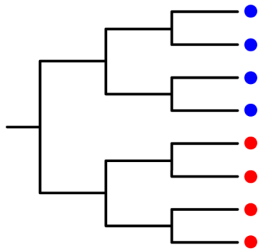# STATS 700-002 Class 6.
Viral Phylodynamics

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Outline

Volz, E. M., Koelle, K., & Bedford, T. (2013). Viral phylodynamics. PLOS Computational Biology, 9(3), e1002947. doi:10.1371/journal.pcbi.1002947.
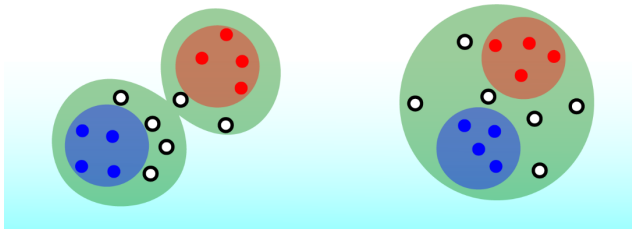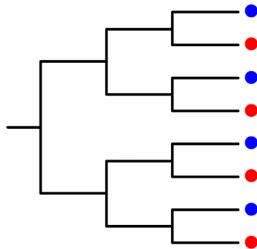
A Structured Host Population

B Unstructured Host Population

Fig. 2. Population structure

Structure: questions

1. Given a tree and some information about leaves, what descriptive analysis (plots or summary statistics) would you use to investigate population structure?

2. Descriptive statistics can be suggestive, but a suitable model is usually more conclusive. What models could you propose? How would you do inference for them?
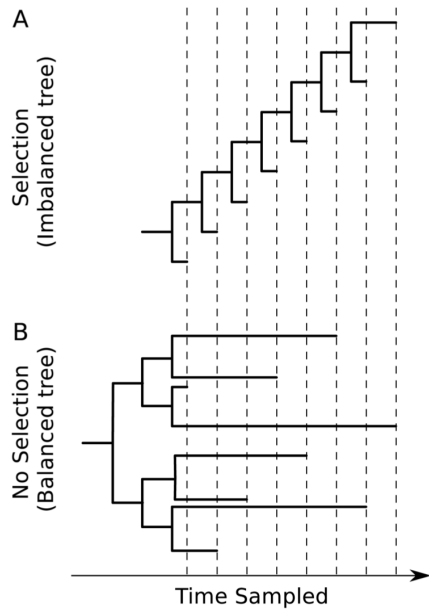
A

Selection
(Imbalanced tree)

B

No Selection
(Balanced tree)

Time Sampled

Fig. 3. Immune escape

Immune escape: questions

1. Immune escape is a property of evolution of the pathogen. What can we learn about immune escape via a compartment model for the host?

2. What aspects of the epidemiology of immune escape can and cannot be addressed in the phylodynamic framework developed so far (compartment models for host dynamics investigated by their likelihood for phylogenetic tree data)?

1 sample from 9 patients
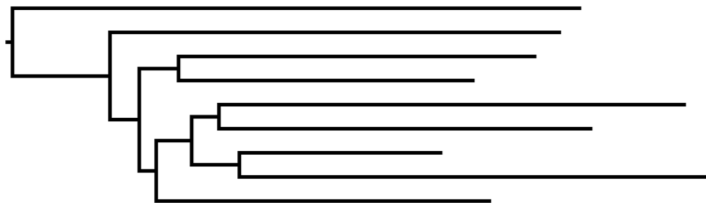
15 samples from 1 patient
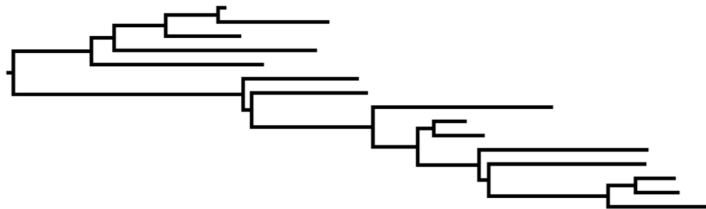
(Fig. 6). What are the challenges and opportunites for studying *within host* phylodynamics rather than *between host*?

Methodology

Beyond the coalescent-based methods described, the authors mention simulation-based approaches, including ABC.

What is ABC and how might it be applied in this context?

Future directions

To what extent has the future fulfilled the predictions of this review paper?