

GREAT LAKES FISHERY COMMISSION

2002 Project Completion Report¹

Review of Procedures for Estimating Wild Production of Chinook Salmon Through Marking Experiments: Evaluation of Needed Sampling of Marked Fish on Lake Michigan

by:

Emily Szalai² and James Bence²

²Dept. Fisheries and Wildlife
Michigan State University
14 Natural Resources Bldg.
Lansing, Michigan 48824-1222

October 2002

¹Project completion reports of Commission-sponsored research are made available to the Commission's Cooperators in the interest of rapid dissemination of information that may be useful in Great Lakes fishery management, research, or administration. The reader should be aware that project completion reports have not been through a peer review process and that sponsorship of the project by the Commission does not necessarily imply that the findings or conclusions are endorsed by the Commission.

**Review of Procedures for Estimating Wild Production of Chinook Salmon Through
Marking Experiments: Evaluation of Needed Sampling of Marked Fish on Lake Michigan**

Completion Report Submitted to Great Lakes Fishery Commission - October 1, 2002

Emily Szalai and James Bence

Department of Fisheries and Wildlife

Michigan State University

14 Natural Resources Building

East Lansing, Michigan 48824-1222

Introduction

Concerns over the balance between prey production and predator demand in Lake Michigan have led to an increased need to understand the population dynamics of both the predator and prey species in the lake (Stewart and Ibarra 1991). Chinook salmon (*Oncorhynchus tshawytscha*) is the predominant open-water predator in Lake Michigan and consumes the bulk of the forage consumed by all of the stocked salmonine species. Chinook salmon has also experienced large mortality events in the 1990s thought to be associated with low food availability. Therefore, management of chinook salmon populations is a key component of managing for a balanced predator-prey system.

Estimates of chinook salmon consumption depend critically on the number of chinook salmon in the Lake Michigan populations. Current estimates of the size of the chinook salmon population rely mainly on the numbers of chinook salmon stocked into the lake and upon estimates of natural reproduction that were generated from a few year classes over a decade ago. Natural production of chinook salmon appears to be important with previous studies suggesting that natural production could account for 20 to 40 % of chinook salmon recruitment (Hesse 1994), but this production could be changing over time. Better estimates of the natural reproduction occurring in the lake would lead to improved estimates of chinook salmon population size and estimates of forage consumption.

Previous studies of natural recruitment of chinook salmon in Lake Michigan have used oxytetracycline (OTC) to mark all hatchery produced chinook salmon. OTC marking produces a mark in the vertebra of the fish that is visible under UV light. The existence of this mark can be used to distinguish fish of hatchery origin from wild-born fish without marks. The proportion of wild fish in the population can be estimated based on samples of the population and the resulting

number of fish with and without OTC marks. Early attempts at using this procedure in Lake Michigan to estimate chinook natural production have had limited success. Problems with inconsistent marking procedures in the hatcheries, a lack of consistent quality control at the hatcheries, and the lack of a coordinated lake-wide sampling plan have hampered to ability to obtain accurate estimates of lake-wide natural recruitment. In order to get good estimates of chinook salmon natural production, consistent marking procedures and quality control and a coordinated lake-wide sampling plan are necessary.

The purpose of this white paper is to provide the Lake Michigan Technical Committee with recommendations regarding a coordinated lake-wide sampling plan to estimate the amount of natural reproduction of chinook salmon in Lake Michigan. Issues regarding OTC marking techniques and quality control have been addressed in the companion white paper (Rutherford 2002). In this paper, we will discuss the potential objectives for the OTC marking projects and the impact these objectives have upon the sampling program. We will discuss the importance of determining marking error rates and how these error rates impact the ability to estimate natural production. Additionally, we will provide recommendations for sampling plans to estimate these marking error rates. Finally, we will discuss three sampling plans for lake-wide recovery of OTC marked chinook and make recommendations of sample sizes.

In this report we present results for specific input parameters such as error rates in classifying OTC marks, true proportions wild in the population, age compositions of the harvest, size distributions at age and sample sizes. We have included a user's manual (Appendix A) and the code of the SAS program (Appendix B) we used to calculate these results to allow the interested reader to apply our approach and determine results under conditions different than those we address here.

OTC sampling procedures

OTC marks are read by viewing a vertebrae of the chinook salmon under ultraviolet light using a dissecting scope. A positive OTC mark will produce a fluorescent ring visible to the reader. Since OTC marks degrade when exposed to visible light, sampling of the chinook must limit the exposure of the vertebrae to direct light. The vertebrae can also be used for age determination, so separate samples of otoliths are unnecessary (Hesse 1994). To obtain samples of the vertebrae, a section of the tail of the chinook salmon must be removed. Hesse (1994) removed a section of at least 5 thoracic vertebrae from below the adipose fin prior to the angler cleaning the fish. However, preliminary sampling done on Lake Huron suggests that anglers are often unwilling to donate a section of the tail from their catch. Therefore on Lake Huron, the vertebrae sample is taken after the angler cleans the fish from the carcass (J. Johnson, personal communication). The sample is then wrapped in aluminum foil, placed in a zip lock bag and frozen for later analysis for OTC marks at the Alpena station.

Previous sampling on Lake Huron also suggests that it is difficult to obtain samples from locations without cleaning stations and sampling should be concentrated in those locations with cleaning stations to maximize the number of fish available for sampling. By targeting tournaments and other events that produce large catches of fish, samples as large as 100 fish in an eight hour day have been collected on Lake Huron (J. Johnson, personal communication). These targeted efforts as opposed to a random selection of locations have eliminated much of the wasted time spent waiting for samples to come in. Sampling on Lake Huron has also suggested that a single individual charged with other sampling duties (recovering coded-wire tags (CWTs)) cannot adequately sample for tails and perform the necessary interviews and sample collections

for the other program. They have found that assigning each sampler an assistant to collect tail samples is necessary to collect the additional tail samples needed for OTC mark detection (J. Johnson, personal communication).

We have estimated the current capacity for reading OTC marks based on the capacity of the Michigan DNR Alpena Station. This facility currently uses a specialized microscope designed for reading of OTC marks. While increases in capacity are possible, they would either involve additional staffing, additional equipment or both. Use of other lower quality equipment carries with it the danger of producing different error rates, and those involved in this work have argued this is a reasonable possibility if lower quality equipment were used. The Alpena station currently has the resources to process approximately 4000 OTC samples a year. This capacity allows approximately 2000 samples lake-wide for Lake Michigan.

Importance of marking error rates

The accuracy of estimating the proportion of wild fish in the chinook salmon population depends critically on the ability to distinguish hatchery and non-hatchery origin fish from one another. This requires both a consistent OTC mark on hatchery fish prior to their release and the ability to detect this OTC mark when the fish are sampled. Rutherford (2002) has documented that problems with mark formation and mark detection have occurred in previous attempts at OTC marking chinook salmon in Lake Michigan and are likely to continue to occur under current OTC marking procedures.

In a scenario where there was no error associated with mark formation or detection, the proportion of unmarked fish observed in the sample is an estimate of the proportion of wild fish in the population. However, with marking and detection errors, the proportion of unmarked fish

no longer represents solely wild fish with no mark but also includes hatchery fish that were not marked and also those hatchery fish where the OTC mark was not detected.

