

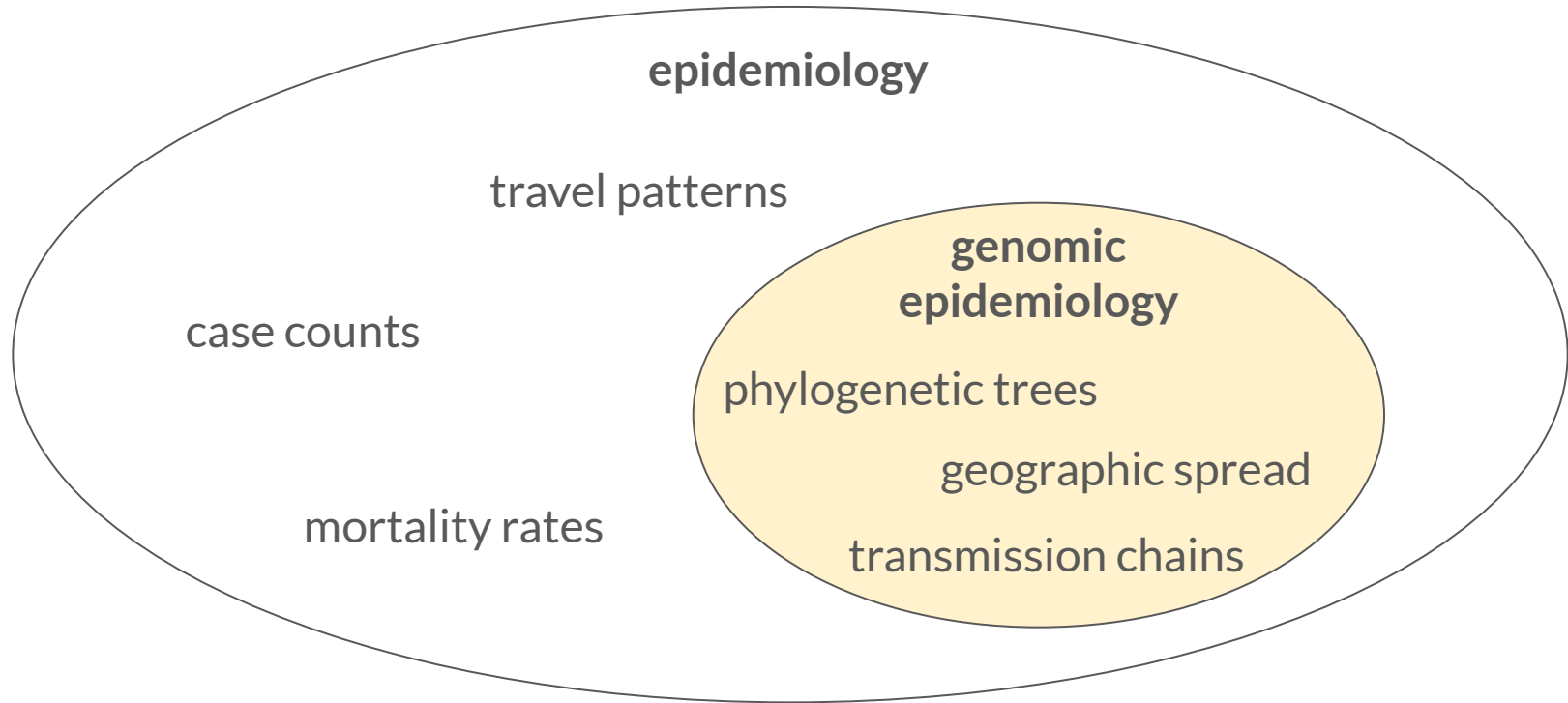


Nextstrain

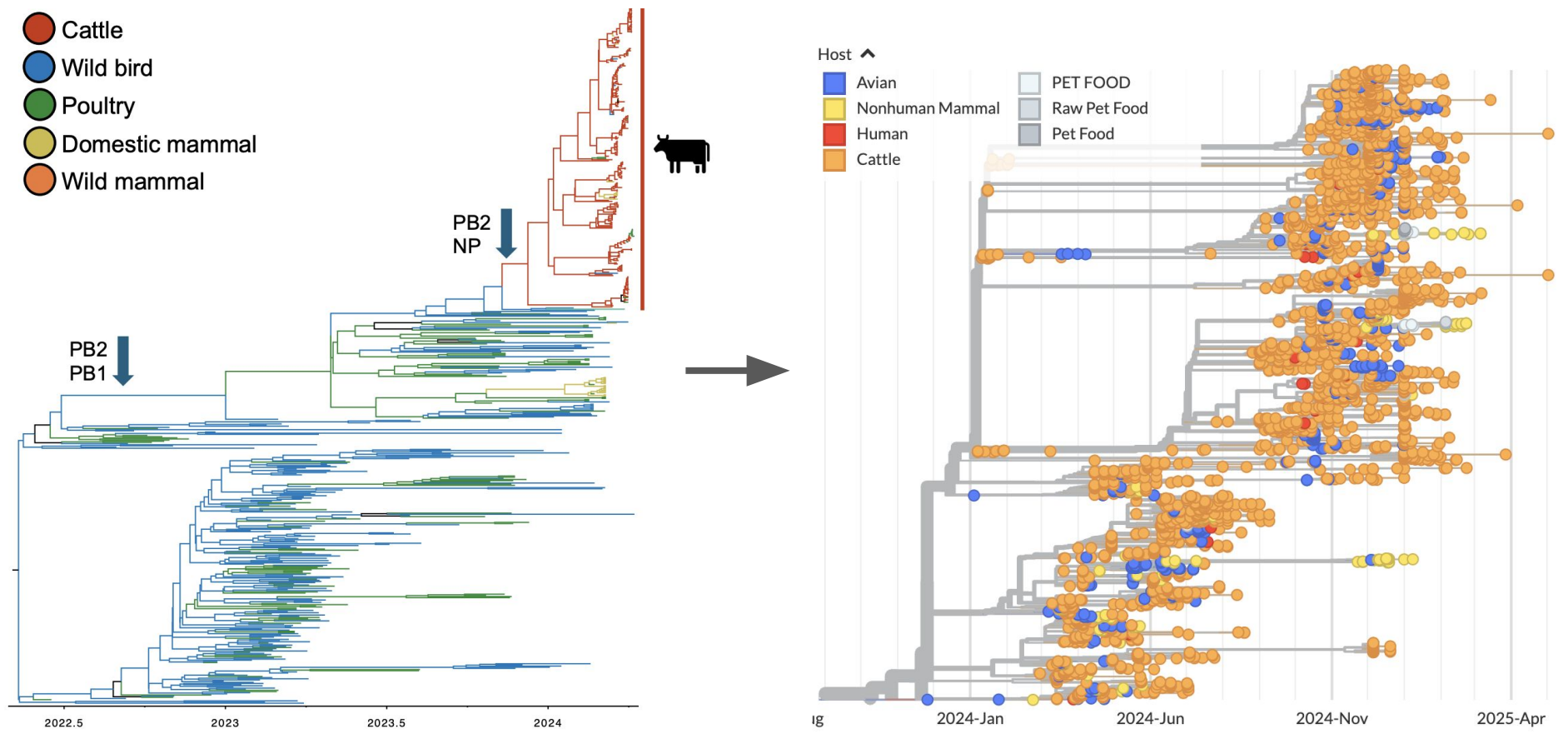
Real-time tracking of pathogen evolution

