Sección temática: Bioinformática

Phylogenetic inference's algorithms.

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Phylogenetic inference consist in the search of an evolutionary tree to explain the best way possible genealogical relationships of a set of species. Phylogenetic analysis has a large number of applications in areas such as biology, ecology, paleontology, etc.

There are several criterias which has been defined in order to infer phylogenies, among which are the maximum parsimony and maximum likelihood. The first one tries to find the phylogenetic tree that minimizes the number of evolutionary steps needed to describe the evolutionary history among species, while the second tries to find the tree that has the highest probability of produce the observed data according to an evolutionary model. The search of a phylogenetic tree can be formulated as a multi-objective optimization problem, which aims to find trees which satisfy simultaneously (and as much as possible) both criteria of parsimony and likelihood. Due to the fact that these criteria are different there won't be a single optimal solution (a single tree), but a set of compromise solutions. The solutions of this set are called "Pareto Optimal".

To find this solutions, evolutionary algorithms are being used with success nowadays.This algorithms are a family of techniques, which aren't exact, inspired by the process of natural selection. They usually find great quality solutions in order to resolve convoluted optimization problems. The way this algorithms works is based on the handling of a set of trial solutions (trees in the phylogeny case) using operators, some of them exchanges information between solutions, simulating DNA crossing, and others apply aleatory modifications, simulating a mutation. The result of this algorithms is an approximation to the set of the "Pareto Optimal" which can be shown in a graph with in order that the expert in the problem (the biologist when we talk about inference) can choose the solution of the commitment which produces the higher interest.

In the case of optimization multi-objective applied to phylogenetic inference, there is open source software tool, called MO-Phylogenetics, which is designed for the purpose of resolving inference problems with classic evolutionary algorithms and last generation algorithms.

REFERENCES

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