

DEPARTMENT OF MATHEMATICS AND COMPUTER SCIENCE
UNIVERSITY OF SOUTHERN DENMARK, ODENSE

COMPUTER SCIENCE COLLOQUIUM

Improving Searches for Evolutionary Trees

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IMADA's Seminar Room

Abstract:

Evolutionary histories, or phylogenies, form an integral part of much work in biology. In addition to the intrinsic interest in the interrelationships between species, phylogenies are used for drug design, multiple sequence alignment, and even as evidence in a recent criminal trial. A simple representation for a phylogeny is a rooted, binary tree, where the leaves represent the species, and internal nodes represent their hypothetical ancestors. For even this simple way to represent evolution, finding the optima for a bimolecular sequences for a fixed set of species is NP-hard. This talk will focus on some of the elegant questions that arise from improving search in this highly structured space. We will also intriguing results about assembling, summarizing, and visualizing the space of phylogenetic trees. This talk assumes no background in biology and all are welcome.

Host: Daniel Merkle