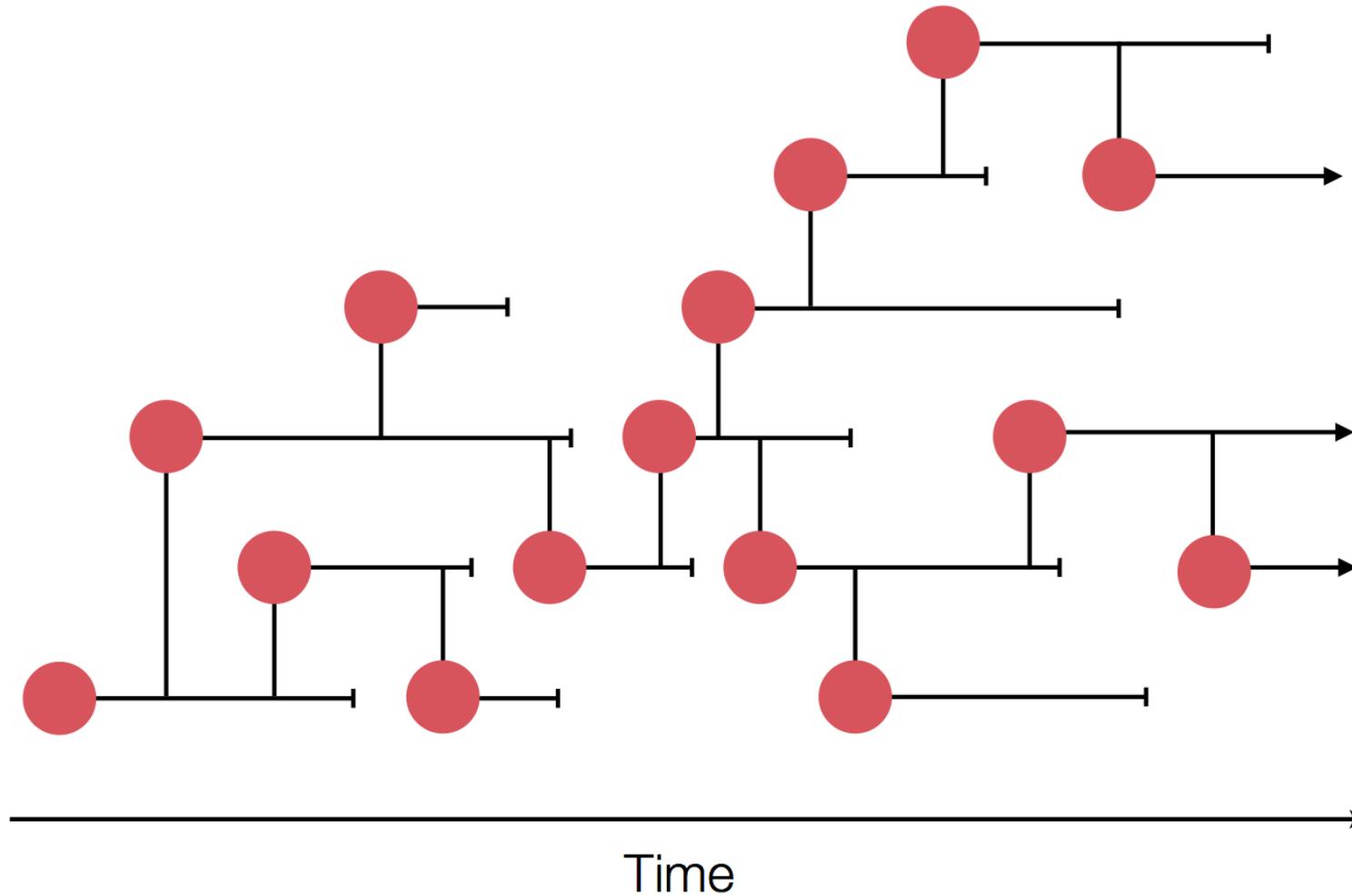


Nextstrain, SARS-CoV-2, and making epidemiologic inferences from sequence data

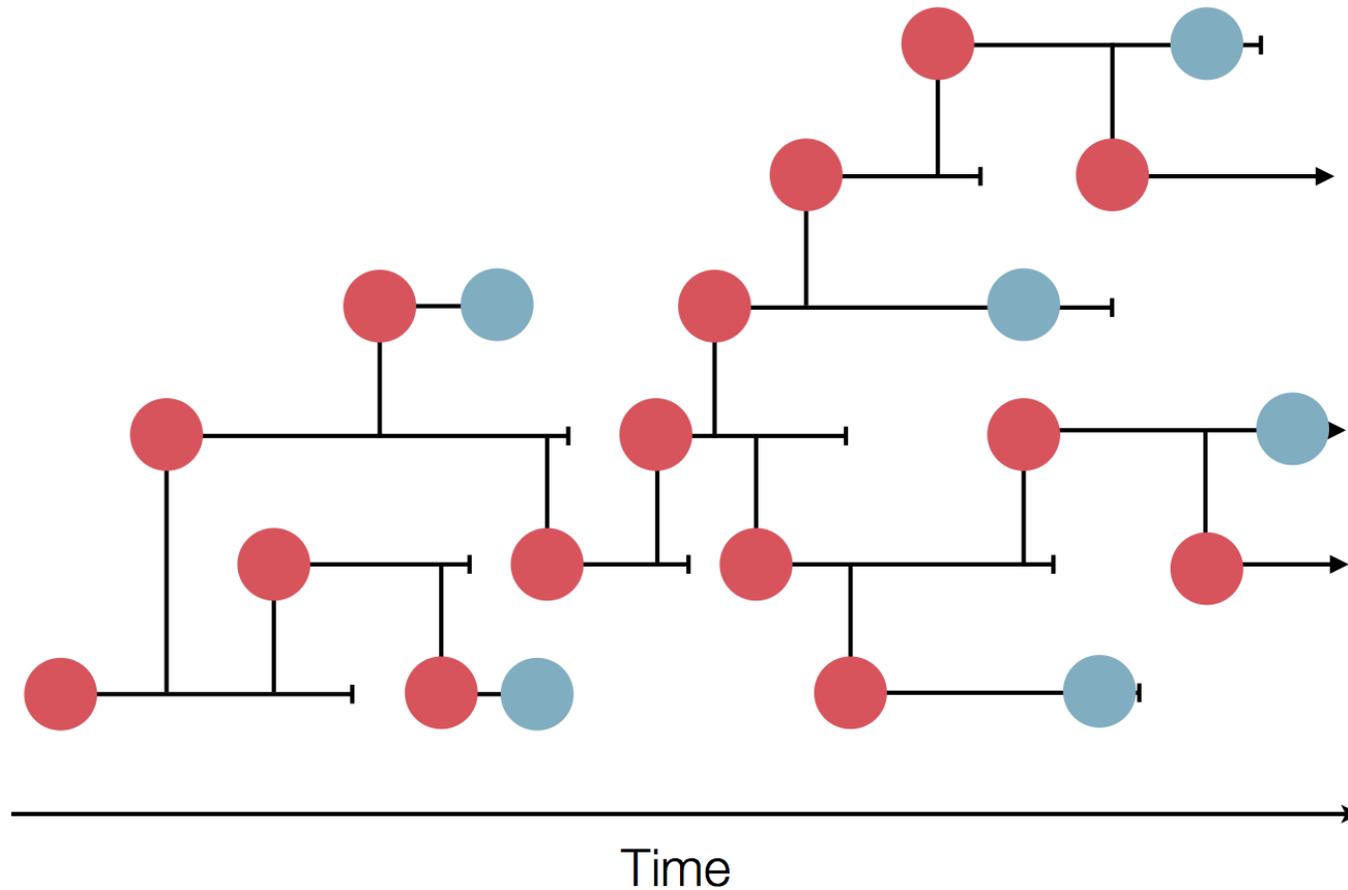
Alli Black
April 3, 2020
StaPH-B Meeting

Genomic epidemiology works because pathogens evolve on the same time scale as infection transmission.