Ignoring the effects of marking and detection errors by treating the proportion of unmarked fish as an estimate of the proportion wild fish can lead to substantial bias in the estimate of the proportion of wild fish. The amount and direction of the bias depends upon the relative abundance of wild and hatchery fish and the classification error rates, i.e. the error rate in classifying hatchery fish as unmarked (false negatives) and the error rate of classifying wild fish as marked (false positives). We will express these error rates as a matrix and will refer to it as the classification error matrix. The classification error matrix contains four elements: the classification rate of wild fish as marked, p_{wm} , the classification rate of wild fish as unmarked, p_{wu} , the classification rate of hatchery fish as marked, p_{hm} , and the classification rate of hatchery fish as unmarked, p_{hu} . An example matrix is

$$T = \begin{pmatrix} p_{wu} & p_{hu} \\ p_{wm} & p_{hm} \end{pmatrix} = \begin{pmatrix} 0.9 & 0.1 \\ 0.1 & 0.9 \end{pmatrix}. \quad (1)$$

The expected proportion of unmarked fish in the population can be calculated as

$$p_u = p_{wu} p_w + p_{hu} p_h \quad (2)$$

where p_w is the true proportion of wild fish in the population and p_h is the true proportion of hatchery fish in the population. If classification errors are ignored, then p_u is treated as an estimate of p_w .

The bias produced by ignoring the classification errors for a variety of classification error matrix can be seen in Table 1. The classification error matrices chosen bracket the expected error rates suggested by Rutherford's (2002) review of past marking studies. When error rates

are even moderate in size (10-20%), the effect of ignoring classification errors is large particularly at low levels of wild fish in the population, e.g. for a true proportion wild of 0.1, the estimated proportion wild ranges from 0.18 to 0.25. In cases of large error rates (40 %), the estimates of proportion of wild in the population are extremely biased with estimates more than four times as large as the true value for a true proportion wild of 0.1. Clearly, ignoring marking and detection errors can have large effects on the accuracy of the estimated proportion wild.

However, the proportion of marked fish estimated from a sample can be corrected for classification errors provided that the classification error matrix is known or can be estimated well. The corrected estimator of the proportion wild and hatchery fish is:

$$\begin{bmatrix} \hat{p}_w \\ \hat{p}_h \end{bmatrix} = T^{-1} \begin{bmatrix} p_u \\ p_m \end{bmatrix} \quad (3)$$

where p_u is the proportion of unmarked fish in the sample, p_m is the proportion marked in the sample, and T^{-1} is the inverse of the classification error matrix. This corrected estimator removes the bias associated with marking and detection errors provided that classification error matrix is well estimated. For the remainder of the paper when we discuss an estimator of the proportion of wild fish, we will be referring to the estimator in equation 3.

Estimating the classification error matrix

As we have discussed previously, the classification error matrix can have large effects on the accuracy of the estimated proportion wild. Therefore, it is very important that the amount of classification error be estimated for the current OTC marking procedure. In order to estimate the classification matrix, samples of known OTC marked and known unmarked fish must be collected and subjected to the same procedures as other fish to determine the misclassification

rates.

The best source of known marked fish is OTC marked fish that have also been marked with code wire tags (CWT). Both Wisconsin and Michigan have double-marked some stocked chinook salmon released into Lake Michigan. Wisconsin releases approximately 25,000 CWT chinook salmon each year (Paul Peeters, personal communication) and Michigan released approximately 160,000 CWT chinook in 2000 and 533,000 CWT chinook in 2001 (Dave Clapp, personal communication). The best source of known unmarked fish is the chinook salmon stocked in Lake Huron by the Ontario Ministry of Natural Resources that are fin clipped but not marked with OTC. There are currently some chinook salmon in Lake Michigan stocked by the state of Wisconsin that are not marked with OTC. These chinook could potentially serve as a source of known unmarked fish with sampling being done at the Wisconsin weirs. However, if there are even a small number of OTC marked chinook stocked by the state of Michigan stray to the Wisconsin weirs, then any estimate of the error rate would be biased. Provided the Lake Huron and Lake Michigan OTC marks are read using the same methods (which we expect to be the case), the misclassification rates of unmarked fish as marked should be similar for these two lakes.

The state of origin (e.g., Wisconsin versus other states) of a fish cannot easily be determined when sampling the chinook harvest for OTC marking, and thus adjusting for classification errors must be based on a single misclassification rate matrix for the entire lake. If all stocked chinook are marked with OTC using the same procedure and this procedure is used for all years of the study, the misclassification matrix could be estimated only once (with updates to the estimates if conditions change or marking procedures change). However, if OTC marking procedures are changed every year, as has occurred in 2000 and 2001, or Wisconsin and

the other states continue to utilize different OTC marking procedure, the sampling plan for the estimation of the misclassification matrix becomes more complicated.

If the protocols for marking chinook salmon by OTC continue to differ among the Lake Michigan states then an average lake-wide misclassification matrix is needed. This could be accomplished by first estimating the misclassification matrix for each method of marking used by the different states separately using double-marked CWT chinook for each method along with the Ontario unmarked, fin clipped chinook. Once the estimates for each method were available, the lake-wide misclassification matrix could be estimated by taking a weighted average of each methods misclassification where each was weighted by the number of fish stocked that had been marked by that method. However, this approach assumes that the survival of fish marked by the different methods (and stocked into different parts of the lake by different jurisdictions) are the same.

There has been some concern that OTC marks deteriorate as a fish ages, thus it may be important to assess how misclassification error rates change across the life of a cohort. For this reason, we recommend that misclassification rates for each age be estimated separately so that the effects of mark deterioration can be determined. This requires that sampling be stratified by length classes to ensure that adequate sample sizes of age-2 and age-3 fish are collected from the harvest. If a consistent marking protocol is used for every year then sampling of the different age classes can be combined in a single year by sampling adjacent cohorts. However, if different OTC marking protocols are utilized in different years then the sampling for age-2 and 3 fish must be from the same cohort and therefore must be collected across years.

Since the classification matrix plays an important role in producing accurate estimates of the proportion of wild fish in the population, it is critical that the sample sizes collected to

estimate the error rates are large enough to provide reasonably precise estimates. Under a simple random sampling scheme, where fish are randomly selected for OTC mark evaluation for the double-marked CWT fish and the Ontario fin clipped fish, the coefficient of variation of the estimated proportion misclassified (i.e., double-marked fish classified as unmarked and fin clipped fish classified as marked) depends upon the sample size by

$$CV = \frac{\sqrt{\left(\frac{p(1-p)}{n}\right)}}{p} \quad (3)$$

where p is the true value of proportion being estimated and n is the sample size. The CV of the estimated proportion declines rapidly with increasing sample sizes at first, but at a sample size of approximately 200 fish the rate that the CV declines with increasing sample size is small (Figure 1). Therefore, we recommend that a sample size of at least 200 double-marked CWT chinook and 200 fin-clipped Ontario chinook be sampled to estimate the classification matrix. In order to adequately sample age-2 and age-3 fish, these samples should be spread across the length distribution to attempt to ensure an equal sampling of each age of fish.

