# SAMPLING INSECT POPULATIONS FOR THE PURPOSE OF IPM DECISION MAKING

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Decision making is a key aspect of current integrated pest management (IPM) programs and will continue to play an important role as IPM programs mature (71, 106). In an IPM context, decision making relies on protocols for deciding on the need for some management action based on an assessment of the state of a pest population (and ideally its natural enemies). These protocols, which we refer to as control decision rules, consist of at least two components and may include a third: (a) a procedure for assessing the density of the pest population, (b) an economic threshold (63);, and (c) a phenological forecast (e.g. 49), which is often necessary to determine the appropriate time to assess population densities. Assessment of pest density usually requires obtaining actual counts of the pests, and therefore, sampling is important. Because sampling is time consuming and expensive, one must know how to gather enough information about pest abundance to be able to make correct decisions without incurring excessive costs.

Decision making in IPM is important for two reasons. First, decisionmaking protocols can be used to reduce pesticide use. Ideally, IPM relies on benign tactics such as biological control, plant resistance, and cultural practices to maintain fluctuating pest populations below economic injury levels. To make biological control work, in many crop-production systems one must begin by reducing the use of broad-spectrum insecticides and miticides; here, decision-making procedures can often help. The second reason why decision making is important in IPM is that if tactics such as biological control and cultural practices fail, pest control can still be accomplished through the effective use of pesticides, and decision-making protocols must be available to determine when to intervene.

The purpose of this paper is to review the sampling component of pestcontrol decision rules. We have provided few mathematical details because, first, the allotted space does not allow a detailed presentation of the mathematics, which can be found elsewhere (57). Second, we wish to present the concepts behind the mathematics in as nonmathematical a form as possible. We also do not attempt to cite all the papers that report on applications of the concepts we review. Where appropriate, we cite illustrative work.

The presentation is divided into five sections. First, we review some of the general aspects of sampling theory. Second, we describe models used to characterize sampling experiments. Third, we review methods that can be used to develop sampling procedures to provide either a density estimate or a classification into two or more categories. All the methods reviewed are sequential, because these are the methods of choice when sampling costs are critical. In the fourth section we comment on two aspects of sampling for decision making that are not well developed or thoroughly understood, yet in our opinion offer future opportunities. Finally, we review how to analyze the effect of sampling uncertainty on decision rule performance.

#### GENERAL ASPECTS OF SAMPLING THEORY

Cochran (15) and Southwood (89) describe the basic principles of sampling; Perry (66) discusses early advances in the theory of sampling that remain important. The reviews by Morris (52) and Strickland (93) remain useful summaries of most of the basic principles of pest sampling. Neither contains a single mathematical formula, while both express a hope that entomologists will become more aware of statistical methodology and more comfortable in using it. Their hopes have been fulfilled in many ways. For example, these articles were written before Taylor published his paper on the variance-mean power law (95) or Iwao described his mean crowding relationship (37); both of these have profoundly affected the practice of insect sampling. Sequential classification sampling was only just beginning to be noticed by entomologists, but now this method is used extensively (e.g. 22). General sampling theory has also been applied in particular instances [e.g. ratio methods to estimate mortality in the field (88)]. To facilitate interdisciplinary work, investigators have attempted to standardize technical terms (24). Kuno (47) summarized many of the advances made during the past thirty years.

Two practical sampling concepts repeatedly encountered by entomologists are (a) randomization and (b) choice of sample unit and how it should be examined. For example, the theoretical necessity of proper randomization for estimating variances may be ignorable ["very little insect sampling is truly random" (52)], but using nonrandom methods should be justified in each instance (e.g. 19). Most sampling procedures used in a decision-making context assume random, independent samples. This assumption is not satisfied when samples are selected by traversing a path through a field and sequential stopping procedures are used. The ultimate effect of violating this assumption depends on the distribution of the organism being sampled. In practice, it may be more important that representative rather than random samples be taken (35). Representative samples can be obtained through systematic sampling; Sampford (77) provides a good discussion of this topic.

The second important consideration is the sample unit and how it should be examined. The advantages of different sample units need to be studied (72, 80, 83, 85, 92) as well as the possible effects of the pests themselves on the sample units (51), or of observer bias or time of day on the value of sample data (81, 86, 108). Shelton & Trumble (84) provide a useful summary of practical considerations.

# MODELS FOR DESCRIBING SAMPLING EXPERIMENTS

The adequacy of the information provided by a sampling scheme is defined by the precision (small variance) and accuracy (lack of bias) of sample estimates or classifications [using Cochran's (15) convention]. To characterize precision and accuracy, one must first describe a sampling experiment, and these descriptions are most conveniently done via mathematical models. Such models are needed for developing specific protocols (e.g. stopping boundaries for sequential estimation) and for evaluating the performance of a proposed plan (e.g. by simulation). The models we discuss here are: (a) models that relate sample variance to sample mean, (b) analysis of variance (ANOVA) models for estimating components of variance in multistage sampling, (c) probability models that define the distribution of individual animals in sample units, and (d) models that describe spatial patterns of counts.

#### Variance-Mean Models

The variance-mean relationships of Taylor (95) and Iwao (37) have been used effectively as foundations for many sampling protocols. These relationships are extremely useful because they permit the prediction of variances for estimated means and this in turn allows development of sequential sampling procedures. Only recently has serious attention been given to the ecological meaning and arithmetic stability over time and space of these relationships (47, 97, 98, 101). Both variance-mean models describe the variance-mean

relationship well, although Taylor's power law (TPL) seems to be more common (96). However, the models' ability to predict what will happen in the future (i.e. their suitability as foundations for pest-management sampling) has been debated. The index, b, of TPL may not be consistent from site to site across a continent (101), or it may depend on pesticide use (100). The size of the sample unit usually has little effect on the exponent of the TPL (96), but on occasion it may (78). However, this relationship remains critically important for the development of sampling procedures (39, 97). Iwao's relationship, based on the empirical observation that the mean crowding index (48) often depends linearly on the mean, seems to have received less critical attention as far as consistency of its parameters, possibly because the TPL is more popular.

Because both dependent and independent variables are subject to sample error, using simple regression to estimate a variance-mean relationship is not ideal. However, if the number of sample units counted for each mean is large and the mean values cover a wide range, simple regression is usually adequate. Perry (65) discusses in detail the fitting of TPL.

