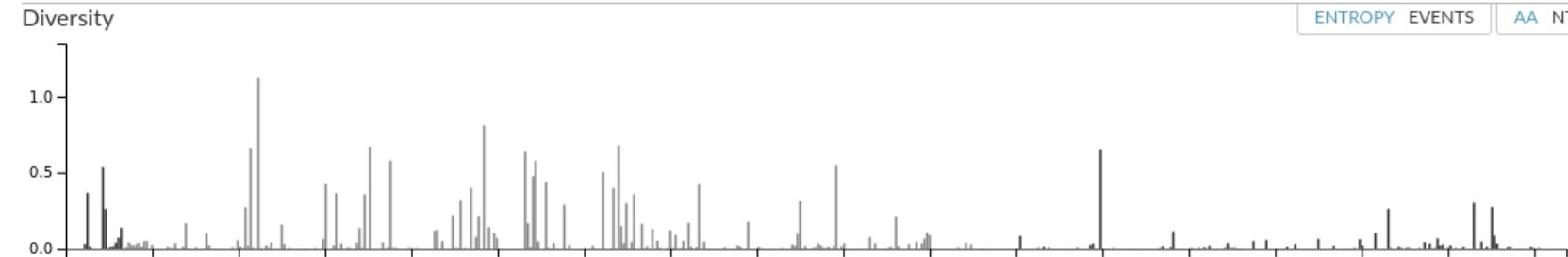
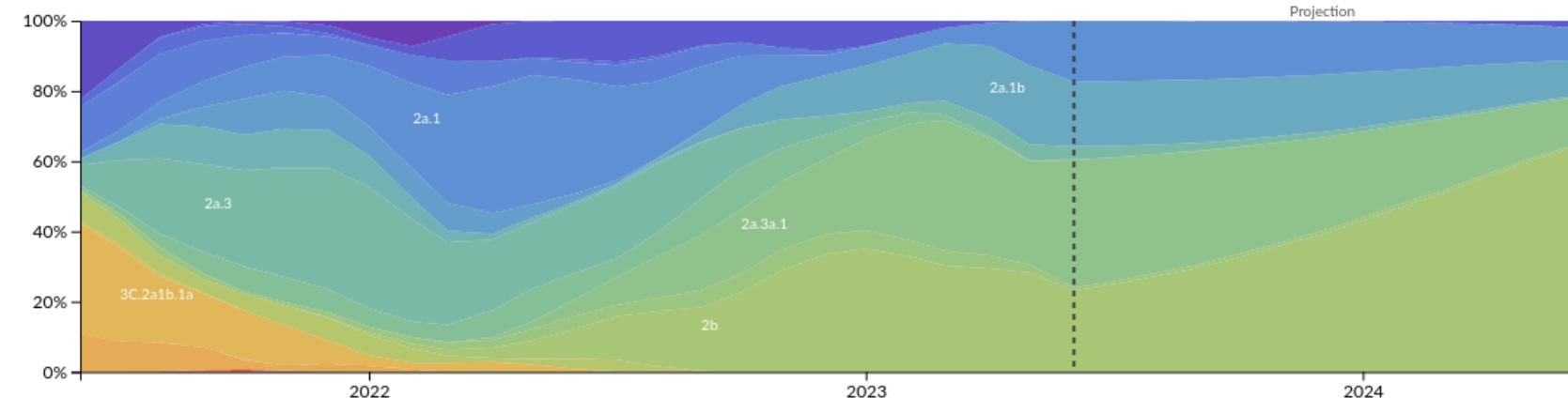
2013-11-11 2023-05-12

[PLAY](#)[RESET](#)**Color By**

Clade

**Filter Data**

Type filter query here...

**Tree Options****Frequencies (colored by Clade)**



DOCS HELP LOGIN <

# Real-time tracking of influenza A/H3N2 evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 1949 of 1949 genomes sampled between Sep 2015 and May 2023.

## Dataset

flu

seasonal

h3n2

h3n2



h1n1pdm

vic

yam

2013-11-11 2023-05-12

▶ PLAY



RESET

## Color By

Clade

## Filter Data

Type filter query here...

## Tree Options

### Layout

RECTANGULAR

RADIAL

UNROOTED

CLOCK

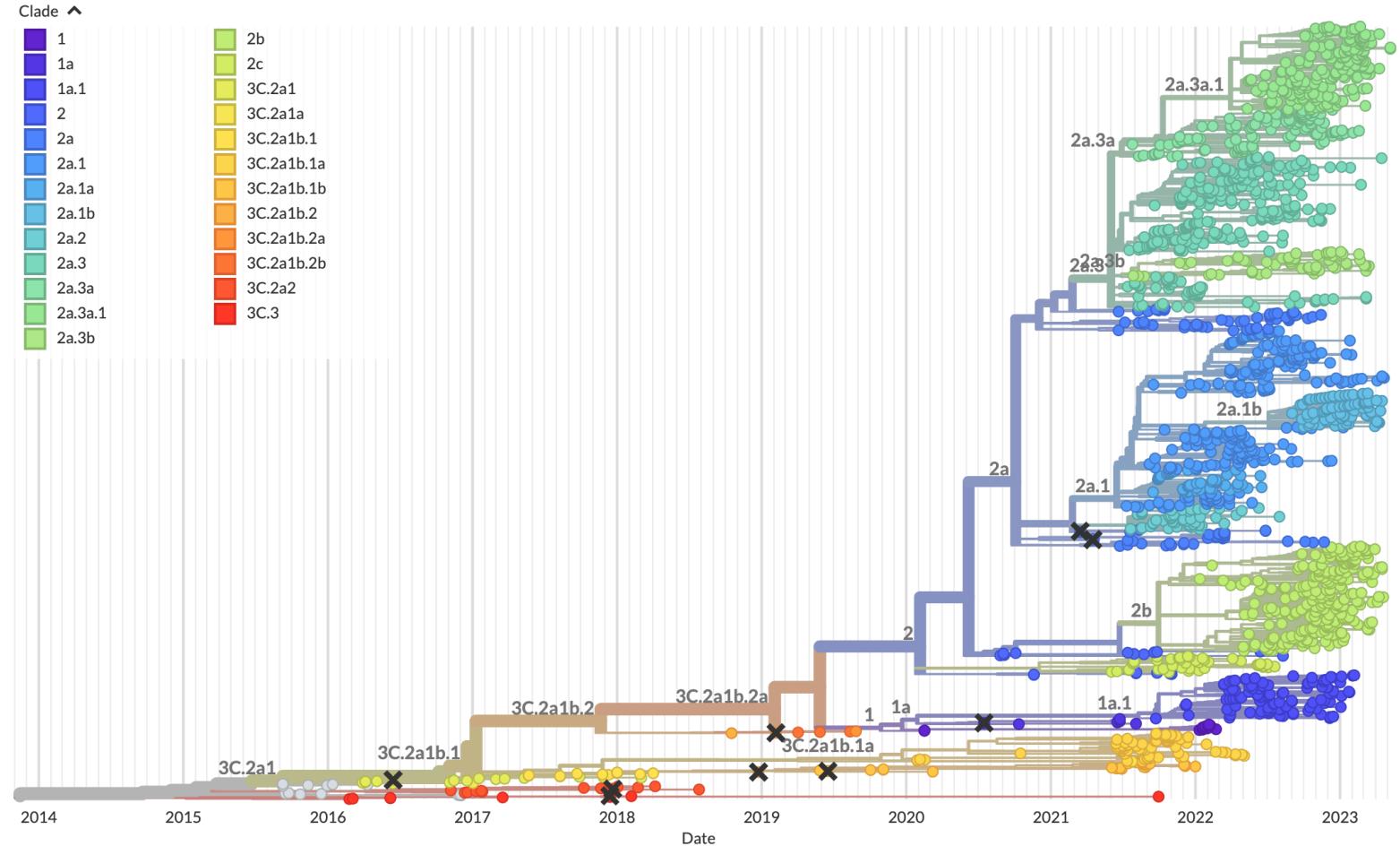
## Phylogeny

### Clade ^

1	2b
1a	2c
1a.1	3C.2a1
2	3C.2a1a
2a	3C.2a1b.1
2a.1	3C.2a1b.1a
2a.1a	3C.2a1b.1b
2a.1b	3C.2a1b.2
2a.2	3C.2a1b.2a
2a.3	3C.2a1b.2b
2a.3a	3C.2a2
2a.3a.1	3C.3
2a.3b	

ZOOM TO SELECTED

RESET LAYOUT





## Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 2027 of 2027 genomes sampled between Jul 2015 and May 2023.

