

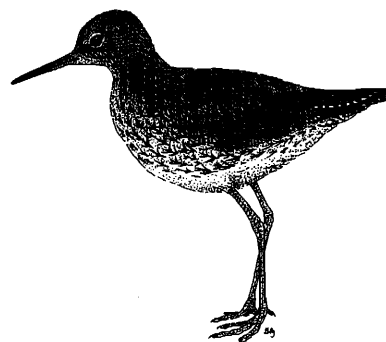
it would certainly be significant if one applied the hypergeometric distribution. However, if p is large or the number of birds remaining unsampled is small, one may miss what is actually significant clumping by using the binomial.

Acknowledgements

I am grateful to Cynthia Greenwood for typing this note and to G.E. Thomas for checking its content.

References

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A potential bias in log-transformed allometric equations

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Citation: Wood, A.G. 1986. A potential bias in log-transformed allometric equations. *Wader Study Group Bull.* 47: 17–19.

Introduction

Many recent studies in avian ecology have used regressions with logarithmic transformations to estimate various biological parameters, particularly metabolic rate (Lasiewski & Dawson 1967, 1969, Zar 1968, Aschoff & Pohl 1970, Kendeigh *et al.* 1977). This paper examines a potential bias resulting from the use of such equations, and presents the appropriate methods for converting estimates from logarithmic equations back to untransformed units.

The problem

In the general case, we have two variables X and Y which are related by the allometric equations:

$$Y = kX^b \quad (1)$$

where k and b are constants. Although the relationship between X and Y is non-linear, the transformed variates $\log X$ and $\log Y$ are connected by the straight line relationship:

$$\log Y - \log k = b \cdot \log X \quad (2)$$

This equation implies a linear relation between the logarithms of X and Y based on three assumptions:

1. The expected value of Y , for a given X is $(E(\log Y) = \log k + b \cdot \log X)$.
2. The variance V of $\log Y$, given $\log X$, is constant.
3. For each value of $\log X$, $\log Y$ is normally distributed.

The parameters of transformed equation (2) can now be estimated using the biological data and standard least-squares regression techniques.

When a logarithmic transformation is used it is usually necessary to be able to express estimated values of Y in

untransformed units. Such a back transformation is not direct, because if the distribution of $\log Y$ at a given $\log X$ is normal, the distribution of Y cannot be normal, but will be skewed. In fact the solution of equation (2) for a given X , and determining the antilogarithm of $\log Y$, yields the median of the skewed distribution of Y rather than the mean (Baskerville 1971). The correction factor (CF) by which this median must be multiplied to obtain the mean of Y , has been derived by a number of authors (Baskerville 1971; Mountford & Bunce 1973, Sprugel 1983), and is calculated from:

$$CF = e^{(V/2)}$$

where V is the variance of $\log Y$, e is the base of natural logarithms 2.718.

In practice V is not known, but can be estimated from the square of the standard error of the estimate of the regression, giving equation (3).

$$CF = e^{(SEE^2/2)} \quad (3)$$

where SEE is the standard error of estimate of the regression. The values for $\log k$ and b in equation (2) also have errors associated with them. However, they can be considered insignificant if a large enough sample size for the regression is obtained.

The value of SEE depends on the base to which logarithms are taken when the values of Y are transformed (Sprugel 1983). To obtain the correct value for the correction factor (CF), SEE must be based on natural logarithms. Therefore, using a base 10 standard error does not give the correct value; this base 10 SEE should be converted to base e (multiply by $\log_{.10} e = 2.303$) and this value used in equation (3).

In energetic studies, estimates are made of a species' metabolic rate from its weight using the following equation,



derived from a number of other species in which the metabolic rate is known:

$$\log(\text{Metabolic rate}) = \log k + b \cdot \log(\text{Body mass})$$

Given the body mass of a species, the antilog of the metabolic rate derived from this equation would give an estimate of the median metabolic rate for that particular mass. Only by multiplying this median by the previously defined correction factor would the mean metabolic rate for the particular body mass be obtained.

Example

As an example of the difference between back transformation to the median and mean from published allometric equations, I will take the non-passerine estimators of basal metabolic rate (BMR) given by Lasiewski & Dawson (1967) and Kendeigh *et al.* (1977). The MBR estimates for Dunlin *Calidris alpina* and Grey Plover *Pluvialis squatarola* are presented in Table 1.

Discussion

From the data in Table 1 it is clear that the inclusion of the correction factor produces a mean estimate of BMR which can be up to 2.3% above that which would normally be used (i.e. the uncorrected median). A further complication in the application of such equations is the question of what body mass should be used? Tuite (1984) showed that the use

of average lean mass rather than average total body mass greatly affects the metabolic rate estimate, and it is probably the average lean mass which best predicts the metabolic rate of a bird.

Basal metabolic rate is commonly used as a base for many energetics studies (Ashkenazie & Safriel 1979, Wood 1984). If there are large discrepancies as to which value of BMR to use, the multiplication of the error through a calculated energy budget will produce an even larger variation in the end result. The correction factor presented here does not appear to give a large change in the estimated BMR values. However, this is one source of error which is known about and can be corrected for: many others cannot yet be quantified.

Acknowledgements

I would like to thank Peter Rothery for the helpful discussion and advice he gave in the preparation of this paper. I am also grateful to Nick Davidson for his help, and to Peter Evans for his comments.

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Table 1. Estimates of BMR (Kcal/bird/day) from allometric equations.

	Dunlin	Grey Plover
Average lean mass (g)	47.0	196.0
BMR from Lasiewski & Dawson (1967) (SEE = 0.068)		
Median	8.58	24.10
Mean	8.69	24.40
% difference	1.2	1.2
BMR from Kendeigh <i>et al.</i> (1977) (SEE = 0.093)		
Median	8.84	25.24
Mean	9.05	25.83
% difference	2.3	2.3

