Vol. 125, No. 1 The American Naturalist January 1985

PHYLOGENIES AND THE COMPARATIVE METHOD

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VOL. 193, NO. 6 THE AMERICAN NATURALIST JUNE 2019

HISTORICAL COMMENT

Revisiting a Key Innovation in Evolutionary Biology: Felsenstein's "Phylogenies and the Comparative Method"

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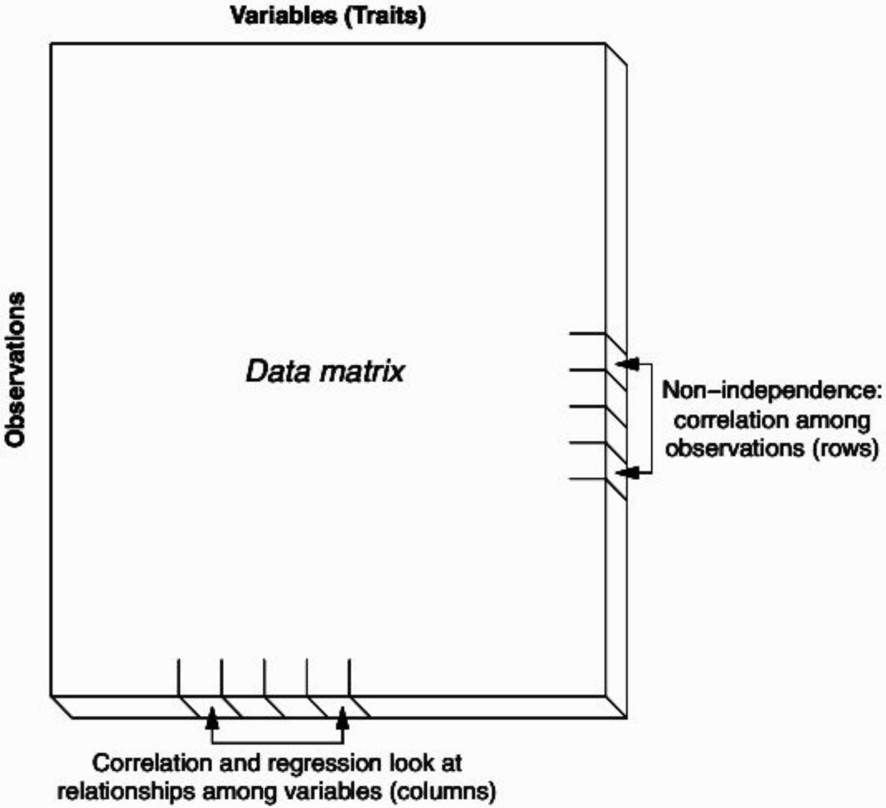


Fig. 1.2 A general depiction of a data set

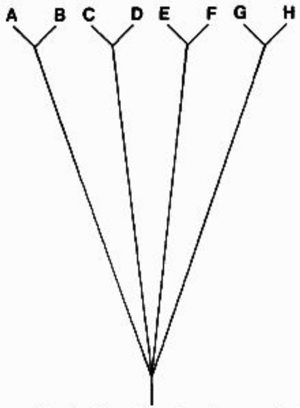


Fig. 3.—Another phylogeny for the 8 species, showing a radiation that gives rise to 4 pairs of closely related species.

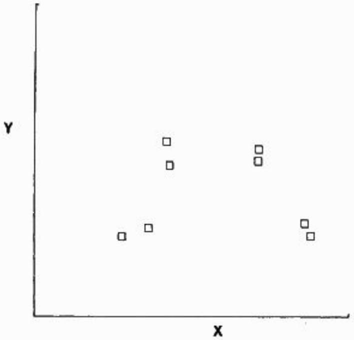


Fig. 4.—A data set simulated using the phylogeny of fig. 3, under a model of random, normally distributed, independent change in each character, where the change in each branch is drawn independently from a normal distribution with mean zero and variance proportional to the length of the branch.

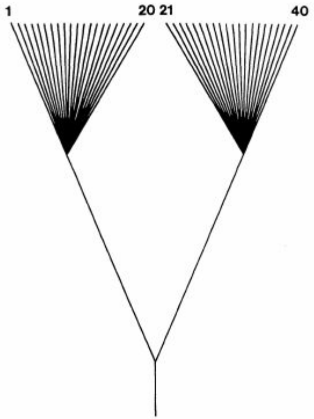


Fig. 5.—A "worst case" phylogeny for 40 species, in which there prove to be 2 groups each of 20 close relatives.

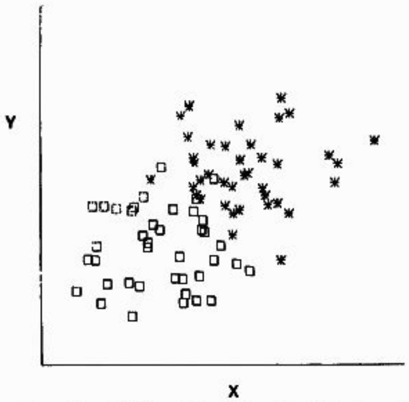
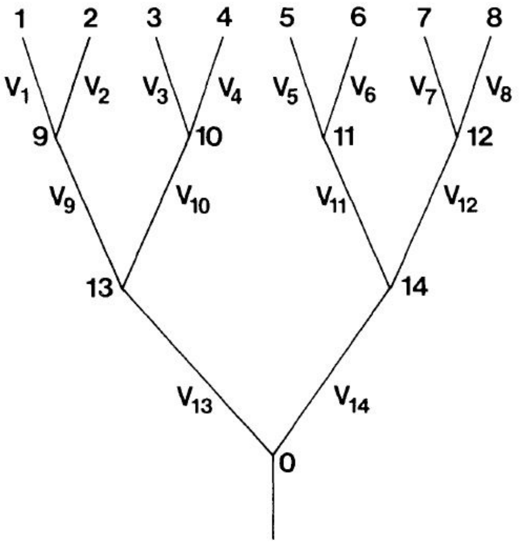


Fig. 7.—The same data set, with the points distinguished to show the members of the 2 monophyletic taxa. It can immediately be seen that the apparently significant relationship of fig. 6 is illusory.



moment the problem of estimating s_X and s_Y, and assume that they are known.

By dividing each contrast by its standard deviation, we have obtained from the original eight species seven pairs of contrasts that can be regarded as drawn independently from a bivariate normal distribution with means zero, variances unity, and an unknown correlation r_{XY} between the members of a pair. Testing independence of the evolution of X and Y reduces to simply testing whether this

The critical point in a PCM-based analysis is to use the correct correlation structure among observations. The more distant the assumed correlation structure from the real one, the more biased the analysis will be. This property explains the statement that “in a comparative analysis a wrong phylogeny is better than no phylogeny at all” (Losos 1994; Martins 1996). Indeed, if the traits evolved on a phylogeny and another phylogeny is used for data analysis, the latter will result in a correlation structure closer to the correct one than assuming no correlation at all (i.e., independence of observations).

From the point of view of data analysis, one problem often encountered in published studies is that the phylogenetic correlation structure of the data is usually not assessed. This certainly comes from the view traditionally defended by most authors that only the phylogenetically controlled analyses are relevant. We now know that this can lead to wrong inference. This seems relatively easy to fix with tests of phylogenetic signal and model selection with information criteria such as the AIC (see Chap. 5).