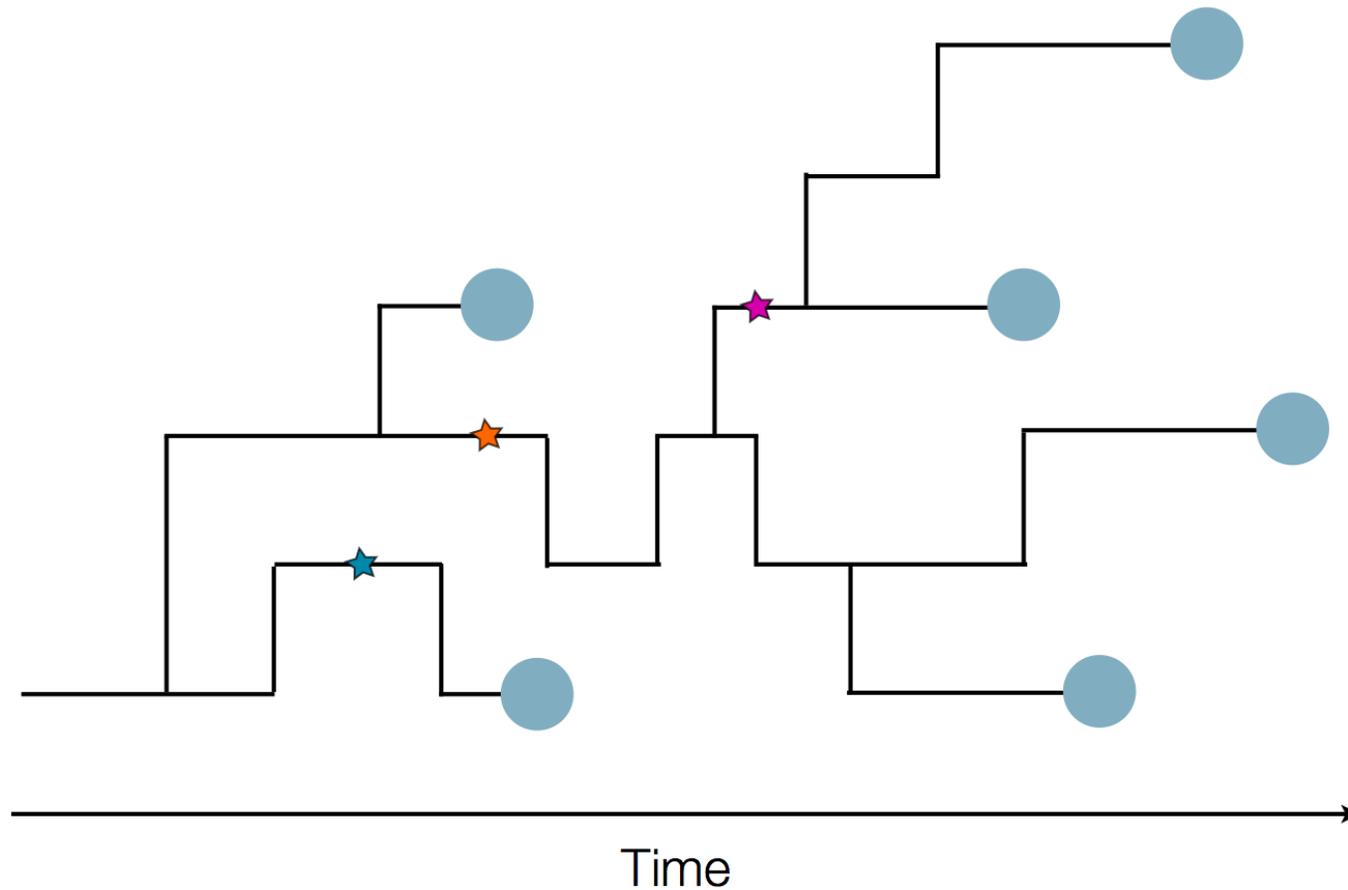
Toy example of a transmission process



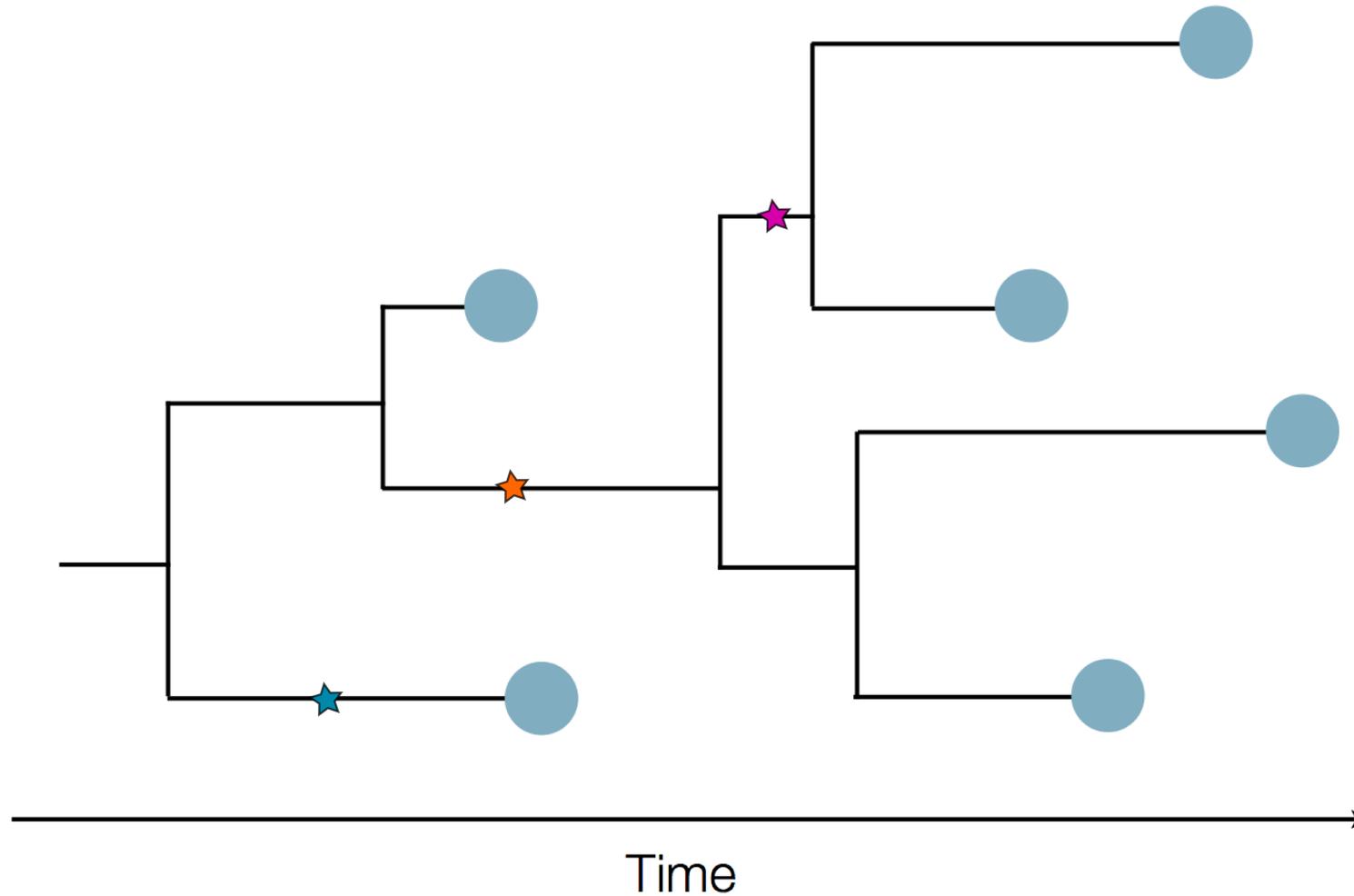
We sample some of the infected people,
usually when they develop symptoms