# Analysis of Variance Models

The variance of a density estimate obtained from multistage sampling (MSS) has more than one source of error. For example, Harcourt & Binns (32) described a multistage sampling experiment for the alfalfa blotch leafminer, *Agromyza frontella*, with stratification within alfalfa stems. For the simplest case of MSS, two-stage sampling, a random sample of *c* primary sample units (e.g. alfalfa stems) is taken, and from each of these, *e* subunits (e.g. leaves) are taken. The variance of the density estimate per subunit is  $V = s_1^{-2}/ec + s_2^{-2}/c$ , where the variance components  $s_1^2$  and  $s_2^2$  are most conveniently estimated using standard analysis of variance (ANOVA) (e.g. 15). Once  $s_1^2$  and  $s_2^2$  are known, *V* can be calculated for any sample size (*e* and *c*). This ANOVA properly relies on homogeneity of variances, which are known to vary with the mean value. Often one can transform the data to remove heterogeneity (e.g. 66), but other direct methods based on variance-mean relationships have recently been proposed.

Kuno (45) used Iwao's relationship to obtain estimates of variance components in terms of the mean values. He incorporated the results from within each ANOVA into the analysis to estimate the three parameters  $\alpha$ ,  $\beta_1$ , and  $\beta_2$ in the models:  $s_1^2 = (\alpha + 1)m + [\beta_1(\beta_2 - 1)/\beta_2]m^2$  and  $s_2^2 = [(\beta_1 - \beta_2)/\beta_2]m^2$ , where *m* represents the mean. Nyrop et al (59) used Taylor's relationship to estimate variance components, based on equating variance components with a TPL function. If a common *b* is justifiable for between and within mean squares in the ANOVA (which should be checked), a good deal of simplification is possible so that  $s_1^2 = a_1m^b$  and  $s_2^2 = a_2m^b$ . In a similar procedure, the mean squares in the ANOVA are equated with TPLs yielding  $s_1^2 = a_1 m^b$  and  $s_2^2 = (a_2 - a_1) m^b / e$ .

#### Probability Models

Probability models are important because they can form a basis for sample protocols and they can also be used to assess the performance of a sampling protocol. The primary difficulty in using probability models to describe sampling data is that the distribution of animals can change with density. Under these circumstances, a variance-mean relationship can be used; however, neither of the variance-mean relationships describes a distribution. This is demonstrated by the development of the Adès distribution (67), one of whose authors is Taylor. One of the (three) parameters of this distribution is effectively the index of the Taylor power law, while the others can vary from population to population and represent the individual distributions. In a similar way, plausible biological reasons explain why the k of the negative binomial distribution (NBD) can be regarded as varying according to a variance-mean law, thus introducing an extra parameter (e.g. 7). These approaches have been compared (41, 68); however, there is no guarantee in practice that the form of a distribution remains consistent as the mean value increases. For example, the distributions of European corn borer, Ostrinia nubilalis can be fitted to the Adès distribution for all mean values, but not to the NBD (67).

Fitting the kinds of distribution encountered in field work is greatly simplified by general computer programs like DISCRETE (27) and MLP (75). Programs to fit the Adès distribution are available from the original authors (68).

#### Spatial Pattern of Counts

Occasionally, plotting the distribution of animal counts over a sample universe is useful. The resulting graph can be important for detecting distributional patterns such as edge-effects that have to be considered when designing a strategy for collecting samples. The data for such a plot are usually obtained by sampling at a grid of points (not necessarily at regular distances). A smooth surface can be obtained by fitting a mathematical model to these data, but this approach is rarely satisfactory because of the difficulty in choosing an appropriate form for the model. However, nonparametric techniques like kriging (e.g. 31) can be used to interpolate between points. For these, the value at any point not on the grid is determined by interpolation using a weighted average of neighboring data values, the weights being derived from a curve relating average covariances between data values to distance between the points they represent. Schotzko & O'Keefe (82) recently used these methods in entomological studies. The methods' usefulness will

reside mainly in the theoretical insights they may give; they require much sampling effort and assume that animals are not disturbed by such intensive sampling. Much mathematical theory has been developed recently on the estimation of spatial pattern (17, 31, 74).

#### SAMPLING METHODS

In this section, we shall assume that mean density (m) is of interest, although other parameters such as the ratio of two population means can be more important (e.g. 56). Four general methods of constructing sampling procedures for use in IPM decision making have been developed. The methods can be ordered in terms of the type of information they yield, whether or not they assume simple random sampling (SRS) or multistage sampling (MSS), the cost of obtaining the information, and the ease with which the procedures can be developed and implemented (Table 1).

Sequential sampling has been proposed for each of these procedures. We shall confine ourselves to sequential methods because they are generally less costly than fixed-sample-size methods. In a sequential method, as data  $(x_i)$  are gathered from sample units, a summary statistic (e.g. the sum of the  $x_i$ ) is updated in such a way that a sample path can be plotted of this statistic against the current sample size. Sampling continues until this path crosses a predetermined stop line at which point sampling stops and the desired information is immediately available. Determining how the sample path is to be generated, and how to calculate the stop line (or lines), are discussed below.

The type of information available from each of these procedures ranges from: (a) a simple dichotomy in which the mean is estimated to be either above or below a predetermined critical value,  $m_t$ , through (b) a trichotomy in which the mean is estimated to lie in one of three intervals (covering all possible values), (c) an enhanced trichotomy in which a point estimate with standard error (SE) is obtained if m is deemed to lie in the middle interval, to (d) a point estimate (with SE) for all situations. As might be expected, the more information obtained, the higher the (sampling) cost. For any given problem, the method chosen must be appropriate to the information required. For example, if a quick decision has to be made whether or not to spray a field with a pesticide, a simple dichotomy is all that is required.

Two modifications can be made to most of the procedures. First, instead of fully sequential sampling, double sampling procedures can be used. Second, binomial or presence-absence counts can be substituted for complete enumeration. These modifications are discussed after reviewing the four methods.