Project objectives and potential sampling designs

The OTC marking project in Lake Michigan could be designed to answer three main objectives regarding natural reproduction of chinook salmon in the lake. Each of these objectives requires a different sampling plan to ensure that samples are collected in a way that will allow the questions of interest to be answered. The three main objectives we have identified for the Lake Michigan OTC marking project are:

1. Estimate the proportion wild in the chinook population
2. Estimate the proportion wild at age in the chinook population

3. Estimate the proportion wild at age in the chinook salmon harvest.

Objectives one and two differ fundamentally from objective three in that they are interested in characteristics of the chinook salmon population in the lake rather than in the harvest. These objectives require that sampling be representative of the population rather than just the harvest. When samples of fish used in the analysis come from the recreational fishery harvest, in essence this requires that sampling of the harvest occur at a time when the population is well mixed. This assumption is necessary to ensure that we can combine estimates from different locations as if they were samples of the same population. If the chinook salmon population was divided into spatially distinct sub-populations, each with a potentially different proportion of wild fish, the sampling design should be stratified by the location of these sub-populations similar to the stratified sampling plan for sampling the harvest to determine the proportion of wild fish in the harvest. This would require that we know both the spatial distribution of each sub-population and the relative size of each sub-population. At this time, this type of information is not available for the Lake Michigan chinook population. Therefore we chose to assume that the chinook salmon population is well-mixed during July. There is evidence from studies of the movement of CWT chinook salmon that suggests this assumption may be appropriate. Analysis of CWT data suggested that there is no spatial aggregation of the CWT chinook recovered in the harvest to the locations where the chinook were released during the mid-summer (Bence unpublished analyses of Michigan DNR data). However, earlier OTC studies done by Hesse (1994) on the eastern shore of Lake Michigan have found a significant difference in the proportion wild at age-3 between samples collected at Ludington, MI and those collected at Grand Haven, MI suggesting that there may be some spatial segregation of the chinook population. However, these differences were detected only when the samples were

combined across all of the months sampled (May-September) and no significant differences were detected in the July samples alone (or any other month). This lack of a significant difference in the July samples collected by Hesse (1994) may suggest that the population is well-mixed during this time and not at others, which causes the significant difference when samples are pooled across all months. However, this hypothesis is not supported by the lack of any significant differences in any other month. The small sample sizes collected by Hesse (1994) in each month at each location preclude any strong conclusions regarding the spatial distribution of wild fish in Lake Michigan.

While we believe the assumption of a well-mixed population during July is reasonable for determination of sample sizes and development of a sampling plan, this is clearly an approximation and it is only prudent to stratify samples spatially so that large spatial differences in the proportion wild could be detected.

An alternative approach to sampling the recreational harvest would be to obtain samples from research surveys. Currently only the Michigan DNR collects such samples in substantial numbers and only from Michigan's waters. Use of these data would also require that the chinook salmon population was well mixed, so that pooled observations would be representative of the lake-wide population. Given such an assumption, our calculations of CVs and recommendations regarding sample sizes would also apply to samples from such a survey.

For inferences about the composition of the chinook harvest, sampling should be spread across the entire fishing season (approximately March-November) to capture a representative sample of the harvest. In addition, such sampling would have to also be spatially stratified because chinook salmon of different origins are clearly aggregated spatially at some times of year (e.g., as they stage prior to spawning runs).

A sampling plan to estimate only the total proportion wild in the lake requires that a simple random sample (SRS) of the population be taken. Although this sample could be taken at only one location (given our assumptions of well mixing), as discussed above it is more prudent to take the sample at several locations to provide spatial coverage across the lake. This will allow the data to be examined for spatial patterns in the proportion of wild fish, provided the sample size is adequate in each location.

If age-specific estimates of the proportion of wild fish in the population are desired, then a stratified sample is necessary to ensure that all age classes are represented in the sample. However, age of the fish is unknown at the time of sampling. Therefore, samples must be stratified by length class so as to provide samples of each age class of interest (SLS). Again, this sampling could be directed at one location at a time when the population is well-mixed, but a wider spatial coverage would provide the ability to examine spatial patterns in the proportion wild at age.

Estimating the proportion wild at age in the harvest requires a more complicated sampling design. Since the amount and composition of the harvest varies across locations and between seasons in a given location, the sampling plan must be stratified by both location and season. Additionally, since age-specific estimates may be desirable, the samples at each location in each season should be stratified by length class to ensure representation of the age classes of interest (HSS). This stratified sampling of the harvest can also produce inferences about the proportion of wild fish in the population if the population is well mixed during one of the seasons sampled. By looking only at the samples collected during this season, estimates of the proportion wild in the population can be produced. However, this may require that larger sample sizes be taken during this season to ensure there is adequate precision in the estimate of the

proportion wild in the population.

Simple Random Sampling

For the simple random sampling design, the main objective of the study is to estimate the proportion of wild fish in the total population (not by age class). In order to determine how sample size affects the uncertainty in the estimates of the proportion wild, several preliminary calculations are necessary. First, with marking and detection errors, the expected proportion of unmarked fish (p_u) in the sample must be calculated from the true proportion wild in the population. This is done by applying equation 1. The expected variance in the estimate of the proportion of unmarked fish (\hat{p}_u) can then be calculated from the expected proportion of unmarked fish in the sample and the size of the sample taken by

$$Var(\hat{p}_u) = \frac{P_u(1-P_u)}{n} \quad (4)$$

which is also the expected variance of the estimated proportion of marked fish (\hat{p}_m). The expected estimate of the proportion wild (\hat{p}_w) can then be calculated from equation 3.

Assuming that the classification error matrix is known, the expected variance of \hat{p}_w can be calculated as

$$Var(\hat{p}_w) = (T^{-1})_{11}^2 Var(\hat{p}_u) + (T^{-1})_{12}^2 Var(\hat{p}_m) + 2(T^{-1})_{11}(T^{-1})_{12} Cov(\hat{p}_u, \hat{p}_m) \quad (5)$$

where $(T^{-1})_{ij}$ is the element of in the row i and column j and $Cov(\hat{p}_u, \hat{p}_m)$ is the covariance of \hat{p}_u and \hat{p}_m . This covariance \hat{p}_u of and \hat{p}_m is

$$Cov(\hat{p}_u, \hat{p}_m) = -\sqrt{Var(\hat{p}_u)Var(\hat{p}_m)} \quad (6)$$

since the correlation between \hat{p}_u and \hat{p}_m is -1. The expected coefficient of variation of \hat{p}_w is

then

$$CV = \frac{\sqrt{\text{Var}(\hat{p}_w)}}{p_w} \quad (7)$$

Figure 2 shows the expected coefficient of variation of the estimated proportion wild in the population for a variety of true proportion wild and sample sizes for two different classification matrices. The first classification error matrix we chose to present, T_1 ,

$$T_1 = \begin{pmatrix} 0.7 & 0.3 \\ 0.3 & 0.7 \end{pmatrix} \quad (8)$$

approximates what we thought might be reasonable to expect the error rates could be under the current marking protocol. The second classification matrix, T_2 ,

$$T_2 = \begin{pmatrix} 0.9 & 0.1 \\ 0.1 & 0.9 \end{pmatrix} \quad (9)$$

represents a near best-case scenario using current OTC technology, where errors in the marking and detection have been minimized.

In all cases, the coefficient of variation for the total proportion wild in the population declines with increasing sample sizes (Figure 2). The coefficient of variation also declines with increasing true proportion wild for the same sample size. The effect of decreasing the amount of classification errors (going from T_1 to T_2) is to decrease the CV of the estimated proportion wild in the population (note the difference in the scales of the y-axes). For the scenario where marking and detection errors have been minimized (T_2), the benefit of increasing sample size above 500 on the CV is minimal for moderate values (0.2-0.4) of the true proportion wild. If the true proportion wild in the population is small (0.05-0.1), then larger sample sizes may be necessary to obtain a desirable level of CV (Figure 2 b). If marking and detection errors remain

high (T_1), the CV of estimates for low levels of wild fish may be unacceptably high even for the largest sample size feasible given the current capacity for reading OTC marks (2000 samples) (Figure 2a). Furthermore, the results suggest diminishing returns with increasing samples size, so that substantial improvement in results are unlikely given such reading errors even with large increases (above current capacity) in recovery and processing of fish for OTC marks.

