Distribution of Aflatoxin in Pistachios. 1. Lot Distributions

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A nonparametric relation is derived between the discrete probability distribution $\{p_i, c_i\}$, assumed for toxin concentration c in individual members of a population, and the probability distribution $\{P_i(n)\}$ of the toxin concentration in n-member samples taken from that population. Here p_i is the probability of an individual member having toxin concentration c_i, while $P_i(n)$ is the probability of an n-sample exhibiting toxin concentration falling in range i of C. An information theoretic basis is given for the number J of indices i required for $\{P_i(n)\}$. The same number of indices is used for $\{p_i, c_i\}$; additional values, if needed, are estimated. $\{P_i(n)\}$ is derived from $\{p_i, c_i\}$ by multinomial Poisson statistics. Conversely, it is shown how $\{p_i, c_i\}$ may be derived from empirical $\{P_i(n)\}$ data when the np_i are small, as is commonly the case for aflatoxin contamination of tree nuts. As a first approximation one obtains $p_i = P_i(n)/n$ and $c_i = n * C_i$, where C_i is the midpoint of range i of C. Higher approximations are evaluated as well. A basis is thus laid for computing $\{P_i(n)\}$ for a sample size differing from that of the sample actually determined. The results are applied to predicting the probability of a sample of any size exceeding a predetermined level C_a.

Keywords: *Low-level contamination; sampling; nonparametric; sample size; tree nuts; aflatoxin*

INTRODUCTION

Edible tree nuts may be infected by a deleterious toxin, aflatoxin, which appears to develop in the orchard on a very few isolated nuts. As a result, very high and variable levels of this toxin may be present on a very small proportion of nuts in a lot. Since the average level of aflatoxin in the lot is of regulatory concern, sampling presents a difficult problem. Sampling protocol for whole nuts (with or without shell) calls for the withdrawal of a sample of predetermined size (typically 4.5 or 22.5 kg), homogenization by grinding and blending, and determination of the concentration C of aflatoxin of a subsample of the ground sample (Park and Pohland, 1989). Analytic and subsampling errors typically result in a coefficient of variation in aflatoxin concentration of 20–30% (Whitaker et al., 1974), but sampling errors are severe; repeated samples may result in values that differ by many orders of magnitude. This is caused by the infrequent appearance of highly contaminated nuts which dominate the sample concentration. It is impractical to select samples large enough to obtain a representative selection of such nuts; hence, lot average concentrations are difficult to estimate. What is wanted is then the probability that C will exceed some preset action or acceptance level, C_a. Although the industry is generally aware of these problems, there is little appreciation that these probabilities depend critically on the sample size, n; certainly the form of the dependence on n does not seem to be understood. There are, in fact, testing protocols in use for which the sample size is taken proportionally to the lot size (FDA, 1986). In summary reports the actual sample size is frequently not reported or available (Wood, 1989). The emphasis is entirely on toxin level.

The relation between sample size, n nuts, sample concentration, C, and the probability, $P_i(n)$, that this concentration falls within a predetermined range [bin i] of C is based on the underlying probability distribution function (pdf), $f(c)$, of aflatoxin concentration, c, in individual nuts. (Throughout this paper, upper case will be used to refer to things related to C, the n-sized sample concentration. The corresponding lower case is used for things related to c, the concentration in a single nut. The dependence of C distributions on the parameter n is shown explicitly.) $f(c)$ is taken as a discrete function, represented as a set $\{p_i, c_i\}$, with probability p_i of a single nut having aflatoxin concentration c_i. The relation of $\{P_i(n)\}$ to $\{p_i, c_i\}$ is derived in the next section. It will allow, in principle, estimation of $\{P_i(n)\}$ by the measurement of a large number of samples, all of size n, followed by the computation of $f(c)$ and the subsequent calculation of $\{P_i(n)\}$ for a different n. [The notation {} will be used to designate a set, here all $P_i(n)$ for a given n and fixed binning. We shall refer to this set as the probability distribution (*not* the pdf).] This concept is then taken one step further to compute the probability, $R(n, C_a)$, of rejecting an n-nut sample. Whitaker and co-workers (Whitaker et al., 1972, 1994) assumed a parametric pdf, the negative binomial, and studied sampling as it applied to peanuts. Experimental data were fitted parametrically, and an adequate fit was found between theoretical and experimental distributions. The present approach is nonparametric in the sense that the same number of parameters is used to describe $f(c)$ as $P_i(n)$ so that no information is lost. Only in estimating the limits of some of the approximations used is a functional form applied.

