

# Phylogenetics for Predicting Virus Evolution

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**Can we anticipate next seasons dominant influenza strain from sequence alignment?**

Paul Wiesenmeyer

# Problem

- Influenza evading immunity
- Pandemics as with SARS-CoV-2
- "Houston, we have aah—CHOO!"
- 3 — 11% of the population catch symptomatic influenza each season. CITATION
- Influenza mutates quickly at  $\sim 2$  mutations / kilobases / year
- No one can tell next seasons circulating influenza strains.
- Antigenic shift can cause sudden epidemics and even pandemics.
- How can we take informed counter measures on a global level?

# Outline for Section 1

## 1. Influenza and Vaccines

### 1.1 Basics

### 1.2 The Hemagglutination Inhibition Assay

## 2. Phylogenetics

### 2.1 The Molecular Clock

### 2.2 Sequence Alignment

### 2.3 Building A Phylogenetic Tree

## 3. *Nextstrain*

### 3.1 How to use the Framework

### 3.2 The Powerful Metadata

### 3.3 Confidence Levels and Limitations

# Influenza and Vaccines

*Influenza—an artful disguise master*

# Basics

*Where does influenza come from?*

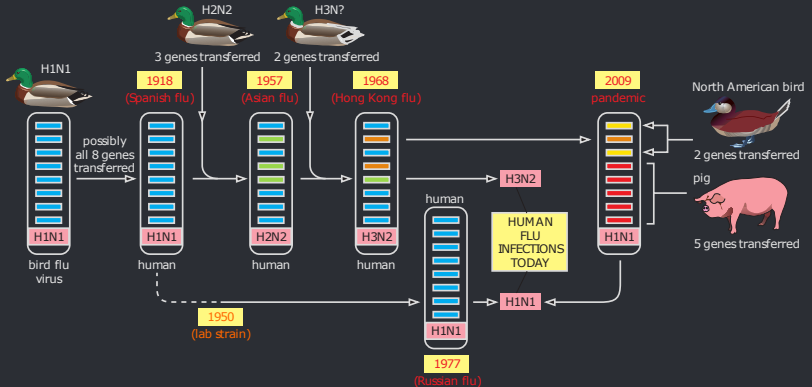


Figure: taken from CITATION Alberts

## The Hemagglutination Inhibition Assay

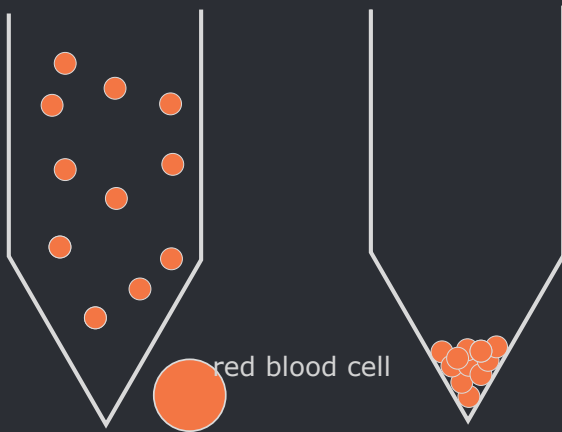


Figure: Red blood cells (RBC) precipitate.

## The Hemagglutination Inhibition Assay

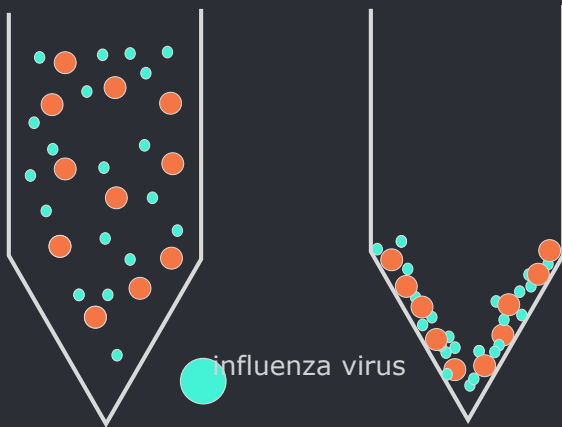


Figure: Influenza Hemagglutinin (HA) coagulates the RBC, forming a mat.

