# TRACKING VIRAL OUTBREAKS IN REAL TIME

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Connect the fields of programming and biology

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- Use real tools for computational biology

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- Use real tools for computational biology
- Explore patterns in virus evolution

#### WHO AM I?

- Ph.D. student in a virus evolution lab at the Fred Hutch
- Professional programmer for 8 years
- M.S. in computer science and biology

#### WHO ARE YOU?

- Rising 10th and 11th grade students
- Programmers?
- Scientists?

#### THE PLAN FOR TODAY

- 1. Introductions
- 2. Reconstructing the Ebola outbreak with freely available tools
- 3. Exploring the Ebola outbreak with Nextstrain

# OUTCOMES FOR THIS WORKSHOP

At the end of this workshop you will know how to:

- Identify viral sequences from online databases
- Construct a multiple sequence alignment
- Build a phylogenetic tree
- Interpret ancestral relationships between organisms in a tree

### ORIGINS OF AN OUTBREAK



# QUESTIONS WE NEED TO ANSWER

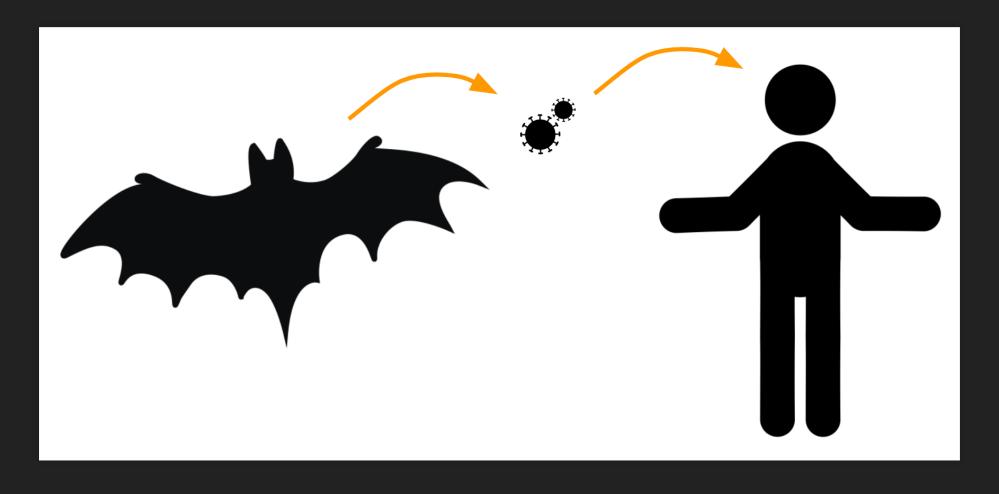
- What is the infectious unit?
- Where is the outbreak?
- How is it transmitted geographically?
- How is it transmitted between people?
- How is it evolving?

### WHERE IS THE OUTBREAK?



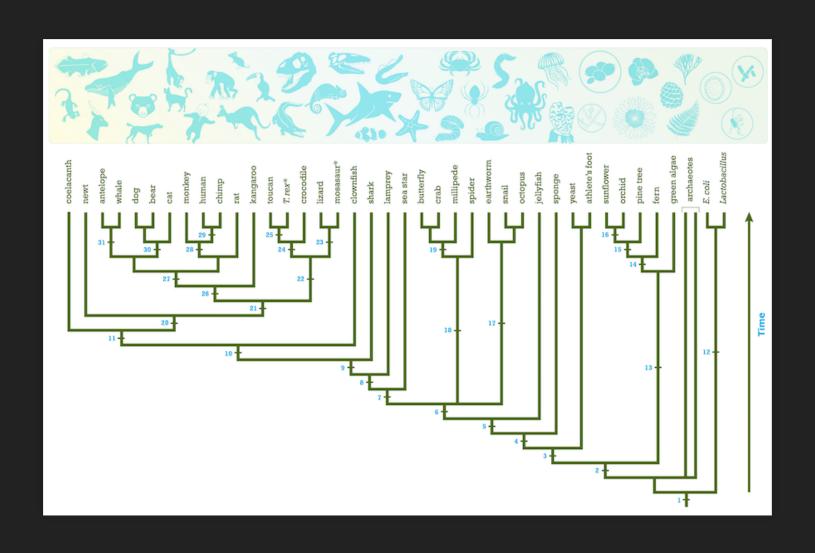
# HOW IS THE VIRUS TRANSMITTED?

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# MUTATIONS CAN ALTER PROTEINS

# MUTATIONS INFORM ANCESTRAL RELATIONSHIPS





#### **EXPLORE ONLINE TOOLS**

https://www.ncbi.nlm.nih.gov/genomes/VirusVariation/Database

Or, Google:

ncbi virus variation database

### FILTER EBOLA SEQUENCES

Select sequence type				
● Protein Nucleotide ✓ Full-length sequences only				
Define search set				
Species	Host	Region/Country	Genome region	Isolation source
Bundibugyo ebolavirus Tai Forest ebolavirus Sudan ebolavirus Reston ebolavirus Zaire ebolavirus  Collection date: Release date:	Unknown Bat Chimpanzee Gorilla Human  to  Month Day Year	any regions Africa Asia Europe  Month Day	Polymerase complex protein Matrix protein Second secreted glycoprotein Small secreted glycoprotein Spike glycoprotein	any abdominal cavity blood cerebrospinal fluid heart
Additional filters				
Add query Show results Collapse identical sequences				

### ALIGN SEQUENCES

- 1. Build sequence alignment
- 2. Browse alignment
- 3. Download alignment ("Fasta plus gaps")
- 4. View alignment at http://msa.biojs.net/app/

#### BUILD A PHYLOGENETIC TREE

- 1. Build phylogenetic tree
- 2. Collapse view to "viewport"
- 3. Explore patterns

# EXPLORE EBOLA OUTBREAK WITH NEXTSTRAIN

https://nextstrain.org/ebola

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https://nextstrain.org/ebola

- Where did Ebola emerge? Where did it expand most rapidly?
- When did the outbreak start?
- What mutations were associated with the outbreak?
- How does the mutation rate of Ebola compare to other viruses?

# BEHIND THE SCENES OF NEXTSTRAIN

https://github.com/nextstrain

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You can contribute to the tools and/or the science

### **THANK YOU!**

More at https://github.com/huddlej/workshop-2018-hutch-explorers