"Phylogenetic trees: exploring maps through the forest of tree-space"

by   Hannah Saugier

Phylogenetic trees are a method for diagramming possible lineages among organisms that biologists have been using for years. However, one of the main problems that biologists have with them is finding the proper model to use. Mathematicians have been trying to help solve this problem by associating a mathematical structure to the tree. Since parts of phylogenetic trees represent various probabilities, we can construct a polynomial ring of the probabilities for various situations; analyzing the images, algebraic varieties, and ideals of these polynomial rings can help biologists determine which model is best for a given set of data. Since our goal is to be able to evaluate the phylogenetic ideal associated with these trees, we need an easy way to find this ideal. Allman and Rhodes have found a very simple way to compute the ideals for binary trees, leaving the non-binary trees to still be explored. I look into the hypothesis that perhaps the variety of a non-binary tree is equal to the intersection of that tree's binary refinements, finding one case where it is true and two where it is not true.