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The main problem in phylogenetics is to reconstruct evolutionary relationships between collections of species, typically represented by a phylogenetic tree. In the statistical approach to phylogenetics, a probabilistic model of mutation is used to reconstruct the tree that best explains the data (the data consisting of DNA sequences from homologous genes of the extant species).

In algebraic statistics, we interpret these statistical models of evolution as geometric objects in a high-dimensional probability simplex. This connection arises because the functions that parametrize these models are polynomials, and hence we can consider statistical models as algebraic varieties.

The goal of the talk is to introduce this connection and explain how the algebraic perspective leads to new theoretical advances in phylogenetics, and also provides new research directions in algebraic geometry. The talk material will be kept at an introductory level, with background on phylogenetics and algebraic geometry. (Received March 09, 2011)