# The Hemagglutination Inhibition Assay

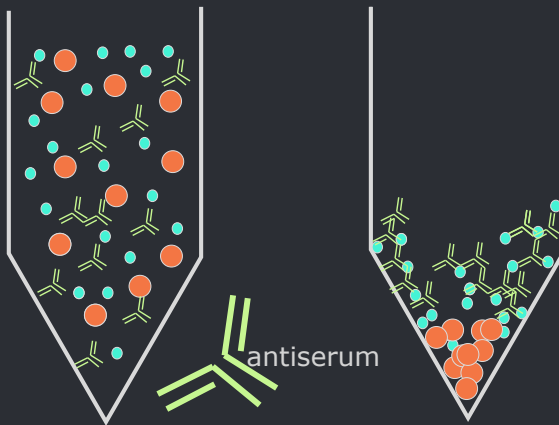


Figure: Antisera of the same *serotype* clump the HA, letting the RBC sink to the bottom. This is an (antiserum) concentration dependent process.



# The Hemagglutination Inhibition Assay

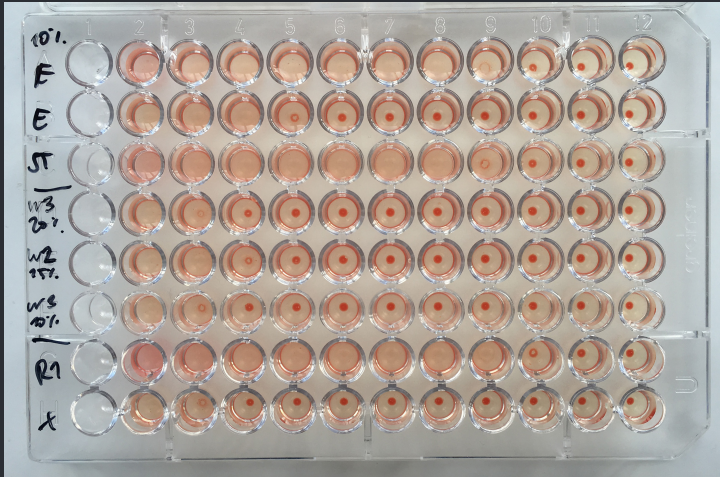


Figure: Here, one antiserum is tested in 12 different dilutions against 8 different virus strains. The highest dilution that prevents agglutination is called the titer.

# Outline for Section 2

## 1. Influenza and Vaccines

### 1.1 Basics

### 1.2 The Hemagglutination Inhibition Assay

## 2. Phylogenetics

### 2.1 The Molecular Clock

### 2.2 Sequence Alignment

### 2.3 Building A Phylogenetic Tree

## 3. *Nextstrain*

### 3.1 How to use the Framework

### 3.2 The Powerful Metadata

### 3.3 Confidence Levels and Limitations

# Phylogenetics

*An old idea*

# Phylogenetics: The Molecular Clock

# Phylogenetics: Sequence Alignment

# Phylogenetics: Building A Phylogenetic Tree

—*from sequenced data*

# Outline for Section 3

## 1. Influenza and Vaccines

### 1.1 Basics

### 1.2 The Hemagglutination Inhibition Assay

## 2. Phylogenetics

### 2.1 The Molecular Clock

### 2.2 Sequence Alignment

### 2.3 Building A Phylogenetic Tree

## 3. *Nextstrain*

### 3.1 How to use the Framework

### 3.2 The Powerful Metadata

### 3.3 Confidence Levels and Limitations

**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 Metadata*

*(this is mirrored in the narrative)*

## Nextstrain: Confidence Levels and Limitations

*(this is mirrored in the narrative)*

## Conclusion

*...and why Nextstrain is awesome*

# References