Victor Lin
Software Developer

Nextstrain is rooted in genomic epidemiology



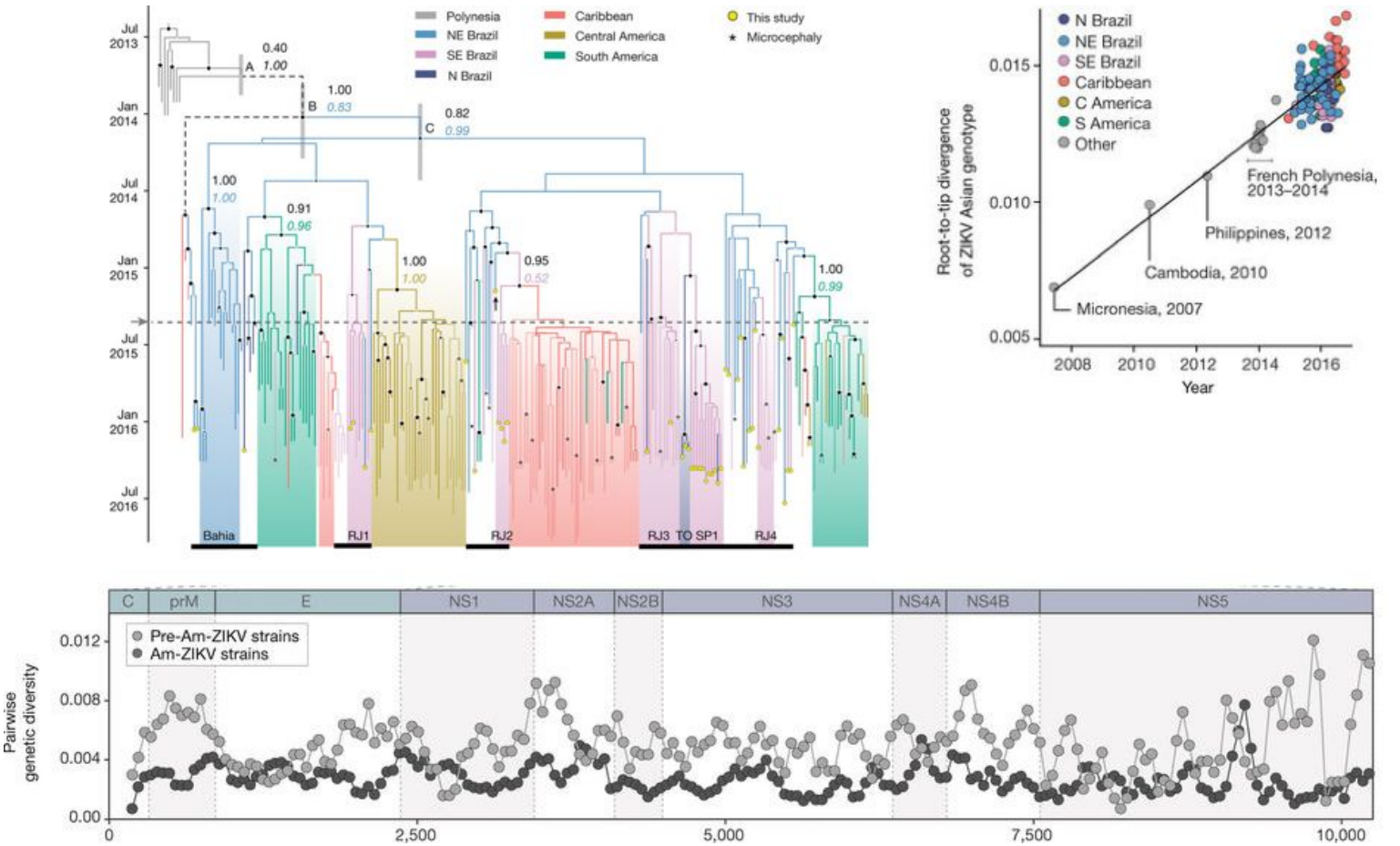
Even with preprints, analyses tend to become frozen snapshots