## Dataset

flu

seasonal

h1n1pdm

ha

ha

na

2012-05-19 2023-05-25

PLAY RESET

## Color By

Clade

## Filter Data

Type filter query here...

## Tree Options

Layout  
RECTANGULAR

RADIAL

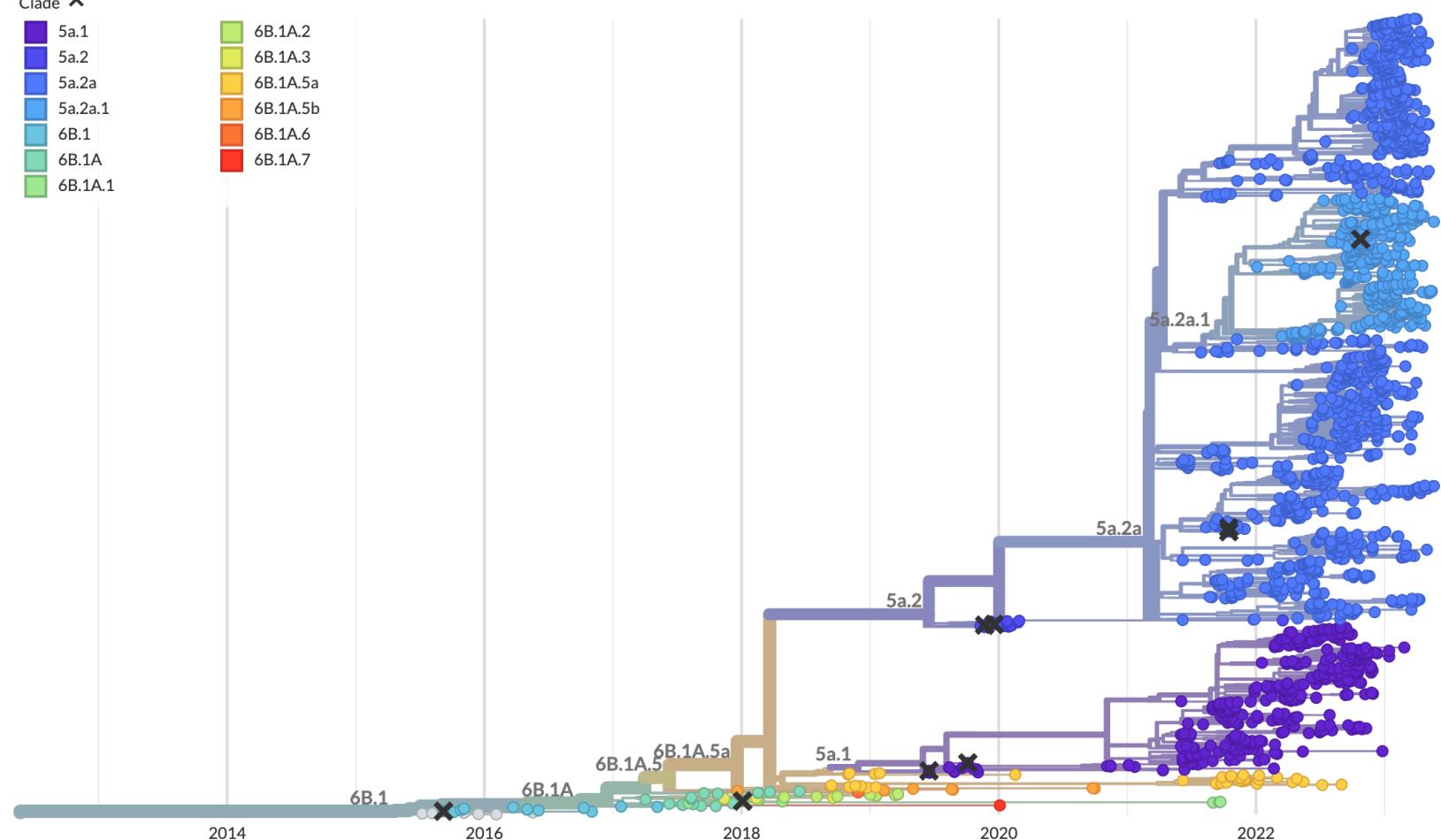
UNROOTED

CLOCK

## Phylogeny

## Clade ^

5a.1	6B.1A.2
5a.2	6B.1A.3
5a.2a	6B.1A.5a
5a.2a.1	6B.1A.5b
6B.1	6B.1A.6
6B.1A	6B.1A.7
6B.1A.1	

 ZOOM TO SELECTED  RESET LAYOUT

flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
Clade

Filter Data  
australia  
Country → Australia  
Division → South Australia  
Division → Western Australia  
sample → A/SouthAustralia/315/2022  
sample → A/SouthAustralia/163/2022  
SCATTER

Branch Length  
TIME DIVERGENCE

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 2027 of 2027 genomes sampled between Jul 2015 and May 2023.

## Phylogeny

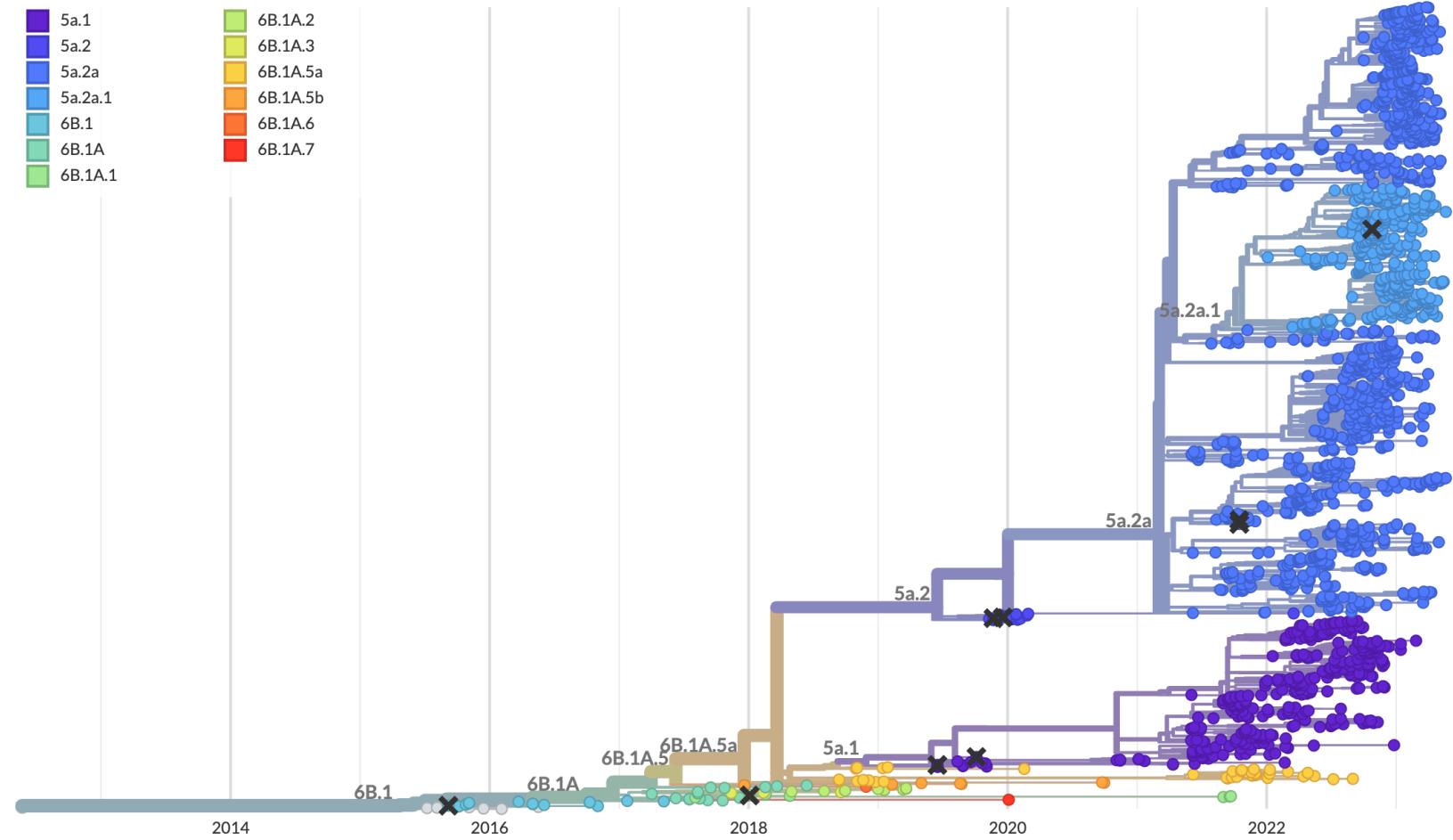
Clade ^

- █ 5a.1
- █ 5a.2
- █ 5a.2a
- █ 5a.2a.1
- █ 6B.1
- █ 6B.1A
- █ 6B.1A.1
- █ 6B.1A.2
- █ 6B.1A.3
- █ 6B.1A.5a
- █ 6B.1A.5b
- █ 6B.1A.6
- █ 6B.1A.7



ZOOM TO SELECTED

RESET LAYOUT



flu

seasonal

h1n1pdm

ha

2y

Date Range

PLAY

RESET

Color By

Filter Data

Type filter query here...

