Phylogenetic distances for neighbour dependent substitution processes

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Abstract:

First, we present a brief introduction to phylogenetics and its mathematical problems.

Then, we consider the most simple nucleotidic substitution process, the Jukes-Cantor model, and we estimate the time elapsed between an ancestral DNA sequence and a present sequence. We provide an asymptotic confidence interval with Delta method and Slutsky's lemma.

After, we do exactly the same with a nucleotidic substitution process with influence, the Jukes-Cantor model with CpG influence, where the rate of substitution at a given site depends on the state of the neighbours of the site.

To finish, we explain the remaining conjectures to extend the results to more general models.