

Random sampling of skewed distributions implies Taylor's power law of fluctuation scaling

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Taylor's law (TL), a widely verified quantitative pattern in ecology and other sciences, describes the variance in a species' population density (or other nonnegative quantity) as a power-law function of the mean density (or other nonnegative quantity): Approximately, variance = $a(\text{mean})^b$, $a > 0$. Multiple mechanisms have been proposed to explain and interpret TL. Here, we show analytically that observations randomly sampled in blocks from any skewed frequency distribution with four finite moments give rise to TL. We do not claim this is the only way TL arises. We give approximate formulae for the TL parameters and their uncertainty. In computer simulations and an empirical example using basal area densities of red oak trees from Black Rock Forest, our formulae agree with the estimates obtained by least-squares regression. Our results show that the correlated sampling variation of the mean and variance of skewed distributions is statistically sufficient to explain TL under random sampling, without the intervention of any biological or behavioral mechanisms. This finding connects TL with the underlying distribution of population density (or other nonnegative quantity) and provides a baseline against which more complex mechanisms of TL can be compared.

delta method | least-squares regression | skewness | variance function

Taylor's law (TL), named after Taylor (1), relates the variance and the mean of population sizes or population densities of species distributed in space and time by a power-law function:

$$\text{variance} = a(\text{mean})^b \quad [1]$$

or equivalently as a linear function when mean and variance are logarithmically transformed:

$$\log(\text{variance}) = \log(a) + b \times \log(\text{mean}). \quad [2]$$

Eqs. 1 and 2 may be exact if the mean and variance are population moments calculated from certain parametric families of probability distributions (e.g., $a = 1$ and $b = 1$ for a Poisson distribution). Eqs. 1 and 2 may be approximate if the mean and variance are sample moments based on finite random samples of observations. Most empirical tests of TL have not specified the random error associated with Eqs. 1 or 2.

TL has been verified for hundreds of biological species and nonbiological quantities in more than a thousand papers in ecology, epidemiology, biomedical sciences, and other fields (2–4). Recently, examples of TL were found in bacterial microcosms (5, 6), forest trees (7, 8), human populations (9), coral reef fish populations (10), and barnacles (11, 12). TL has been used practically in the design of sampling plans for the control of insect pests of soybeans (13, 14) and cotton (15).

Scientific studies of TL largely focus on the power-law exponent b (or slope b in the linear form), which Taylor believed to contain information about how populations of a species aggregate in space (1). Empirically, b often lies between 1 and 2 (16). Ballantyne and Kerckhoff (17) suggested that individuals' reproductive correlation determines the size of b . Ballantyne (18) proposed that $b = 2$ is a consequence of deterministic population growth. Cohen (19) showed that $b = 2$ arose from exponentially

growing, noninteracting clones. Kilpatrick and Ives (20) proposed that interspecific competition could reduce the value of b . Other models that implied TL were the exponential dispersion model (21–23), models of spatially distributed colonies (24, 25), a stochastic version of logistic population dynamics (16), and the Lewontin–Cohen stochastic multiplicative population model (8). The diversity of empirical confirmations suggests that no specific biological, physical, technological, or behavioral mechanism explains all instances of TL. Such empirical ubiquity suggests that TL could be another of the so-called universal laws (26) like the laws of large numbers (27) and the central limit theorem (28). For example, independently of the present study, Xiao et al. (29) showed numerically (not analytically) that random partitions and compositions of integers led to TL with slopes often between 1 and 2, as commonly observed in empirical examples of TL.

The present work was kindred in spirit and intent, although distinct in technical approach and results. Here we demonstrated that, when independently and identically distributed (iid) observations are sampled in blocks (not necessarily of equal size) from any nonnegative-valued skewed probability distribution with four finite moments, TL arises. We do not assert this is the only way TL arises. If these conditions are not satisfied in an empirical confirmation of TL, other mechanisms are likely to be in play. Under these assumptions (iid sampling in blocks from a skewed probability distribution with four finite moments), we derived analytically the explicit approximate formulae for the TL slope (b in Eq. 2), intercept [$\log(a)$ in Eq. 2], and standard error (SE) of the slope estimator [$s(b)$, see *Theorem in Results*]. In simulated random samples from probability distributions, these theoretical formulae approximated well the TL parameters. An empirical example using basal area densities of red oak trees in a temperate forest showed that our theory explained some published

Significance

One of the most widely confirmed empirical patterns in ecology is Taylor's law (TL): The variance of population density is approximately a power-law function of the mean population density. We showed analytically that, when observations are randomly sampled in blocks from a single frequency distribution, the sample variance will be related to the sample mean by TL, and the parameters of TL can be predicted from the first four moments of the frequency distribution. The estimate of the exponent of TL is proportional to the skewness of the distribution. Random sampling suffices to explain the existence and predict the parameters of TL in well-defined circumstances relevant to some, but not all, published empirical examples of TL.