Currently selected filter categories:

1x Country

Tree Options

Layout

RECTANGULAR

RADIAL

UNROOTED

CLOCK

SCATTER

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 329 of 2027 genomes sampled between Aug 2015 and Apr 2023. Filtered to [Australia \(329\)](#) .



ZOOM TO SELECTED

RESET LAYOUT

## Phylogeny

Clade ▲

- |         |          |
|---------|----------|
| 5a.1    | 6B.1A    |
| 5a.2    | 6B.1A.1  |
| 5a.2a   | 6B.1A.2  |
| 5a.2a.1 | 6B.1A.5a |
| 6B.1    | 6B.1A.5b |

flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
Clade

Filter Data  
Type filter query here...

Year/month → 2023-01

Year/month → 2023-02

Year/month → 2023-03

Year/month → 2023-04

Year/month → 2023-05

genotype HA1 104Q

genotype HA1 104R

genotype HA1 105L

genotype HA1 105M

# Real-time tracking of influenza A/H1N1pdm evolution



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Showing 329 of 2027 genomes sampled between Aug 2015 and Apr 2023. Filtered to [Australia \(329\)](#) .



ZOOM TO SELECTED

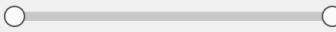
RESET LAYOUT

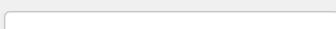
## Phylogeny

Clade ▲

- |         |          |
|---------|----------|
| 5a.1    | 6B.1A    |
| 5a.2    | 6B.1A.1  |
| 5a.2a   | 6B.1A.2  |
| 5a.2a.1 | 6B.1A.5a |
| 6B.1    | 6B.1A.5b |

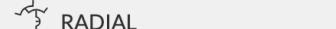
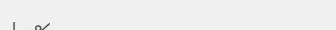
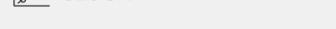
flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
 Clade

Filter Data  
  
Type filter query here...

Currently selected filter categories:  
  


Tree Options  
Layout  
 RECTANGULAR  
 RADIAL  
 UNROOTED  
 CLOCK  
 SCATTER

# Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

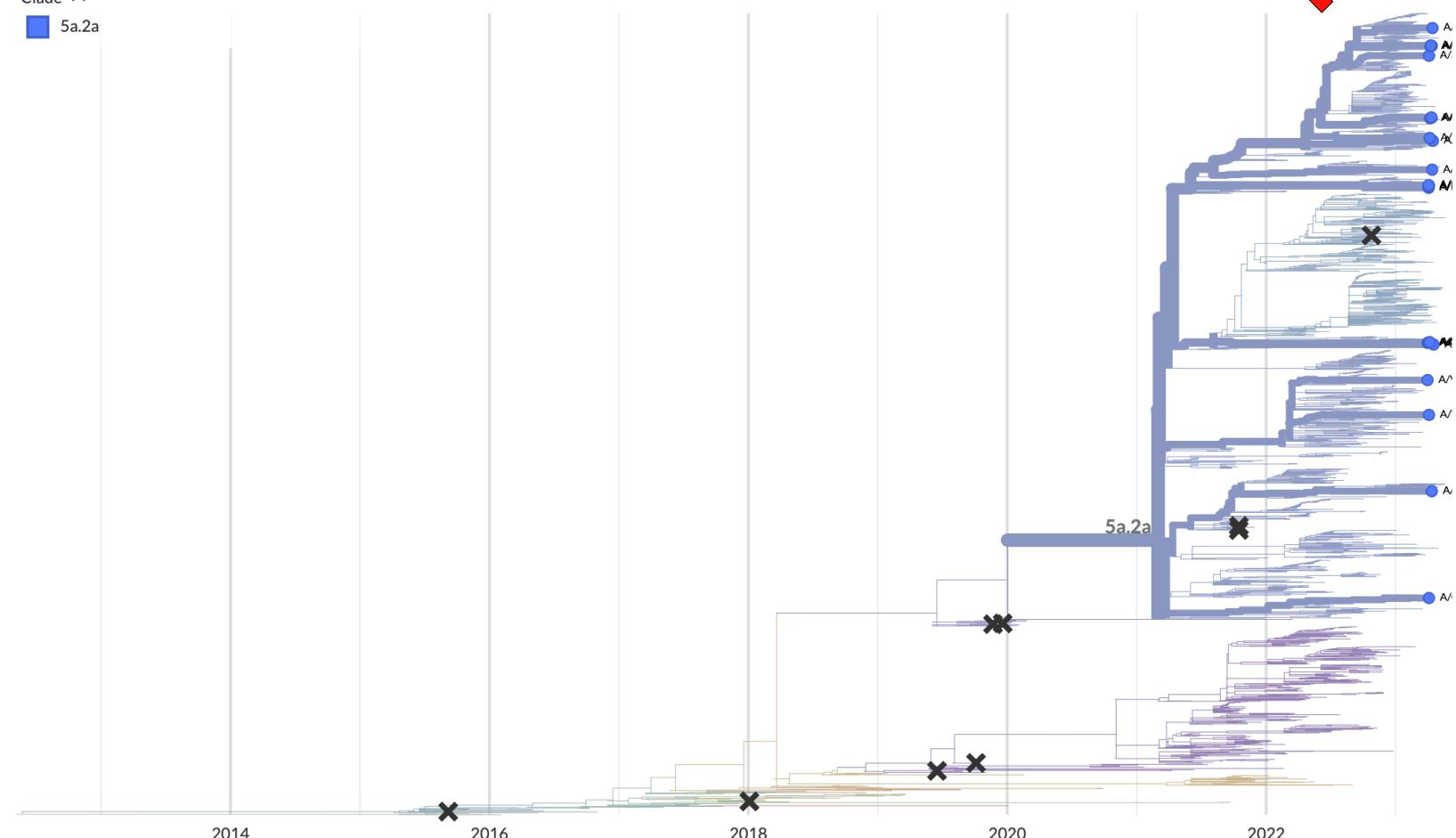
Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to  Australia (329)   n  2023-04 (82)  .

## Phylogeny

Clade 

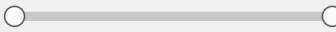
 5a.2a

 ZOOM TO SELECTED 





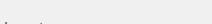
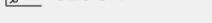
flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
Clade

Filter Data  
Type filter query here...

Currently selected filter categories:  
1 x Country    
1 x Year/month  

Tree Options  
Layout  
RECTANGULAR   
RADIAL   
UNROOTED   
CLOCK   
SCATTER 

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)   n [2023-04 \(82\)](#)  .

Phylogeny

Clade

5a.2a

mouse over on a branch – do not click!



