

# **Phylogenetics for Predicting Virus Evolution**

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**Anticipating next seasons influenza strains**

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## Problem



HOUSTON,  
we have a — CHOO!

- Estimated 3 – 11% of the population catch symptomatic influenza each season [Tokars et al., 2018]
- Influenza evolves rapidly and evades immunity and vaccines
- Epidemics and pandemics caused by RNA recombination events
- Science is slow responding to health issues

# Problem

- $\sim 8$  months from submission to publication of a medical paper [AAMC, 2018]
- $\sim 6$  months from vaccine strain selection to distribution:



Figure 1: [Bedford, 2015]

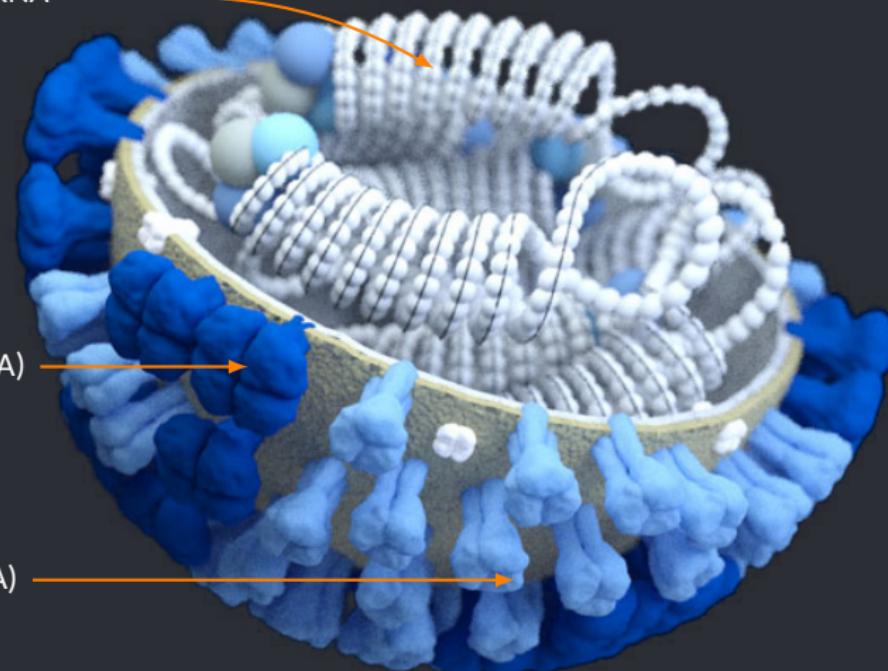
# Outline

1. Influenza
2. Phylogenetics
  - 2.1 The Molecular Clock
  - 2.2 Sequence Alignment
  - 2.3 Inferring the tree
  - 2.4 Predicting Virus Evolution
  - 2.5 The Hemagglutination Inhibition Assay
3. Predicting the next strain of influenza
  - 3.1 Results
4. *Nextstrain*
  - 4.1 How to use the Framework
  - 4.2 The Powerful Meta Data
  - 4.3 Confidence Levels and Limitations

# Influenza

*—a closer look*

8 single stranded RNA



Neuraminidase (NA)

Hemagglutinin (HA)

# Influenza

*—the recent history*

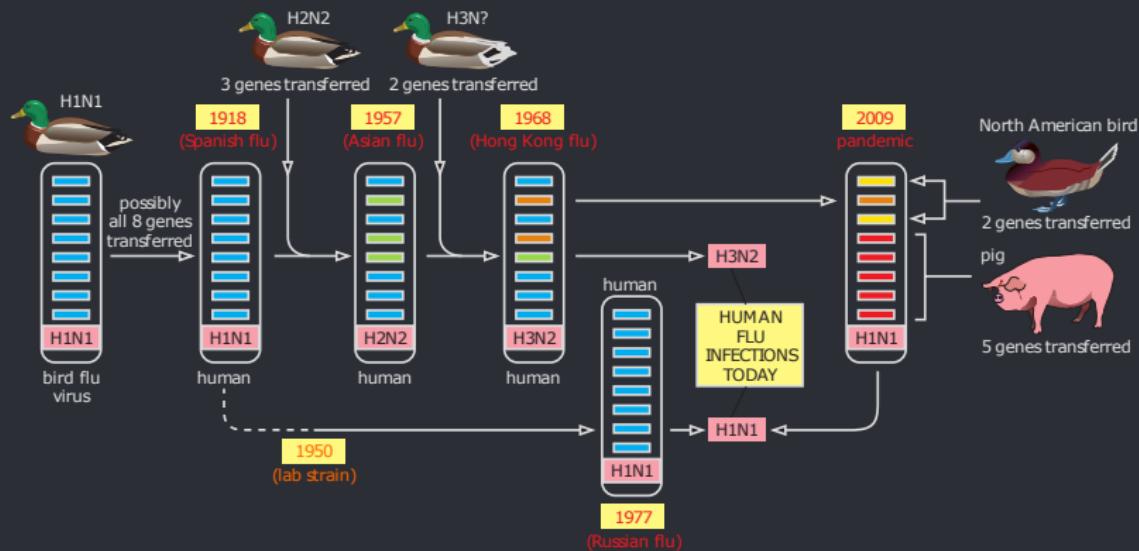


Figure 2: taken from [Alberts, 2015]