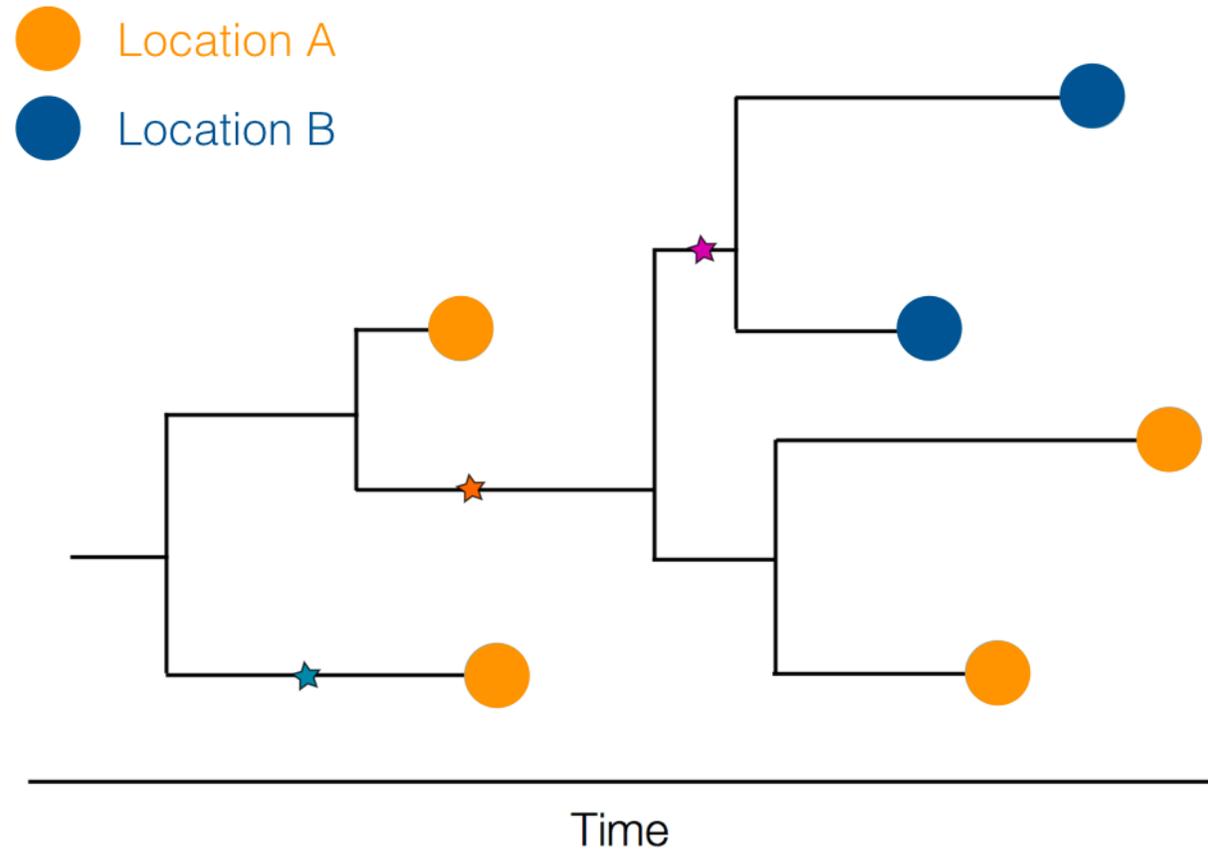
We sequence their infection, looking for unique and shared mutations



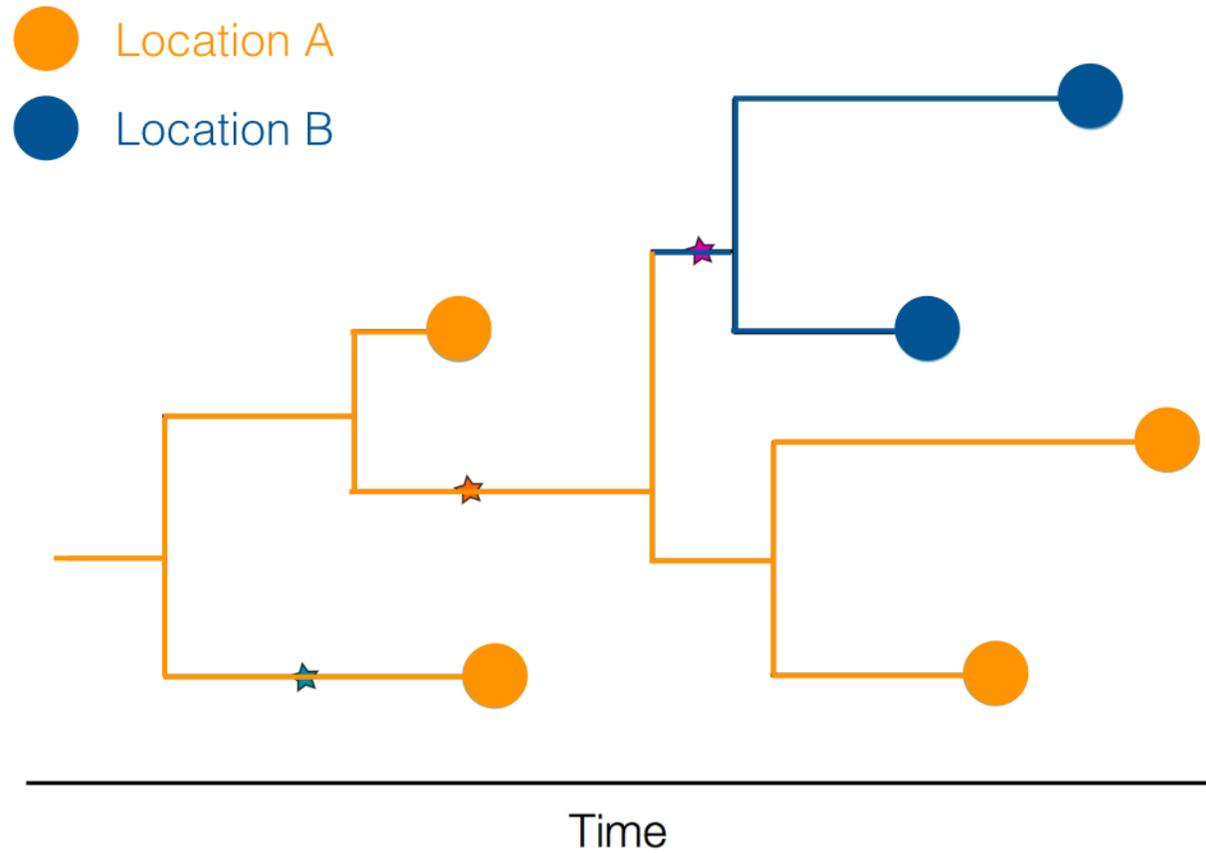
The tree actually ends up looking like this