ZOOM TO SELECTED

RESET LAYOUT

Number of descendants: 95

Homoplasic mutations: A992G

No amino acid mutations

Divergence: 0.0392

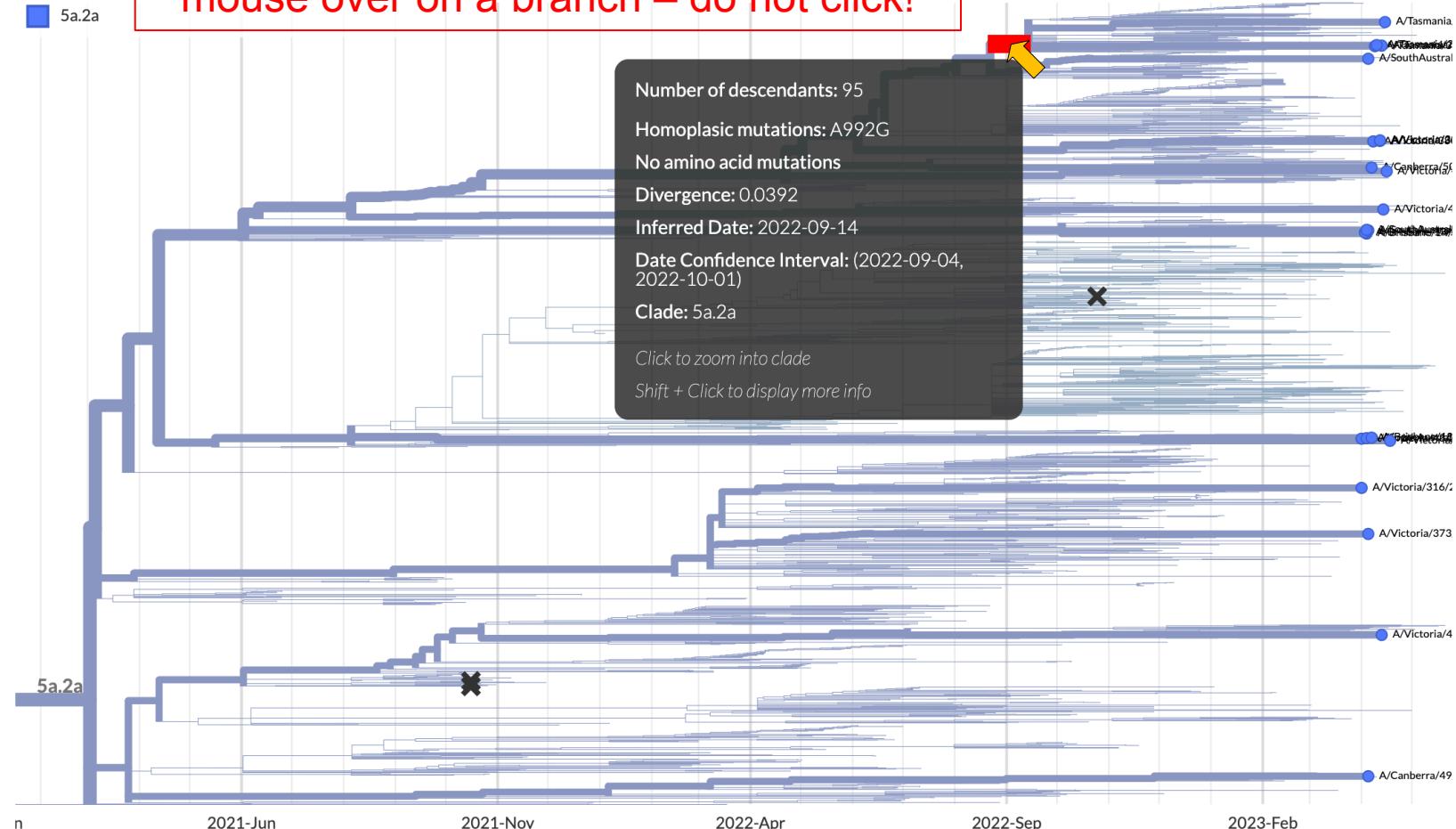
Inferred Date: 2022-09-14

Date Confidence Interval: (2022-09-04, 2022-10-01)

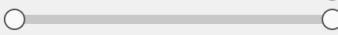
Clade: 5a.2a

Click to zoom into clade

Shift + Click to display more info

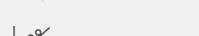
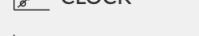


flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
Clade

Filter Data  
Type filter query here...  
Currently selected filter categories:  
1 x Country    
1 x Year/month  

Tree Options  
Layout  
 RECTANGULAR  
 RADIAL  
 UNROOTED  
 CLOCK  
 SCATTER

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)   n [2023-04 \(82\)](#)  .

Phylogeny

Clade

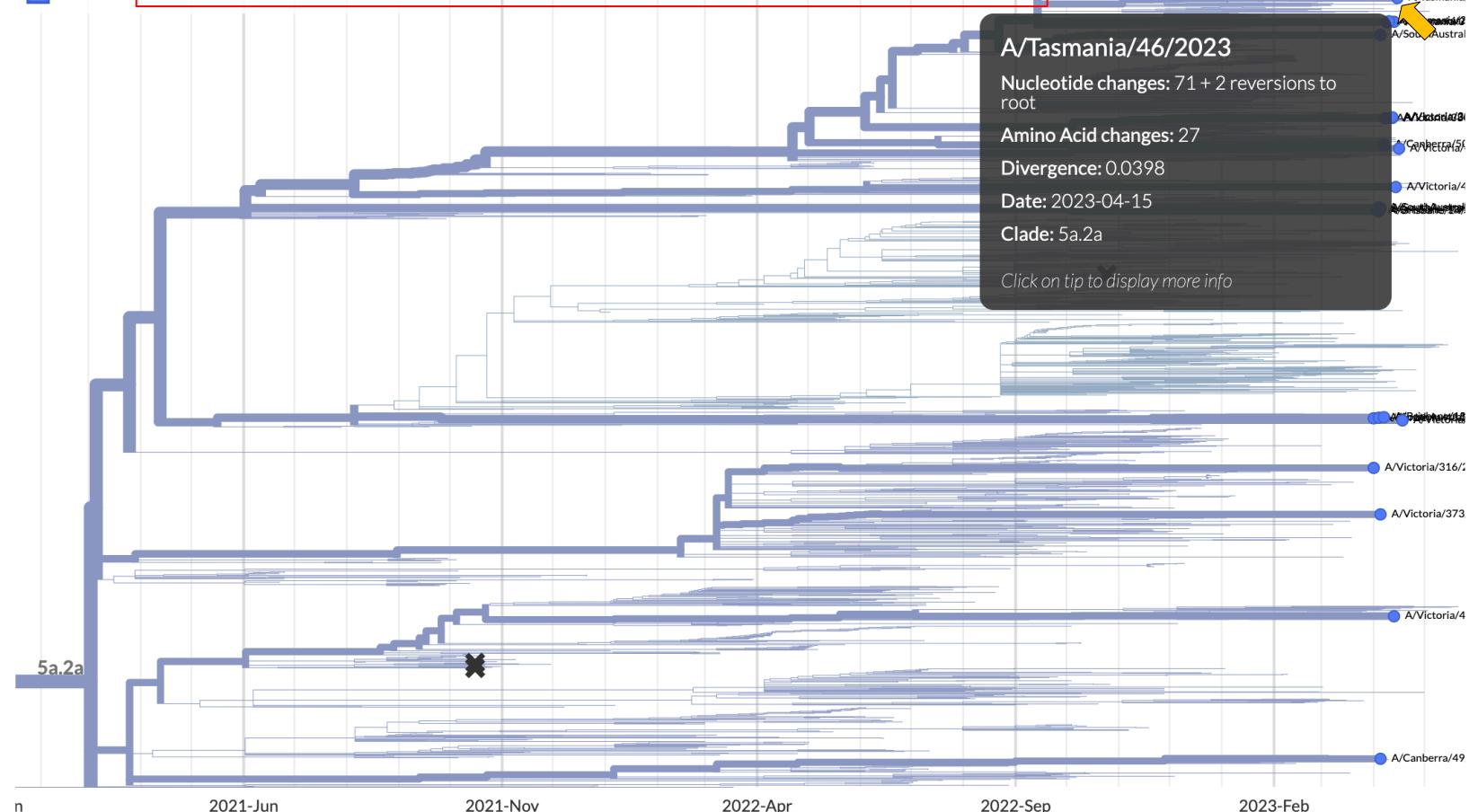
5a.2a



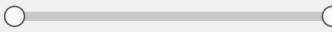
ZOOM TO SELECTED

RESET LAYOUT

mouse over on a terminal node – do not click!



flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
Clade

Filter Data  
Type filter query here...

Currently selected filter categories:  
1 x Country    
1 x Year/month  

Tree Options  
Layout  
RECTANGULAR  
RADIAL   
UNROOTED  
CLOCK  
SCATTER

# Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)   n [2023-04 \(82\)](#)  .