# Influenza

—*the phylogeny*

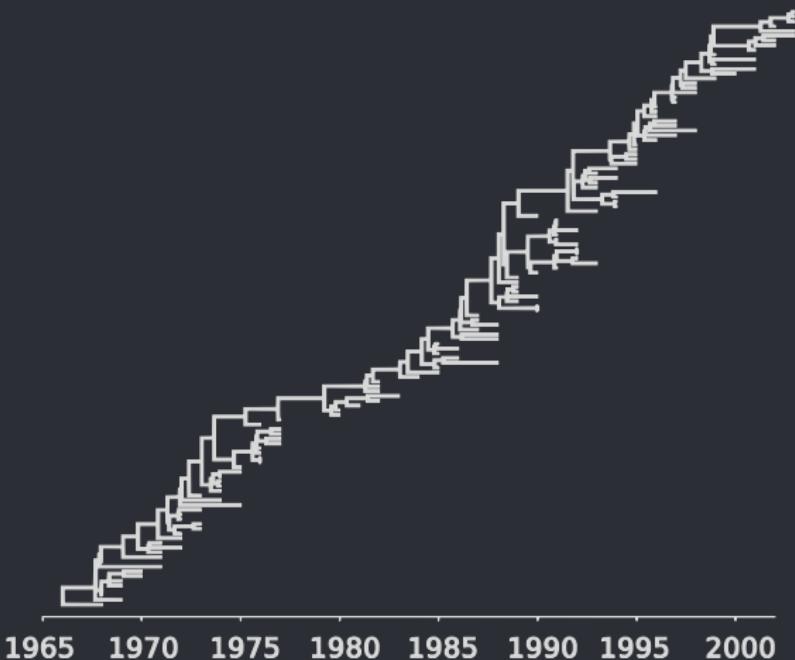


Figure 3:

# Influenza

*A virus that does not change escape vehicle will get caught*



Figure 4: It's like getting more and more stars, having to switch escape vehicle constantly