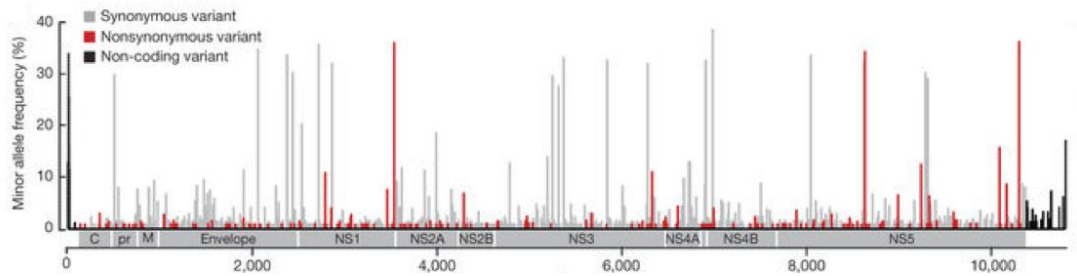
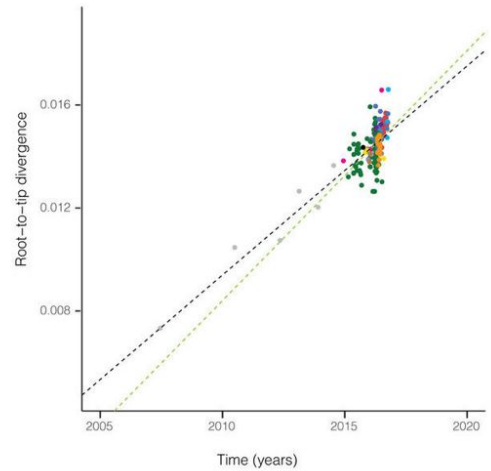
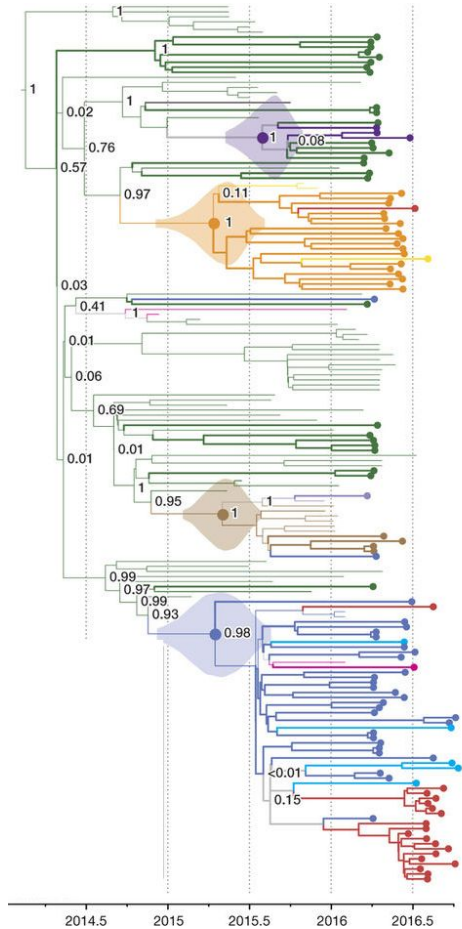
Nguyen et al. (2024 bioRxiv, 2025 Science)

nextstrain.org/avian-flu/h5n1-cattle-outbreak

Core phyldynamic plots tend to be tree, map, genomic diversity and clock



Core phylodynamic plots tend to be tree, map, genomic diversity and clock



Nextstrain aims for continually updated views of these plots

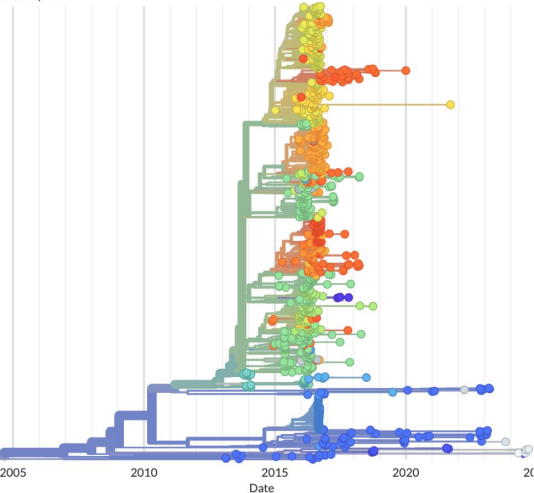
Real-time tracking of Zika virus evolution

Built with [nextstrain/zika](#). Maintained by [the Nextstrain team](#). Data updated 2025-04-28. Enabled by data from [GenBank](#) and [USVI](#).

Showing 1037 of 1037 genomes sampled between Feb 2013 and Sep 2024.