Each of the four methods can be based on either a variance-mean relationship or a specific probability model. In all cases, however, probability models

Method	Result	Selection of sample units	Sampling cost	Complexity*
Two level classification	$m^{\rm b} \leq m_t^{\rm c}$ or $m > m_t$	SRS <sup>d</sup>	Lowest	Easy
Three level classification	$m \le m_{1t},$ $m_{1t} < m \le m_{2t},$ or $m > m_{2t}$	SRS	Low	Intermediate
Variable intensity	$m \le m_{1t},$ $m > m_{2t}, \text{ or }$ $m \pm d^{\text{f}}$	MSS <sup>e</sup>	High	Most difficult
Estimation	$m \pm d$	SRS	Highest	Easy

Table 1 Attributes of sampling plans used in IPM decision making

<sup>a</sup>Complexity in implementation.

<sup>b</sup>Estimated mean.

 $c_t =$  Threshold.

<sup>d</sup> Simple random sample. <sup>e</sup> Multistage sample.

<sup>f</sup> Specified value.

must be used to analyze the performance of a particular plan. Some of the methods have been (or can be) modified to incorporate a temporal dimension. These modifications are discussed in a separate section.

# Two-Level Classification

The general problem in sequential classification is to classify the unknown population density,  $m_{1}$  into one of two specified sets: either above or below a critical value  $m_t$ . A plan is assessed by two basic criteria: (a) how accurately does it perform the classification (i.e. for any value of m above or below  $m_t$ , what is the probability that a correct classification is made), and (b) how quickly is the decision made (i.e. how many samples are required)? These are generally displayed as (a) an operating characteristic (OC) curve that shows the probability of the procedure deciding (whether correctly or not) that  $m \leq m$  $m_{t}$  for any value of  $m_{t}$  and (b) an average sample number (ASN) curve that shows the expected sample size required to reach a decision. Typically, an OC curve is near 1 when m is much less than  $m_t$ , near 0.5 when m is near  $m_t$ , and near 0 when m is much larger than  $m_t$ . A typical ASN curve is high when m is near  $m_t$ , and decreases to moderate or small values when m is far or very far from  $m_t$ . Before embarking in practice on a decision-making protocol based on sequential classification, these (or equivalent) properties should be studied to see if the protocol is too expensive (ASN) or not worth using because its discriminating power (OC) is poor. It is therefore unfortunate that papers proposing sequential classification methods have often tended to present only the mechanics (stop lines) of their procedures and not the performance criteria (OC and ASN).

Two methods of sequentially classifying population densities have found extensive use in IPM. One is based on the distributional theory of  $x_i$  in the field [Wald's sequential probability ratio test, SPRT (103)] and the other on a variance-mean relationship (38).

Initial development of the SPRT was in terms of simple hypothesis testing. The null hypothesis,  $H_0$ , that  $m = m_0$  was to be tested against the alternative hypothesis,  $H_1$ , that  $m = m_1$  ( $m_0 < m_t < m_1$ ), and no other values of m were to be considered. If the probabilities of wrongly rejecting  $H_0$  and  $H_1$  were to be  $\alpha$  and  $\beta$ , respectively, Wald (103) showed how to calculate stop lines, and generalizing the analysis to allow for any value of m, gave approximate formulae for the OC and ASN curves. Specific sampling plans for IPM have been reviewed by Fowler & Lynch (22).

To develop a sequential sampling plan based on the SPRT, the distribution of sample observations must be described by a probability model with one unknown parameter. Models frequently used in IPM are the Poisson and the negative binomial (NBD). The Poisson has a single unknown parameter, the mean m, but the NBD has two parameters, m and the dispersion parameter k. To use the NBD, one generally assumes that k is known and constant. These requirements, and similar ones for other distributions, impose some restrictions on the applicability of the SPRT (see below), but even when they are not strictly met, they do not necessarily prevent use of the SPRT. If an appropriate model can be found to describe the distribution of sample counts, the SPRT has two advantages over the second sequential classification method. First, the OC and ASN functions are rapidly approximated by easily computed formulae (23). Second, the SPRT has the property that among all sequential tests with OC values for  $m_0$  and  $m_1$  equal to  $1 - \alpha$  and  $\beta$ , respectively, it minimizes the ASN values for these means (104). In general, SPRT plans require on average only 40-60% as many observations as equally reliable fixed-sample-size methods, and sample-size reductions as high as 86% have been reported (91).

Before implementing a sequential classification sampling plan based on  $\cdot$  Wald's SPRT, the four parameters noted above must be specified:  $m_0$ ,  $m_1$ ,  $\alpha$ , and  $\beta$ . The best way to view these is as parameters that can be manipulated in order to define an acceptable SPRT, as defined by its OC and ASN curves.

One of the frequently noted limitations of the SPRT is the requirement that the only parameter allowed to change from one sample location or time to another is the mean density. For the NBD, this means that the dispersion parameter k must remain constant. However, as is well known, the dispersion of animal populations frequently changes as a function of density. Changes in the dispersion of sample observations may or may not significantly affect the OC and ASN of a SPRT, and these effects should be determined (possibly by simulation) before discounting the use of the SPRT in a sequential sampling program. Under some situations, the OC and ASN functions for a SPRT based on the NBD are not very sensitive to even rather large changes in k (105).

The second sequential method used to classify population densities is based on a confidence interval about the threshold density. This procedure was first proposed by Iwao (38) and has the desirable attribute that it can be developed without having to consider any nuisance parameter (e.g. k of the NBD). The only requirement for determining the stop limits is that the variance can be modeled as a function of the mean (e.g. TPL) and thereby predicted for the threshold density. With this procedure, null and alternative hypotheses are constructed as:  $H_0$ ,  $m \le m_t$ ; and  $H_1$ ,  $m > m_t$ . Stop limits are constructed by computing a standard confidence interval about  $m_t$  in terms of the total number of organisms found in n observations.

However,  $\alpha$  no longer has the same meaning as for a fixed-sample-size confidence interval, and error rates can differ considerably from the nominal values (61). There is a mathematical theory for approximating the OC and ASN associated with a sequential sampling plan based on Iwao's approach (87), but computer simulation is often easier to use (57). Thus, while no probability model for the sample observations is required to construct the stop lines, a probability model is required to determine the OC and ASN. If the NBD is used, the value of k can be estimated from TPL as  $k = m^2/(am^b - m)$ . Variability in the variance-mean relationship (see e.g. 101) should be included in the calculations.

