

# Numerical Taxonomy, Convergence, and Evolutionary Reduction

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Let us be clear from the beginning—I am writing to criticize *numerical taxonomy*, not quantitative systematics. I am sure that measurement and mathematical methods will and should be much more widely employed in systematic studies. It should also be understood that *numerical taxonomy*, by which I mean specifically the doctrine and methods outlined by Sokal and Sneath (1963) in their book of this title, is to me not without interest, import, and potential usefulness for systematic biology. But I intend to show that in at least one important respect, numerical taxonomy is headed in the wrong direction.

I am not going to attempt to deal with mathematical questions, and I am going to skip over the obvious objections based on the difficulty of properly analyzing characters, so that I can get to the subject that interests me most. While considering this fault in numerical taxonomy, I hope to bring the criticism around to a more constructive position by hinting at an approach to systematics that the numerical taxonomists might find worth trying.

The aspect I have chosen to discuss deals with phyletic *convergence*, a term that I here interpret broadly to include the finer-grained phenomenon, *parallelism*. Michener and Sokal (1957) make the following statement:

Possible parallelisms present a difficult problem. The amount of evolution, after divergence from a common stem, of two forms that have evolved in a parallel manner, would be underestimated by our method, as well as by customary systematic methods.

The authors claim that their studies of saturniid moths and megachilid bees show relatively few parallel characters.

We believe that much of the difficulty due to parallelisms is eliminated in our study by the large number of characters used. Parallelism or convergence affecting only a few characters would not greatly influence our measure of relationship.

It hardly needs to be added that convergence or parallelism affecting a *large* proportion of the characters used would seriously upset the conclusions of the numerical taxonomist, as well as those of many a traditional phylogeny-builder. Perhaps it was uneasiness about evolutionary convergence that led Sneath and Sokal (1962) to pose this rhetorical question.

Suppose an absurdly extreme overall convergence had occurred so that two forms were almost indistinguishable and could readily and successfully hybridize: What is the purpose of separating them on grounds of ancestry when in all other attributes they are the same?

We accept this question as “absurdly extreme” indeed (at least at the metazoan level), but we answer it anyway: We separate the two forms if we know their ancestry, because the *history* of this situation is of overriding biological importance. It should be borne in mind that systematic biology is not merely an arrangement for gathering and filing data on the diversity of living organisms; it is also, with genetics and ecology, one of our main hopes of understanding how evolution occurs. That understanding is clearly fragmentary right now, despite the advances of Darwin and the geneticists.

Let us examine the case of the convergence that may not be “absurdly” extreme but is at least extreme enough to threaten taxonomic judgment. In the group I work on (the ants), the old tribe Dacetini has contained convergent elements of three separate tribes, and genera actually repre-