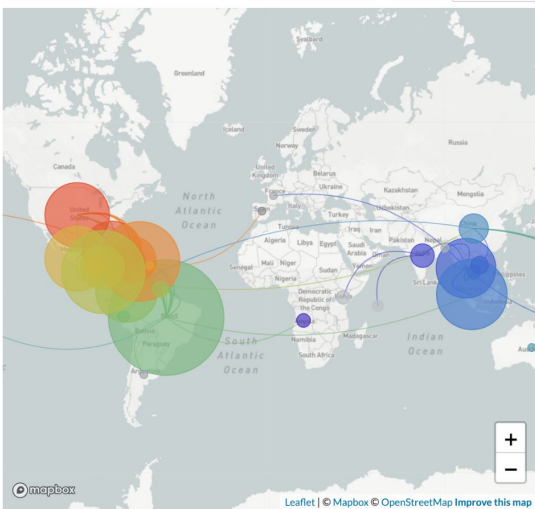
Phylogeny

country ▾



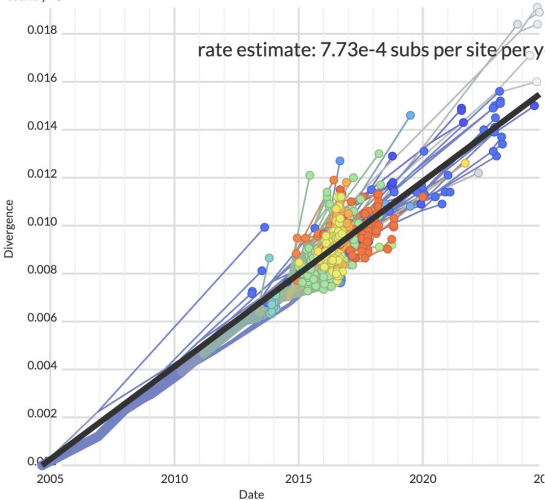
Transmissions

RESET ZOOM



Phylogeny

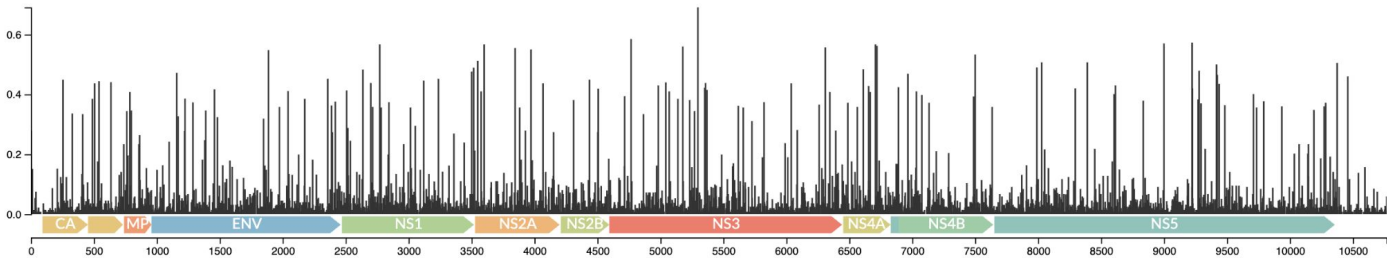
country ▾



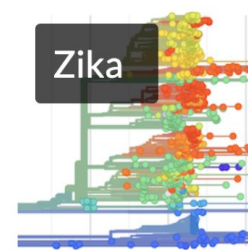
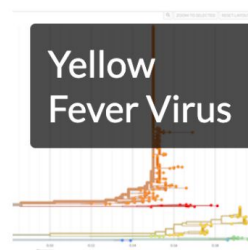
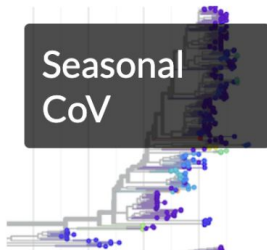
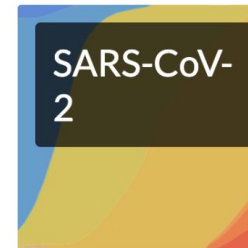
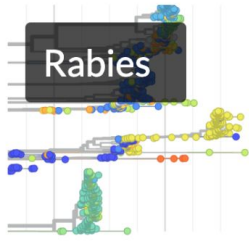
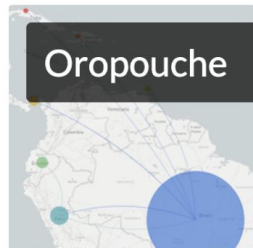
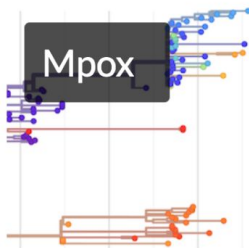
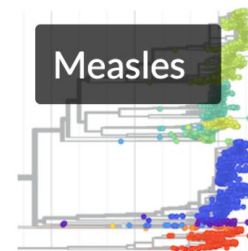
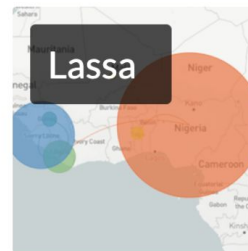
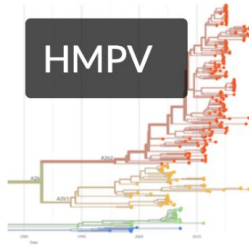
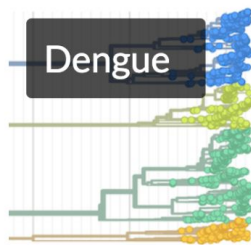
Nucleotide diversity of genome

RESET LAYOUT

ENTROPY EVENTS ⓘ



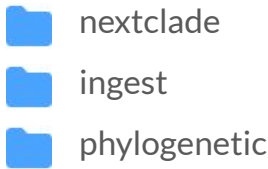
Pathogens with regularly updated global analyses



Each core pathogen consists of a package of resources

- **Open source pathogen repository**

github.com/nextstrain/mpox



- **Curated data**

data.nextstrain.org/files/workflows
/mpox/sequences.fasta.xz
/mpox/metadata.tsv.gz

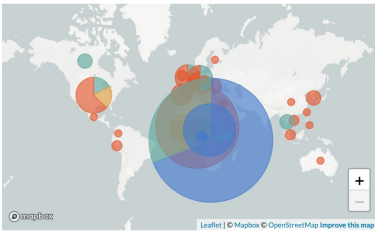
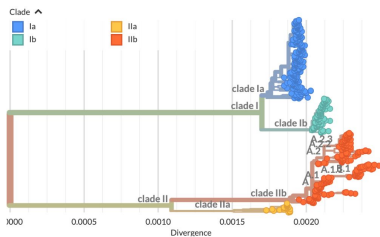
```
> SEQ_1
TATGGGTAGAATTA
> SEQ_2
CGTGAGCTTAACGC
```

id	date	region
SEQ_1	2023-03-01	Asia
SEQ_2	2024-10-17	Africa
SEQ_3	2025-04-05	Europe

- **Phylogenetic datasets**

nextstrain.org/mpox
/all-clades
/clade-I

...



