it would certainly be significant if one applied the hyper-
geometric distribution. However, if \( p \) is large or the num-
ber of birds remaining unsampled is small, one may miss what
is actually significant clumping by using the binomial.

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A potential bias in log-transformed allometric equations
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Introduction
Many recent studies in avian ecology have used regressions
with logarithmic transformations to estimate various biologi-
cal parameters, particularly metabolic rate (Lasiewski &
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 logarith-
ic 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:
\[ Y = kX^b \]  
where \( k \) and \( b \) are constants. Although the relationship be-
tween X and Y is non-linear, the transformed variates logX
and LogY are connected by the straight line relationship:
\[ \log Y - \log k = b \log X \]  
This equation implies a linear relation between the logaithms
of X and Y based on three assumptions:
1. The expected value of Y, for a given X is
   \( E(\log Y) = \log k + b \log X \).
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 (Basker-
ville 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:
\[ CF = e^{\left( \frac{V}{2} \right)} \]
where \( V \) is the variance of \( \log Y \), \( e \) is the base of natural loga-
rithms 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).
\[ CF = e^{\left( \frac{\text{SEE}^2}{2} \right)} \]  
where \( \text{SEE} \) is the standard error of estimate of the regression.
The values for logk and b in equation (2) also have errors
associated with them. However, they can be considered in-
significant if a large enough sample size for the regression
is obtained.

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

\[ \log(\text{Metabolic rate}) = \log k + b \log(\text{Body mass}) \]

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.

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**References**