We can also add additional data, like geographic information

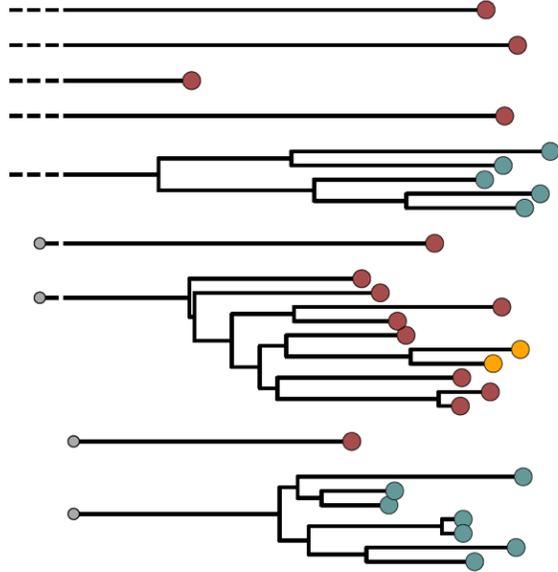


And infer patterns of change in that trait across the tree



When we combine the sequence data with other data, such as geographic information, we can describe various aspects of transmission.

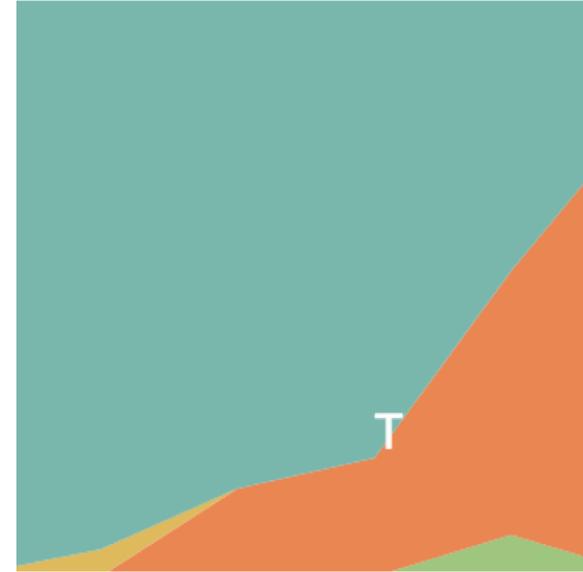
Introductions and transmission chains



Spatial patterns and source-sink dynamics



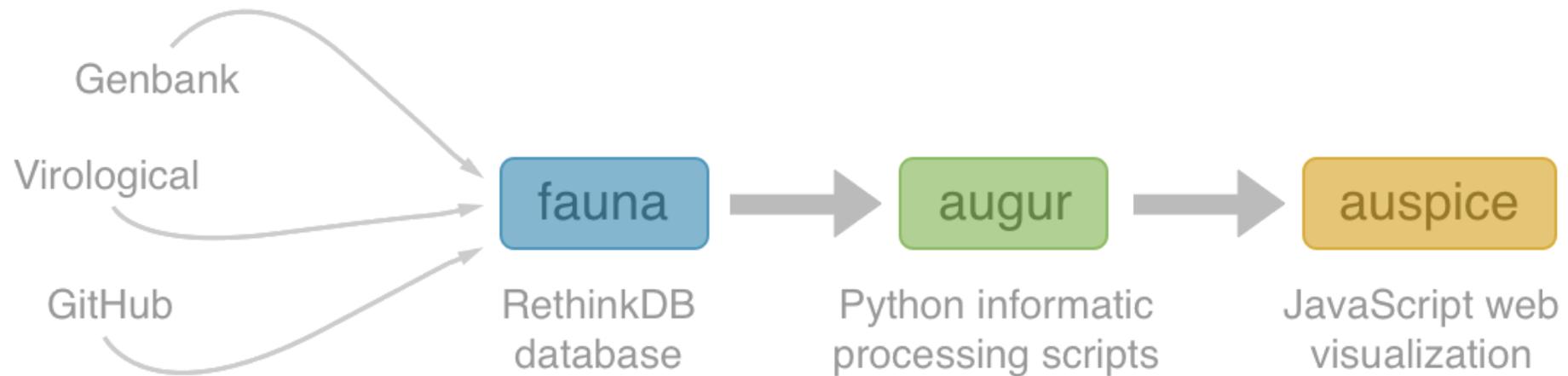
Emergence of adaptive variants



So how does Nextstrain fit in to all this?