- **Nextclade reference dataset**

clades.nextstrain.org

Sequence name	QC	Clade	Outbreak	Lineage	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.
MT903339	N M P C F S	IIb	hMPXV-1	A	9	0	0	99.8%	20	767
ON843165	N M P C F S	IIb	hMPXV-1	B.1.5	68	0	75	100.0%	88	100
KJ642617	N M P C F S	IIb			41	1	0	99.8%	55	797
Yambuku_DRC_1985	N M P C F S	Ia			815	0	0	100.0%	3133	3172
Ivory_Coast_2012	N M P C F S	IIa			555	0	0	100.0%	261	3087

Nextstrain-maintained pathogen analyses

These data represent analyses and situation-reports produced by the [core Nextstrain team](#).
Explore analyses produced by others on the [Groups](#) and [Community](#) pages.


We aim to provide a continually-updated view of publicly available data to show pathogen evolution and epidemic spread. The pipeline used to generate each dataset is available on [our GitHub page](#) or by loading a dataset and clicking the "built with" link at the top of the page.

Showcase resources: click to filter the resources to a pathogen



Filter by keywords in dataset names


Sort pathogens by: ☒ alphabetical ☐ most recently updated

 **avian-flu (influenza)** Most recent snapshot: 2024-09-14

Quick links: [h5n1/ha/2y](#) [h5nx/ha/2y](#) [h7n9/ha](#) [h9n2/ha](#)
➤ show 49 more datasets

- [avian-flu|h5n1-cattle-outbreak|genome](#) ↻ every few days (n=51)
- | [ha](#) ↻ every few days (n=25)
- | [mp](#) ↻ every few days (n=25)
- | [na](#) ↻ every few days (n=25)

- [avian-flu|h5n1-cattle-outbreak|np](#) ↻ every few days (n=25)
- | [ns](#) ↻ every few days (n=25)
- | [pa](#) ↻ every few days (n=25)
- | [pb1](#) ↻ every few days (n=25)

 **dengue** Most recent snapshot: 2024-09-10

- [dengue|all|E](#) ↻ every few days (n=50)
- | [genome](#) ↻ every few days (n=96)
- | [denv1|E](#) ↻ every few days (n=49)

- [dengue|denv11](#) ↻ weekly (n=10)
- | [denv2|E](#) ↻ every few days (n=49)
- | [genome](#) ↻ every few days (n=95)

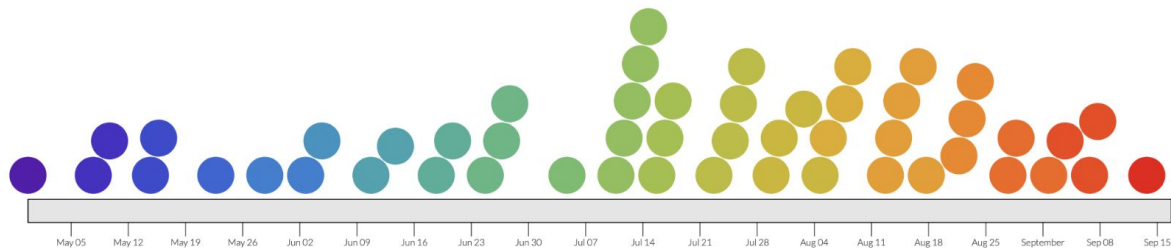
- [dengue|denv3|genome](#) ↻ every few days (n=96)
- | [denv4|E](#) ↻ every few days (n=49)
- | [genome](#) ↻ every few days (n=96)

Nextstrain-maintained pathogen analyses

avian-flu | h5n1-cattle-outbreak | genome

51 snapshots spanning 5 months: 2024-04-30 - 2024-09-14 (click to view the latest available snapshot)

Over the past two years this dataset's been updated consistently every ~2 days.



Each circle represents a previous snapshot of the dataset. **Mouse-over the light-grey axis box** to identify the latest available snapshot for any given date, and click to load the snapshot.

Alternatively, **hover over dots** to show the date the analysis was shared and **click on a dot** to load that particular snapshot.

Note: circles represent update date which may differ from when the analysis was run. An updated dataset doesn't necessarily mean there was new data. Finally, there may be a very recent upload which is newer than 2024-09-14 which is not shown on this page (loading the "latest available snapshot" will always fetch the latest version).

Showcase

Filter by

Sort path



• avian



• deng

• | genome ↻ every few days (n=96)

• | denv1|E ↻ every few days (n=49)

• | genome ↻ every few days (n=96)

• | denv2|E ↻ every few days (n=49)

• | genome ↻ every few days (n=95)

• | denv3|E ↻ every few days (n=49)

• | denv4|E ↻ every few days (n=49)

• | genome ↻ every few days (n=96)

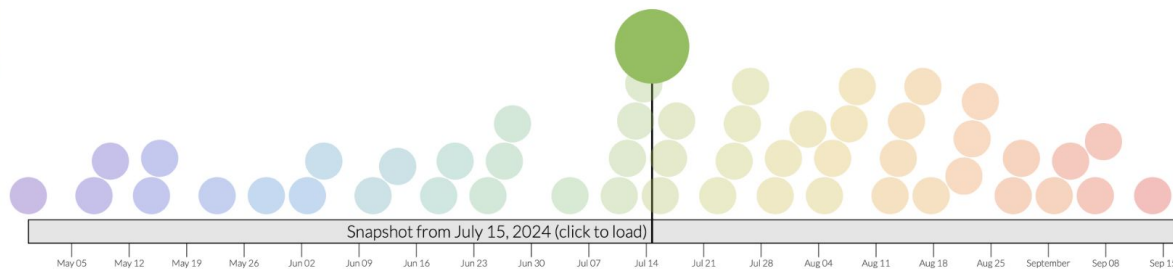
Nextstrain-maintained pathogen analyses

avian-flu | h5n1-cattle-outbreak | genome

51 snapshots spanning 5 months: 2024-04-30 - 2024-09-14 ([click to view the latest available snapshot](#))

Over the past two years this dataset's been updated consistently every ~2 days.

nextstrain.org/avian-flu/h5n1-cattle-outbreak/genome@2024-07-15



Each circle represents a previous snapshot of the dataset. **Mouse-over the light-grey axis box** to identify the latest available snapshot for any given date, and click to load the snapshot.

