

Phylogenetics for Predicting Virus Evolution

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

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Outline for Section 1

1. Motivation

- 1.1 Viruses evolve – but what's the problem?
- 1.2 How do we measure virus evolution?
- 1.3 But wait!—wouldn't a graph make more sense?

2. A powerful data synthesis

- 2.1 The lab approach to vaccines: HI assay
- 2.2 The computer scientist's approach: Sequence alignment
- 2.3 Constructing a phylogenetic tree
- 2.4 What predictions can we make?

3. Going forward: the Metadata

- 3.1 Visualizing spread and evolution on a world map

4. Making the project smart: Building a community

Outline for Section 2

1. Motivation

- 1.1 Viruses evolve – but what's the problem?
- 1.2 How do we measure virus evolution?
- 1.3 But wait!—wouldn't a graph make more sense?

2. A powerful data synthesis

- 2.1 The lab approach to vaccines: HI assay
- 2.2 The computer scientist's approach: Sequence alignment
- 2.3 Constructing a phylogenetic tree
- 2.4 What predictions can we make?

3. Going forward: the Metadata

- 3.1 Visualizing spread and evolution on a world map

4. Making the project smart: Building a community

Outline for Section 3

1. Motivation

- 1.1 Viruses evolve – but what's the problem?
- 1.2 How do we measure virus evolution?
- 1.3 But wait!—wouldn't a graph make more sense?

2. A powerful data synthesis

- 2.1 The lab approach to vaccines: HI assay
- 2.2 The computer scientist's approach: Sequence alignment
- 2.3 Constructing a phylogenetic tree
- 2.4 What predictions can we make?

3. Going forward: the Metadata

- 3.1 Visualizing spread and evolution on a world map

4. Making the project smart: Building a community

Outline for Section 4

1. Motivation

- 1.1 Viruses evolve – but what's the problem?
- 1.2 How do we measure virus evolution?
- 1.3 But wait!—wouldn't a graph make more sense?

2. A powerful data synthesis

- 2.1 The lab approach to vaccines: HI assay
- 2.2 The computer scientist's approach: Sequence alignment
- 2.3 Constructing a phylogenetic tree
- 2.4 What predictions can we make?

3. Going forward: the Metadata

- 3.1 Visualizing spread and evolution on a world map

4. Making the project smart: Building a community