# Phylogenetics

*An old idea*

Haeckel, Darwin

# Phylogenetics

## Concept: The Molecular Clock

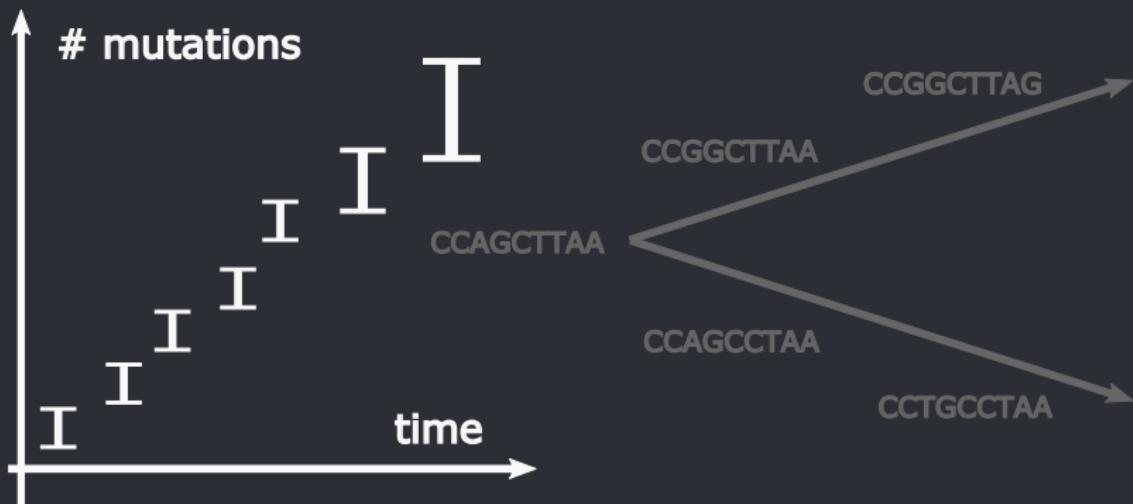


Figure 5: Linear time-mutation relationship

# Phylogenetics

Concept: The Molecular Clock

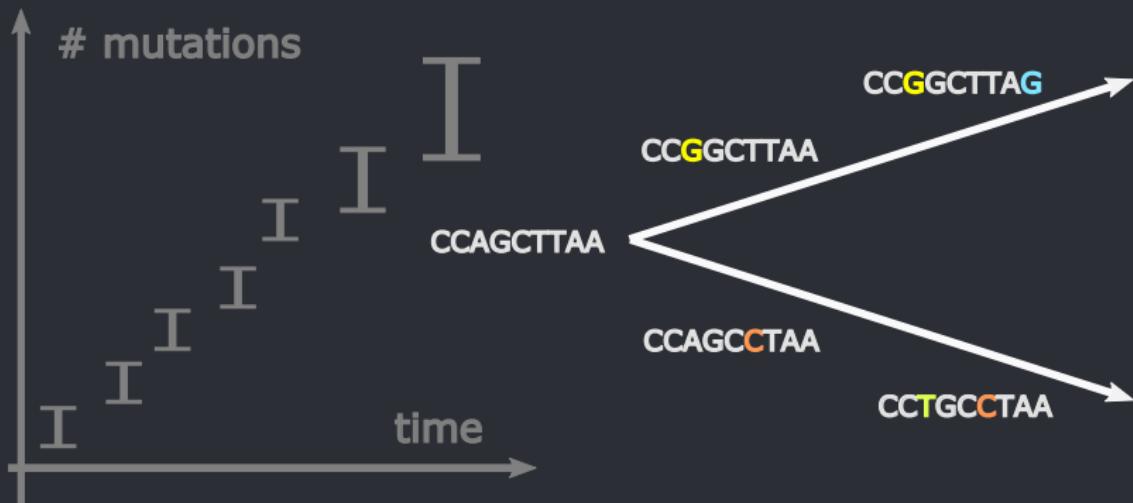


Figure 6: Linear time-mutation relationship

Corroborated by genetic equidistance.

Limited by complete turnover time.

# Sequence Alignment

*An example algorithm*

# Inferring the tree

## *Basic Principles*

Parsimony — Ockhams razor, Cost function

Epidemiological: Is there a geographical region?

Genealogical: Is there a certain type of Mutation?

Immunological: Hemagglutinin inhibition cartography

(Denote the scales here: Molecule/Cell/Population)

Vision: Bring these levels together

# The Hemagglutination Inhibition Assay

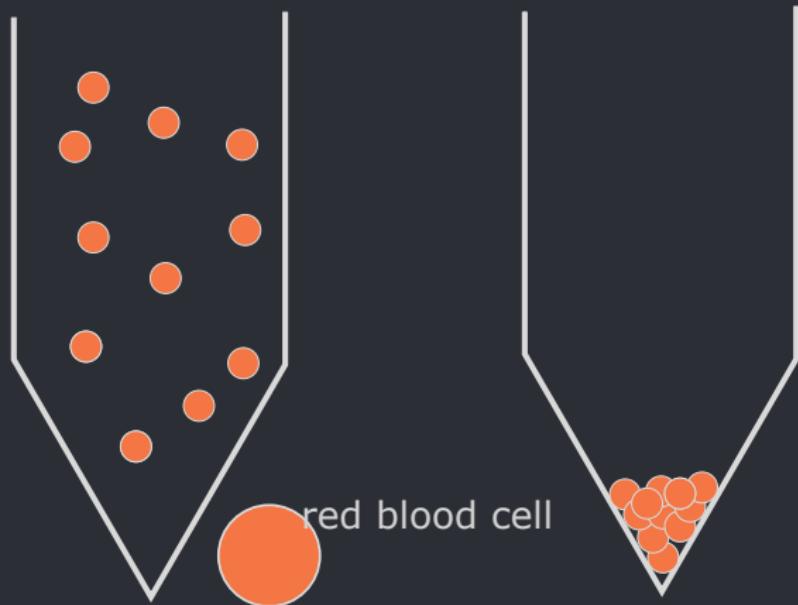


Figure 7: Red blood cells (RBC) precipitate.

## The Hemagglutination Inhibition Assay

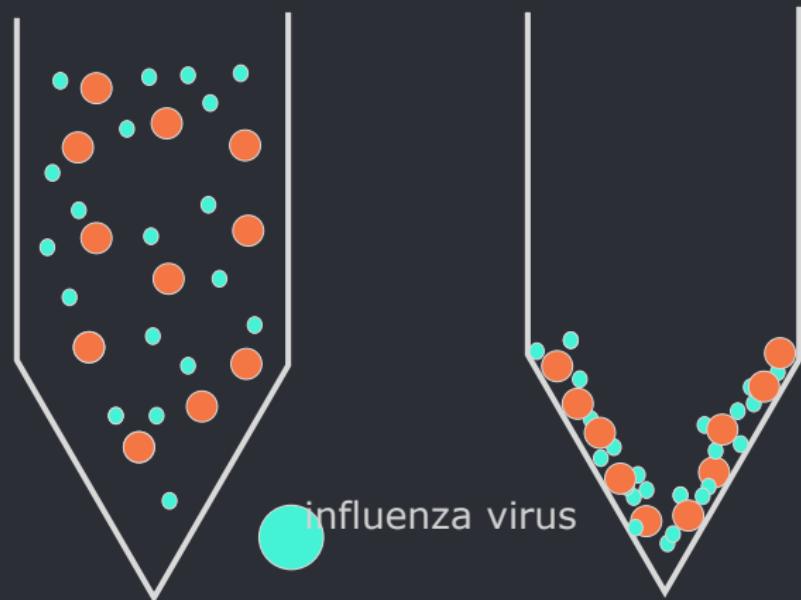


Figure 8: Influenza Hemagglutinin (HA) coagulates the RBC, forming a mat.