Stratified Random Sampling by Length

The presence of year-to-year variation in the amount of wild production of chinook salmon makes it valuable to be able to estimate age-specific proportions of wild chinook in Lake Michigan. To obtain estimates of the proportion wild by age class requires that the sampling plan is designed to adequately sample all of the age classes of interest. This can be accomplished by using a stratified sampling design. However, when sampling chinook salmon, we cannot determine the age of the fish prior to sampling the tail of the fish. Therefore, we will use length as a surrogate for age in the stratification. We chose to use the same length bins as the chinook salmon diet protocol to stratify our sampling. This sampling protocol uses three length bins, less than 37 cm, 38 to 57 cm, and greater than 58 cm. However, since the smallest length bin corresponds to age-0 chinook and age-0 chinook are rarely caught in the harvest, we eliminated this length bin and used only the two larger length bins. To calculate the expected sample size for each age, we applied a reverse age-length key to convert the sample size in each length bin to a sample size in each age class. We ignored age-5 chinook salmon since they account for such a small proportion of the population. Our reverse age-length key was calculated using the length and age information from the creel survey from 1985 to 1999 and was

$$A = \begin{pmatrix} 1 & 0 \\ 0 & 0.55 \\ 0 & 0.42 \\ 0 & 0.03 \end{pmatrix}$$

We chose to focus on sampling plans that had the same sample size in each length bin and we expressed the sample size to be collected as a vector, S , where the first element is the sample size for the 38-57 cm length bin and the second element is the sample size for the greater than 58 cm length bin.

The expected sample size for each age for a variety of sample sizes can be seen in Table 2. These expected sample sizes can then be used to calculate the expected coefficient of variation in the estimates of the proportion of wild fish at age using equations 4-7. Again, we chose to present the expected CV of the estimated proportion wild at age for the two example classification error rate matrices, T_1 and T_2 . We chose not to present the results for age-4 because even at the maximum lake-wide sample size (2000) expected CVs were extremely large in most cases. Results for age-4 can be obtained by applying the SAS program (Appendix B).

Again, the effect of the amount of marking and detection error on the expected uncertainty in estimates of the proportion wild at age is large. By decreasing classification error rates from 30% to 10%, the CV of the proportion wild at age declines by at least 50% for all sample sizes and true proportions wild (Figures 3 and 4). The amount of classification error rate is extremely important for low values of the true proportion wild at age in the population (≤ 0.1) where CVs remain high (≥ 0.5) with classification error rates of 30% for most ages even at the maximum possible sample size (Figure 3 a and b). The CV also increases with each age because the sample size at age decreases with increasing age (Figures 3 and 4).

For moderate classification error rates (T_1) and moderate values (0.2-0.4) of the true

proportion wild in the population, CVs for the proportion wild of age-1, -2, and -3 fish are all below 0.25 for sample size greater than 1500 fish and for age-1 and -2 fish are below 0.25 for sample sizes greater than 1000 fish (Figure 3 c-e). For smaller values of the true proportion wild (0.05-0.1), CVs never decline below 0.25 for sample sizes less than the maximum of 2000 fish (Figure 3 a and b). For smaller classification error rates (T_2), at moderate values of the true proportion wild in the population, CVs for the proportion wild at -for age-1, -2, and -3 fish are below 0.25 for sample sizes greater than 1000 fish and for age-1 and -2 fish are below 0.25 at sample sizes greater than 500 fish (Figure 4 c-e). For smaller classification error rates (T_2) and lower values (0.05-0.1) of the true proportion wild in the population, sample sizes of 1500 or greater fish are required for any of the CVs to reach 0.25 and in the cases of the true proportion wild in the population of 0.05, a CV of 0.25 is never reached (Figure 4a and b).

Stratified random sampling of the harvest

In order to have estimates of the proportion wild in the harvest rather than the population, the sampling plan must be designed to account for the differences in harvest between locations and seasons around the lake. For this reason, we recommend that sampling to estimate the proportion wild in the harvest be stratified by both location and season along with length class to ensure that adequate samples of each age class are obtained.

Following Benjamin and Bence (in press), the lake was divided into seven regions, which followed the boundaries of the statistical districts (Smith et al. 1961). The Green Bay region consists of Wisconsin statistical districts WM1 and WM2 as well as Michigan statistical district MM1. However, since none of these statistical districts provide a significant chinook fishery, we did not include this region in the sampling design. This left us with six regions for stratification.

The north region encompasses Michigan statistical districts MM2, MM3, and MM4. The Northeast region includes Michigan statistical districts MM5 and MM6. The northwestern region includes Wisconsin statistical districts WM3 and WM4. The southeastern region includes Michigan statistical districts MM7 and MM8. The southwestern region includes Wisconsin statistical districts WM5 and WM6. The Indiana-Illinois region includes all waters within Illinois and Indiana state boundaries.

Tables 3, 4, and 5 show the average harvest (in numbers) reported in the creel database for each statistical district by month. The majority of the chinook salmon harvest occurs in June, July and August in most locations. We chose to stratify the harvest samples into three seasons, an early, mid and late season. The early season would include all chinook caught through mid-June. The mid season sample would span mid-June through the end of July. This sample could also be used to estimate the proportion wild at age in the population. The late season sample would span August through the end of the fishing season. This stratification would ensure that the population would be well-mixed during the mid-season sample so that the data could also be used to estimate the proportion wild at age in the population.

The expected CV of the proportion wild at age in each season and location can be calculated as before using equations 4-7. The expected CV of the proportion wild in the harvest averaged across ages, locations and seasons can also be calculated by specifying the age composition of the harvest, the proportion of the harvest that occurs in each location and the proportion of harvest that occurs at each location. We calculated the average age composition of the harvest for 1990-2000 from the most recent catch at age models for Lake Michigan chinook salmon , which was

$$P = \begin{pmatrix} 0.25 \\ 0.39 \\ 0.31 \\ 0.05 \end{pmatrix}$$

We also approximated the proportion of harvest that occurs in each season at each location by

$$S = \begin{pmatrix} 0.25 \\ 0.5 \\ 0.25 \end{pmatrix}$$

Finally, we calculated the average proportion of the harvest that was caught in each region for 1985-2000 from the creel database, which was

$$H = \begin{pmatrix} \textit{North} \\ \textit{Northeast} \\ \textit{Northwest} \\ \textit{Southeast} \\ \textit{Southwest} \\ \textit{IN / IL} \end{pmatrix} = \begin{pmatrix} 0.02 \\ 0.33 \\ 0.17 \\ 0.27 \\ 0.16 \\ 0.05 \end{pmatrix}$$

These quantities were used to average across ages, seasons, and locations to produce an estimate of the proportion wild in the harvest. The expected CV was then calculated using the rule:

$$CV = \frac{\sqrt{\sum_i p_i^2 \text{Var}(\hat{p}_{wi})}}{\hat{p}_w}$$

where p_i is the proportion of the harvest in the i th category (e.g. i th season) and $\text{Var}(\hat{p}_{wi})$ is the variance of \hat{p}_w in the i th category (e.g. i th season).

