Bioinformatic techniques for sequence analysis

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My lab works, in part, on the development and testing of bioinformatic approaches to sequence analysis. Recently, we have developed software to identify amino acid replacements involving significant changes in biochemical properties. Here I describe this software, TreeSAAP which reconstructs ancestral sequences using maximum likelihood. Then compares ancestral sequences to derived sequences and categorizes the amino acid replacements in terms of intensity of change relative to 31 different biochemical properties. Finally, I describe a new distributed technology approach to perform phylogenetic analyses in parallel and document the parameters associated with increases in speed using this parallel computational approach.