LOT DISTRIBUTION

Contamination at a Single Level. To derive the relation expressing $P_i(n)$ in terms of $f(c)$, it is instructive to first consider the case where all contaminated nuts have the same aflatoxin level, c_1, and occur with a probability p_1, a fraction $p_0 = 1 - p_1$ being noncontaminated. This case was first treated by Schade et al. (1975). If one selects an n-nut sample from such a lot, the probability of such a sample containing x_1 contaminated nuts is given by a binomial distribution which may be approximated by a Poisson distribution (Feller, 1957, p 142)

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$$\boldsymbol{P}(n, x_1) = \exp(-np_1) * (np_1)^{x_1}/x_1! \quad (1)$$

The Poisson approaches the binomial distribution as $n \rightarrow \infty$, with np fixed. However, even for n as low as 10, term for term the two distributions differ by less than 0.021 when $p = 0.1$ and $x < 2$ and much less when p is smaller or x is larger. In experimental work on tree nuts sample sizes as small as 10 are not uncommon. While the binomial is more accurate and converges to zero more rapidly as x increases, it requires two parameters, n and p, while the Poisson requires but one, np. Hence, the latter is easier to describe, generalize, and investigate. It is used here.

Such an n-nut sample will have a sample concentration (w/w basis)

$$C = x_1 * c_1 * w / (n * w) = x_1 * c_1/n \quad (2)$$

where w is the weight/nut. When np_1 is small, the likelihood of obtaining a sample with a single contaminated nut, $P(n, 1)$, will be approximately proportional to np_1, while the probability of obtaining a sample with higher concentration, $x_1 > 1$, will vanish, since it involves higher powers of np_1. The mean of the C distribution becomes $E(C) = E(x_1) * c_1/n = (np_1) * c_1/n = p_1 * c_1$, the sampling variance $V_s(C) = V(x_1) * (c_1/n)^2 = np_1 * (c_1/n)^2 = p_1 * c_1^2/n$, where E is the expectation function. From the coefficient of variation indicated in the previous section, the variance due to subsampling and analysis, V_{ssa}, amounts to $(25\%)^2 * (np_1 * c_1/n)^2 = 0.0625\ (p_1 * c_1)^2$. In the analysis to follow, np_1 will be <1, hence V_{ssa} can be ignored. The probability of an uncontaminated sample, $P_0(n)$, is given by $\exp(-np_1) = \exp[-E^2(C)/V(C)]$. From $E(C)$, n, and $P_0(n)$ or $V(C)$, one could deduce p_1 and c_1.

Distributed Contamination. When one measures C for a set of n-sized samples taken from a single lot of tree nuts or from a set of lots with distributions believed to be the same, one finds that the C distribution does not match the one predicted above; in particular, $P_0(n)$ is smaller than that predicted above. The above concepts need to be generalized to more than a single level of contamination. The number of levels J which need to be considered is determined by the number of distinguishable levels of C. This number depends on the dynamic range and precision of C. The dynamic range of C is limited by the minimum detectable level C_0 of aflatoxin (currently approximately 0.03 ng/g) and the maximum level C_{max} sustainable by a single nut (which appears to be about 10^6 ng/g or a little more) or approximately 7.5 decades. The precision was indicated above to be approximately 25%, from which it follows that a half-decade in C (approximately a factor of 3) covers ± 2 SD ($1 \pm 2 * 25\%$ or 0.5–1.5). Thus, the experimental data can be expressed as $J \approx 7.5/0.5 = 15$ independent probabilities $P_i(n)$, corresponding to J logarithmic bins B_i of fixed size $\Delta = \log_{10} C_i^+/C_i^- = 0.5$, where C_i^+ and $C_i^- = C_{i-1}^+$ are the limits of B_i. The probability of an uncontaminated sample, $C < C_0$, becomes $P_0(n) = 1 - \sum_{i>0} P_i(n)$.