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estimates of the TL slope when the assumptions of the theory were satisfied, and also successfully predicted the TL slope when the assumptions of the theory were shown to be mildly violated. Our results showed that TL may arise without any complicated mechanisms, and provided simple assumptions (skewed and iid observations) against which empirical applications of TL can be tested.

Results

Analytical Results. Suppose X is a nonnegative real-valued random variable with cumulative distribution function F , finite mean $E(X) = M > 0$, finite variance (or second central moment) $var(X) \equiv E(X^2) - [E(X)]^2 = V > 0$, and finite third and fourth central moments $E[(X - M)^h] = \mu_h$, $h = 3, 4$. Consider $N > 2$ “blocks” or sets of iid observations (random samples) of X . Let x_{ij} denote observation i of block j , $i = 1, \dots, n_j$, assuming the number of observations in block j satisfies $n_j > 3$, $j = 1, \dots, N$. The total number of observations is $n_1 + n_2 + \dots + n_N$. For block j the sample mean of observations and the expectation and variance of the sample mean are, respectively, $m_j = (x_{1j} + \dots + x_{n_j j})/n_j$, $E(m_j) = M$, $var(m_j) = V/n_j$. The unbiased sample variance of observations in block j and its expectation and variance are, respectively,

$$v_j = \frac{1}{n_j - 1} \sum_{i=1}^{n_j} x_{ij}^2 - \frac{n_j}{n_j - 1} m_j^2,$$

$$E(v_j) = V, \quad var(v_j) = \frac{1}{n_j} \left(\mu_4 - \frac{n_j - 3}{n_j - 1} V^2 \right).$$

The formula for $var(v_j)$ is from Neter et al. (30). As $n_j \rightarrow \infty$, $Prob\{m_j = 0\} \rightarrow 0$ and $Prob\{v_j = 0\} \rightarrow 0$ by Chebyshev’s tail inequality (31). We assume that n_j is large enough that $m_j > 0$ and $v_j > 0$.

In this theory, the variation between blocks in the sample mean and the variation between blocks in the sample variance are small because every block is randomly (iid) sampled from the same distribution. Because any two smoothly varying functions can be locally linearly related, the logarithm of the sample variance of a block can be approximated as a linear function of the logarithm of the sample mean of that block. The theorem below quantifies this qualitative observation.

In empirical examples, if the variation of sample means among blocks is too large to arise from random sampling alone (e.g., if ANOVA rejects homogeneity of block means), then the assumptions of the theorem do not apply, and it remains to be determined empirically whether the theorem’s conclusions apply, as if the theorem’s assumptions were close enough to reality. We give empirical examples, based on published data, where the theorem’s assumptions do, and do not, hold and the conclusions do hold in both situations.

By definition, the coefficient of variation of X is $CV = V^{1/2}/M$, the skewness is $\gamma_1 = \mu_3/V^{3/2}$, and the kurtosis is $\kappa = \mu_4/V^2$. Most empirical tests of TL estimated the intercept $\log(a)$ and the slope b of TL using ordinary least-squares regression of $\log(v_j)$ as the dependent variable and $\log(m_j)$ as the independent variable, and we analyze this practice. We do not assume that the sample mean is an error-free estimate of the population mean: the theorem deals with a relation among sample moments.

Definition: Suppose a random variable Y is a function of a random sample of size n from a distribution F , and suppose the expectation $E(Y)$ exists. Then the expression $Y \approx K$, where K is a constant independent of the random sample, is defined to mean that, for some $p > 0$, $E(Y) = K + o(n^{-p})$, where $o(n^{-p})$ refers (in Landau’s little- o notation) to any function $f(n)$ such that $\lim_{n \rightarrow \infty} f(n)/n^{-p} = 0$ (e.g., see ref. 31, p. 121).

