

FACULTY MENTOR Mirarab, Siavash

PROJECT TITLE The evolution within - are clonal trees different from phylogenetic trees?

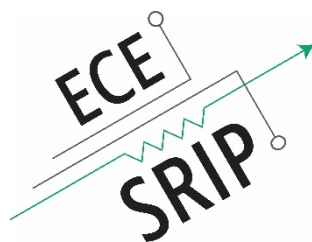
PROJECT DESCRIPTION

Evolutionary trees, or phylogenies, are important tools in any attempt to understand biological processes. Traditional approaches for studying evolutionary trees have assumed that ancestral states are not sampled in a given dataset of sequence data. Many of the emerging types of datasets, including those from the immune system and from cancer cells, violate this assumption. Accordingly, some authors have argued that instead of traditional phylogenetic trees, new types of "clonal" trees need to be estimated, allowing for assignment of observed data to internal nodes (as opposed to only to leaves). Whether this distinction is important in theory or in practice remains poorly tested. In this project, we will use simulations and ideally also theoretical analyses to find out whether clonal trees and phylogenies are distinct in ways that matter in practice.

INTERNS NEEDED 1 MS Student and possibly 1 Undergrad Student

PREREQUISITES

Knowledge of programming required. ECE 286 (my grad course, Algorithms for scalable biological data analysis) for the MS student.



FACULTY MENTOR Mirarab, Siavash

PROJECT TITLE New methods for inference of unbalanced phylogenetic trees

PROJECT DESCRIPTION

Evolutionary trees, or phylogenies, are important tools in any attempt to understand biological processes. Traditional models used in phylogenetics typically use as prior models of tree shape that expect the shape of the phylogeny to be balanced. Many of the emerging types of data sets, including HIV and other viruses and genomic repeats, are known to have very unbalanced trees. Our lab has recently developed a new model of tree evolution, parameterized with a single parameter to control how balanced an expected tree should be (apriori). In this project, we will develop phylogenetic inference tools to incorporate expectations of this model in phylogenetic inference tools. A phylogenetic inference tool typically finds the tree that has the highest likelihood of generating some observed data, but Bayesian methods can also incorporate prior information. Whether implemented as a Bayesian prior or some heuristic approach, we will develop methods that can incorporate expectations of the tree shape into phylogenetic inference methods.

INTERNS NEEDED 1 MS student, who will be collaborating with my PhD student

PREREQUISITES

Knowledge of programming and ECE 286 (my grad course, Algorithms for scalable biological data analysis).