## The Hemagglutination Inhibition Assay

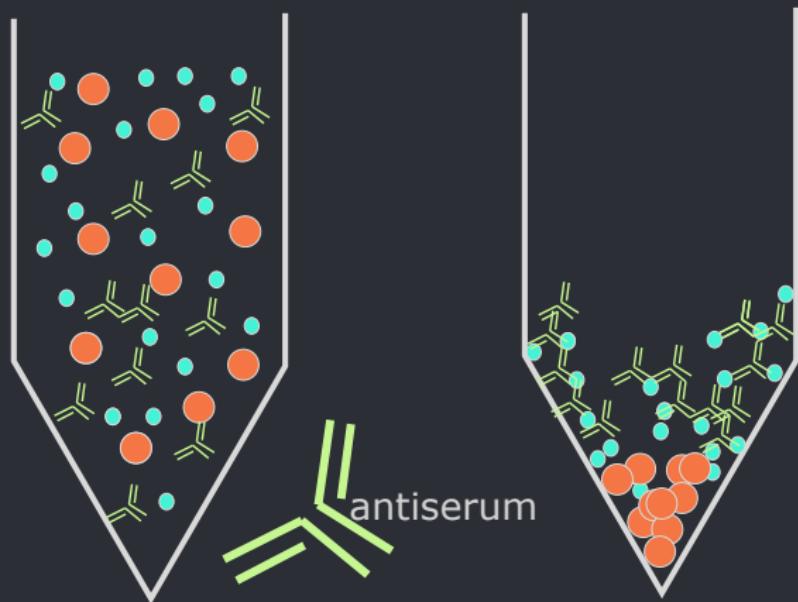


Figure 9: Antisera of the same *serotype* clump the HA, letting the RBC sink to the bottom. This is an (antiserum) concentration dependent process.

# The Hemagglutination Inhibition Assay

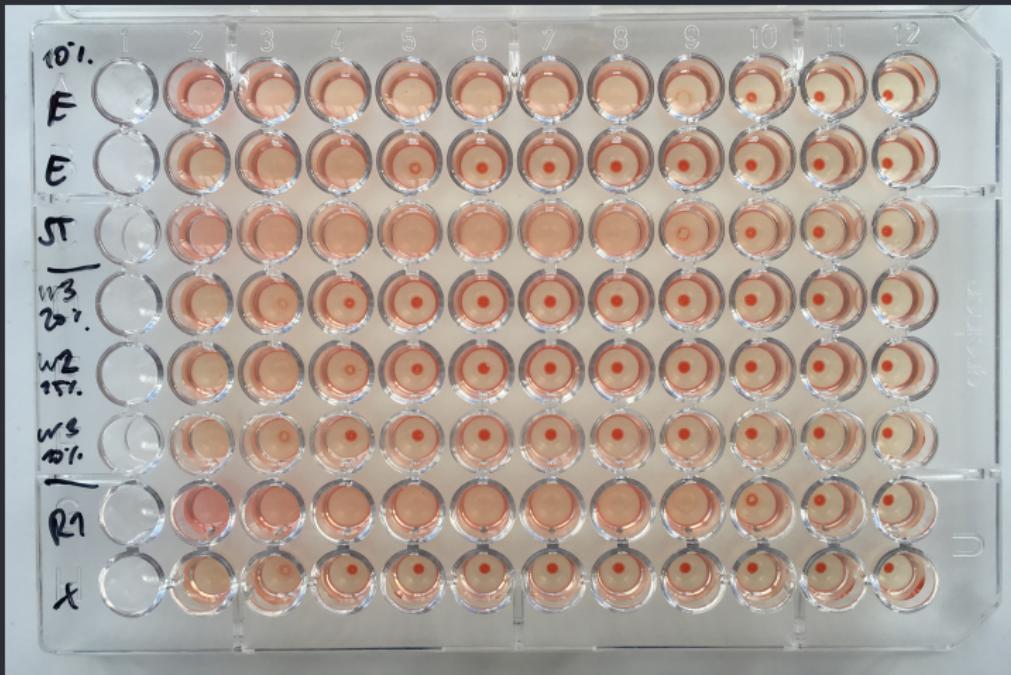
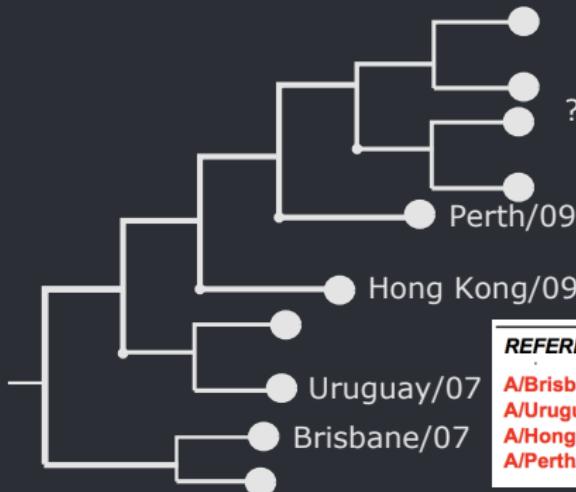


Figure 10: Here, one antiserum is tested in 12 different dilutions against 8 different virus strains. The highest dilution that prevents agglutination is called the titer.