Theorem. Suppose the nonnegative real-valued random variable X has finite first four moments, with strictly positive mean and strictly positive variance. Suppose that $n_j > 3$ observations x_{ij} ($i = 1, \dots, n_j$) of X are randomly assigned to block j ($j = 1, \dots, N$), $N > 2$, and all

of the observations, which number $\sum_{j=1}^N n_j$ in total, are iid. Let m_j, v_j be the sample mean and the sample variance, respectively, of the n_j observations in block j , and suppose n_j is large enough that m_j and v_j are strictly positive. Let \hat{b} and $\widehat{\log(a)}$ denote the least-squares estimators, respectively, of b and $\log(a)$ in TL, namely, $\log(v_j) = \log(a) + b \times \log(m_j)$, $j = 1, \dots, N$ (Eq. 2). Let $s(\hat{b})$ denote the SE of the least-squares slope estimator \hat{b} . Then, in the limit of large N and large n_j ,

$$\hat{b} \approx \frac{cov(m_j, v_j)}{MV} \bigg/ \frac{var(m_j)}{M^2} = \mu_3 M / V^2 = \gamma_1 / CV, \quad [3]$$

$$\widehat{\log(a)} \approx \log V - \frac{\gamma_1}{CV} \cdot \log M, \quad [4]$$

$$s(\hat{b}) \approx \sqrt{\frac{M^2(\mu_4 V - V^3 - \mu_3^2)}{(N-2)V^4}} = \sqrt{\frac{\kappa - 1 - \gamma_1^2}{(N-2)(CV)^2}}. \quad [5]$$

Proof of this Theorem is given in SI Text. Because $CV > 0$, Eq. 3 shows that random sampling in blocks of any right-skewed distribution (one with $\gamma_1 > 0$) generates a positive TL slope.

Squaring both sides of Eq. 5 yields the estimated variance of \hat{b} . Because any variance is nonnegative, the numerator of the variance estimate ($\kappa - 1 - \gamma_1^2$) is nonnegative. Eq. 5 thus provides an alternative proof and adds a new interpretation of the inequality $\kappa - 1 - \gamma_1^2 \geq 0$ that was obtained by Rohatgi and Székely (32).

Numerical Simulations. We illustrate our theory of TL using six probability distributions, five of which are positively skewed. We created six square matrices (here $N = n$) to mimic the blocks commonly found in ecological field data. Each column can be viewed as a block containing n observations (rows). For each matrix, we plotted (Fig. 1) the log of the sample variance v_j of each column j on the ordinate against the log of the sample mean m_j on the abscissa, $j = 1, \dots, N$.

For each of the five positively skewed distributions, an approximately linear relationship with positive slopes was observed (Fig. 1A–E). The lognormal slope (Fig. 1E) was larger than most estimates observed in ecological applications. For the shifted normal distribution, which had zero skewness, no relationship between the log sample variance and the log sample mean was observed (i.e., analytically $b = 0$ and numerically and by regression $\hat{b} = 0$) (Fig. 1F).

To illustrate our Theorem numerically, we applied the theoretical formulae (Eqs. 3–5) to each of the six probability distributions and analytically computed the predicted values of the slope and intercept in Eq. 2, and the SE of the slope estimator. The first four moments used in the formulae are standard results for these distributions. For each distribution, we also generated 10,000 random copies of the n ($= 100$) by N ($= 100$) matrix and fitted a linear regression and a quadratic regression to the $\log(m_j)$ and $\log(v_j)$, $j = 1, \dots, N$ from each random copy. We obtained an approximate sampling distribution for each parameter of TL and for the quadratic coefficient c in the hypothetical quadratic relationship $\log(\text{variance}) = \log(a) + b \times \log(\text{mean}) + c \times [\log(\text{mean})]^2$. Medians and 95% confidence intervals (CIs) of TL parameters, SE of the slope estimator, and the quadratic coefficient were calculated respectively from the 50, 2.5, and 97.5% quantiles of the sampling distribution of the corresponding linear and quadratic regression point estimates. To test the robustness of our theory, the $n \times N$ observations in each matrix were used to calculate sample estimates of the first four moments of the corresponding probability distribution, as if the first four moments were not known a priori but were based on a sample. These estimates were then plugged into the formulae (Eqs. 3–5) to evaluate the theoretical TL slope, intercept, and SE of the slope estimator. Their medians and 95% CIs were similarly