We again present the expected CV using a variety of true proportions wild in the harvest and the classification error matrices T_1 and T_2 . We divided the total lake-wide sample size evenly between the six locations, three seasons and two length bins so that each length bin, season and location combination had the same sample size. We do not present the results for age-

4 due to the extremely large CVs. Again, the amount of classification error has a large effect on the CV of the estimates with the CV decreasing by approximately 50% when the classification error rate declines from 30 to 10% (Figures 5 and 6). In all cases the CV of the estimates of the proportion wild at age in each season and location is much higher than the CV for the estimated proportion wild at age in the population because the sample size used to calculate the former is much smaller despite a similar lake-wide sample size (Figures 3, 4, 5 and 6). With moderate classification error rates, T_1 , the expected CV never decreases below 40% for any true proportion wild up to the maximum sample size. With reduced classification errors (T_2), the expected CV of the estimates declines to 25% only for the largest sample size and moderate values (0.3-0.4) of the true proportion wild. In order to estimate the proportion wild at age in the harvest for each season and location well, the capacity to read OTC marks would need to be substantially increased.

We can also examine the expected CV of an estimate of the proportion wild in the harvest averaged across ages, seasons and locations. The results are shown in Figure 7. Again, reducing classification error rates from 30 to 10% reduces the expected CV by approximately 50%. For classification error matrix T_1 , CVs of below 0.25 are expected from lake-wide sample sizes greater than 1000 for most values of the true proportion wild. For classification error matrix T_2 , a similar level of precision can be obtained from lake-wide sample sizes of approximately 400 fish.

Recommendations

1. Marking and detection error rates are extremely important to acknowledge in OTC mark evaluation. Failure to account for errors in the classification of fish (i.e. scoring all unmarked

fish as wild) can lead to large biases in the estimates of the proportion wild fish. We recommend that the Lake Michigan Technical Committee evaluate the classification error rates for the OTC marking procedure adopted for the chinook salmon natural reproduction evaluation study.

2. To evaluate classification error rates for an OTC marking protocol, samples of known unmarked and known marked adult chinook are needed. If the Wisconsin and the other states continue to utilize different OTC marking protocols, then samples of known marked fish are necessary for both methods being used. Sources of known unmarked fish are Ontario fin clipped chinook for Lake Huron and Wisconsin CWT fish stocked into Lake Michigan prior to 2001. Sources of known marked fish are CWT fish that were marked with OTC from both Wisconsin and Michigan in 2001. Sample sizes of at least 200 of type of known marked and unmarked fish are necessary to determine the classification error rates with precision.

3. We recommend that the classification error rates be evaluated by age to determine if OTC marks fade with increasing age of the fish. To accomplish this, we recommend that the samples of known marked and unmarked fish be collected from different lengths chosen to capture similar numbers of age-1, -2, and -3 chinook.

4. Sampling for OTC marks to estimate the proportion wild in the population or harvest should be concentrated at locations where large numbers of chinook salmon are harvested. This can be accomplished either by targeting tournaments or sampling at locations during times that are known to produce large harvests. Sampling should also be concentrated at locations that have cleaning stations as anglers have been reluctant to allow a tail sample to be taken from their catch prior to cleaning their fish in Lake Huron.

5. We recommend that at least two individuals collect samples for the OTC project at a given location if coupled with the current sampling activities (such as obtaining biological samples

from other species or recovery of CWT fish). In Lake Huron, they found that one individual could not efficiently collect OTC samples along with CWT sampling.

6. We recommend that the Lake Michigan Technical Committee concentrate their efforts on estimating the proportion wild at age. Sampling only to estimate the proportion wild in the total population does not provide any information on how year class strength varies temporally, a key uncertainty in chinook salmon population dynamics. Additionally, we recommend that the LMTC not attempt to estimate the proportion wild in both the harvest and the population at the same time due to the large number of samples required to estimate both with precision. A larger investment in the maximum number of samples that can be processed would be needed to accomplish both of these goals successfully.

7. The amount of classification error is very important in influencing the amount of uncertainty in the estimated proportions at age. Substantial efforts should be made to minimize these errors. If classification error rates are as large as 30-40%, there exists the possibility that the current capacity to process OTC samples is not large enough to ensure adequate precision in the estimates of the proportion wild at age. If classification error rates can be lowered to approximately 10%, then samples sizes of 1000 – 1500 fish will most likely be adequate to estimate the proportion wild at age with a CV of 25% or less.

8. We recommend that the samples for the stratified sampling of the population be taken from different locations around the lake (perhaps from each region described above), so that patterns in the proportion wild at age across the lake can be examined. To accomplish this objective, sample sizes in each region should be as large as possible within the constraints of the number of OTC samples that can be read (currently 2000 samples).

Acknowledgements

This work would not have been possible without the assistance of a number of people associated with the Lake Michigan Technical Committee and its associated agencies. We would like those individuals who provided us the information that made this report possible, including David Clapp (MDNR), Brad Eggold (WDNR), Rob Elliott (USFWS), Dave Fielder (MDNR), Jim Johnson (MDNR), John Kubisiak (WDNR), John Netto (USFWS), Paul Peters (WDNR), Ed Rutherford (UM), and Michael Wilberg (MSU).

References

- Benjamin, D.M. and J.R. Bence. In press. Spatial and temporal changes in the Lake Michigan Chinook Salmon fishery, 1985-1996. Michigan Department of Natural Resources, Fisheries Division, Fisheries Research Report.
- Hesse, J.A. 1994. Contribution of hatchery and natural chinook salmon to the eastern Lake Michigan Fishery. M.S. Thesis submitted to Michigan State University.
- Rutherford, E. 2002. Review of procedures for estimating wild production of chinook salmon through marking experiments: assessment of methods for marking fish.
- Smith, S.H., H.J. Buetner, and R. Hile. 1961. Fishery statistics of the Great Lakes. Great Lakes Fishery Commission Tech. Rep. 2. 24 p.
- Stewart, D.J., and M. Ibarra. 1991. Predation and production by salmonine fishes in Lake Michigan, 1978-1988. Canadian Journal of Fisheries and Aquatic Sciences 48: 909-922.

Table 1. The effects of ignoring classification error on the expected estimates of the proportion of wild fish (p_w) for different classification error matrices (T).