The lot distribution is now modeled as a collection of nuts with a fraction p_i having aflatoxin concentration c_i, $i = 1, \ldots, J$ and a fraction p_0 uncontaminated. Mathematically, this amounts to using for a pdf

$$f(c) = p_0 * \delta(c) + \sum_{i>0} p_i * \delta(c - c_i) \quad (3)$$

where $\delta(c - c_i)$ is the Dirac δ function which integrates to unity for any range that includes c_i and to zero otherwise. Again, the fraction of uncontaminated samples is given by $p_0 = 1 - \sum_{i>0} p_i$. The c_i are placed at the center of the B_i but, for reasons discussed below, an offset, $\log n$, is used to index c_i, i.e. $\log c_i \equiv \log n + 0.5 \log (C_i^+ * C_i^-)$, i.e. the spacing of $\log c_i$ is again Δ. (There is no biological basis for restricting the contamination levels to J discrete levels. However, the error in using δ functions is no worse than the precision with which C can be measured.) If an n-nut sample is drawn at random from such a lot, the probability of obtaining x_1 nuts of type 1, x_2 nuts of type 2, etc., in the sample is given by a multinomial distribution which is approximated by a product of Poissons (Feller, 1957, p 162).

$$\boldsymbol{P}(n,x_1,x_2,\ldots,x_J) = \exp(-np_1) * (np_1)^{x_1}/x_1! * \exp(-np_2) * (np_2)^{x_2}/x_2! * \ldots \exp(-np_J) * (np_J)^{x_J}/x_J! \quad (4)$$

This sample will exhibit a sample concentration

$$C = (x_1 * c_1 + x_2 * c_2 + \ldots + x_J * c_J)/n \quad (5)$$

as long as the weight/nut is independent of i [strictly, units of c are ng of aflatoxin/weight of average nut (in g)].

Finally, to obtain $P_i(n)$, one considers all combinations of $x_1, x_2, \ldots, x_J$ for which C, as computed using eq 5, falls into bin B_i, computes $\boldsymbol{P}(n,x_1,x_2,\ldots,x_J)$ for each combination by use of eq 4, and sums the $\boldsymbol{P}$'s. Formally

$$P_i(n) = \sum\ldots,x_1, x_2,\ldots x_J \boldsymbol{P}(n; \ldots, x_1, x_2, \ldots x_J) \mid C_i^- < C < C_i^+ \quad (6)$$

The index notation in eq 6 takes explicit account of the fact that nuts at $c_i < n * C_i^-$ may well contribute toward C, as long as x_i is large enough. In particular, nuts for which $c_i < n * C_0$, $i < 0$, may contribute toward B_i. (The index $i = 0$ remains reserved for uncontaminated nuts.) Strictly, eq 3 should include $i < 0$ terms in the sum as well. Such terms appear only to second order, however (see below). On the other hand, $i > J$ need not be considered, as $c_i < C_{max}$. Expression 6, upon substitution of eqs 4 and 5, is then the expression of the $P_i(n)$ in terms of n and $\{p_i, c_i\}$. This sample probability, while laborious to compute, will only depend on the set of np_j and the bin limits. The approach is then exactly the same as for the single-level contamination case. One estimates $\{P_i(n)\}$ from the fraction of samples in each bin B_i. [No distinction is made here between $\{P_i(n)\}$ and the estimate thereof. Which is meant will be clear from the context.] Next one computes $\{p_i, c_i\}$ as described below, which, in turn, allows the computation of the $\{P_i(n)\}$ at any other n through the use of eq 6.

From eqs 5 and 6 one has $E(C) = \sum_i p_i * c_i$ and $V(C) = \sum_i p_i * c_i^2/n$. [In evaluating $V(C)$, the covariance terms $-n * p_i * p_j$ (Wilks, 1962, p 139) are negligible since $p_i \ll 1$, all $i > 0$ (see also below)]. Algebra yields $(n * \sum_i p_i) * V(C) - E^2(C) = \sum_{i,j} p_i * p_j * (c_i - c_j)^2 > 0$. Combining the last expression with $P_0(n) = \exp(-n * \sum_{i \neq 0} p_i)$, one has, for any distributed contamination, $P_0(n) < \exp(-E^2(C)/V(C))$.

