Computational methods in phylogenetic algebraic geometry and constructing phylogenetic tree using flattenings

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Abstract

Phylogenetic algebraic geometry is concerned with certain complex projective algebraic varieties derived from finite trees. Real positive points on these varieties represent probabilistic models of evolution. For small trees, we recover projective geometric objects, such as toric determinantal varieties and their secant varieties, but larger trees lead to new and totally unknown regions. This talk gives an introduction to this subject and explain computational method for this area using Macaulay 2, singular, maple program.
Also we introduce a new and statistically consistent algorithm for phylogenetic tree construction that uses the singular value decompositions of flattenings of statistical models. Our fundamental tool is Singular Value Decomposition (SVD). Starting with an mutiple sequence alignment of n DNA sequences, we show that SVD gives us to decide whether a split of the taxa occurs in their phylogenetic tree, assuming only that evolution follows a tree model. Using this fact, we have developed an algorithm to construct a phylogenetic tree by computing only $O(n^2Wlog n)$ SVDs relating to the hierarchy of flattenings. In total our computational order is $n^2Wlog n (m^2)^3 L$. Furthermore we have obtained more efficient tree construction algorithm comparing to the previous one which Ericksson has got.