## Phylogeny

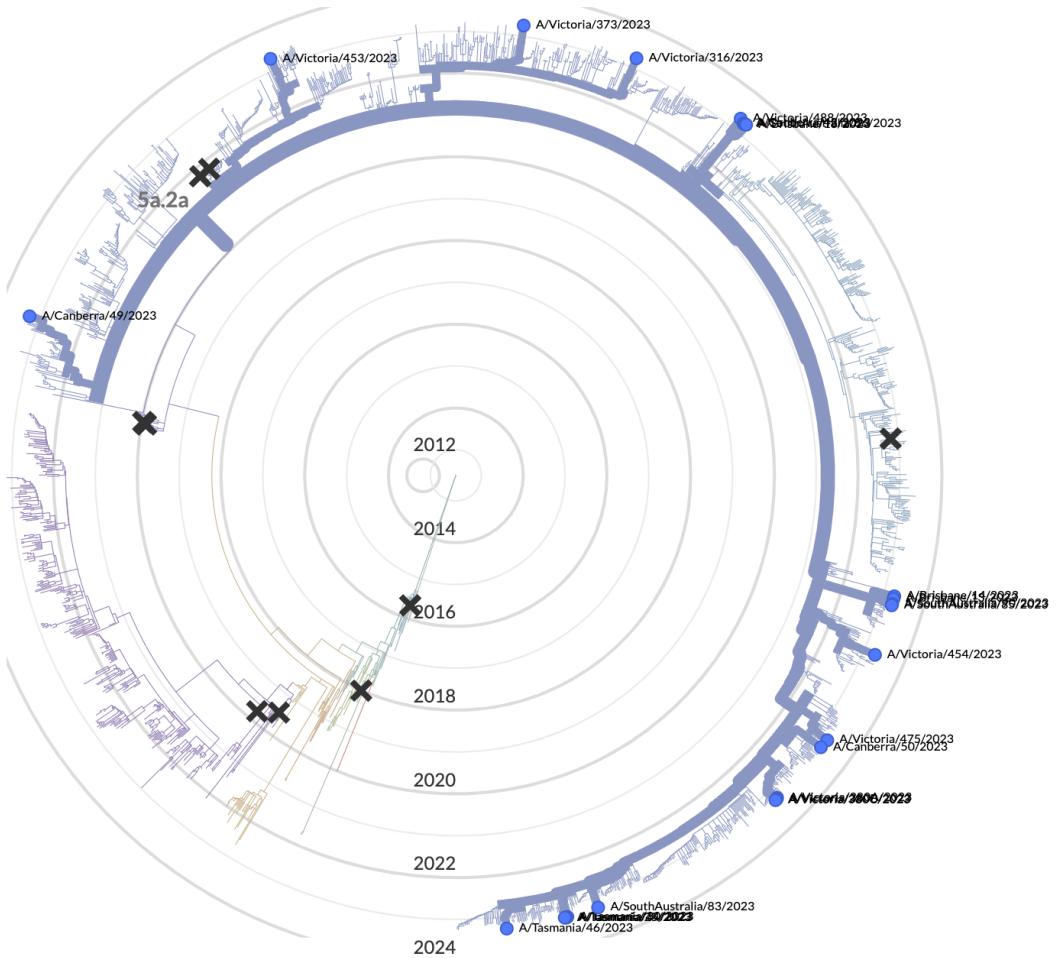
Clade ▲

5a.2a

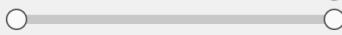


ZOOM TO SELECTED

RESET LAYOUT



flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  


Clade

Filter Data  


Type filter query here...

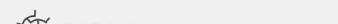
Currently selected filter categories:

1 x Country  

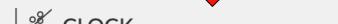
1 x Year/month  

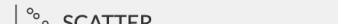
Tree Options  


Layout  
 RECTANGULAR

 RADIAL

 UNROOTED 

 CLOCK

 SCATTER

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)   n [2023-04 \(82\)](#)  .

## Phylogeny

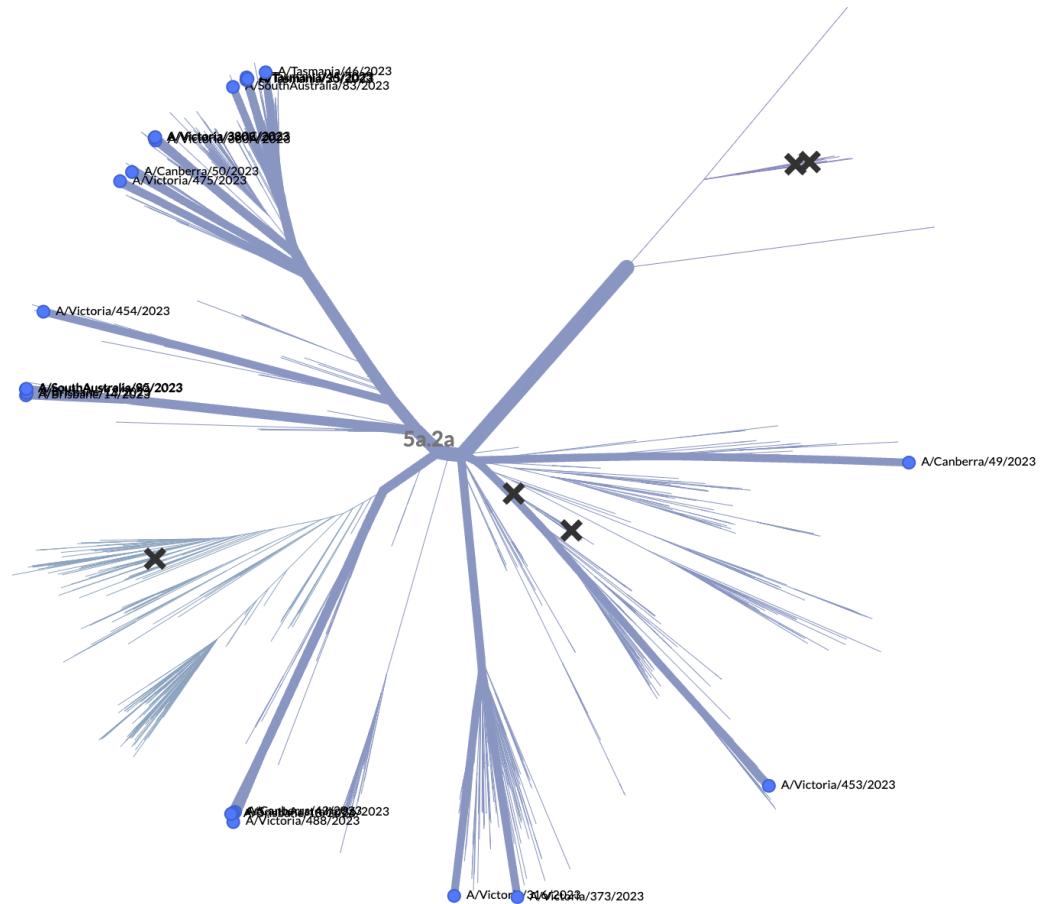
Clade 

 5a.2a

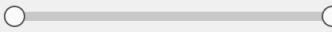


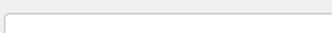
ZOOM TO SELECTED

RESET LAYOUT

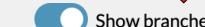


flu  
seasonal  
h1n1pdm  
ha  
2y

Date Range  
  
2012-05-19 2023-05-25  
PLAY RESET

Color By  
 Clade

Filter Data  
  
Currently selected filter categories:  
1 x Country   
1 x Year/month 

Tree Options  
Layout  
 RECTANGULAR  
 RADIAL  
 UNROOTED  
 CLOCK   
 Show branches

# Real-time tracking of influenza A/H1N1pdm evolution



Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to  n .

