Alain Guénoche (IML)

Arbre consensus unique ou multiple ?

Abstract

The aim of this paper is to frame a method to decide if, given a set of phylogenetic trees, there is only one consensus tree, or if several consensus trees, corresponding to several subsets of trees, can be detected. The proposed method is also a way to decide if some given gene trees are congruent, that is sufficiently compatible to admit a single consensus tree, or not. In this latter case the different consensus trees are depicted and can be compared to infer horizontal transfers.