Russell Schwartz

Professor
School of Computer Science
Department of Biological Sciences
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Research Topic

Computational Biology

Research Problem

How can we use present-day genomes to infer an evolutionary history?

Problem Statement

Given a set of genomes, construct a evolutionary history that minimizes both the distances between genomes and the number of inferred(historical/hypothetical) genomes.

A genome is the symbolic representation of the DNA of a single individual.

An evolutionary history is a tree containing observed present-day genomes as leaves and hypothetical common ancestors as parent nodes.

Problem Description

The theory of evolution implies common ancestors for all life on earth. Until recently, fossil records were the only tools for discovering exactly what those common ancestors were and exactly how species evolved from those ancestors. Computational phylogenetics offers an alternative. By collecting genetic information about present-day species and populations, Dr. Schwartz uses graph theoretic concepts to infer both missing common ancestors and the evolutionary links connecting them to present day populations.

Computer Science Perspective

Computational phylogenetics provides interesting problems for both theoreticians and algorithm designers. Perfect phylogenies, which can only be guaranteed when there are no constraints on the ‘missing’ nodes, are computationally infeasible. However, by placing some reasonable constraints on the missing nodes, near-perfect phylogenies can be computed efficiently.

Actively Involved Discipline:

A discipline is an actively involved discipline if there is an actively involved individual who belongs to that discipline.

An actively involved individual is an individual who has received credit in any related publications or presentations or who is mentioned by the principal investigators, either through verbal or written communications, online or offline, digital or analog.

Disciplines actively involved

Machine Learning
Bioinformatics
Operations Research
Genetics

Description of Disciplines Involved
Genetics
Evolution
Sociology

References
Presenter web page:
http://www.cs.cmu.edu/%7Erussells/
SCIMP: Scan for Imperfect Phylogenies:
http://pyrolysine.bio.cs.cmu.edu/Beta/

By Jfolson
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