Alternatively, **hover over dots** to show the date the analysis was shared and **click on a dot** to load that particular snapshot.

Note: circles represent update date which may differ from when the analysis was run. An updated dataset doesn't necessarily mean there was new data. Finally, there may be a very recent upload which is newer than 2024-09-14 which is not shown on this page (loading the "latest available snapshot" will always fetch the latest version).

| genome ↻ every few days (n=96)

| denv1|E ↻ every few days (n=49)

| genome ↻ every few days (n=96)

| denv2|E ↻ every few days (n=49)

| genome ↻ every few days (n=95)

| denv3|E ↻ every few days (n=49)

| denv4|E ↻ every few days (n=49)

| genome ↻ every few days (n=96)

Full genome analysis of the ongoing influenza A/H5N1 cattle outbreak in North America

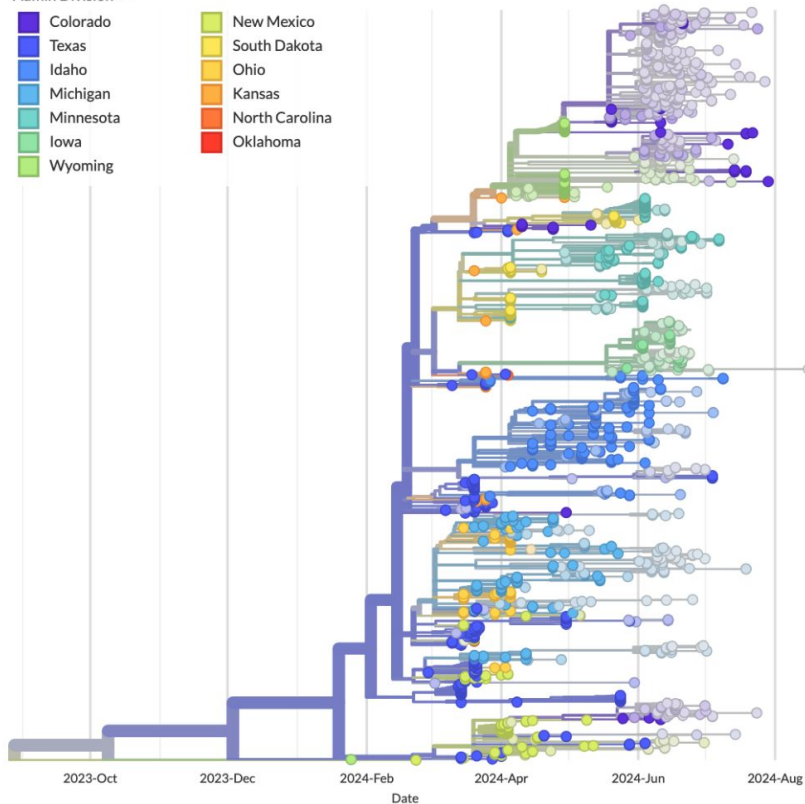
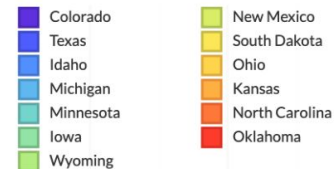


Built with [nextstrain/avian-flu](#). Maintained by [Louise Moncla](#) and the [Nextstrain team](#). Data updated 2024-09-16. Enabled by data from [USDA](#), [Andersen Lab](#) and [GenBank](#).

Showing 1465 of 1465 genomes sampled between Jan 2024 and Aug 2024.

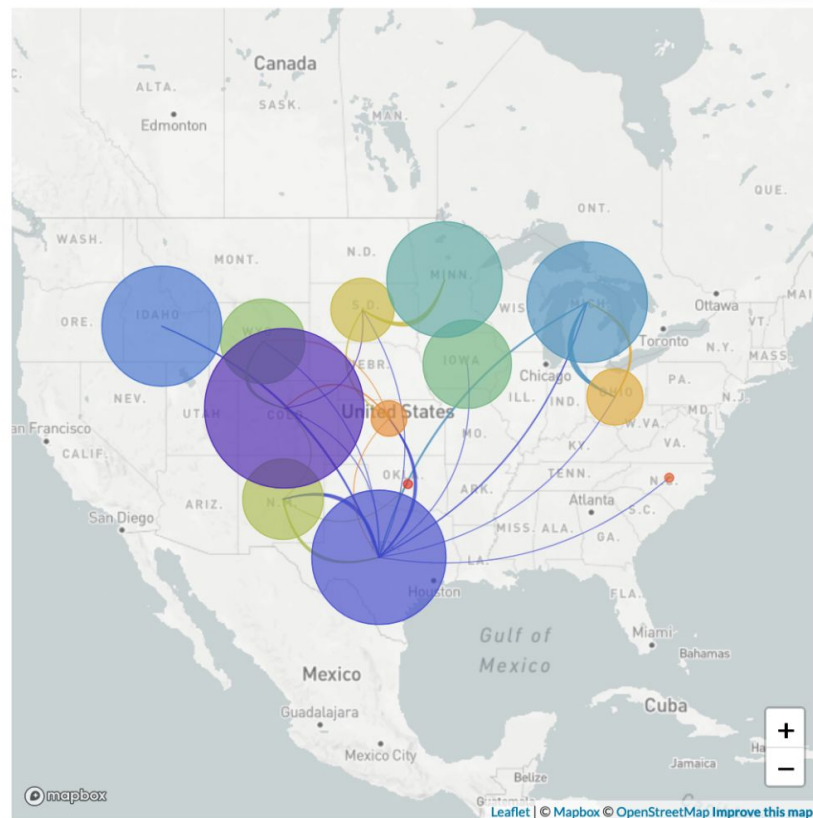
Phylogeny

Admin Division ^



Transmissions

RESET ZOOM



Full genome analysis of the ongoing influenza A/H5N1 cattle outbreak in North America



