

# The Anâtaxis phylogenetic method. I. Optimal trichotomies under fuzziness constraints : homoplasy and heterogeneity of evolutionary rate over phyletic lineages

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*Erratum*

THE ANÂTAXIS PHYLOGENETIC METHOD. I. OPTIMAL TRICHOTOMIES  
 UNDER FUZZINESS CONSTRAINTS, HOMOPLASY AND HETEROGENEITY  
 OF EVOLUTIONARY RATE OVER PHYLETIC LINEAGES

BY

**Gabriel BITTAR & Leigh CARTER**

Part of this paper, published in Archs Sci. Genève 50:153-168, was defectuous because of the utilisation of an older version of the text in part of it, which led to an error dating from a time where the trichotomy-inference algorithm used to reconstruct in the Anâtaxis program the Dissimilarities to trichotomies correspondence table at p. 166 was wrong. Moreover the presentation was not practical. The corrected and improved table is presented in this Erratum.

Besides, the explanation text in pp. 164-5, from “Then there is the more complex case...” up to the end of p. 165 should read in the wollowing way:

Then there is the more complex case with one relatively large dissimilarity, and two relatively small and (roughly) identical dissimilarities, e.g.  $\Delta_{ba} \approx \Delta_{ca} \ll \Delta_{cb}$ . In this case, there is no solution without homoplasy if one is to keep with the  $\Delta_{oc} \approx \Delta_{ob} \ll \Delta_{oa}$  conditions. In fact, b and c being symmetrical, there are two alternative solution: either a and c group together, with a and b partially homoplastic to one another, or a and b group together, with a and c partially homoplastic to one another. There is another, albeit less parsimonious, couple of alternative solutions: again either a and c group together, but this time with c and o partially homoplastic to one another and terminal branch c having evolved relatively rapidly, or again a and b group together, but this time with b and o partially homoplastic to one another and terminal branch b having evolved relatively rapidly.

Is the second set of solutions, those involving a hypothesis of heterogeneity of substitution rates in addition to a hypothesis of homoplasy, really less plausible than the first, apparently more parsimonious, set of solutions? In other words, could the added condition of rate heterogeneity (distorsion of the molecular clock) be compensated by the fact that there is a bigger probability of partial homoplasy between two lineages the older their date of divergence (and divergence from outgroup lineage o is the oldest one in our rooted tetrachotomies)?

The answer is not easy, one of the reasons being that the molecular clock is a source of much controversy, both theoretical and empirical (see e.g. GOODMAN, 1981; GOJOBORI *et al.*, 1982; DOVER, 1987, OHTA, 1987; WOLFE *et al.*, 1987; ZUCKERKANDL, 1987; CACCONI & POWELL, 1990; EASTEAL, 1990). Our personal experience with real data (NADOT *et al.*, 1995; SOUZA-CHIES *et al.*, 1996; BITTAR *et al.*, 1996; PAWLOWSKI *et al.*, 1996; BITTAR & VEUTHEY, in preparation; and BITTAR, unpublished data) leads us to think that the second set of solutions is not necessarily to be rejected out of hand, but in the present state of affairs the question of rate heterogeneity is still basically a question of opinion.

Finally (we are still analysing the  $\Delta_{oc} \approx \Delta_{ob} \approx \Delta_{oa}$  sub-table) there is the case where the three dissimilarities are all clearly different from one another, e.g.  $\Delta_{cb} \ll \Delta_{ca} \ll \Delta_{ba}$ . Again in this case, it is not possible to avoid doing a hypothesis of homoplasy. In terms of parsimony of the hierarchically-ordered evolutionary hypotheses, the most likely solution is the tree  $(a, (b, c))$ , either with  $a$  and  $c$  partially homoplastic to one another, or with the  $b$  terminal branch having evolved relatively rapidly and in a way partially homoplastic to  $o$ .

Clearly, there are many cases where there is no solution without doing a hypothesis of homoplasy: thus, it is a useful feature for a dissimilarity-matrix method to give such warnings of possible or probable homoplasy (which Anâtaxis does), homoplasy that can then be checked more rigorously with a careful analysis of character states, e.g. with the help of program MacClade 3.06 (MADDISON & MADDISON, 1992).

Whatever, the correspondence table approach is flexible enough for freely allowing alternative evolutionary scenarios if one does not adhere to those presented here. It may also be noted that, clearly, Anâtaxis could give, as many distance-matrix methods do, phenetic branch lengths simply based on the level of divergence between any two lineages, with *ad hoc* accompanying hypotheses; but also, and more interestingly in our opinion, it can offer for each branch of the evolutionary tree, in really phylogenetic terms, a qualitative estimation of possible rate heterogeneity, which may then be compared with the phenetic branch length.

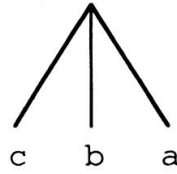
For concluding, it would be ideal to have an exhaustive dissimilarities-to-tree table, where all possible phyletic scenarios, for any  $(\Delta_{oa}, \Delta_{ob}, \Delta_{oc}, \Delta_{cb}, \Delta_{ca}, \Delta_{ba})$  sextuplet, would appear, with each possible solution having a probability value between 0 and 1 (presently, the most likely scenario is affected with probability 1, the other scenarios with probability 0); then Anâtaxis would be able, in a probabilistic "fuzziness" way, to propose a spectrum of solutions rather than a single global tree... but this is easier to say than to implement.

**Dissimilarities to trichotomies correspondence table**

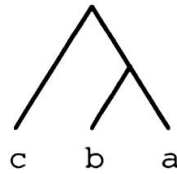
OUT-IN :  $\hat{\Delta}_{oc} = \hat{\Delta}_{ob} = \hat{\Delta}_{oa}$  (o = outgroup)

z homopl. x = z partially homoplastic with x  
'+' for relatively rapid transformation rate

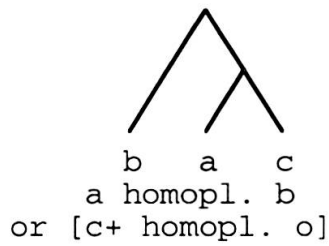
$\hat{\Delta}_{ba} \approx \hat{\Delta}_{ca} \approx \hat{\Delta}_{cb}$



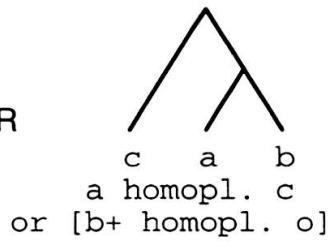
$\hat{\Delta}_{ba} \ll \hat{\Delta}_{ca} \approx \hat{\Delta}_{cb}$



$\hat{\Delta}_{ba} \approx \hat{\Delta}_{ca} \ll \hat{\Delta}_{cb}$



OR



$\hat{\Delta}_{cb} \ll \hat{\Delta}_{ca} \ll \hat{\Delta}_{ba}$

