

if we ask old questions in old ways, we are likely to encounter frustration in our attempts to apply the reparameterized version of the Richards function to our data. Some of the reasons are given in the commentary by Brisbin et al. (1987).

The parameters one ought to be able to estimate are the rate of growth (Ricklefs 1967), the asymptote, and the shape of the curve. Most studies have focused on growth rate, largely because Ricklefs's (1967) analysis made it feasible to extract this information from a wide variety of growth data sets. In ornithology, at least, the asymptote has not been of much interest, because it is usually assumed to be close to the adult mass, which is usually readily obtained by weighing adults. It is not necessary that the asymptote remain underutilized.

The shape of the curve has rarely been addressed. In fact, deviations generally have been treated as noise rather than useful information. This has been particularly important to toxicologists and risk analysts, for whom extrapolation of sigmoid dose-response curves back toward the origin has been an active undertaking in the past 5 yr (Van Ryzin 1981). From the work of Brisbin et al. (1986) it is apparent that the shape parameter itself may provide important biological information, and researchers may choose to investigate this, even at the expense of the more traditional growth rate. Thus, some species may concentrate growth early, showing a short lag phase, whereas others may show negligible growth before a growth spurt. Stressors may act, for example, by prolonging the lag phase, a result readily identifiable if one studies the shape parameter.

It is here that the paradigm enters, for to investigate the shape parameter, it is essential to design studies that can yield sufficient information so that the iterative solutions can estimate the parameters of interest.

As Brisbin et al. (1987) mention, traditional studies of growth often end when the young birds fledge (or when the investigators find it impractical to recapture them). The problem emerges that the procedures fail to converge in an iterative solution when the data set is too sparse or terminates prematurely. A variety of artificial techniques have been discussed that might salvage particular situations, for example, creating artificial asymptotic data points. Most researchers, however, find this undesirable.

The value of the paradigm, therefore, is that it points the way to new study designs that will assure a data set worthy of the powerful new techniques. As a tool for analyzing pre-existing data sets, researchers are likely to be disappointed, and will turn to more traditional analyses. One should be careful, however, not to allow such frustrations to color one's understanding of the importance of new study designs and new analyses.

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A Historical Explanation for Polyandry in Wilson's Phalarope

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Early in the 20th century, A. O. Treganza recognized that great numbers of phalaropes were present at Great Salt Lake, Utah, in early summer. Because information about phalarope biology was then rudimentary, Treganza considered these flocks to represent nonbreeders, rather than postbreeders involved in a molt migration (Jehl 1981, *Natl. Geogr.* 160: 520; Jehl in press, *Ornis Scandinavica* 18). His

interpretation, coupled with a lack of anatomical and physiological knowledge and an uncritical acceptance of scientific "authority," led W. L. Dawson (1923, *The birds of California*, San Diego, California, South Moulton Co., pp. 1090-1091) to concoct a marvelous hypothesis about a topic of much recent interest to biologists: the evolution of polyandry. Dawson's explanation reflects the passions and prejudices of the time, and should not be allowed to molder in the archives of avian science.

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"According to a physician friend of Mr. Treganza's, who, pending the completion of his studies, desires his name withheld, the females of Wil-

son's Phalarope are excessively afflicted with diseased ovaries. Thus, hundreds, perhaps thousands, of non-breeding females are found during the summer in the vicinity of Salt Lake, and examination shows that invariably these non-breeders are possessed of diseased and non-functioning organs. As a result of this condition, which affects perhaps two-thirds of the entire number of females, the males, if they would breed at all, must accept at least one rival, or male partner, in their family relation.

"But one who knows Phalaropine character soon suspects that this ovarian disease, which is forcing polygamy upon the race, is in itself an effect rather than a cause. The cause is the ex-

cessive development of the sex instinct in female Phalaropes. The female of *Steganopus* [*Phalaropus*] *tricolor* is a wanton who no reasonable indulgence will satisfy . . . It is, without doubt, this strange excess of *libido* which has brought the females of the species first to their musky perfection of size and power, and then, lacking outlet, has deranged the sex organs themselves."

Half a century hence, our successors will no doubt find similar amusement in ideas devolving from our present ignorance.

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DNA Hybridization and Avian Systematics

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The "revolution in molecular approaches to taxonomic problems" noted by Houde (1987) is in its infancy, and neither its methods nor its concepts are yet perfected. Those who have used the methods and contributed to the data are keenly aware of their limitations, and their strengths. Since 1957 the authors of this commentary have participated in the preparation of some 70 publications pertaining to avian systematics based on the properties of proteins or DNA. We have tried various methods with varying degrees of success in a continuing effort to reconstruct the phylogeny of birds. We appreciate Houde's positive comments about DNA hybridization and our results to date. His critique contains valid points, but it does not acknowledge our current position on molecular evolutionary rates, and it is flawed by confusion about exactly what DNA hybridization measures and, thus, about the properties of the data. Our current understanding of these subjects differs from our earlier views, such as those Houde may have discussed with Sibley in 1982 (as noted by Houde 1987: 29). In this commentary we will try to clarify the issues, correct misconceptions, and state our present position on several questions.

Rates of molecular evolution.—Since 1984 we have

been aware that rates of single-copy nuclear DNA (scnDNA) evolution differ among avian lineages and between birds and mammals, and we have engaged in experiments designed to determine the occurrence and extent of such differences (Bledsoe 1987; Catzeflis et al. 1987; Sheldon 1987a, b; Sibley and Ahlquist 1987; Sibley et al. 1987). The laboratory work for these papers was carried out between 1984 and 1987. While these publications were being processed, we presented the evidence for different average genomic rates in seminars and lectures, including the International Ornithological Congress in June 1986 and recent A.O.U. annual meetings.

Although the existence of different average genomic rates (AGRs) is clear, it is also clear that such variation alone does not introduce ambiguity into phylogenetic reconstructions, provided appropriate clustering algorithms are used. Thus, Houde is incorrect in claiming that the reconstruction of phylogenies from DNA hybridization data depends on the existence of the same average rate along all branches. This misunderstanding is so basic to Houde's arguments about the shortcomings of DNA hybridization studies that many of his other points are rendered irrelevant.

The relationship between polarity and divergence.—Houde (pp. 17–18) stated that the dissimilarity measures produced by DNA hybridization comparisons are "inherently phenetic," and he referred to a footnote (p. 18) concerning apomorphy and plesiomorphy in relation to distance values. He implied that, in the absence of knowing the actual nucleotide substitutions and their relative apomorphy, there will always be ambiguity in phylogenetic reconstructions from distance data. We agree with Houde that "In-

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