## Three-Level Classification

Sampling plans that classify population density into three levels (tripartite plans) provide the next higher level of information. Such sampling plans are constructed by simultaneously considering two simple two-level classification schemes that can be developed using either the SPRT or Iwao's stop limits. Fowler (21) describes this process using the SPRT. For example, if two critical densities,  $m_{t1}$  and  $m_{t2}$  ( $m_{t1} < m_{t2}$ ), are to be classified, joint consideration of two sets of hypotheses allows classification according to:  $m \le m_{t1}$ ,  $m_{t1} < m \le m_{t2}$ , and  $m > m_{t2}$ . In situations in which the most satisfactory action for  $m_{t1} < m \le m_{t2}$  is to take a second look after a few days, the flexibility of such a tripartite plan is attractive.

Simulation must be used to construct OC and ASN functions for tripartite classification schemes. These functions are somewhat different from those for a simple two-level plan in that there are two OC curves, one corresponding to the conclusion that  $m \le m_{t1}$  and the other to the conclusion that  $m_{t1} < m \le m_{t2}$ . The first OC curve has a standard shape, but the second is bell shaped with a peak approximately mid-way between  $m_{t1}$  and  $m_{t2}$ . The ASN function is bimodal with peaks located approximately at  $m_{t1}$  and  $m_{t2}$ .

#### Variable-Intensity Sampling

Variable intensity sampling (VIS) (33, 34) offers the next level of information by providing either a classification of density or an estimate of density if the density is within a fixed distance from a threshold value. The objectives behind VIS are twofold. First, samples are taken from throughout the sample universe to ensure a representative sample. This procedure is especially important in situations where heterogeneity in pest density is suspected. The second objective is to sample more intensively when the mean is close to the economic threshold and less intensively when it is far from this value. The second objective is similar to that of other sequential classification methods: to be as economical as possible. Because VIS is designed to meet both objectives, it is very appealing and, when possible, should be more widely used. The biggest drawback to VIS is that it is more difficult to implement than other sampling procedures because the decision to continue sampling is not simply yes or no; instead, the number of samples to be taken at a particular sampling location in a field is a function of the cumulative number of samples and the current estimate of mean density. Tables can sometimes be produced that allow relatively easy determination of updated sampling intensity (34, 59), but often a programmable calculator or computer is required.

The method works in the following way. First, the number of sites to be sampled (c) and the maximum number of elements to be sampled at each site  $(e_{\max})$  are determined. The maximum total sample size  $n = ce_{\max}$  can be determined by estimating maximum available sampling time or by specifying bounds on the range of densities for which the maximum sample size will be used. At the first site,  $e_{\max}$  elements are sampled. Based on the outcome of this sampling, the number of elements e to be sampled at the next and all subsequent sites is determined. If the estimated mean density is considerably less than or greater than the threshold, e is reduced from  $e_{\max}$ . Samples are taken at the next site using the appropriate sampling intensity and the overall mean is recomputed. Based on this estimate, the number of elements to be sampled may be revised again. This procedure continues until all sites have been visited.

Revision of the number of samples to take at each site proceeds as a two-step process. First, the estimated mean density is compared with a nominal confidence interval that brackets the threshold  $(m_t)$ . If the density estimate falls within this interval, the maximum number of samples is taken. If the density estimate lies outside this interval, the element sample size is adjusted so that the overall sample size will estimate the mean, with either an upper or lower  $1 - \alpha$  confidence limit equal to the threshold  $m_t$ .

VIS protocols can be developed using all of the probability models previously described (e.g. TPL, nested variance, NBD) but they are most appropriate when a nested variance structure exists. One can assess the performance of VIS procedures using simulation (33, 34, 59).

#### Estimation

Estimation procedures provide the most information about the population being sampled. They are relatively easy to implement, but they may incur greater sampling costs than classification procedures. The fundamental questions to be addressed in designing a sampling procedure whose purpose is to provide an estimate of population density is how many observations are required and how can they best be allocated to achieve a desired degree of precision. Two common ways are used to express the precision of a density estimate. First, the standard error of an estimated mean may need to be within a certain value of the mean. This value may be a specific numerical value or a proportion of the mean equivalent to specifying a certain coefficient of variation of the mean, cv. Second, the estimated mean may need to lie within a certain interval around the true mean density with a specified confidence probability. These methods use essentially the same formulae and provide a way of computing the required sample size, n, as a function of the mean and variance (40).

The variance is usually not known, but using a relationship such as TPL in these formulae yields n in terms of m, the mean density being sampled. This term still cannot be used for a fixed-sample-size plan, but the relationship between n and m can be rewritten to define sequential stop lines as the basis for sequential estimation procedures (30, 43). As samples are processed, the cumulative number of animals found is compared with the stop line. When the total exceeds the stop limit, sampling is terminated with the expectation that the specified precision has been reached.

Sequential estimation procedures that make use of variance-mean relationships do not depend on any particular distribution for computing stop lines. Procedures have also been developed for specific distributions; they are usually based on Bayes theory and the minimization of losses defined in terms of sampling costs and desired precision (109), but some use stopping boundaries that are specific to a given distribution (44). Kuno (43) proposed a method for estimating the mean of a NBD with a known value of k. He derived a stopping boundary by specifying that the precision of the estimate of m must have a predetermined cv. Binns (6) and Rudd (76) derived a similar boundary, and Binns (6) showed that the distribution of the estimated mean was independent of n. This finding is important because it guarantees that the cv and confidence interval will not vary unaccountably as can happen with other boundaries.

If a sequential estimation procedure is done many times, the estimates on each occasion generate a distribution. This distribution has a mean and cv of its own that should be distinguished from the mean and cv based on the data of a single sample. The precision of a sequential procedure can be defined in terms of either of these cv values: the cv based on the distribution of the estimates (CVD) can be used to predict the precision on any future occasion;

the cv based on the sample data (CVS) defines how precisely the mean was estimated on that occasion. The values of these cv values may not be the same.

Sequential estimation procedures that are based on specifying a cv and that use an empirical variance-mean relationship such as TPL will not yield estimates whose CVSs are equal to the specified cv each time they are used (36, 101), because first, while TPL may fit the data well, variability and hence uncertainty remains in the variance-mean relationship. Second, the stop lines are based on expected values of random observations and the required average precision will be attained only in the long run: the decision to stop sampling will often be made well before or after the expected number of samples is collected. Another often-overlooked point is that the estimated mean is biased, although the magnitude of this bias is usually modest (5, 44).