Sparse Approximation. What is needed is the inverse of eq 6, an expression for $\{p_i, c_i\}$ in terms of $\{P_i(n)\}$, since the latter can be estimated from experiment. Because of the presence of the $p_{i<0}$ terms, discussed above, there are more p_i than $P_i(n)$. A unique inversion does not exist. However, it will follow below that $i < 0$ terms are only of interest to second order,

and hence the $\{p_{i<0}\}$ may be estimated from the $\{p_{i>0}\}$ without actually solving for them. Even with this proviso, inversion is difficult as these expressions are nonlinear (exponential in eq 6 or polynomial of order n if the multinomial expression is used). There exists, however, a common situation when the equations separate and become linear. If the sample size n is chosen to be small compared to $1/p_i$ for all i except $i = 0$, then all $np_i \ll 1$, $i > 0$, and $\boldsymbol{P}(n,x_1,x_2,...)$ will substantially vanish for all cases except when one of the $x_i = 1$ and all of the other $x_i = 0$, since all of the latter will involve products of the np_i. The only terms contributing in eq 6 will correspond to samples that contain only a single contaminated nut. This is, of course, but a generalization of the single-level contamination, discussed above, where $\boldsymbol{P}(n, 1)$ dominated $\boldsymbol{P}(n, >1)$ when np_1 was small. (Note that the use of the Poisson approximation requires that all $p_i \ll 0.1$ to keep the necessary $n > 10$. Otherwise, the multinomial expression must be used.) If a single nut is the sole nut that is contaminated at level c_i, eqs 5 and 6 reduce to

$$C_i = c_i/n \quad \text{or} \quad c_i = n * C_i \tag{5'}$$

where $P_i(n) = \exp(-n * \sum_{j>0} p_j) * np_i \approx np_i$ or

$$p_i = P_i(n)/n \tag{6'}$$

We refer to the situation described by eqs 5′ and 6′ as "sparse". Expression 5′ is the basis for choosing logarithmic binning and the shift of the index i between the log c and log C axis. Expression 6′ reflects the fact that an n-sized sample is n times as likely to contain this nut. Equation 6′ does not apply to uncontaminated nuts; p_0 is given by $1 - \sum_{i>0} p_i$. In brief, in the sparse limit, if log $P_i(n)$ is plotted against log C, then log p_i can be obtained by shifting right and down by log n. A direct consequence of eqs 5′ and 6′ is the relation between $P_i(n)$'s at two different sample sizes. A little algebra yields

$$P_i(n_2)/{n_2}^{1-\gamma} = P_i(n_1)/{n_1}^{1-\gamma} \tag{7'}$$

if $\gamma = \log(P_i(n)/P_{i-1}(n))/\log(C_i/C_{i-1})$ is constant between C_i and $(n_2/n_1) * C_i$.

Note that in the sparse approximation J is reduced by log n and the $p_{i<0}$ do not appear at all. No samples can be expected to exhibit $C > C_{max}/n$ and, indeed, no such samples have ever been reported for tree nuts. Conversely, no evidence would be obtained for individual nuts containing aflatoxin concentration less than $n * C_0$. To obtain data on nuts at low aflatoxin contamination, very small samples, even single nuts ($n = 1$), would need to be analyzed to avoid dilution.

Limits of the Sparse Approximation. While the sparse approximation will always hold in the limit as $np_i \to 0$ for all $i > 0$, it is of interest to know to what extent it may be used in practice, i.e. how much of an error is made in using eq 6′ instead of eq 6. Equation 6′ uses but a single term of eq 6 and approximates the exp function as unity. To evaluate this error, consider a specific bin B_i and ask which c_j's must be considered in computing the total sample aflatoxin content to cause it to fall into B_i [and hence contribute toward $P_i(n)$]. In general, no $c_j, j > i$, need to be considered since even a single such nut would cause the sample to fall into a bin $B_j, j > i$. Levels $c_j, j < i$, may contribute, however. How likely combinations containing such nuts are will depend on the np_j, as well as on Δ. One needs to estimate just how many j are needed to include all combinations of importance. If np_j is not too large and c_j/c_i is small enough, it would take an inordinate number of lightly contaminated nuts to affect $P_i(n)$ and this would be very unlikely. As a result, the sum 6 converges rapidly if treated as a series in the j index. In practice, $i \geq j \geq i - 4$ is sufficient to obtain a good estimate of $P_i(n)$ for the parameter ranges considered.