# The Hemagglutination Inhibition Assay

*How this used to be looked at*

# The Hemagglutination Inhibition Assay



REFERENCE VIRUSES	A/Bris	A/Uru	A/HK	A/Perth
A/Brisbane/10/2007	2560	2560	80	<
A/Uruguay/7/16/2007	1280	2560	<	<
A/Hong Kong/1985/2009	80	160	1280	640
A/Perth/16/2009	<	40	640	640

Figure 11: Mapping the chart to the tree constructed from sequences

# The Hemagglutination Inhibition Assay

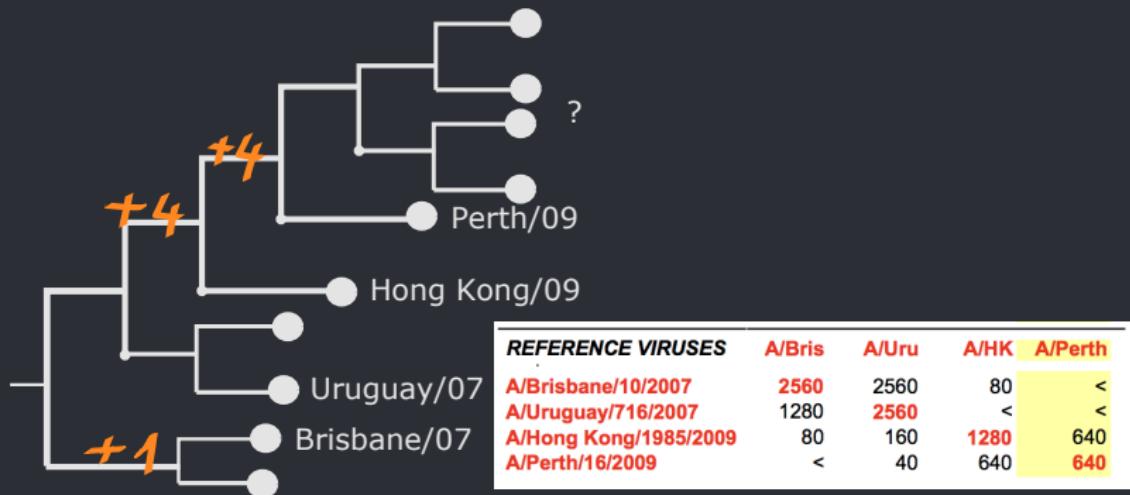
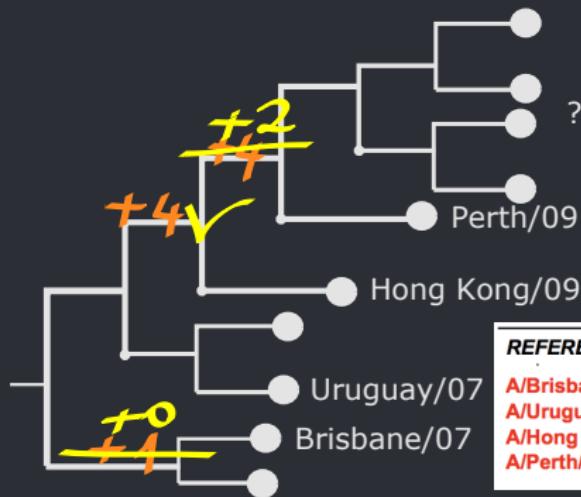


Figure 12: Here, one antiserum is tested in 12 different dilutions against 8 different virus strains. The highest dilution that prevents agglutination is called the titer.

# The Hemagglutination Inhibition Assay

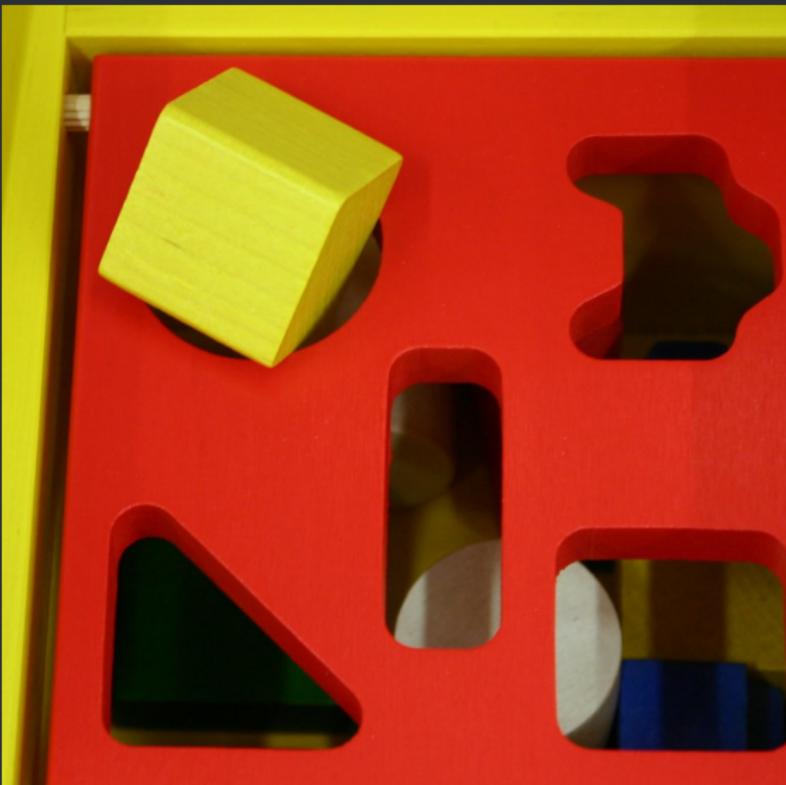


REFERENCE VIRUSES	A/Bris	A/Uru	A/HK	A/Perth
A/Brisbane/10/2007	<b>2560</b>	2560	80	<
A/Uruguay/716/2007	1280	<b>2560</b>	<	<
A/Hong Kong/1985/2009	80	160	<b>1280</b>	640
A/Perth/16/2009	<	40	640	<b>640</b>

Figure 13: Here, one antiserum is tested in 12 different dilutions against 8 different virus strains. The highest dilution that prevents agglutination is called the titer.

