PH.D. PRELIMINARY ORAL EXAMINATION

Thursday, November 17th
12:40p.m. @ 223 Atanasoff

Jucheol Moon
Major Professor: Oliver Eulenstein

Tree Assembly: Inferring Large-Scale Phylogenetic Trees

A species tree is a rooted binary tree where each leaf is labeled by a taxon in a set of species; the tree represents the ancestor–descendant relationships between species. Studying a species tree not only holds enormous promise for advancements in the field of evolutionary biology, but also benefits many other research areas including molecular biology, conservation biology, medical sciences, and agronomy. My research work has been focused on the median tree problem under the gene duplication measure, called the gene duplication problem. The gene duplication measure is defined as the minimum number of gene duplications necessary to explain the discordance between a gene tree and a species tree. I will present an efficient fixed parameterized algorithm that can compute exact species trees with up to 6,561 taxa in 3 hours or less, while a general dynamic programming algorithm can do so with up to 22 taxa within 17 hours on a standard workstation. Another direction of my research work has been studied a median tree problem under the Robinson-Foulds (RF) metric, called the RF problem. I will introduce a clique-based formulation of the RF problem and a graph-theoretic heuristic that is fundamentally different from standard heuristics of median tree problems.

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