Nextstrain aims to:

- (1) *perform rapid and flexible phylodynamic analysis and*
- (2) *facilitate interactive visualization*

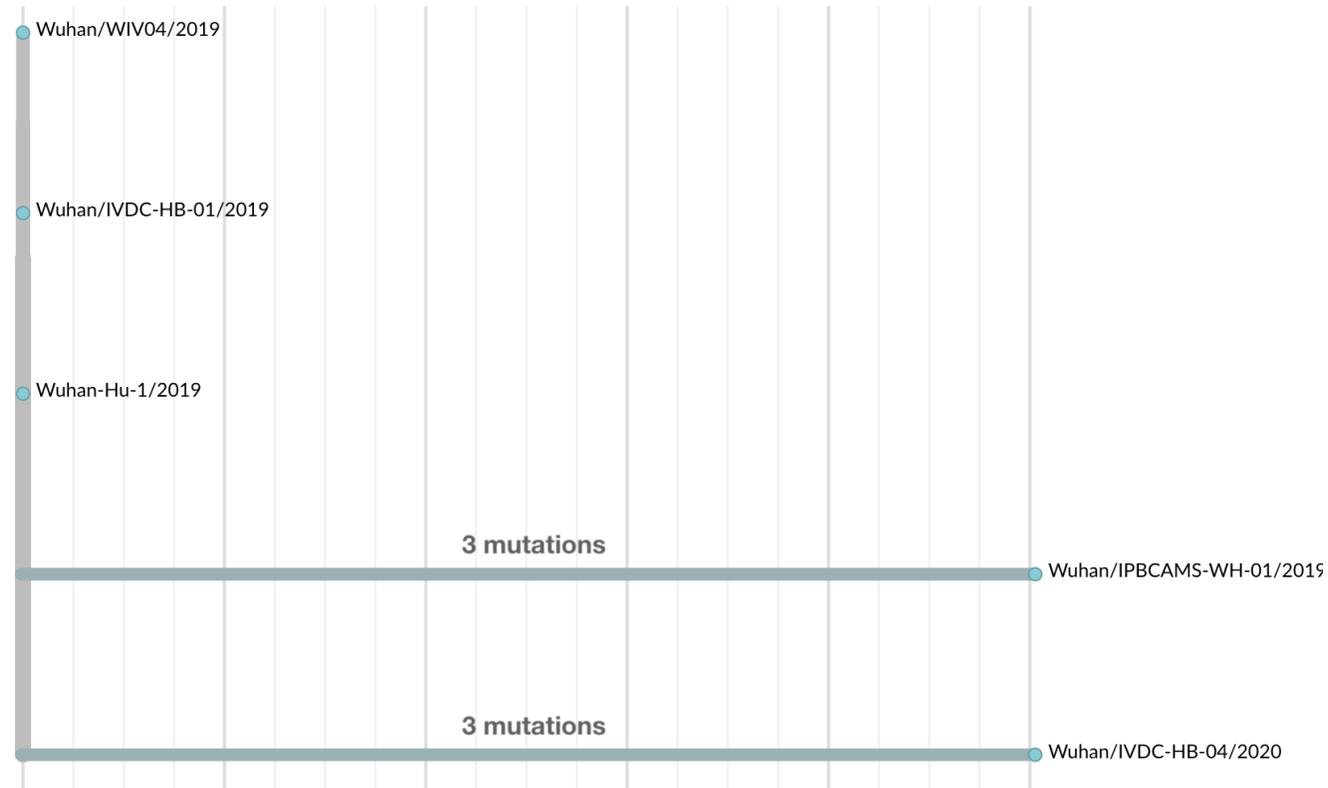


Nextstrain is two things

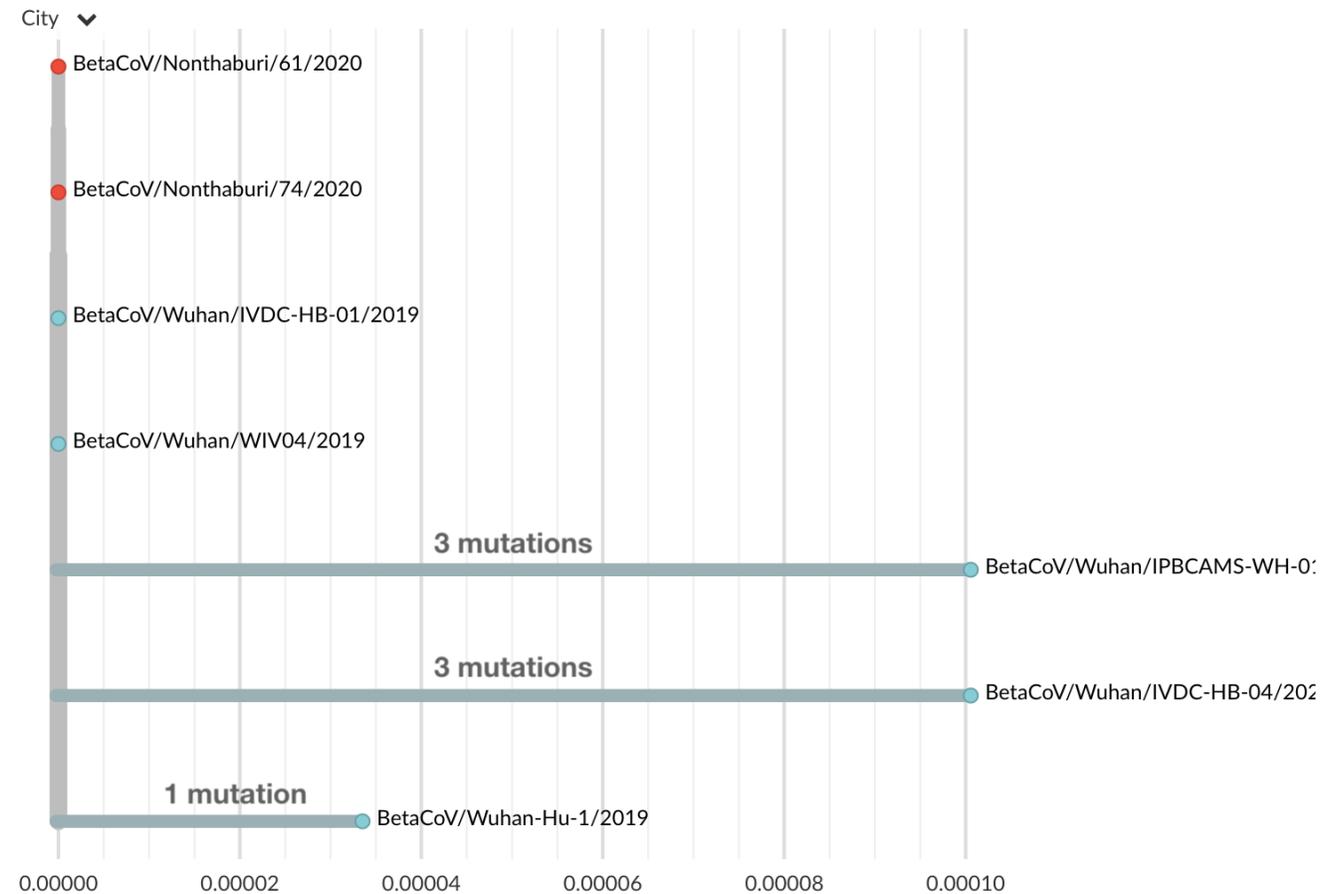
- a bioinformatics toolkit and visualization app, which can be used for a broad range of datasets