# The Hemagglutination Inhibition Assay

*The asymmetry makes sense, think of it like this but with more dimensions*



## Formulas I

$T_{a\beta}$  ..... HI titer of virus  $a$  against antiserum  $\beta$  (virus  $b$ )

$H_{a\beta}$  .....  $\log_2$  relative titer (we'll use this one)

$$H_{a\beta} = \log_2 T_{b\beta} - \log_2 T_{a\beta} \quad (1)$$

$\hat{H}_{a\beta}$  ..... predicted  $\log_2$  relative titer

$v_a$  ..... avidity of virus  $a$  (=greediness)

$p_\beta$  ..... potency of antiserum  $\beta$  (=effectiveness)

$D_{a\beta}$  ..... genetic component of titer drop

$$\hat{H}_{a\beta} = v_a + p_\beta + D_{ab} \quad (2)$$

## Formulas II

What remains is split up into a sum over individual mutation contributions:

$$D_{ab} = \sum_{i \in (a \dots b)} d_i \quad (3)$$

Where the sum is over the path connecting virus  $a$  and virus  $b =$  antiserum  $\beta$ . Now we want

$$\hat{H}_{a\beta} \stackrel{!}{=} H_{a\beta} \quad (4)$$

so we minimize a cost function  $C$  of the whole tree:

$$C := \sum_{a,\beta} (\hat{H}_{a\beta} - H_{a\beta})^2 + \lambda \sum_i d_i + \gamma \sum_a v_a^2 + \delta \sum_\alpha p_\alpha^2 \quad (5)$$

