We will introduce a variation on the quartet puzzling model of reconstructing evolutionary trees from DNA sequence data. Instead of using maximum likelihood methods to infer the best four taxa tree, we examine the use of phylogenetic invariants in this key step. This model is a step toward using invariants to construct trees for data samples involving a large number of taxa. We will describe the results of preliminary investigations into the accuracy of this model. (Received September 15, 2011)