

Department of Mathematics and Statistics
Colloquium Lecture Series

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**A Method of Finding a Likely Evolutionary Tree
for a Group of Taxa Using Algebraic Geometry**

In biology evolutionary trees are commonly used to illustrate similarities and differences between species. However, given a group of species, how does one decide which evolutionary tree best describes the evolutionary history of those species?

Today, with the growing availability of DNA sequence data, DNA is commonly used to infer evolutionary relationships. Since these sequences can be described simply, mathematical methods of analyzing the similarities and differences can be used.

Given a set of taxa, finding an evolutionary tree that best describes the evolutionary history of these taxa can be reduced to a question about observed pattern frequencies in aligned sequence data. A simple model implies polynomial constraints on these pattern frequencies and these constraints can be found using ideas from Algebraic Geometry. We will discuss an application of this method to the simplest interesting case, and possible improvements that can be made.

Monday, April 20, 2009

Bunnell 410

4:00–5:00

Refreshments after the talk in Chapman 101A