# Results

## *tree model*

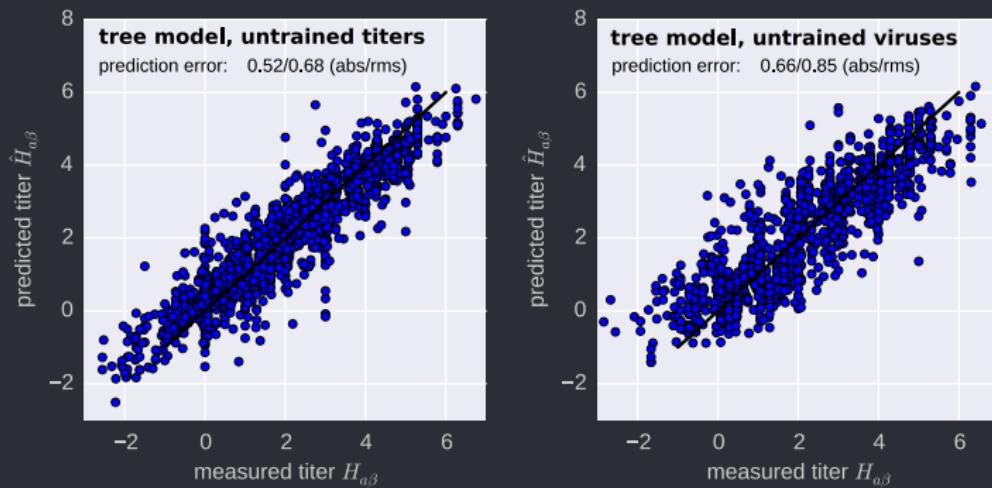


Figure 15: a

# Results

## *tree model hist*

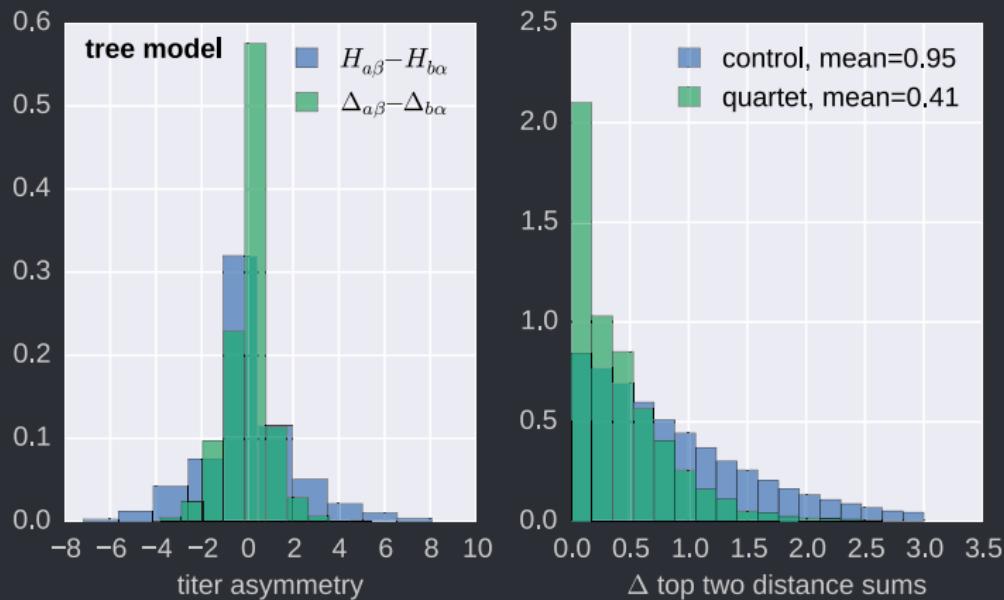


Figure 16: a

# Results

## *recent antigenic evolution*

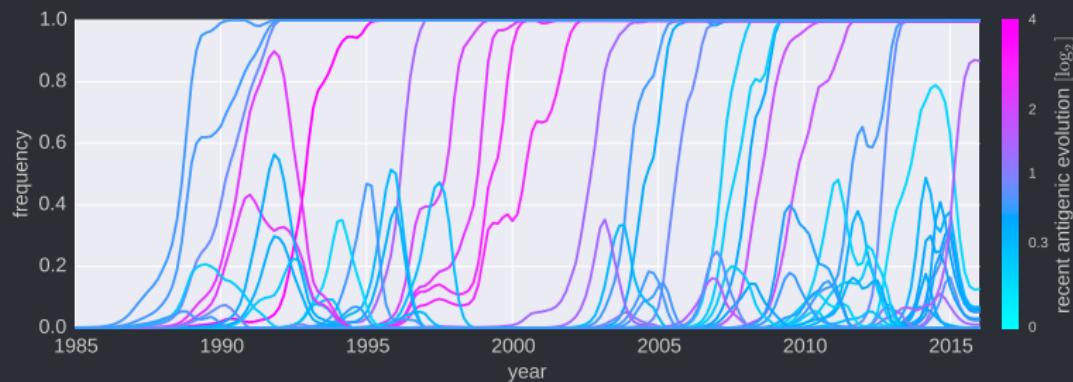


Figure 17: a

# Results

*fraction frequency threshold color bar*

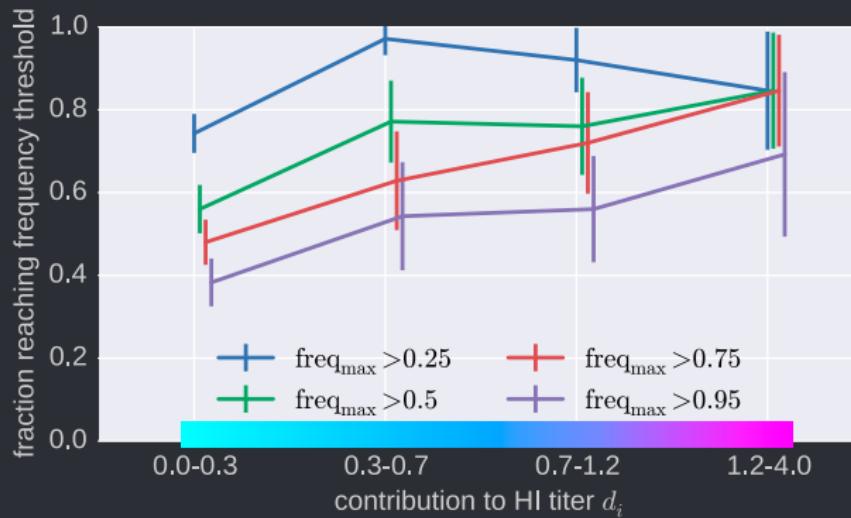


Figure 18: a

# Results

## *cumulative antigenic change*

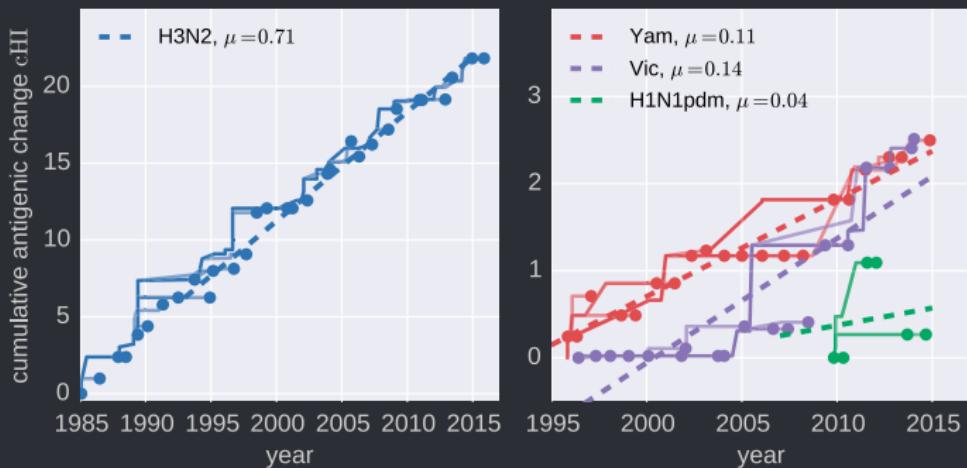


Figure 19: a

## Results

*distance to season year*

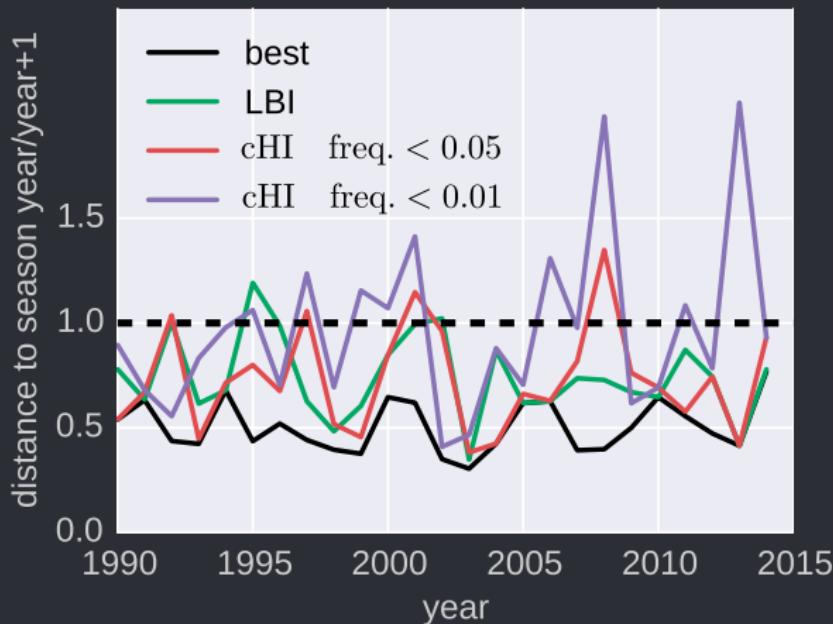


Figure 20: a

## Results

*years antigenic advance*

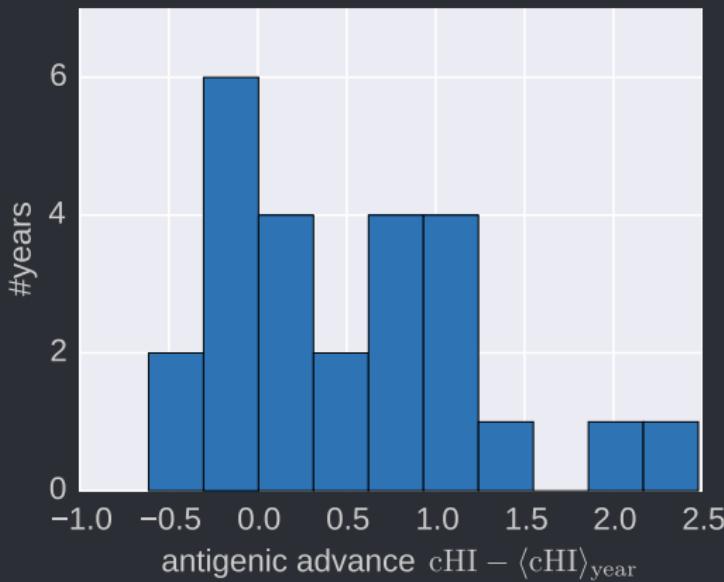


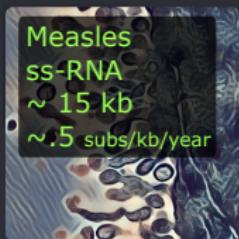
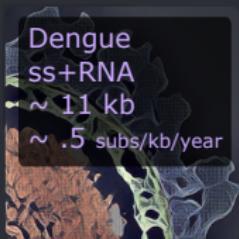
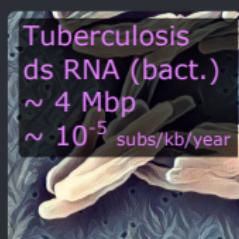
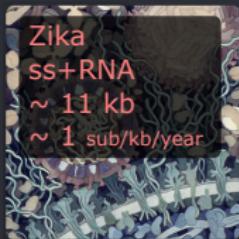
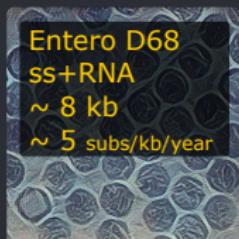
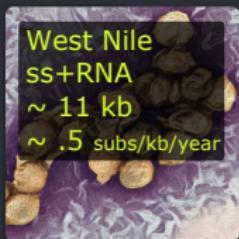
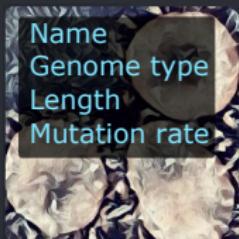
Figure 21: a

*Nextstrain*

*Mending pieces together*

Please visit [nextstrain.org/narratives/](https://nextstrain.org/narratives/)

# Nextstrain: How to use the Framework (this is mirrored in the narrative)



## **Nextstrain: The Powerful Meta Data**

*(this is mirrored in the narrative)*

## *Nextstrain: Confidence Levels and Limitations*

*(this is mirrored in the narrative)*

## Multi Scale Evolution

If a single event mutation occurs, say **D 186 G** in the HA genome, it is subject to multi scale evolutionary selection:

- this RNA instance vs. the other RNA strands in the same cell
- this cell's mutated viruses vs. other viruses inside the host
- this host's viruses vs. viruses in rest of the population
- this population vs. other populations

These scales are difficult to separate. At the population level *epidemiological* processes may dominate.

# Conclusion

*...and why Nextstrain is awesome*

# References I

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- [Alberts, 2015] Alberts, B. (2015).  
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