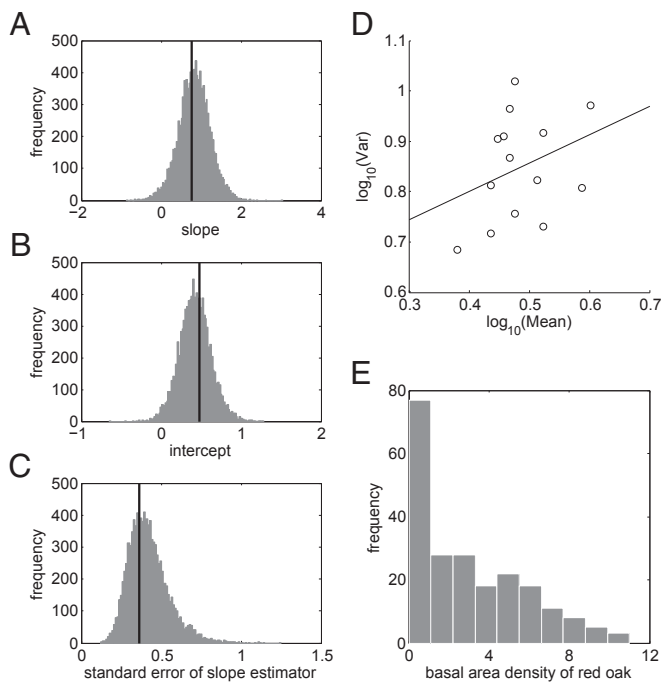


Fig. 2. Testing TL using basal area density of RO in BRF. (A–C) Histograms of the slope, intercept, and SE of the slope estimator, respectively, estimated by regression from 10,000 random assignments of observations into blocks, with the theoretically predicted values marked by the solid vertical lines. (D) A least-squares regression (solid line) of the dependent variable $\log(\text{variance})$ as a linear function of the independent variable $\log(\text{mean})$ under one realization of random groupings. Each open circle represents a mean and a variance calculated over observations within a single block. (E) The histogram of basal area density of RO at 218 sampling points is right-skewed.

Discussion

Our results show that random sampling of a distribution in blocks leads to TL. Moreover, the first four moments of the distribution and the number of blocks predict the TL parameters and the SE of the slope estimator. No biological or physical mechanisms need be invoked to explain TL under this form of sampling. In the empirical example of RO, the 95% CI of the TL slope calculated from our theory (0.0146, 1.5975) overlapped the range of 1–2 commonly but not universally observed in ecological data (36). Our examples show that this model has relevance to some, but not all, published empirical examples of TL.

Our random sampling model does not purport to be a universal explanation of TL in all or most circumstances. For example, when the mean population densities in large samples of different species of widely different body masses range over seven or more orders of magnitude (37), the differences in mean and variance of population density probably cannot be attributed to random sampling variation from a single underlying distribution. However, when the mean population densities range over little more than one order of magnitude (ref. 11, p. 12, figure 7), the invariance of TL parameters under different regimes of population dynamics might be accounted for by our sampling model.

In our numerical examples, the discrepancy between the theoretical prediction and the regression estimate of TL slope b under random sampling was largest for the lognormal distribution, which also had the least realistic values of \hat{b} (Fig. S1E). A possible reason is that $s(\hat{b}) = 0.6660$ for the lognormal distribution was twice as large as $s(\hat{b})$ for any of the other four skewed distributions, the second largest being 0.3194 for the gamma distribution (Table 1), whereas the sample sizes for all of the distributions were the same $n = 100$. In addition, because the fourth moment of lognormal distribution grows exponentially as a function of the parameter σ^2 , our estimates of the variance for

the lognormal distribution were likely to be least reliable among the estimates for the skewed distributions [see formula for $\text{var}(v_j)$ in *Results, Analytical Results*]. Among tested distributions, the fourth central moment of the lognormal distribution was at least 90 times the fourth moment of any other distribution. Evidently, in the lognormal example, we did not simulate enough linear regressions to sample adequately the full range of variation of the parameters. Nevertheless, when applied to the 10,000 random copies of $n \times N$ lognormal observations, our formula provided a robust theoretical estimate of b compatible with that from the regression (Table 1).

Previous works have analyzed TL in relation to frequency distributions. For example, Taylor (2) observed that insect populations at progressively higher densities conformed to different frequency distributions (e.g., Poisson, negative binomial, and lognormal) with identical slope parameter b , but he did not explain why TL arises from these distributions. Our results connect TL with the underlying probability distribution but do not explain why the distribution of observations (e.g., Fig. 2E) was right-skewed. Future studies on TL and other general empirical scaling patterns should give attention to the role of population distributions in understanding these patterns.