- a collection of real-time pathogen analyses kept up-to-date on the website nextstrain.org

The most recent pathogen analysis we support is SARS-CoV-2.

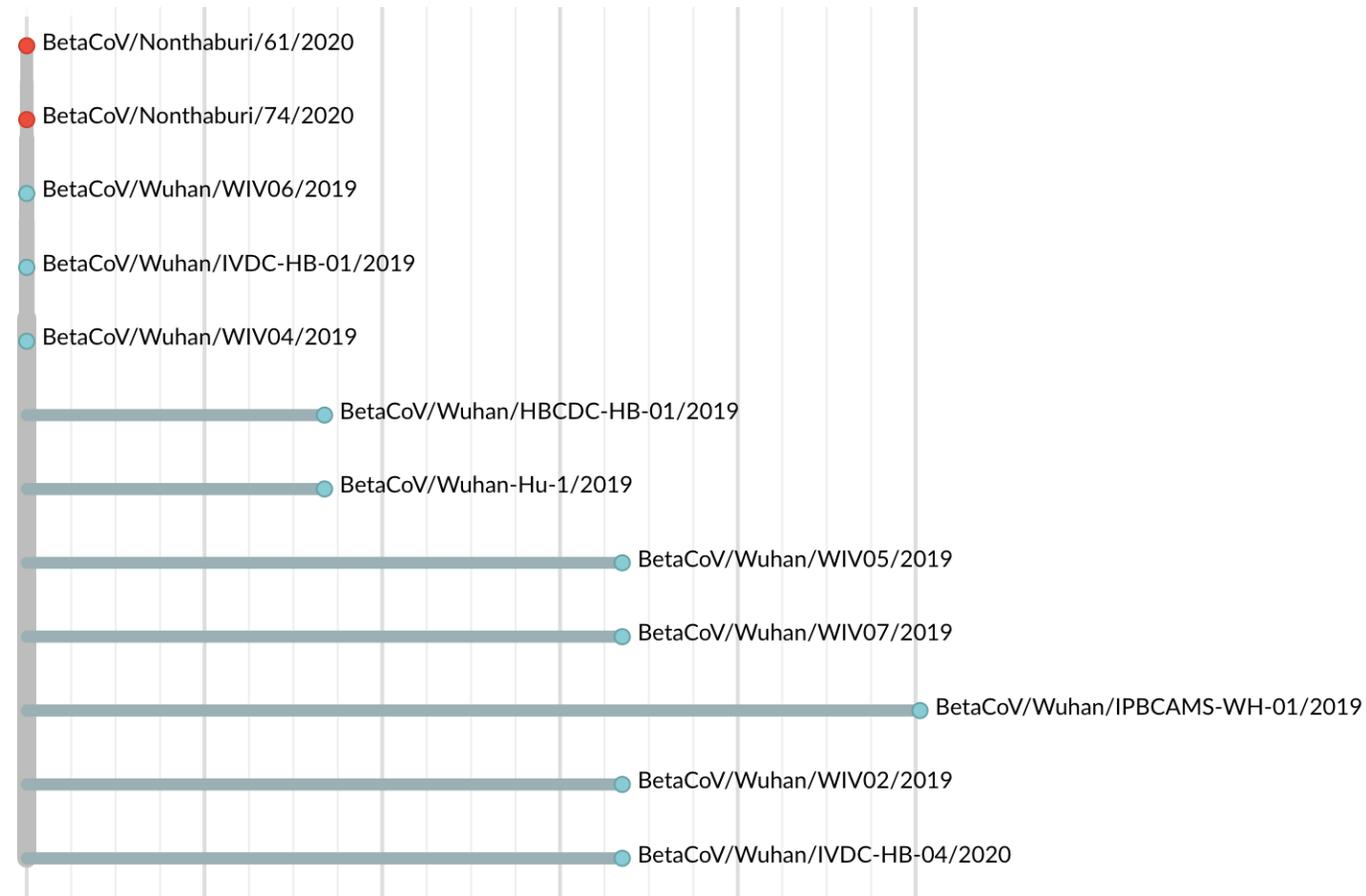
Jan 11: Initial 5 nCoV genomes from Wuhan showed fairly limited genetic diversity



