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Jesus Alberto Leyva* (jesus_leyva@brown.edu), 69 Brown Street Box 3852, Providence, RI 02912. *Monte Carlo Methods for Phylogenetic Analysis*. Preliminary report.

The research conducted in our lab is concerned primarily with the study and application of mathematical models for the purposes of analyzing phylogenetic data. Phylogenetics is defined as the branch of genetics concerned with the study of the evolutionary relationships between organisms and the overall tree models that allow us to better understand just how organisms interact. This is achieved by generating phylogenetic trees with predetermined structures so that if any errors are to arise in the algorithm they will be easier to detect than if the algorithms were tested with real data. Naturally, there are complexities that need to be taken into consideration when looking into developing test data such as the intended nuclear-mutation-rate matrices involved as well as the ideal node lengths involved in the test tree that is to be used. (Received January 10, 2014)