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UNIQUE ROBUSTNESS PROPERTIES OF BALANCED MINIMUM EVOLUTION

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Background. In a classic paper in computational phylogenetics, Atteson (1999) studied the *robustness* of a number of methods for phylogenetic reconstruction. Informally, this is the ability to withstand noise without compromising the reconstruction of the correct tree.

For methods which reconstruct a tree based on a matrix of distances between taxa, the notion of robustness can be made very precise. The input distances can be seen as estimates of the “correct” evolutionary distances $\mathbf{D}^T = [d_{ij}^T]$ in the unknown evolutionary tree T for the taxa under consideration (where d_{ij}^T is simply the length of the path between i and j in T). In an ideal world, the input distances coincide with those in \mathbf{D}^T , in which case any sensible method is able to reconstruct the correct tree T from \mathbf{D}^T . If, more realistically, the input distances equal $\mathbf{D}^T + \boldsymbol{\epsilon}$, reconstruction of the correct topology of T can only be guaranteed if the noise terms $\boldsymbol{\epsilon}$ are sufficiently small. The robustness of a tree reconstruction method can be measured by the maximum “size” for $\boldsymbol{\epsilon}$ still allowing correct reconstruction of the topology of T .

Atteson (1999) showed that there is a theoretical upper bound Θ_T on $\|\boldsymbol{\epsilon}\|_\infty = \max_{i,j} |\epsilon_{ij}|$ beyond which no method can always reconstruct the correct tree topology (Θ_T is half the length of the shortest branch in T). However, he also proved that a number of algorithms, including neighbor-joining, are guaranteed to reconstruct the topology of T whenever $\|\boldsymbol{\epsilon}\|_\infty < \Theta_T$. Because no method can do better than that, these methods are said to have *optimal robustness*.

Results. Since the most important factor in determining the accuracy of tree reconstruction is the optimization principle used to evaluate alternative trees, we have recently started to investigate the robustness of a number of principles (which can be defined as the robustness of an algorithm reconstructing the optimal tree with respect to that principle).

For example, we have recently shown that *balanced minimum evolution* (BME), the principle underlying neighbor-joining, has optimal robustness, whereas another version of minimum evolution based on least squares has very limited robustness. This difference may partly explain the well-documented gap in reconstruction accuracy between these two approaches.

Here, I will announce a result that considerably strengthens the result above: I show that BME is in fact the *only* principle with optimal robustness, among all *linear* optimization principles, i.e., those that score tree topologies on the basis of linear functions of the input distances (each function usually represents the total branch length associated with a topology) — this includes all minimum evolution principles in the line initiated by Rzhetsky and Nei (1992). In other words, I show that a necessary (as well as sufficient) condition for a linear minimum evolution principle to have optimal robustness is that the coefficients of its tree-length functions coincide with those of BME (and therefore the principle itself coincides with BME).

Finally, I will deal with the practical relevance of this result. In particular the strengths and weaknesses of Atteson’s definition of robustness will be discussed.