Jan 17: Additional 2 nCoV genomes from Thailand travel cases also lacked diversity



Jan 19: Additional 5 nCoV genomes from Wuhan still showed limited diversity



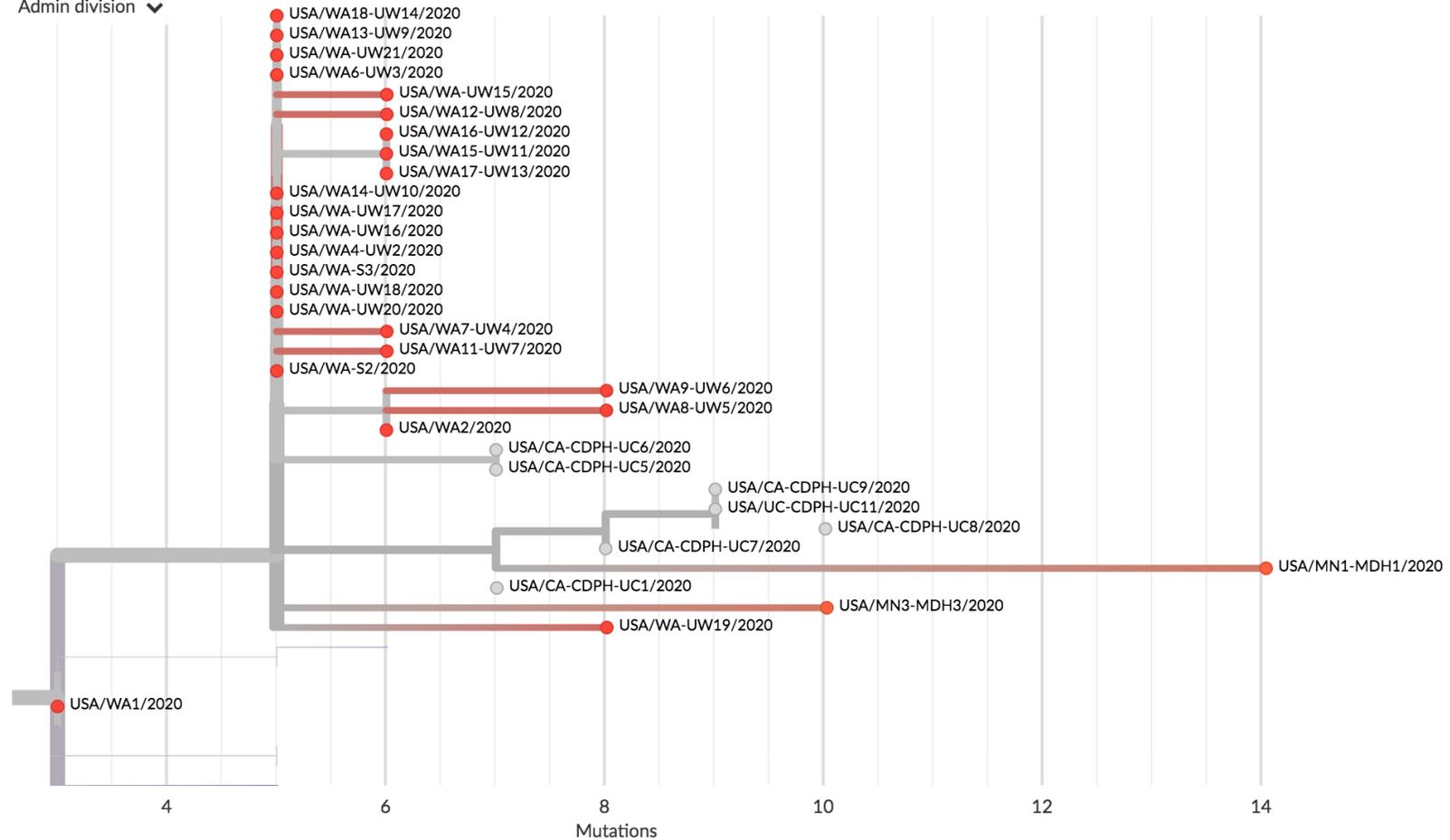
Other ways in which Nextstrain can potentially inform public health action?

Seattle, mid-March

Phylogeny

RESET LAYOUT

Admin division ▾



Europe, mid- to late-March