The performance patterns of sequential estimation procedures based on requiring the estimated mean to lie within a certain interval around the true mean have also been studied (44). For both normal and nonnormal distributions, the obtained probabilities can be significantly below the specified ones. This decrease is greater when the width of the confidence interval, l, divided by the standard deviation, s, (l/s) declines.

For example, a simulation experiment that aimed at 25% cv was done using Green's (30) method for m = 2,5,8 and two TPL formulae ( $s^2 = 4m^{1.1}$  and  $s^2$  $= 4m^{1.9}$ ). This figure was compared with the equivalent stop lines for Binns' NBD method, for the Poisson distribution [a horizontal line (107)], and for a straight-forward fixed sample size. Figure 1 shows the stop lines for m = 5. The reason for choosing these boundaries is to exemplify the effect on the estimates as the boundary slope at the expected crossing point goes from vertical (fixed sample size) through Green's or Binns' slopes to horizontal (Poisson). The results (Table 2) for the zero slope are not good because the distributions are not Poisson (k = 0.61, 1.35, 2.04 for m = 2, 5, 8 and b =1.1; k = 0.31, 0.31, 0.32 for m = 2, 5, 8 and b = 1.9). When the slope at the expected crossing point is low for any method, the estimates are biased. CVD and average CVS are similar, but CVD tends to be larger when the slope is smaller. Average CVS is always less (but only slightly) than the prescribed value. These results exemplify some characteristics of sequential estimation methods; more work remains to be done before all general properties are known.

Of these four methods, only Green's requires no more than knowledge of TPL (or equivalent). Methods based on the NBD perform as expected only if the value of k is known. Using an underestimate of k results in better precision than expected (and the taking of more samples), while using an overestimate results in lower precision (6). If k is not known, one can follow a two-stage procedure in which one first estimates k using the method of moments as k =



Figure 1 Stop lines for three sequential estimation sampling programs.

 $m^2/(s^2 - m)$  after a certain number of samples have been processed and then continues sampling using this estimated value of k. This procedure works quite well (57).

# Double Sampling

Double sampling is occasionally more convenient and useful than full sequential sampling. The basic principle is to take an initial sample and use the information so obtained to decide on the size of a second sample or whether to take a second sample at all. Two reasons are generally given for using double sampling: (a) to try to gain some of the advantages of sequential sampling for classification without checking a table or chart after every sample unit (e.g. 62), or (b) to obtain an estimate of, say, mean density with some predetermined precision when the precision depends on some other quantity (e.g. variance) that is unknown (e.g. 90). A third reason is to ensure a better representation of the population than may be possible under sequential sampling, by a proper disposition of the initial sample.

Because of mathematical difficulties, the assumption of a normal distribution is usually necessary, which implies that at least moderate sample sizes must be used. This requirement could reduce the effectiveness of the method. For example, Nyrop & Wright (62) used 25 as a minimum sample size with an additional 25 samples taken if required. However, if normality is assumed for smaller sizes, a plan with first and second sample sizes equal to 15 and 35 rather than 25 and 25 produces approximately the same OC, but on average requires 10–20% fewer samples because of the greater chance of stopping after the initial sample. This result should be compared with that found by Cox (16), who showed that for estimation, the first sample should be as large

			Stop lines based on												
			Green			NBD			Fixed sample size		Poisson				
b <sup>b</sup>	m°	Ma	2°	CVD	CVS <sup>g</sup>	М	S	CVD	CVS	М	CVD	CVS	М	CVD	CVS
1.1	2	2.10	2	27	24	2.02	-6	24	24	2.00	24	24	2.12	27	24
1.1	5	5.25	5	25	23	5.04	-14	24	23	4.98	24	23	5.35	26	23
1.1	8	8.52	9	26	23	8.17	-51	24	23	8.09	24	24	8.57	28	24
1.9	2	2.01	-19	24	24	2.01	-14	24	24	2.00	25	24	2.12	27	24
1.9	5	5.00	-45	24	24	4.99	-81	24	24	4.97	24	24	5.28	28	24
1.9	8	7.93	-79	24	24	7.90	-390	23	24	7.87	24	24	8.40	29	24

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Table 2 Comparison of sequential procedures for estimating the mean<sup>a</sup>

<sup>a</sup>Based on 1000 simulations each.

<sup>b</sup>Exponent for TPL;  $s^2 = am^b$ , a = 4.0.

<sup>c</sup>True mean.

<sup>d</sup>Average estimate of the mean.

<sup>e</sup>Slope of the boundary at the expected crossing point.

f cv of the distribution.

<sup>8</sup>Average of the sample cv.

as possible provided it is not larger than the sample size that would be recommended if the precision were known beforehand.

For classification, cost and complexity are similar for double and sequential sampling. For estimation, however, double sampling replaces the predetermined stopping boundary with a procedure that requires a programmable calculator or computer to obtain the required sample size (e.g. 12). Thus, double sampling for estimation is more complex.

#### Binomial Sampling

Sampling can sometimes be made easier and less time-consuming by substituting binomial counts for complete counts. Binomial sampling is founded on defining a relationship between the density of organisms (*m*) per sample unit and the proportion of sample units with more than *T* organisms  $(1 - P_T)$ , where T = 0, 1, 2, ... Here, *T* is referred to as a tally threshold although it has also been referred to as a "cutoff number" (9). Historically, T = 0 has been used most often, but there may be compelling reasons to use some other tally threshold. Apparently, Anscombe (3), Kono & Sugino (42), and Pielou (69) were first to apply binomial sampling to ecological work, although researchers had long known that the proportion of sample units containing no individuals could be used for estimation purposes (e.g. 99).

Binomial sampling is appealing because it is usually faster and therefore less costly on a per-sample unit basis (110). In addition, binomial sampling is the most feasible field sampling method for many organisms. The trade-off with binomial sampling is increased uncertainty with respect to estimated densities or classification decisions.

All binomial sampling plans are based on a model that expresses the relationship between the mean density and the proportion of sample units with more than T organisms. Two approaches have been used: one is based on the empirical observation that  $\log(-\log P_T)$  and  $\log m$  are linearly related over wide ranges of m (28, 42), while the other is based on a theoretical distribution of the animals (3, 69). For both decision making and estimation, the goodness of fit of these models to base data is critical in terms of bias and precision (8, 57). To save space, we discuss decision making based only on a theoretical distribution (NBD) and estimation only in terms of the empirical model. These indicate the general procedures and their problems for other contexts.