True p_w	T						
	$\begin{pmatrix} 0.6 & 0.4 \\ 0.4 & 0.6 \end{pmatrix}$	$\begin{pmatrix} 0.7 & 0.3 \\ 0.3 & 0.7 \end{pmatrix}$	$\begin{pmatrix} 0.8 & 0.2 \\ 0.2 & 0.8 \end{pmatrix}$	$\begin{pmatrix} 0.9 & 0.1 \\ 0.1 & 0.9 \end{pmatrix}$	$\begin{pmatrix} 0.95 & 0.05 \\ 0.05 & 0.95 \end{pmatrix}$	$\begin{pmatrix} 0.7 & 0.2 \\ 0.3 & 0.8 \end{pmatrix}$	$\begin{pmatrix} 0.95 & 0.2 \\ 0.05 & 0.8 \end{pmatrix}$
0.05	0.41	0.32	0.23	0.14	0.095	0.225	0.238
0.1	0.42	0.34	0.26	0.18	0.14	0.25	0.275
0.2	0.44	0.38	0.32	0.26	0.23	0.3	0.35
0.3	0.46	0.42	0.38	0.34	0.32	0.35	0.425
0.4	0.48	0.46	0.44	0.42	0.41	0.4	0.5

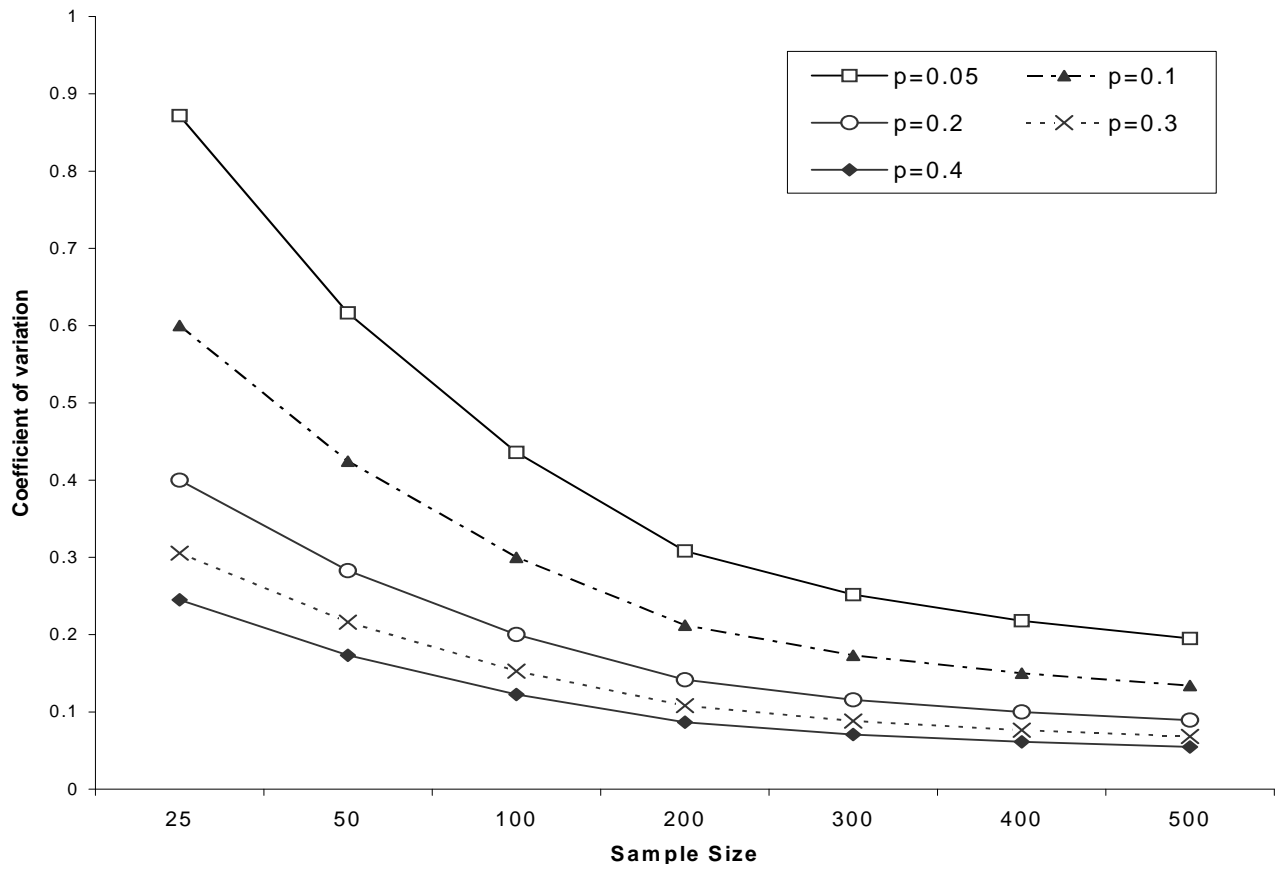


Figure 1. Effects of sample size on the coefficient of variation of a proportion estimated using Simple Random Sampling.

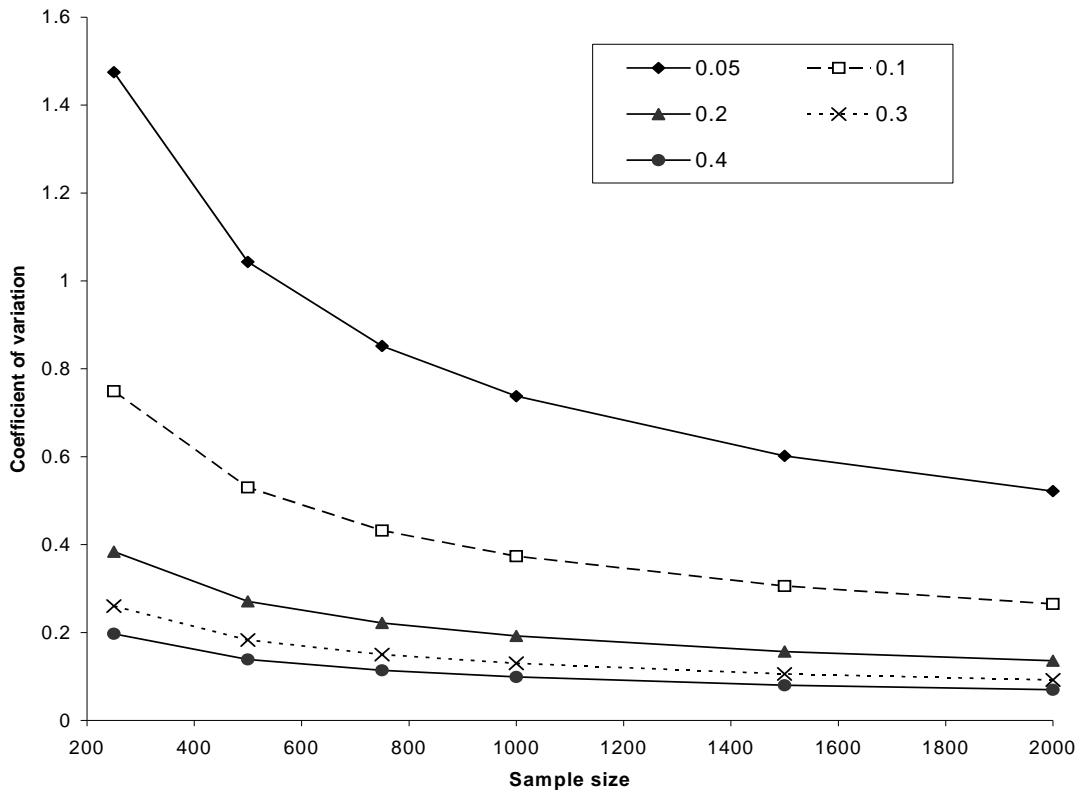


Figure 2a. Expected coefficient of variation for the total proportion wild in the population sampled using Simple Random Sampling for a variety of true proportions wild and sample sizes with the classification error matrix, T_1 .

