



**L.H. BAKER CENTER FOR BIOINFORMATICS AND
BIOLOGICAL STATISTICS AND IGERT
SEMINAR SERIES**

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Department of Computer Science,

**"The Multi-State Perfect Phylogeny Problem:
The Chordal Graph Approach."**

The Multi-State Perfect Phylogeny Problem is a natural extension of the Binary Perfect Phylogeny (or compatibility) Problem, allowing evolutionary characters to take on more than two states. The basic problem is to determine whether multi-state data can be derived on a multi-state perfect phylogeny. In population genetics terminology, the binary problem is to determine if data fits the "infinite-sites" model, while the multi-state problem is to determine if data fits the "infinite-alleles" model. The problem is of interest due to prior elegant mathematical and algorithmic results (the key algorithmic result was obtained at Iowa State by Agarwala and Fernandez-Baca), and due to non-binary, but integer, population genomic data that is increasingly becoming available.

In 1975, Buneman showed a how to view the multi-state perfect phylogeny problem as a problem of triangulating non-chordal graphs, but that result has not been widely exploited (until now) despite a robust and continuing literature on the problem of triangulating non-chordal graphs. In this talk, I discuss our recent work on exploiting the chordal graph approach to study multi-state perfect phylogeny problems. I will talk about two sets of results. The first set of results concerns problems that extend the utility of the multi-state perfect phylogeny model. The second set of results concerns generalization of the famous "four-gametes test" that characterizes the compatibility of binary data.

Date: Thursday, November 19th

Time: 12:40—1:40PM

Room: Gilman Hall Room 1352