Built with [nextstrain/avian-flu](#). Maintained by [Louise Moncla](#) and [the Nextstrain team](#). Data updated 2024-09-16. Enabled by data from [USDA](#), [Andersen Lab](#) and [GenBank](#).

Showing 1465 of 1465 genomes sampled between Jan 2024 and Aug 2024.

Phylogeny



ZOOM TO SELECTED

RESET LAYOUT

Transmissions

RESET ZOOM

In addition to this cattle outbreak specific view, we have broader views of H5N1 evolution available as:

- [nextstrain.org/avian-flu/h5n1/ha/2y](#)
- [nextstrain.org/avian-flu/h5n1/na/2y](#)
- etc...

(click outside this box to return to the app)

View this dataset on other platforms:

Filter by Host (n=4)

Clicking on the following links will take you to an external site which will attempt to load the underlying data JSON which you are currently viewing. These sites are not part of Nextstrain and as such are not under our control, but we highly encourage interoperability across platforms like these.

Filter by Region (n=1)

nextclade

Use this tree as a nextclade reference dataset which allows you to add new sequences (via drag-and-drop) and see them placed on the tree. Note that manually curated datasets may be better suited to your use case, see [clades.nextstrain.org](#) for all reference datasets or read the [Nextclade Web documentation](#) for more details.

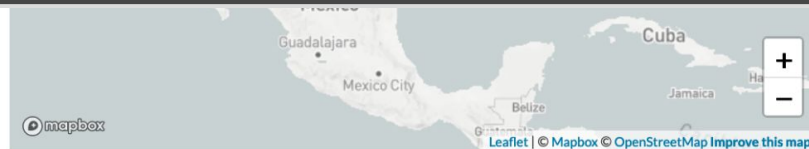
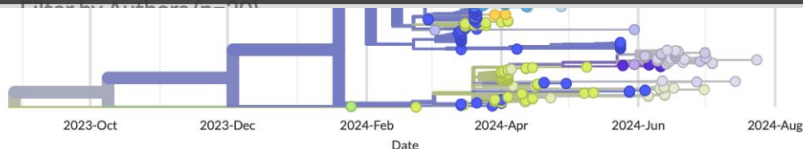
taxonum.org

Visualise this dataset in Taxonium ([learn more](#)).

microbetrace.cdc.gov

View this data in MicrobeTrace ([learn more](#)). Note that trees with over 500 tips may have trouble loading (this one has 1465).

Filter by Subtype (n=1)





Nextstrain

Real-time tracking of pathogen evolution

Name	Data stored on...	Accessed via...	Visibility	Managed by...
Nextstrain-maintained pathogens	nextstrain.org	nextstrain.org	Public	the Nextstrain team
Nextstrain Community	Your own GitHub repo	nextstrain.org/community/...	Public	You, via GitHub
Nextstrain Groups	nextstrain.org	nextstrain.org/groups/...	Public or private	You, via the Nextstrain CLI
Public URLs	Anywhere HTTPS-accessible	nextstrain.org/fetch/...	Public	You, via your web host
auspice.us ("auspicious")	Your computer	auspice.us	Private	You, via your file manager
Custom Auspice servers	Wherever you choose	Your own server's URL	Your choice	You, however you choose

Scalable Sharing with Nextstrain Groups

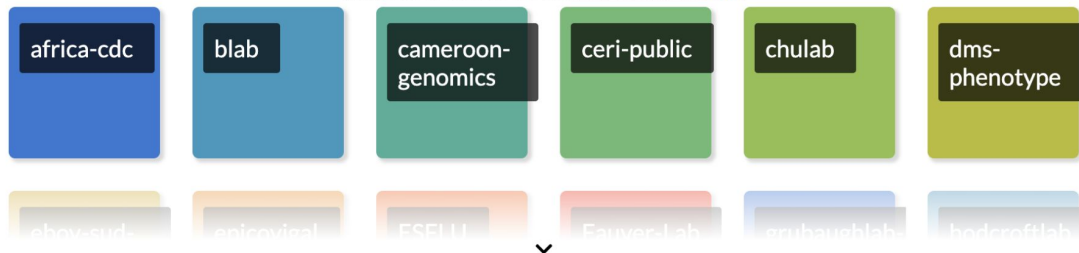
We want to enable research labs, public health entities and others to share their datasets and narratives through Nextstrain with complete control of their data and audience. Nextstrain Groups is more scalable than community builds in both data storage and viewing permissions. Datasets in a public group are accessible to the general public via [nextstrain.org](#), while private group data are only visible to logged in users with permission to see the data. A single entity can manage both a public and a private group in order to share data with different audiences.

For more details about Nextstrain Groups, [please see our documentation](#). For an alternative approach to sharing data through [nextstrain.org](#) which leverages GitHub repositories, please see [Community data sharing](#).

Nextstrain Groups is still in the early stages and require a Nextstrain team member to set up and add users. Please [contact us at hello@nextstrain.org](mailto:hello@nextstrain.org) and we'd be happy to set up a group for you.

Available groups

Click on any tile to view the different datasets and narratives available for that group. These groups are all public, to see private groups please [log in](#).



