

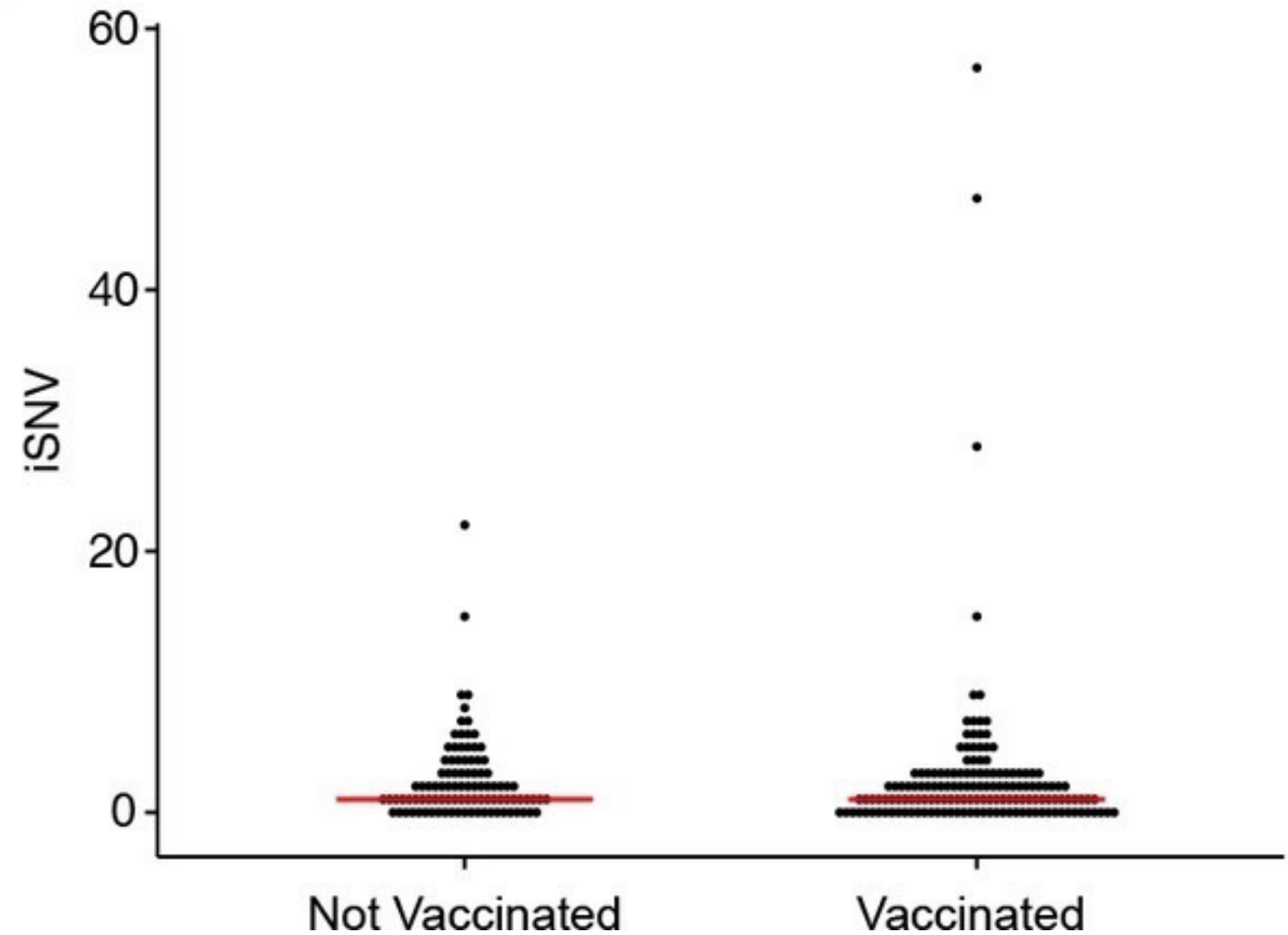
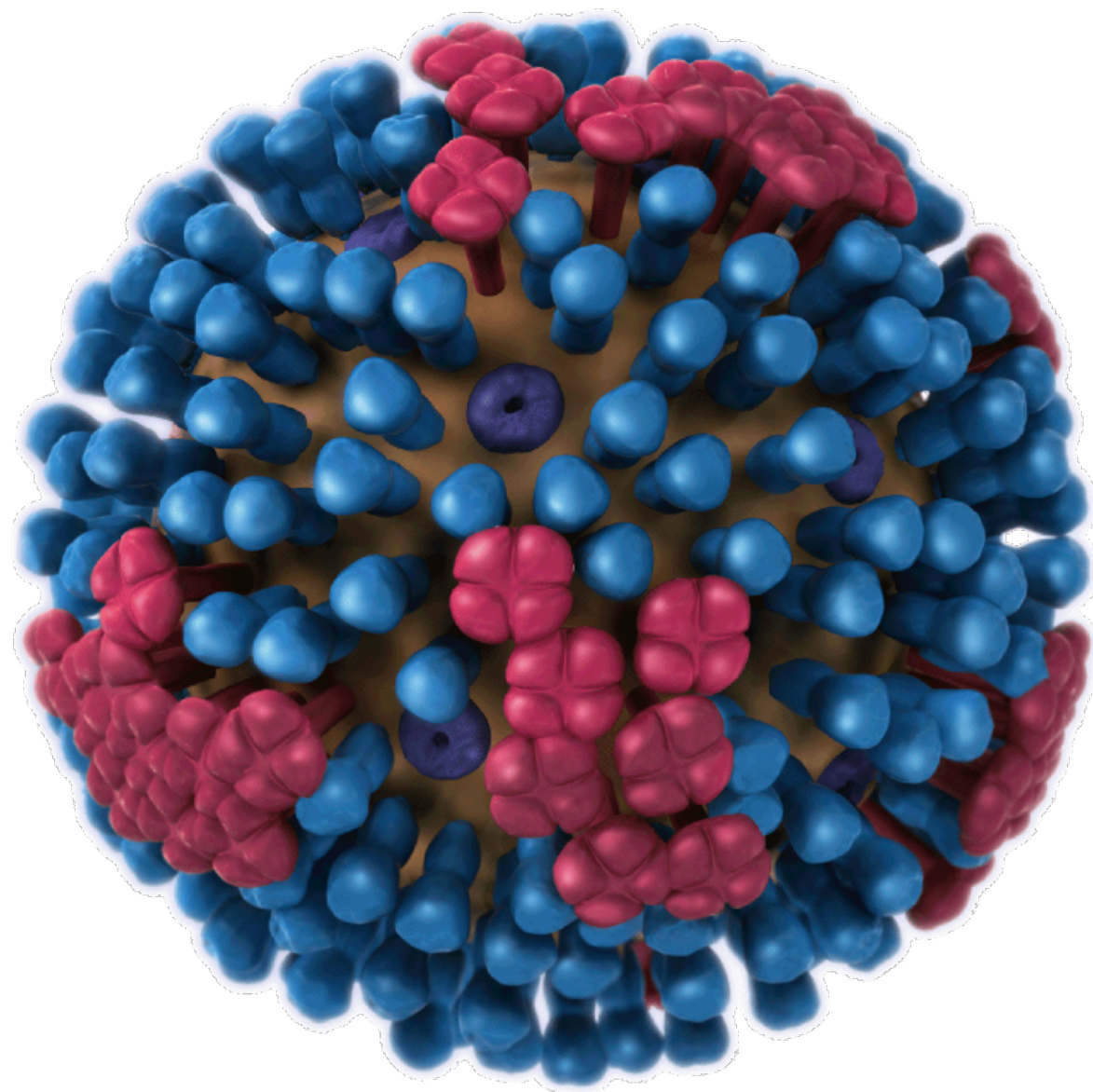
Dataset:

422 sequences

Ann Arbor, MI

Three Influenza A subtypes

Low genetic diversity



Goal: Infer ML phylogenies from genetically homogenous populations