## Phylogeny

Clade 

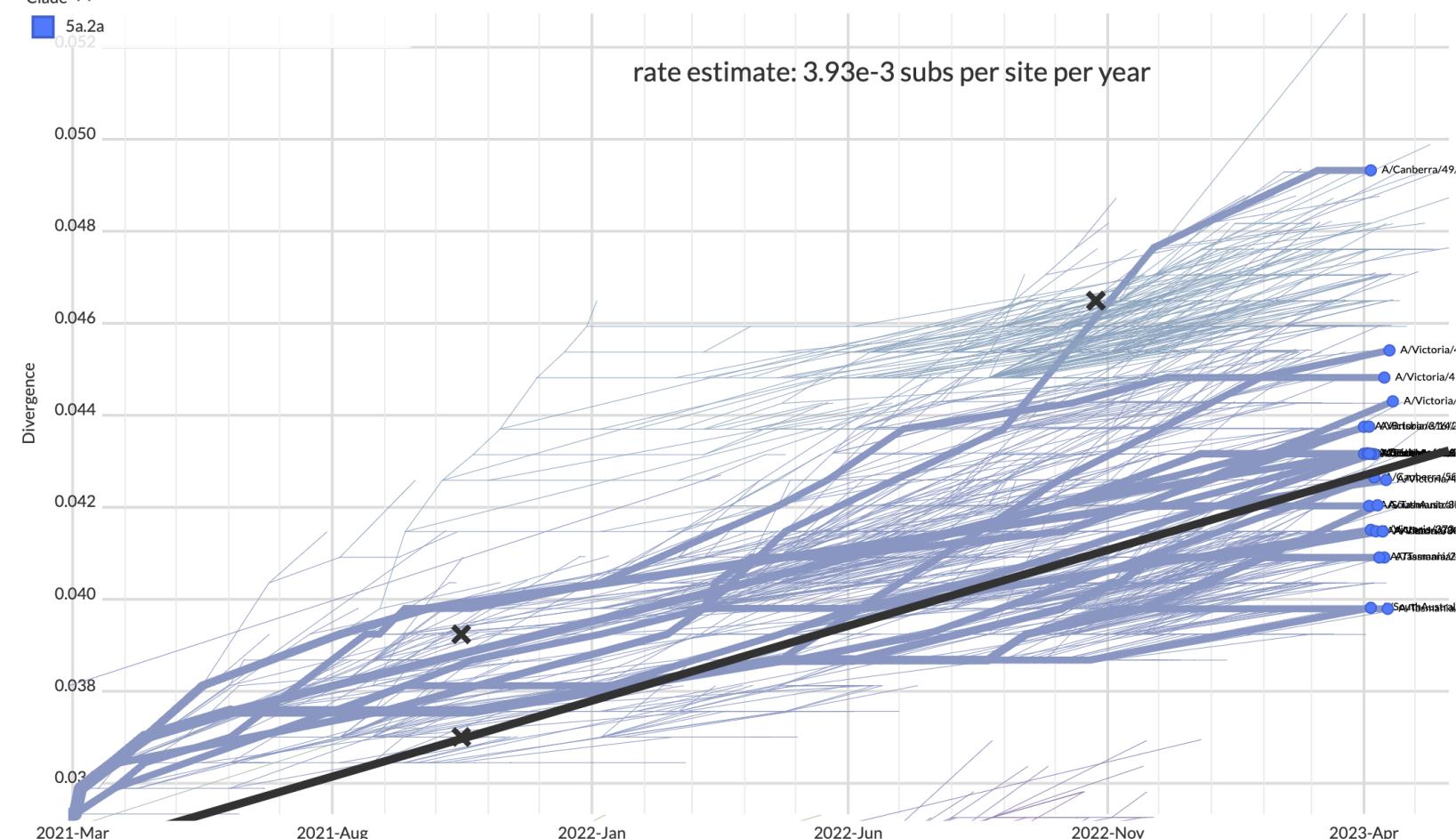
 5a.2a  
0.052



ZOOM TO SELECTED

RESET LAYOUT

rate estimate: 3.93e-3 subs per site per year



# Nextclade: analysis of viral genetic sequences

Nextclade is an open-source project for viral genome alignment, mutation calling, clade assignment, quality checks and phylogenetic placement.

Nextclade consists of a set of related tools:

- Nextclade Web - a web application available online at [clades.nextstrain.org](https://clades.nextstrain.org)
- Nextclade CLI - a command-line tool

Both tools are powered by the same algorithms, they consume the same inputs and produce the same outputs, but they differ in the user interface, the features included, and the degree of customization. It is recommended to start with Nextclade Web and later proceed to CLI tools if you have more advanced use-cases (for example, repeated batch processing, bioinformatics pipelines).



# Nextclade

v3.3.1

Clade assignment, mutation calling, and sequence quality checks

## Provide sequence data

[File](#) [Link](#) [Text](#) [Example ▾](#)



Drag & drop files  
or folders

FASTA

Select files

## Selected reference dataset [i](#)



Suggest automatically

Reset

Suggest



### Influenza A H3N2 HA

official

Reference: A/Darwin/6/2021 (EPI1857216)

Updated at: 2024-02-22 16:12:03 (UTC)

Dataset name: nextstrain/flu/h3n2/ha/EPI1857216

[Load example](#)

[Change reference dataset](#)

[Run](#)



# Nextclade

v3.3.1

Clade assignment, mutation calling, and sequence quality checks

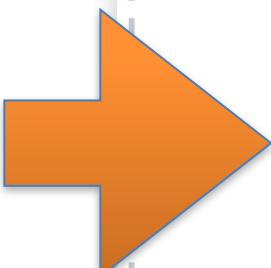
## Provide sequence data

[File](#) [Link](#) [Text](#) [Example ▾](#)



Drag & drop files  
or folders

Select files



## Selected reference dataset



Suggest automatically

Reset

Suggest



### Influenza A H3N2 HA

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# Nextclade

v3.3.1

Clade assignment, mutation calling, and sequence quality checks

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Dataset name: nextstrain/flu/h3n2/ha/EPI1857216

[Load example](#)

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# Nextclade v3.3.1

Clade assignment, mutation calling, and sequence quality checks

## Provide sequence data

[File](#) [Link](#) [Text](#) [Example ▾](#)Drag & drop files  
or folders

Select files

## Selected reference dataset i



Suggest automatically

Reset

Suggest



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Reference: A/Darwin/6/2021 (EPI1857216)

Updated at: 2024-02-22 16:12:03 (UTC)

Dataset name: nextstrain/flu/h3n2/ha/EPI1857216

[Load example](#)[Change reference dataset](#)[Run](#)

#	i	Sequence name	QC	Clade	Subclade	short-clade	RBD mutations	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC	
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	
0	7	✓ A/Massachusetts/2/2024	M P F S	3C.2a1b.2a.2a.3a	J.2	2a.3a.1	0.00	12(+1-1 0)	25	0	0	100.0%	0	19	0	0	
1	6	✓ A/Idaho/21/2022	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	11	0	0	100.0%	0	19	0	0	
2	2	✓ A/Utah/2/2022	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	11(+0-1 0)	10	0	0	100.0%	0	19	0	0	
3	0	✓ A/Wyoming/1/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	7	0	0	100.0%	0	19	0	0	
4	1	✓ A/California/48/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	10	0	Non-ACGTN (0)		19	0	0		
5	3	✓ A/Maine/19/2022	M P F S	3C.2a1b.2a.2b	G.2	2b	1.00	12(+0-0 0)	18	0	0	100.0%	0	19	0	0	
6	10	✓ A/Tennessee/22/2023	M P F S	3C.2a1b.2a.2a.3a	J.2	2a.3a.1	1.00	12(+1-1 0)	25	0	0	100.0%	0	19	0	0	
7	8	✓ A/Illinois/25/2023	M P F S	3C.2a1b.2a.2a.3a	J.2	2a.3a.1	0.00	12(+1-1 0)	22	0	0	100.0%	0	19	0	0	
8	9	✓ A/Illinois/3/2024	M P F S	3C.2a1b.2a.2a.3a	J.2	2a.3a.1	0.00	13(+1-0 0)	24	0	0	100.0%	0	19	0	0	
9	15	✓ A/Florida/4/2021-egg	M P F S	3C.2a1b.2a.2a.3	G.1.3	2a.3	0.00	13(+1-0 0)	14	0	0	100.0%	0	19	0	0	
10	11	✓ A/Nebraska/5/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	11(+0-1 0)	9	0	0	100.0%	0	19	0	0	
11	12	✓ A/California/61/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	7	0	0	100.0%	0	19	0	0	
12	16	✓ A/Iowa/10/2024	M P F S	3C.2a1b.2a.2a.3a	J.2	2a.3a.1	0.00	12(+1-1 0)	26	0	0	100.0%	0	19	0	0	
13	13	✓ A/Washington/15/2020	M P F S	3C.2a1b.2b	E.2	3C.2a1b.2b	4.00	13(+1-0 0)	37	0	0	100.0%	0	19	0	0	
14	14	✓ A/Michigan/6/2021	M P F S	3C.2a1b.2a.2c	G.3	2c	1.00	12(+0-0 0)	13	0	0	100.0%	0	19	0	0	

