

## Sequence Analysis of Alu Repeated Elements for Primate Phylogenetic Tree Construction

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Phylogenetic tree construction can be a particularly challenging and time-intensive process. This study employs a novel computational approach to phylogenetic tree construction, using the Alu repeating element, a SINE. Repetitive elements including Short and Long Interspersed Nuclear Elements (SINEs/LINEs) have successfully been applied as accurate tools for phylogenetic analysis, as they are predominately unidirectional and homoplasy-free. However, previous analysis of phylogenetic relationships using these repeating elements has been limited to a small number of isolated repeats among relatively few organisms.

As a highly repetitive sequence, the Alu element and its associated subfamilies can provide detailed analysis on evolutionary divergence among species in the Order Primates. This study identified shared sequences as Alu repeating elements that were conserved in both location and base-pair sequence between the primate genomes of interest. These shared sequences, derived from the Genome Library at the University of California San Diego, were analyzed to construct individual phylogenetic trees for each of the 49 Alu subfamilies. As this method solely requires the sequence analysis of available primate genomes, this serves as a cheaper and more time-efficient approach to phylogenetic tree construction for the Order Primates relative to biochemical and anatomical analysis.