BINOMIAL SAMPLING AND DECISION MAKING The most critical aspect of binomial sampling in pest management is knowledge of the formula relating the binomial proportion  $(P_T)$  obtained from field sampling to the mean density (m). To describe the spatial distribution of animals in the field adequately, a theoretical distribution usually requires at least one parameter other than the

mean. Thus, a relationship based on a theoretical distribution must account for the extra parameter, for example, the aggregation parameter k of the NBD. The consequences of being uncertain of the value of k are described for decision-making by Binns & Bostanian (9, 11): an inappropriate choice of Tcould result in misleading recommendations.

Wilson & Room (113) used TPL to estimate k by the method of moments, letting k be a function of m, so that  $P_0$  could also be written as a function of m. However, some problems still remain: estimating k by the method of moments is not very efficient for moderate to large values of m (4, 18, 89); the values of k do not always lie close to their expected values based on TPL (e.g. 54); and the standard errors of a and b in the TPL and the biological variation about TPL may be large and adversely affect the estimation of k. Thus, the solutions suggested by Binns & Bostanian (11) remain relevant if accurate and precise decision making is desired. They showed that by changing T to reflect knowledge of the critical threshold  $(m_t)$ , one can adjust binomial sampling so that the probabilities of making a wrong decision are considerably reduced, while retaining most of the benefits of presence-absence sampling. OC and ASN curves can be calculated for sequential binomial sampling, allowing for the effect of variation around the TPL on the estimate of k (J. P. Nyrop & M. R. Binns, in preparation). Weighted averages of the basic formulae for a binomial SPRT are calculated (by numerical interpolation) with weights proportional to an assumed normal distribution around the TPL. Based on these curves, the properties of decision-making based on Wilson & Room's (113) formula can be improved by adjusting the tally threshold according to  $m_t$ . This improvement is exemplified in Table 3, which is based on mite-count

		Tb	= 0			T = 7				
	$\alpha, \beta = 0.2$		$\alpha \beta = 0.01$		$\alpha \beta = 0.2$		$\alpha \beta = 0.01$			
OC	m <sup>c</sup>	ASN	m	ASN	m	ASN	m	ASN		
0.9	2.2	13	2.5	77	2.8	7	4.3	60		
0.8	2.8	16	3.0	9 <b>9</b>	3.6	7	4.6	70		
0.7	3.3	18	3.5	112	4.2	8	4.8	75		
0.6	3.8	20	3.9	119	4.7	8	5.0	80		
0.5	4.4	20	4.4	122	5.2	7	5.2	78		
0.4	5.1	20	5.0	120	5.7	7	5.4	76		
0.3	5.9	20	5.7	113	6.4	7	5.6	75		
0.2	7.1	19	6.7	100	7.2	6	5.8	65		
0.1	9.3	16	8.5	80	8.7	5	6.2	53		

 Table 3
 Operating characteristic (OC) and average sample number (ASN) values for binomial sequential sampling plans<sup>a</sup>

<sup>a</sup> TPL:  $s^2 = 3.33m^{1.39}$ , SPRT parameters:  $m_0 = 3.5$ ,  $m_1 = 7.5$ ,  $\alpha$ ,  $\beta$  as indicated.

<sup>b</sup>Tally threshold. <sup>c</sup>True mean. data from Quebec apple orchards. Changing the tally threshold can result in a considerably lower ASN; for T = 0, decreasing  $\alpha$  or  $\beta$  beyond a certain point does not materially improve the OC but merely increases the ASN. These findings are consequences of the basic theory of the SPRT and of recent work in binomial sampling (8, 57).

BINOMIAL SAMPLING AND ESTIMATION When a binomial scheme is based on an empirical relationship, different problems arise. One of the most important results from the fact that the relationship is empirical, namely that there must be some unknown (biological) variance about the relationship that has nothing to do with sampling error. Even if very large individual samples are obtained over a wide range of mean densities, the points representing them will not lie exactly on the line depicting the relationship. Thus, the necessary elements of the variance of a m predicted by the model are (a) the binomial sampling variance of the estimate of  $P_T$ , (b) the variances of the estimated parameters of the fitted model, and (c) the biological variance about the model. Several formulae have been suggested for estimating the variance of m; these do not always include every element (28, 46, 55). Binns & Bostanian (10) simplified the problem by equating the mean square error from regression (they used simple linear regression to fit the model) with the biological variance, thus including sample error from the original base data set. Schaalje et al (79) pointed out that this simplification could be misleading and demonstrated that one can use TPL to help estimate the biological variance separately from the sample error [the idea is analogous to that used by Wilson & Room (113) for estimating k using TPL]. They (79) described a method based on large-sample-size (statistical) theory for the calculations. Ordinary regression theory is technically inappropriate because the independent variable,  $\log(-\log P_T)$ , contains sample error (G. B. Schallje, personal communication). However, the practical effect will not be important provided that the range of the independent variable is much wider than its sample error could possibly be, as seems to be the case in all published accounts. Because one need not therefore reject the regression method for estimating the line, one can use a relatively simple method for estimating the biological variance, incorporating the ideas of Schaalje et al (79). The sample error for a mean value  $m_i$  based on TPL and sample size  $n_i$  is  $am_i^b/n_i$ , so the total variance (including biological variance,  $\sigma^2$ ) of log  $m_i$  is approximately  $(am_i^b - 2)/n_i + c_i + \frac{1}{2} (am_i^b - 2)/n_i + \frac{1}{2$  $\sigma^2$ . Thus, a weighted regression analysis can be done in which an iterative algorithm can be used to find the maximum-likelihood estimate of  $\sigma^2$ . The calculations are relatively simple if MLP (maximum likelihood program) (75) is used. For example, the mean square error found in the unweighted regression for Tetranychus urticae on strawberries by Binns & Bostanian (10) was 0.4489. Using weighted regression as above  $(n_i = 35)$ , the biological variance is estimated to be 0.2056. Although reduced by more than 50%, this value is still the major component in the error of the estimate of log m. More work is being done on this problem (G. B. Schaalje, personal communication).

Binomial sampling is attractive and widely used because of its potential economic savings and simplicity of operation. The main hurdles lie in the development of practical plans. Here, the difficulties are mostly in preparing formulae for the variance and bias of estimates, incorporating components of error in the OC and ASN, and choosing the optimum procedure based on these.

