

A statistically consistent coalescent-based k -mer method for phylogenetic tree reconstruction

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Phylogenetic tree reconstruction methods

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Alignment-based methods

Multiple sequence alignment



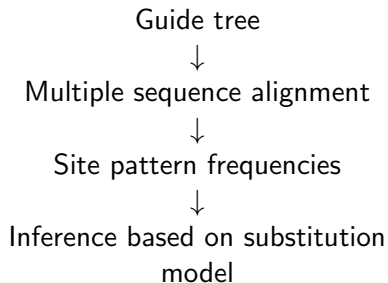
Site pattern frequencies



Inference based on substitution
model

Phylogenetic tree reconstruction methods

Alignment-based methods



Coalescent-based expected k -mer vector distance

