Phylogenetic networks are often necessary to represent the history of a group of species, where a tree is expanded by hybridization edges to explain gene flow or horizontal gene transfer. However, methods to infer phylogenetic networks are still limited. I will first present a new method to test the goodness-of-fit of the coalescent process on a particular tree (or network), to explain the variation in gene trees obtained from molecular sequences. Second, I will present a statistical method to infer phylogenetic networks from sequence data in a pseudolikelihood framework. Our method has a computational advantage over other methods, because calculations are broken down into smaller problems that are easily parallelizable.