# ASPECTS OF SAMPLING FOR DECISION MAKING REQUIRING FURTHER STUDY

Two aspects of sampling for decision making have received relatively little theoretical attention, yet are potentially very useful and warrant further study. The first aspect is motivated by the temporal dynamics of populations. Because pest management is often a continuous process, temporal changes in animal abundance should be explicitly considered in sampling programs. When a temporal dimension is incorporated into the sampling problem, problematic and acceptable population densities (i.e. those above or below an economic threshold) are no longer single points but form trajectories in time. The shapes of these trajectories are influenced by patterns of density change and by variation in economic thresholds, if any. Overall population abundance can grow or decline through reproduction, death, immigration, or emigration. Furthermore, densities of a particular life stage may change independently of overall population density through phenological maturation of the population (25). The second aspect is motivated by the fact that a community of species is often present along with the specific pest being controlled. Thus, one may need to consider two or more pests simultaneously or determine the abundance of a pest and its natural enemies together.

#### Sampling over Time

One can sample population processes through time for the purpose of decision making in two ways: independent estimates or classifications can be made at different points in time, or successive samples in time can be used jointly to characterize the population process. The expected pattern of the population trajectory, the ability to define acceptable and problematic population trajectories, and practical objectives should dictate which approach is used.

A time dimension can be included in a sampling program when independent estimates or classifications are made at each sampling time by using the most recent sample result, by adjusting the time interval between samples, and by using knowledge of the dynamics of the sampled population. Wilson (111) and Wilson et al (112) used sample estimates and nonlinear regression models to determine when the next sample should be taken. We (1) have developed tripartite sampling plans for European red mite, *Panonychus ulmi*, in apple orchards that classify the population into one of three categories: (a) treatment required, (b) treatment not needed and sampling required in 7-10 days, and (c) treatment not needed and sampling required in 11-15 days. Criteria used to classify the population into the last category were determined by assuming exponential growth and finding the density that would result in densities close to the action threshold after the resample interval.

Cumulative use of successive samples in time to classify a population trajectory began to be formalized as "time sequential sampling" by Pedigo & van Shaik (64), who allowed the  $m_0$  and  $m_1$  of a SPRT to be functions of time  $(\tau)$  following models of critical pest abundance so that  $m_0(\tau)$  and  $m_1(\tau)$  correspond to acceptable and problematic population trajectories. With this procedure, stop limits are constructed for each successive sample point in time based on  $m_0(\tau)$ ,  $m_1(\tau)$ , and the SPRT probabilities  $\alpha$  and  $\beta$ . Formulae for the stop limits are similar to those for a SPRT done once in time except that counts taken through time are weighted to reflect changes in the differences between the means for the null and alternate population trajectories.

The properties of such schemes cannot in general be derived from standard SPRT formulae. For example, suppose the population trajectories can be defined by exponential growth curves,  $m(\tau) = \exp(r\tau)$ , and in particular,  $m_0(\tau) = \exp(0.04\tau)$  and  $m_1(\tau) = \exp(0.07\tau)$ , where  $\tau$  is measured in days. Assuming that a reasonable sample size is used each time, a normal distribution provides an adequate approximation with variance based on TPL. If an average variance (V) is used at each time, stop lines similar to those of Pedigo & van Shaik (64) can be determined. The general form of the stop lines is wc $= h_0 + b(\tau)$  and  $wc = h_1 + b(\tau)$ . The intercepts  $h_0$  and  $h_1$  are  $\log[\beta/(1-\alpha)]$ and  $\log[(1 - \beta)/\alpha]$  respectively. The term  $b(\tau)$  is the sum up to time  $\tau$  of  $[m_1(\tau')^2 - m_0(\tau')^2]/2V$ . The summed weighted counts (wc), with weights equal to  $[m_1(\tau') - m_0(\tau')]/V$ , are compared with the stop lines. Table 4 shows OC and ASN values determined via simulation for r ranging from 0.01 to 0.10, five day intervals, and  $s^2 = 4m^{1.9}$ . The procedure using V is close to that using a full model in which different variances for  $m_0(\tau)$  and  $m_1(\tau)$  were used, but the full model is computationally much more difficult. Note that the achieved  $\alpha$  and  $\beta$  (0.05, 0.12) are much less than the nominal values of 0.2 and 0.2.

Another way to integrate successive samples in time is to use a standard model and, beginning at the start of the season, to update the model based on information gleaned from successive samples in a Bayesian type of analysis (70). We have attempted to use this approach when sampling simulated populations with known distributions and have found it difficult to operate. Part of the reason for this difficulty seems to be that estimates obtained at the beginning of the season retain undue influence as the season progresses. Some sort of inverse weighting may help solve this problem, as in industrial quality

r	Full r	nodel <sup>b</sup>	Average variance <sup>c</sup>		
	OC	ASN	OC	ASN	
0.01	1.00	4.1	1.00	3.9	
0.02	1.00	4.2	1.00	4.2	
0.03	0.98	4.4	1.00	4.4	
0.04	0.95	5.0	0.97	5.1	
0.05	0.68	5.1	0.79	5.6	
0.06	0.38	4.7	0.33	5.6	
0.07	0.12	4.4	0.16	4.7	
0.08	0.06	3.5	0.10	4.2	
0.09	0.02	3.5	0.01	3.9	
0.10	0.01	3.4	0.03	3.6	

**Table 4** Sample OC and ASN values for time sequential sampling to compare exponential growth, exp(rt), based on a normal approximation<sup>a</sup>

<sup>a</sup>SPRT probabilities equal to 0.2 at r = 0.04 and r = 0.07; 100 simulations each.

<sup>b</sup> Normal distribution, TPL  $s^2 = 4m^{1.9}$ , sample size 20.

<sup>c</sup> As footnote b, but using an average variance for the weight and intercept.

control (e.g. 50). The same objection may apply to time-sequential sampling, so a similar adjustment may be necessary there.

Linear control systems appear at first to be an attractive alternative approach to updating sample information (e.g. 114). However, the number of parameters in such a system is large and the variance matrices must be estimated (the effect of which is hard to gauge). More importantly, however, linear systems may not be able to mimic nonlinear systems well over a protracted period of time, especially if there are long intervals between sample dates.

