Abstract: Phylogenetics studies the evolutionary relationships between different organisms, and its main goal is the inference of the Tree of Life. Usual statistical inference techniques like maximum likelihood and bayesian inference through Markov chain Monte Carlo (MCMC) have been widely used, but their performance deteriorates as the datasets increase in number of genes or number of species. I will present different approaches to improve the scalability of phylogenetic inference: from divide-and-conquer methods based on pseudolikelihood, to computation of Frechet means in BHV space, finally concluding with neural network models to approximate posterior distributions in tree space. The proposed methods will allow scientists to include more species into the Tree of Life, and thus complete a broader picture of evolution.