Genome annotation 3

Genome annotation 3



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Done. Total sequences: 24. Succeeded: 24

C File Filter Download Print

#	i	Sequence name	QC	Clade	Abbreviated clade name	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
0	0	Nucleotide substitutions rel. to reference (22)							22	0	0	97.1%	0	0
1	1	G 170 A	A 231 C	G 338 T	G 525 A	T 620 C	G 627 A	C 636 G	A 742 C	22	0	0	97.1%	0
2	2	G 847 A	A 968 G	A 994 G	T 1023 C	T 1040 C	T 1199 C	A 1323 G	T 1347 C	28	0	0	97.1%	0
3	3	G 1349 A	C 1601 T	G 1616 A	A 1646 G	C 1659 T	G 1664 A			24	0	0	97.1%	0
4	4	Aminoacid substitutions rel. to reference (8)							27	0	0	97.1%	0	0
5	5	HA1: K 54 Q							22	0	0	97.1%	0	0
6	6	HA1: V 152 I							21	0	0	97.1%	0	0
7	7	HA1: A 186 T							26	0	0	97.1%	0	0
8	8	HA1: Q 189 E							26	0	0	97.1%	0	0
9	9	HA1: E 224 A							25	0	0	97.1%	0	0
10	10	HA1: R 259 K							19	0	0	97.1%	0	0
11	11	HA1: K 308 R							21	0	0	97.1%	0	0
12	12	HA2: I 91 V							23	0	0	97.1%	0	0
13	13	Private mutations rel. to tree (2)							25	0	0	97.1%	0	0
14	14	A/South_Australia/85/2023	M P F S	6B.1A.5a.2a	5a.2a	7(+0 -0 0)	25	0	0	97.1%	0	0	0	0
15	15	A/Canberra/43/2023	M P F S	6B.1A.5a.2a	5a.2a	7(+0 -0 0)	25	0	0	97.1%	0	0	0	0
16	16	A/South_Australia/86/2023	M P F S	6B.1A.5a.2a	5a.2a	7(+0 -0 0)	23	0	0	97.1%	0	0	0	0

Genome annotation ?



50

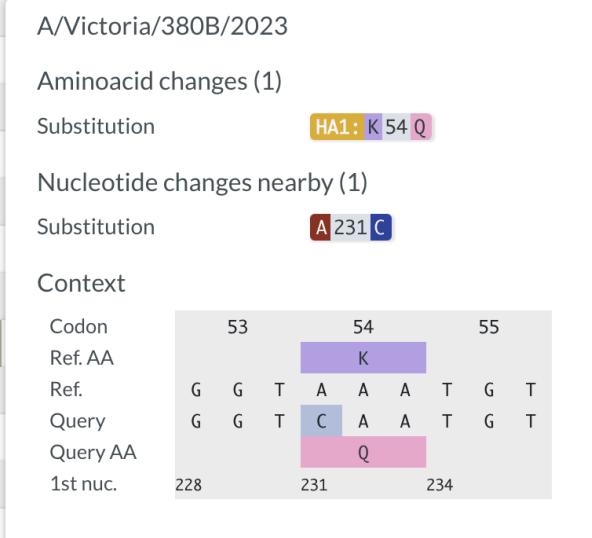
100



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Done. Total sequences: 24. Succeeded: 24

QC	Clade	Abbreviated clade name	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC		Gene HA1	
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	22	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	22	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	28	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	6(+0-1 0)	24	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	27	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	22	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	22	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	21	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	26	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	26	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	25	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	19	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	21	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	23	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	25	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	25	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	25	0	0	97.1%	0	0	0	0			
M P F S	6B.1A.5a.2a	5a.2a	7(+0-0 0)	23	0	0	97.1%	0	0	0	0			



Genome annotation ?

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50 100 150 200 250 300



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Done. Total sequences: 50. S...

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#	i	Sequence name	QC	Clade	Subclade	short-clade	RBD mutations	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC	
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	
0	7	✓ A/Massachusetts/2/2024	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	0.00	12(+1-1 0)	25	0	0	100.0%	0	19	0	0	
1	6	✓ A/Idaho/21/2022	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	11	0	0	100.0%	0	19	0	0	
2	2	✓ A/Utah/2/2022	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	11(+0-1 0)	10	0	0	100.0%	0	19	0	0	
3	0	✓ A/Wyoming/1/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	7	0	0	100.0%	0	19	0	0	
4	1	✓ A/California/48/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	10	0	Non-ACGTN (0)		19	0	0		
5	3	✓ A/Maine/19/2022	M P F S	3C.2a1b.2a.2b	G.2	2b	1.00	12(+0-0 0)	18	0	0	100.0%	0	19	0	0	
6	10	✓ A/Tennessee/22/2023	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	1.00	12(+1-1 0)	25	0	0	100.0%	0	19	0	0	
7	8	✓ A/Illinois/25/2023	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	0.00	12(+1-1 0)	22	0	0	100.0%	0	19	0	0	
8	9	✓ A/Illinois/3/2024	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	0.00	13(+1-0 0)	24	0	0	100.0%	0	19	0	0	
9	15	✓ A/Florida/4/2021-egg	M P F S	3C.2a1b.2a.2a.3	G.1.3	2a.3	0.00	13(+1-0 0)	14	0	0	100.0%	0	19	0	0	
10	11	✓ A/Nebraska/5/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	11(+0-1 0)	9	0	0	100.0%	0	19	0	0	
11	12	✓ A/California/61/2021	M P F S	3C.2a1b.2a.2a.1a	G.1.1.1	2a.1a	1.00	12(+0-0 0)	7	0	0	100.0%	0	19	0	0	
12	16	✓ A/Iowa/10/2024	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	0.00	12(+1-1 0)	26	0	0	100.0%	0	19	0	0	
13	13	✓ A/Washington/15/2020	M P F S	3C.2a1b.2b	E.2	3C.2a1b.2b	4.00	13(+1-0 0)	37	0	0	100.0%	0	19	0	0	
14	14	✓ A/Michigan/6/2021	M P F S	3C.2a1b.2a.2c	G.3	2c	1.00	12(+0-0 0)	13	0	0	100.0%	0	19	0	0	
15	18	✓ A/Wisconsin/7/2024	M P F S	3C.2a1b.2a.2a.3a.	J.2	2a.3a.1	0.00	12(+1-1 0)	24	0	0	100.0%	0	19	0	0	

Genome annotation ?



50



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Done. Total sequences: 50. Succeeded: 50

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Type filter query here...

Currently selected filter categories:

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## Layout

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SCATTER

## Branch Labels

clade

 Show all labels

## Tip Labels

Sample Name

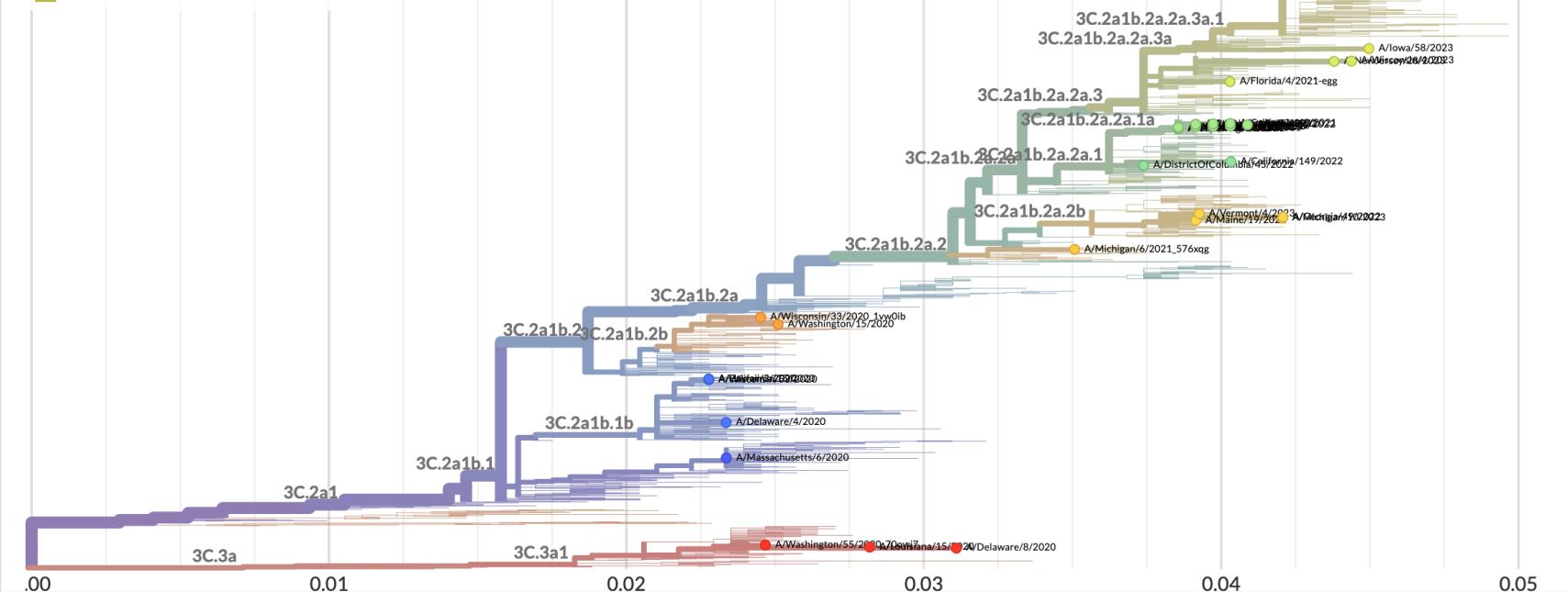
Filtered to [New \(50\)](#) i X Delete.