Genomic epidemiology of mpox clade I viruses: INRB build

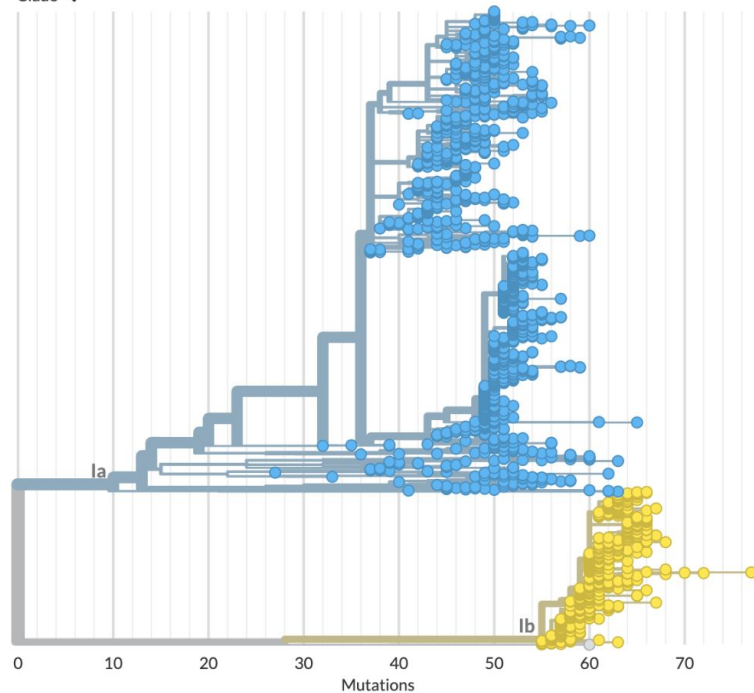


Built with [nextstrain/mpox](#). Maintained by [INRB](#) and [Nextstrain team](#). Data updated 2025-02-08. Enabled by data from INRB, DRC and [GenBank](#).

Showing 1804 of 1804 genomes sampled between Dec 1970 and Jan 2025.

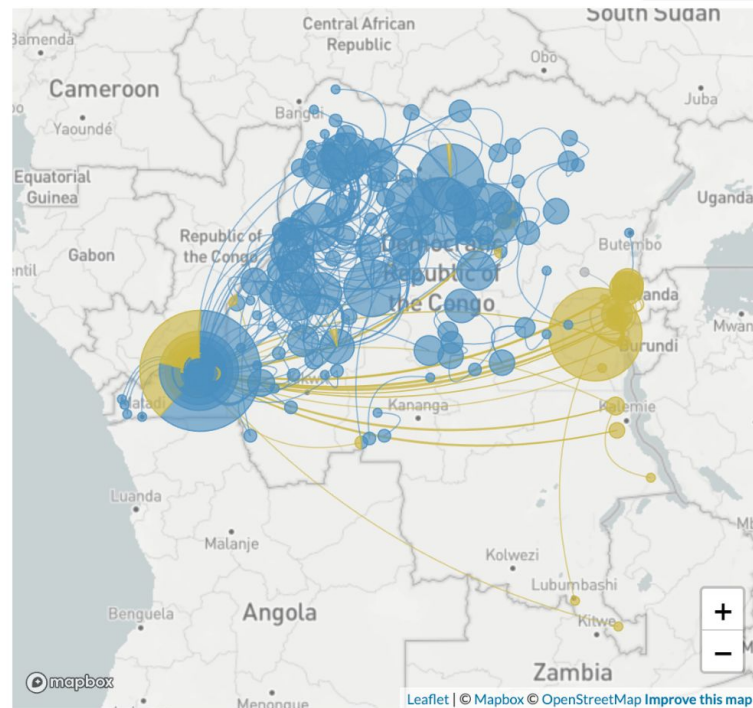
Phylogeny

Clade ▾



Transmissions

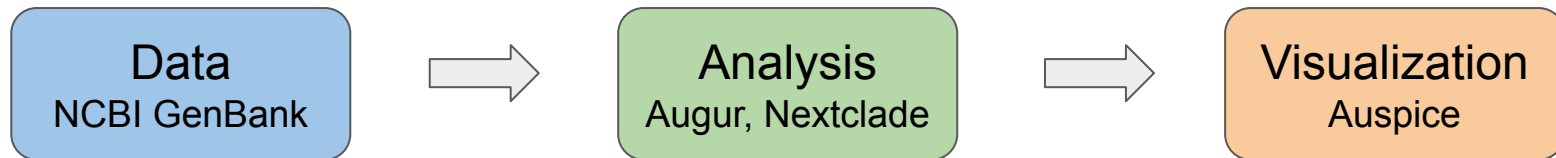
RESET ZOOM





Nextstrain

Real-time tracking of pathogen evolution



Nextstrain architecture

- Software:
 - Bioinformatics toolkit
 - Visualization app
- Real-time pathogen analyses at nextstrain.org



Nextstrain

Real-time tracking of pathogen evolution

Future directions

- Support larger datasets in phylogenetic analyses
- Support frequencies analyses and visualization
- Increase coverage of pathogens with real-time monitoring (e.g. ebola, tuberculosis)
- Facilitate running pathogen workflows with user data, config



Nextstrain

Real-time tracking of pathogen evolution

Resources

- Tutorials: docs.nextstrain.org
- Discussion board: discussion.nextstrain.org
- Email: hello@nextstrain.org
- Nextstrain Office Hours (email for details)



Trevor Bedford,



Richard Neher,



Ivan Aksamentov,



John SJ Anderson,



Kim Andrews,



Jennifer Chang,



James Hadfield,



Emma Hodcroft,



John Huddleston,



Jover Lee,



Victor Lin,



Cornelius Roemer,



Thomas Sibley