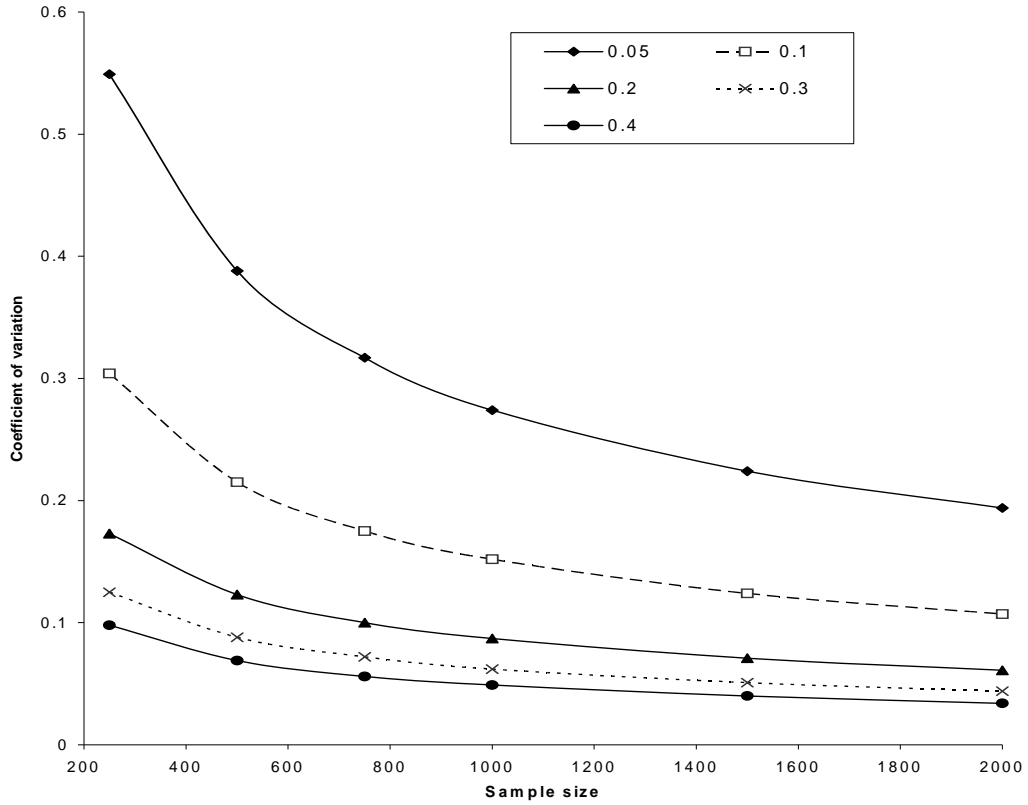


Figure 2b. Expected coefficient of variation for the total proportion wild in the population sampled using Simple Random Sampling for a variety of true proportions wild and sample sizes with the classification error matrix, T_2

Table 2. Expected sample sizes per age class for stratified sampling in two length bins, 38-57 cm and greater than 58 cm.

Age	$S = \begin{pmatrix} 125 \\ 125 \end{pmatrix}$	$S = \begin{pmatrix} 250 \\ 250 \end{pmatrix}$	$S = \begin{pmatrix} 500 \\ 500 \end{pmatrix}$	$S = \begin{pmatrix} 750 \\ 750 \end{pmatrix}$
1	125	250	500	750
2	68.75	137.5	275	412.5
3	52.5	105	210	315
4	3.75	7.5	15	22.5

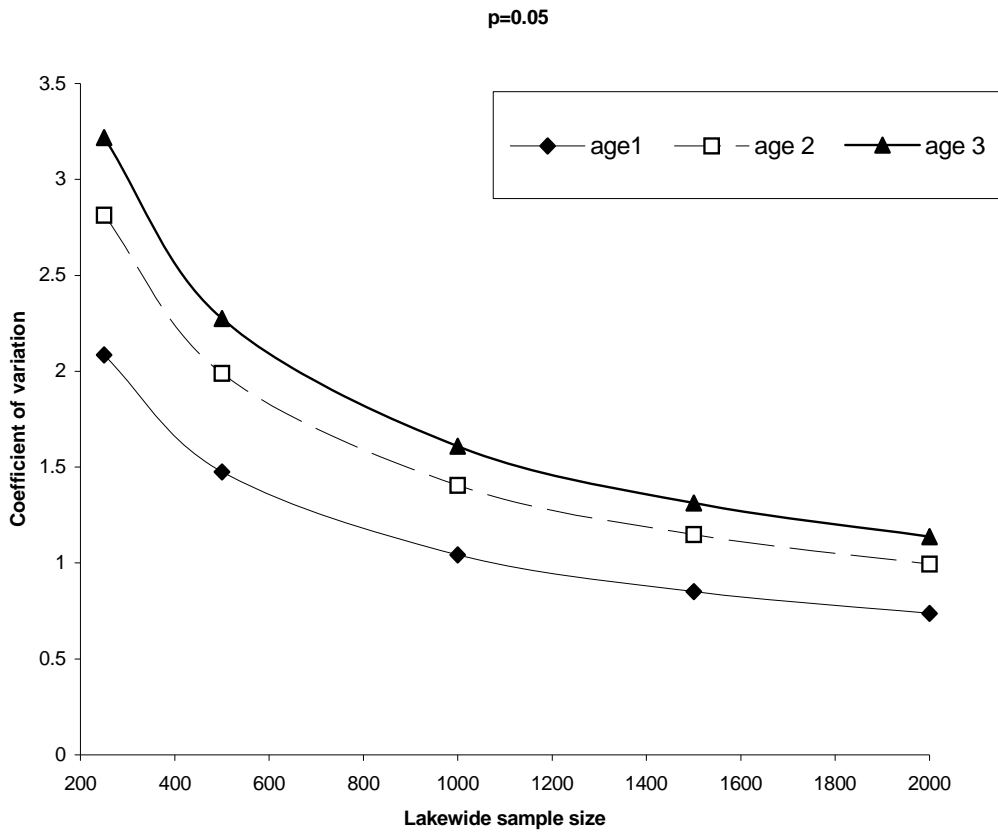


Figure 3a. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_1 and $p_w = 0.05$. The lake-wide sample size was divided evenly between the two length bins.