Table 1. $P_i(n)$, Exact Value (Expression 6)/ Sparse Approximation (Expression 6′)

$\Delta = \log_{10} 2.0$	γ 0.0	0.2	0.4	0.6	0.8
np_i					
0.05	0.97	1.00	1.03	1.09	1.20
0.1	0.94	0.98	1.04	1.16	1.37
0.2	0.86	0.91	1.00	1.16	1.44
0.3	0.76	0.82	0.90	1.03	1.21
0.4	0.67	0.71	0.76	0.83	0.85

$\Delta = \log_{10} 3.16$	γ 0.0	0.2	0.4	0.6	0.8
np_i					
0.05	0.97	0.99	1.01	1.04	1.13
0.1	0.95	0.97	1.01	1.10	1.41
0.2	0.89	0.93	1.02	1.25	1.98
0.3	0.83	0.88	1.01	1.33	2.00
0.4	0.77	0.83	0.97	1.28	1.63

$\Delta = \log_{10} 5.0$	γ 0.0	0.2	0.4	0.6	0.8
np_i					
0.05	0.98	0.98	0.98	1.01	1.13
0.1	0.95	0.96	0.98	1.08	1.42
0.2	0.90	0.93	1.01	1.23	2.11
0.3	0.86	0.89	1.02	1.30	2.40
0.4	0.81	0.86	0.99	1.32	2.16

It has not been possible to analytically evaluate this parametric dependence. It was therefore done numerically. A c++ code was written to exhaustively evaluate all terms arising from $i \geq j \geq i - 4$. Three parameters were considered. The quantity np_i expresses the rapidity of convergence of the Poisson or, in effect, n. $\Delta = \log c_i/c_{i-1}$. The size of p_j at lower bins is expressed as $\gamma \equiv -\log(p_j/p_{j-1})/\log(c_j/c_{j-1})$, averaged over $j = 0, ..., 4$. The ranges explored were $0 \leq np_i \leq 0.4$, $0 \leq \gamma \leq 0.8$, and $\log 2 \leq \Delta \leq \log 5$. These ranges, by and large, cover all cases of practical interest in tree nuts. A value of np_i less than 0.2 is generally what is wanted. The extension to 0.4 covers extreme cases. Unpublished data for pistachios suggest a value of 0.4 for γ, although in limited regions of c values as large as 0.8 may occur [see Schatzki (1995)]. As indicated above, the size of Δ will be set by the analytic and subsampling precision; $\Delta = \log 2$ would correspond to $(V_{ssa})^{0.5} = 17\%$, log 5 to 33%. The code systematically and exhaustively covers all possible combinations and may be obtained in source form from Appendix A (supplementary material) or from the anonymous ftp server aggie.pw.usda.gov as file pub/dropbox/Pin.cpp. It evaluates eq 6 at the rate of 100 000 nut combinations/min, running on a PC486DX/25, when compiled under BorlandC (Borland International, Inc., Scotts Valley, CA). The results, expressed as the result of evaluating eq 6 instead of using eq 6′, are shown in Table 1. These results were obtained using the Poisson expression (eq 1). A recomputation of the entries, using instead of the Poisson the binomial distribution with $n = 10$ and $\Delta = \log_{10} 3.16$, showed that entries changed less than 3%.

The results of Table 1 can be used to estimate the region of applicability of eq 6′ or to correct eq 6′. [In practice, the value of np_i to use would be estimated from $P_i(n)$, the value of γ from $\log P_j(n)/P_{j-1}(n)$, averaged over $j = 0, ...4$, before correction.] The calculations leading to Table 1 also reveal that combinations containing *any* nuts at c_i or c_{i-1} contribute 50% or more to $P_i(n)$ if $P_i(n) \leq 0.4$, within the parameter ranges explored. This verifies the assertion that within this range it is indeed true that sample aflatoxin content is largely due to but a few highly contaminated nuts rather than many lightly contaminated ones. This information is of importance to research in aflatoxin elimination as it indicates how much can be gained by removing only highly contaminated nuts.

ACCEPTANCE TESTS AND SAMPLE SIZE

The acceptance level, C_a, is generally set by the buyer or regulator as the desired maximum lot average, $E(c)$. As noted, the measured sample concentration, C, has a large variance and is thus a poor indicator of $E(c)$ unless np_i is large, all $i > 0$, which is seldom the case. Two situations arise. It nuts are plentiful, but analysis cost is high, one needs to know what the chances are of a lot being rejected on the basis of a single analysis, expressed as $R(n,C_a)$. The opposite situation arises when the total material available for analysis, given by $N * n$, is limited. In this case, one seeks the optimum way of dividing the $N * n$ nuts, i.e. should N or n be large.