The usefulness of TL in inferring biological information about population aggregations is a subject of continuing scientific debate. Alternative mean–variance relationships have been proposed as competitors of TL (25, 38, 39). It has been argued that sampling error and sampling coverage may lead to TL-like patterns as statistical artifacts (40) and to substantially biased TL parameters (41). Our results offer another statistical mechanism that leads to TL.

Methods

Throughout, $\log = \log_{10}$. P represents the P value and α is the significance level of any hypothesis testing (except when α is used as a parameter of the gamma distribution).

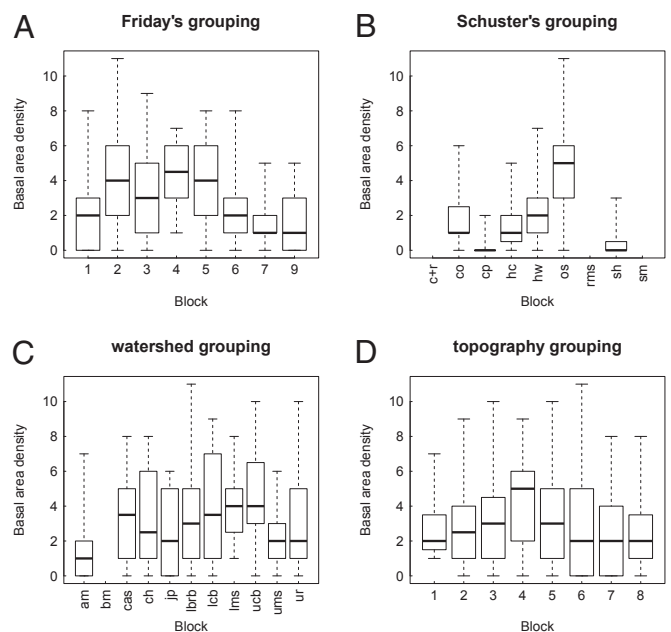


Fig. 3. Boxplots of basal area density of RO in BRF, according to four biological methods of assigning plots to blocks. In each boxplot, the median is the bold black bar, the box covers the interquartile range, and the whiskers cover the entire range of basal area density within a block. One-way unbalanced ANOVA tests of the null hypothesis of no difference between blocks in mean basal area density rejected the null hypothesis ($P < 0.05$) for all grouping methods except for the topography grouping. (A) Friday's grouping. (B) Schuster's grouping. (C) Watershed grouping. (D) Topography grouping.

Traditionally, when tested against empirical data, TL has been taken to be confirmed if the fitted linear regression Eq. 2 had statistically significantly nonzero linear coefficient b (with $P < \alpha$; here $\alpha = 0.05$), and if a least-squares quadratic regression between the independent variable $\log(\text{mean})$ and dependent variable $\log(\text{variance})$ did not yield a statistically significant quadratic coefficient c ($P > \alpha$). The use of the doubly logarithmic scale in the testing of TL and other bivariate allometric relationships (e.g., scaling of metabolic rate with body mass) has been questioned (39, 42–44) and defended (45, 46).

Our numerical examples combined the ordinary least-squares regression approach with random sampling. Specifically, in multiple realizations, we sampled from a single probability distribution, grouped observations into blocks, calculated the mean and the variance of observations per block, recorded the parameters and quadratic coefficient estimates from the corresponding linear and quadratic regressions (47, p. 155), respectively, for each realization, and constructed CIs of the parameters using percentiles of the corresponding approximate sampling distributions obtained from all realizations.

In the empirical example of RO trees, we randomly grouped observations into blocks and obtained TL parameters from linear regression fitted to repeatedly randomly grouped samples. We also analyzed biologically based groupings (33) of these trees that gave rise to TL. Linear and quadratic

regressions were performed using the MATLAB (The MathWorks, Inc.) function “regress.”

The analytical formulae for the TL parameter estimators and the SE of the slope estimator were derived using the delta method (48, 49). The delta method, which is commonly used by statisticians, relies on Taylor series expansions (not the same Taylor as in Taylor’s law) for moments of functions of random variables. To implement the delta method we relied on a moment estimate of the difference between population mean and sample mean by Loève (50) and the consistency of sample estimators (*SI Text*). The delta method is increasingly accurate as the variation around the point of expansion becomes smaller. Because the variation in sample means and sample variances is small when sufficiently large random samples are blocked, the delta method yields quite accurate approximations to TL parameters estimated from linear regression.

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