Enabled by data from

## Phylogeny

Clade ^

<span style="color: blue;">█</span> 3C.2a1b.1a	<span style="color: yellow;">█</span> 3C.2a1b.2a.2a.3a.1
<span style="color: blue;">█</span> 3C.2a1b.1b	<span style="color: yellow;">█</span> 3C.2a1b.2a.2b
<span style="color: green;">█</span> 3C.2a1b.2a.2a.1	<span style="color: orange;">█</span> 3C.2a1b.2a.2c
<span style="color: green;">█</span> 3C.2a1b.2a.2a.1a	<span style="color: orange;">█</span> 3C.2a1b.2b
<span style="color: green;">█</span> 3C.2a1b.2a.2a.3	<span style="color: red;">█</span> 3C.3a1
<span style="color: yellow;">█</span> 3C.2a1b.2a.2a.3a	





Nextclade

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Done. Total sequences: 50. Succeeded: 50

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Filter Data i

Type filter query here...

Currently selected filter categories:

1 x Node type eye trashTree i

## Layout

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## Branch Labels

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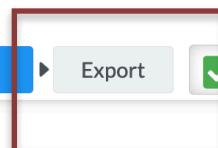
 Show all labels

## Tip Labels

Sample Name

Filtered to [New \(50\)](#) eye trash.

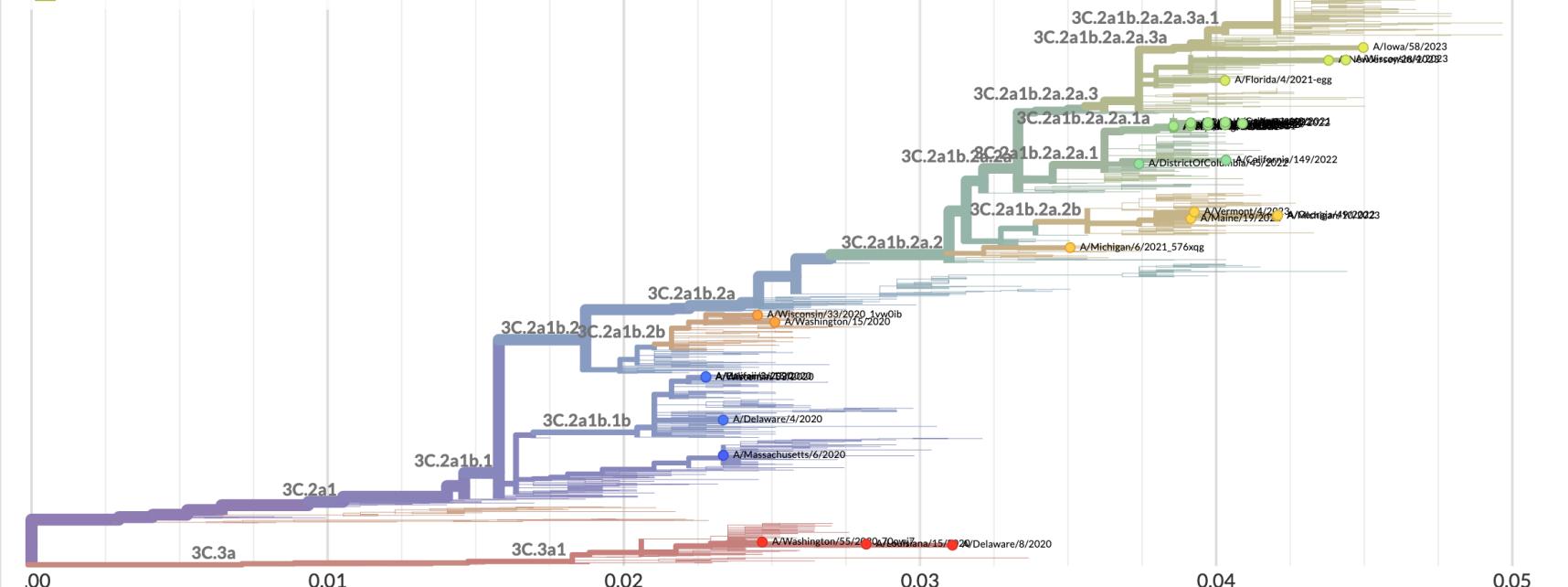
Enabled by data from GISAID



## Phylogeny

Clade ^

<span style="color: blue;">■</span> 3C.2a1b.1a	<span style="color: yellow;">■</span> 3C.2a1b.2a.2a.3a.1
<span style="color: blue;">■</span> 3C.2a1b.1b	<span style="color: yellow;">■</span> 3C.2a1b.2a.2b
<span style="color: green;">■</span> 3C.2a1b.2a.2a.1	<span style="color: orange;">■</span> 3C.2a1b.2a.2c
<span style="color: green;">■</span> 3C.2a1b.2a.2a.1a	<span style="color: orange;">■</span> 3C.2a1b.2b
<span style="color: green;">■</span> 3C.2a1b.2a.2a.3	<span style="color: red;">■</span> 3C.3a1
<span style="color: green;">■</span> 3C.2a1b.2a.2a.3a	





## Download output files

[Files](#)[Column config](#)**nextclade.json**

Results of the analysis in JSON format.  
Contains detailed results of the analysis, such as clades, mutations, QC metrics etc., in JSON format. Convenient for further automated processing. Note that this format is unstable and can change without notice.

**nextclade.ndjson**

Results of the analysis in NDJSON format.  
Contains detailed results of the analysis, such as clades, mutations, QC metrics etc., in NDJSON format (newline-delimited JSON). Convenient for further automated processing. Note that this format is unstable and can change without notice.

**nextclade.csv**

Summarized results of the analysis in CSV format.  
Contains summarized results of the analysis, such as clades, mutations, QC metrics etc., in tabular format. Convenient for further review and processing using spreadsheets or data-science tools.

[Configure columns](#)**nextclade.tsv**

Summarized results of the analysis in TSV format.  
Contains summarized results of the analysis, such as clades, mutations, QC metrics etc., in tabular format. Convenient for further review and processing using spreadsheets or data-science tools.

[Configure columns](#)**nextclade.auspice.json**

Phylogenetic tree with sequences placed onto it, in Auspice JSON v2 format.  
Can be viewed locally with Nextstrain. Available at [Auspicify](#).



**nextclade.nwk**

Phylogenetic tree with sequences placed onto it, in Newick format.  
Can be viewed in most tree viewers, including: [icytree.org](#) or [auspice.us](#).

**nextclade.aligned.fasta**

Aligned sequences in FASTA format.  
Contains aligned sequences in FASTA format.

**nextclade.peptides.fasta.zip**

Aligned peptides in FASTA format, zipped  
Contains results of translation of your sequences. One FASTA file per gene, all in a zip archive.

**nextclade.zip**

All files in a zip archive.  
Contains all of the above files in a single zip file.



# Hands on Exercise with NextClade

- Use the genomes you generated to run Nextclade
- Run on:
  - SC2 (From Galaxy)
  - Influenza (From INSaFlu)