In the single-analysis case, $R(n, C_a) = \sum_i' P_i(n)$, where the primed sum runs from the bin containing C_a to ∞. The dependence of $R(n, C_a)$ on C_a alone can be obtained directly from the empirical probability distribution which estimates the $\{P_i(n)\}$, assuming it is available; none of the calculations presented here are needed. The present calculations find use in obtaining the dependence of $R(n, C_a)$ on n. At low n, where eq 6′ applies, one has $R(n, C_a) = n * \sum_i' p_i$. As n is increased, the first factor increases proportionally, but the primed sum decreases as it extends over a more and more restricted range of $c > n * C_a$. Use of eq 6′, along with the knowledge that $\gamma < 1$ in all observed cases, indicates that the rejection rate will increase with n, but less than proportional to n. When n is somewhat larger, expression 6 can be used instead of eq 6′ to evaluate $P_i(n)$ and thus $R(n, C_a)$. No simple expression results and numerical integration must again be applied. The general conclusions still follow. At yet larger n the convergence of expression 2, or its extension, is no longer of practical use. The sample mean remains the lot average concentration, while the variance decreases as $1/n$. It follows that the rejection rate will approach 1 as $n \rightarrow \infty$ if and only if the lot average exceeds C_a. If it does not, $R(n, C_a)$ may peak as n increases but must eventually approach zero.

When one has a limited number of nuts to analyze, is there something to be gained by analyzing them as N small n-sized samples? If C_k is the sample concentration measured on the kth sample, one would estimate the lot average from $\sum_k C_k/N$. Since $E(C_k) = \sum_i p_i * c_i$, $E(C) = N * E(C_k)/N = \sum_i p_i * c_i$, independent of n or N. Further, the square of the standard error of $C = \sum_k V(C_k)/N^2 = \sum_k \sum_i (p_i * c_i^2/n)/N^2 = N * \sum_i (p_i * c_i^2)/n /N^2 = \sum_i (p_i * c_i^2)/(n * N)$ and hence also independent of the division of the samples. Running many small samples thus does not help in defining the lot average but is essential if one wishes to obtain information about the variance of this average or about the aflatoxin lot distribution or if one wants information at small c.

NOMENCLATURE

*	multiplication. Multiplication is never implied, except for $np_i \equiv n * p_i$
B_i	the ith bin of C
c_i	$n * (C_i^+ * C_i^-)^{0.5}$, ith aflatoxin level of single nuts in the lot, in ng of aflatoxin/wt of average nut (g)
C	aflatoxin concentration in a sample, w/w basis
C_0	detection limit
C_a	highest sample concentration at which a lot will be accepted
C_i^+, C_i^-	upper and lower bounds of bin B_i
exp (z)	exponential function, e^z
$E()$	expectation value, $E^2() = E() * E()$
$f(c)$	probability distribution function (pdf) of contamination of single nuts in the lot
i	bin index
J	number of distinguishable levels of C, upper limit of i
ln, log	logarithm base e and base 10, respectively
n	number of nuts in a sample
N	number of samples
p_i	fraction of contaminated single nuts at aflatoxin level c_i
$P_i(n)$	probability that an n-nut sample will fall into bin B_i
$P_i(n)$	fraction of N n-nut samples that fell into bin B_i
$P_0(n)$	probability that an n-nut sample will have undetectable aflatoxin
$\boldsymbol{P}(n, x)$	probability of choosing an n-nut sample with x contaminated nuts, the Poisson distribution
$R(n,C_a)$	probability of rejecting an n-nut sample when the acceptance level is C_a
$V()$	variance
V_s	sampling variance
V_{ssa}	subsampling and analytic variance (Whitaker et al., 1974)
w	weight/nut
x_i	number of contaminated nuts in a sample at aflatoxin level c_i
γ	$-\log(p_i/p_{i-1})/\Delta$
Δ	width of logarithmic bins in C; thus, $\log C_i/C_{i-1} = \log c_i/c_{i-1}$
{}	indicates a set

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Supplementary Material Available: Source form of code to compute eq 6 as a function of Δ, γ, and p_i. (8 pages). Ordering information is given on any masthead page.

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