In general, procedures that make joint use of counts from successive points in time are only useful when the population trajectory being sampled is reasonably smooth and generally follows the patterns described by the null and alternate hypotheses. This is because these procedures make use of previous and current data to estimate or classify the population. If previous counts are not well related to the current situation, they are of little use. When the above-mentioned conditions do not apply, independent classifications or estimates should be made each time.

## Simultaneous Sampling of Two or More Species

The need for sampling two or more species can arise in at least two ways: a crop may be attacked by two or more pests that, for control or sampling considerations, must be sampled simultaneously, or the abundances of a pest and its natural enemies may need to be estimated together.

The researcher can deal with the first situation in three ways. (a) A

sampling distribution model could be constructed for the pest group as a whole and sample estimates of the group (e.g. lepidopterous larvae) obtained instead of estimates for each species (34). Similarities in the sampling distribution of the target populations determine the feasibility of this approach. If these distributions are widely different, a composite model will likely not be acceptable. However, even when the distributions are different, the effect of these differences on the performance of a group-sampling plan should be determined through simulation. (b) A plan could be developed for the animal with the most variable sampling distribution, and this plan applied to all the species. (c) Provided that the species being sampled can be identified, dynamic sampling distribution models for each species could be coded on a hand-held computer. We know of no actual surveys that have used this technique.

For sampling a pest and its natural enemies, although these solutions could be used to estimate densities, another potential indicator is the ratio of pests to natural enemies (56). Classifying or estimating a ratio is more difficult than classifying or estimating a mean because the sampling distribution of a ratio is complex. With small samples, the distribution tends to be skewed and the estimate can be biased. When the mean densities are moderate or high. sample sizes are large (n > 30), and the coefficients of variation for both numerator and denominator are small (<0.1), the estimate should be approximately normal with negligible bias. Buonaccorsi & Liebhold (13) provide formulae for variance estimates, confidence intervals, and bias estimates of ratio estimators when the numerator and denominator are independent. Cochran (15) discusses when the numerator and denominator are correlated. More recent studies have examined sampling distributions of the ratios of binomial parameters (26). Although the asymptotic sampling theory of ratios is reasonably well developed, little use has been found for ratios in sampling for decision making.

Time-sequential sampling also provides a framework for sampling population processes that are influenced by natural enemies. Estimating or classifying the abundance of natural enemies may not be necessary if their effect on pest dynamics can be ascertained. Sampling a population trajectory through time can provide this information and the methods described above might be used. However, we know of no instance in which this type of work has been done.

# INFLUENCE OF SAMPLE UNCERTAINTY ON DECISION RULE PERFORMANCE

Information provided through sampling has an element of uncertainty, and sampling incurs costs. As a result, it is critical to ask whether a decision rule based on sampling actually results in better IPM decision making. There are a number of ways by which to judge whether better IPM decision making is being accomplished. However, reduced pest-control costs, reduced losses from pests, and reduced use of chemical pesticides are commonly agreed upon indicators.

Empirical historical experience, experiments, and mathematical models can all be used to study decision rule performance. The empirical approach has been used almost exclusively in the past, but although there can be much wisdom in it, gains to IPM are unlikely to arise if this method is used alone. With the experimental approach, properly designed experiments must be done to obtain comparative data on pest control costs and effectiveness with and without a decision rule. While this approach is conceptually straight forward, it may be impractical: paired (similar) sites must be used; there must be adequate replication; and data must be collected over a wide range of pest densities. Therefore, modeling is the only practical approach. Furthermore, the relative effects of different decision rule components (i.e. sampling plan, economic threshold) on rule performance can only be studied via modeling.

Various models of IPM decision making have been proposed (53), but decision theory models (73) seem to be most appropriate for studying the effect of sampling uncertainty on decision rule performance. Decision theory models can be used to select the best management strategy when the information on the state of a system is uncertain and to determine the value of sampling experiments in improving information content. When used in the latter capacity, the measure of interest is the expected net gain from sampling. Expected net gain is the difference between the value of sample information and cost of collecting data. The value of sample information is equal to the expected savings as a result of basing treatment decisions on sample data.

Although it is desirable for the expected net monetary gain from sampling to be positive, this is not always necessary (60). It may suffice for net gain to be zero or not too far below zero, provided appreciable reductions in pesticide use or some other benefits result. We outline below how to calculate expected net gain from sampling using decision theory analysis. Mathematical descriptions and use of the analysis to identify optimal strategies are described elsewhere (2, 53, 57, 58, 73).

The first step in the analysis is to determine the best control strategy to use when no sample information is available. We use average or expected values as judgement criteria, although minimization of a worst-case scenario, or minimization of variance, can also be used (53, 94). The net crop loss is calculated for given pest density and management strategy, and a weighted average over all pest densities (the expected loss) is obtained, with weights proportional to the assumed long-term probability distribution of pest density. The management strategy with the smallest expected loss is the best strategy in the absence of sampling.

The second step is to determine the expected loss when management actions are dictated by sampling. The general principles are exemplified by the simple situation where only one decision is made: namely, to intervene or not to intervene. The net crop loss is calculated for given pest density and both decision actions, as above. Then the net crop loss with sampling for given pest density is calculated as the weighted average of those for the two different actions, weighted by the probabilities of the actions (the probability of recommending no intervention is given by the OC curve). The overall expected loss is obtained, as before, as the weighted average over all pest densities; this is the expected loss dictated by sampling. The value of the sample information is the difference between the expected loss dictated by sampling and losses incurred when the optimal strategy with no sampling is used. Net gain from sampling is the difference between the value of the sample information and the cost of collecting the data. If sampling costs vary according to pest density (e.g. with sequential sampling), these costs are also weighted by the long-term probability distribution of pest density.

Decision theory models have been used to study several situations in which sample data are used in decision making (e.g. 14, 20, 29, 60, 102). However, given the large number of sampling procedures developed and decision rules constructed for use in IPM programs, the number of reported analyses is very small. This is unfortunate because important insights, including the need for further research, can be gained from conducting the analysis. Decision theory analysis requires models for a number of complex processes. While these models may not be well defined, the ability to make the computations on a microcomputer allows study of the effect of various assumptions that in turn will promote rational development of decision rules. Perhaps most importantly, development of theoretical models for analyzing decision rules forces practitioners to adopt a teleological perspective when developing sampling plans for use in pest management.

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