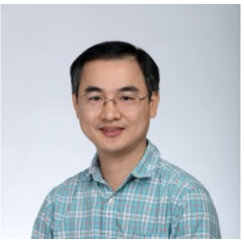
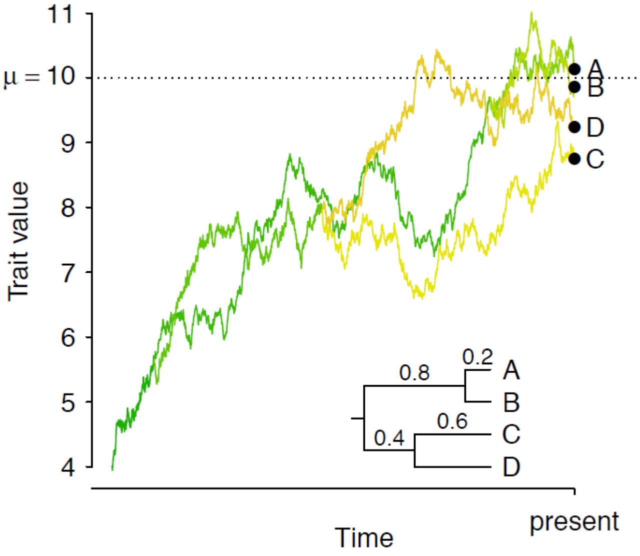
Lam Ho

Statistics



Dr. Ho is interested in statistical theory and methods for stochastic models in evolutionary biology and epidemiology.

Phenotypic evolution: Phylogenetic models arise in biology when sampled species are related to each other according to an evolutionary tree. Under these models, a phenotype evolves along a phylogeny according to stochastic processes. His main goal is developing statistical methods for learning about the process governing the evolution. The proposed methods will provide rigorous tools for answering many important questions in macroevolution such as whether all species are descended from a common ancestor, how humans migrated out of Africa, and how HIV-1 spread in central Africa.



Infectious disease epidemics: Stochastic models are popular tools for studying the spread of many infectious diseases including measles, HIV, and Ebola. These models stratify the population into groups according to health status and assume that the dynamic of these groups follows a continuous-time Markov process. He aims to design efficient inference methods for studying the trajectory of infectious disease epidemics. The proposed methods will be able to provide essential information for controlling infectious disease epidemics by measuring the severeness of an ongoing outbreak and predicting future risks.

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