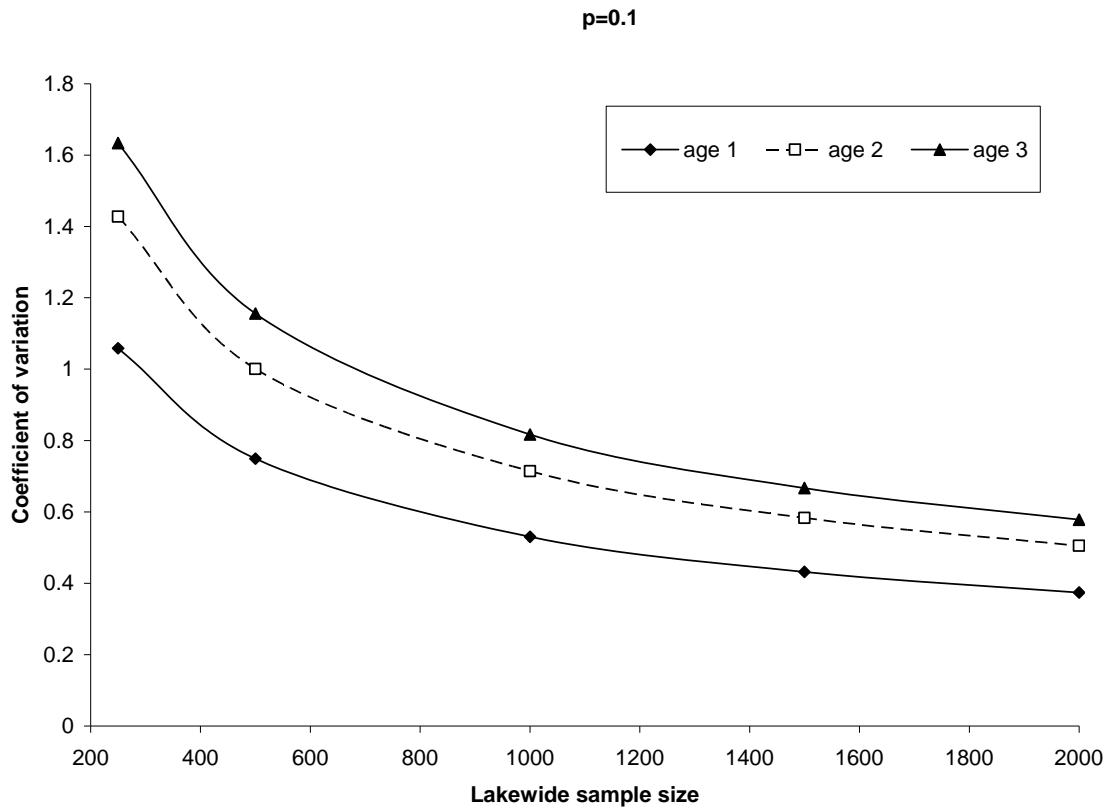


Figure 3b. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_1 and $p_w = 0.1$. The lake-wide sample size was divided evenly between the two length bins.

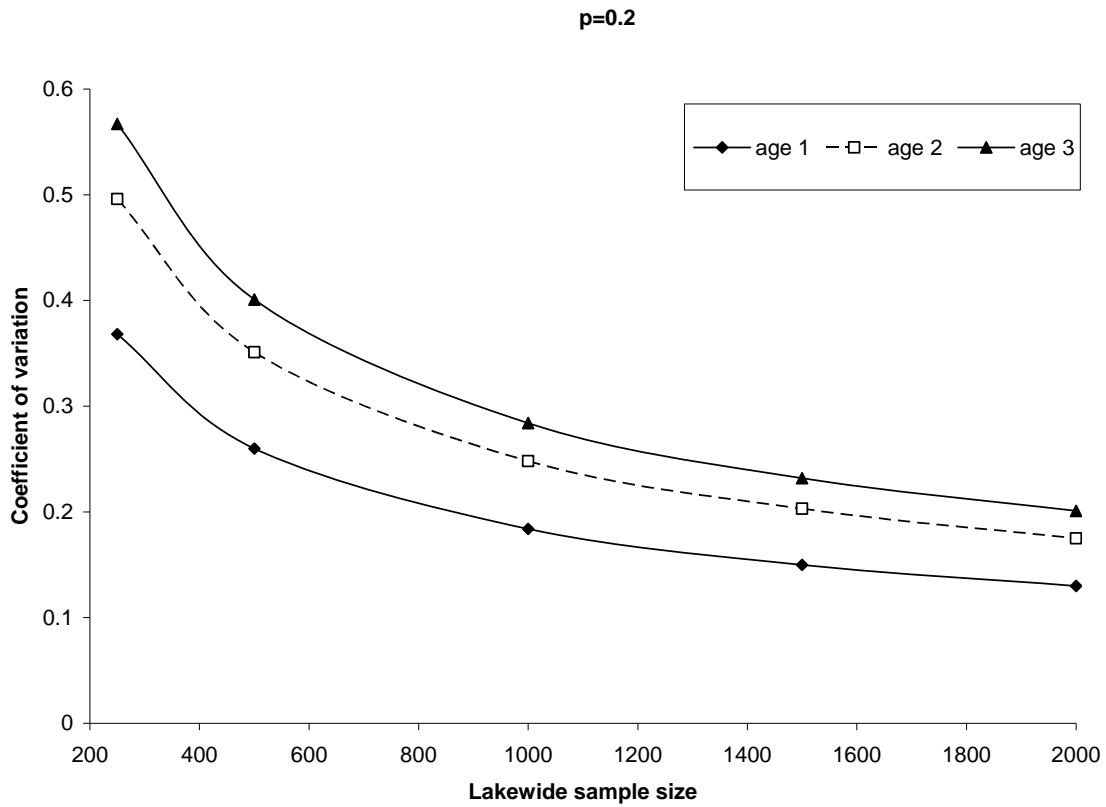


Figure 3c. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_1 and $p_w = 0.2$. The lake-wide sample size was divided evenly between the two length bins.

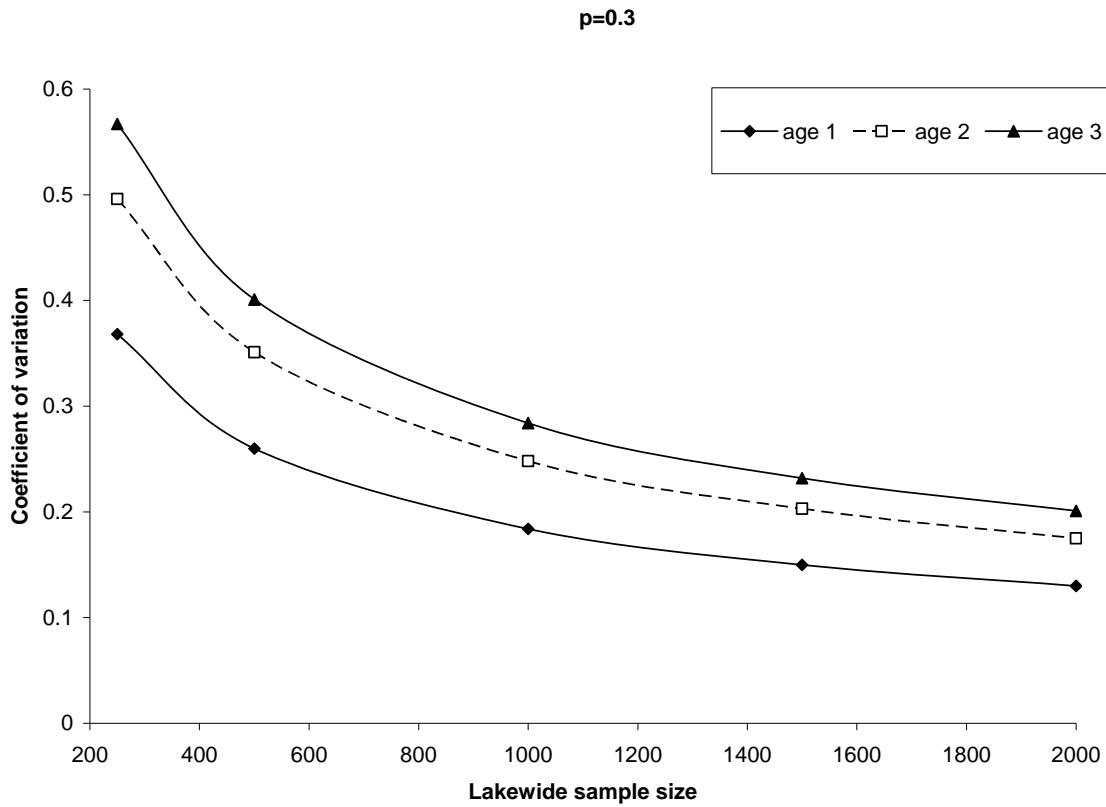


Figure 3d. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_1 and $p_w = 0.3$. The lake-wide sample size was divided evenly between the two length bins.

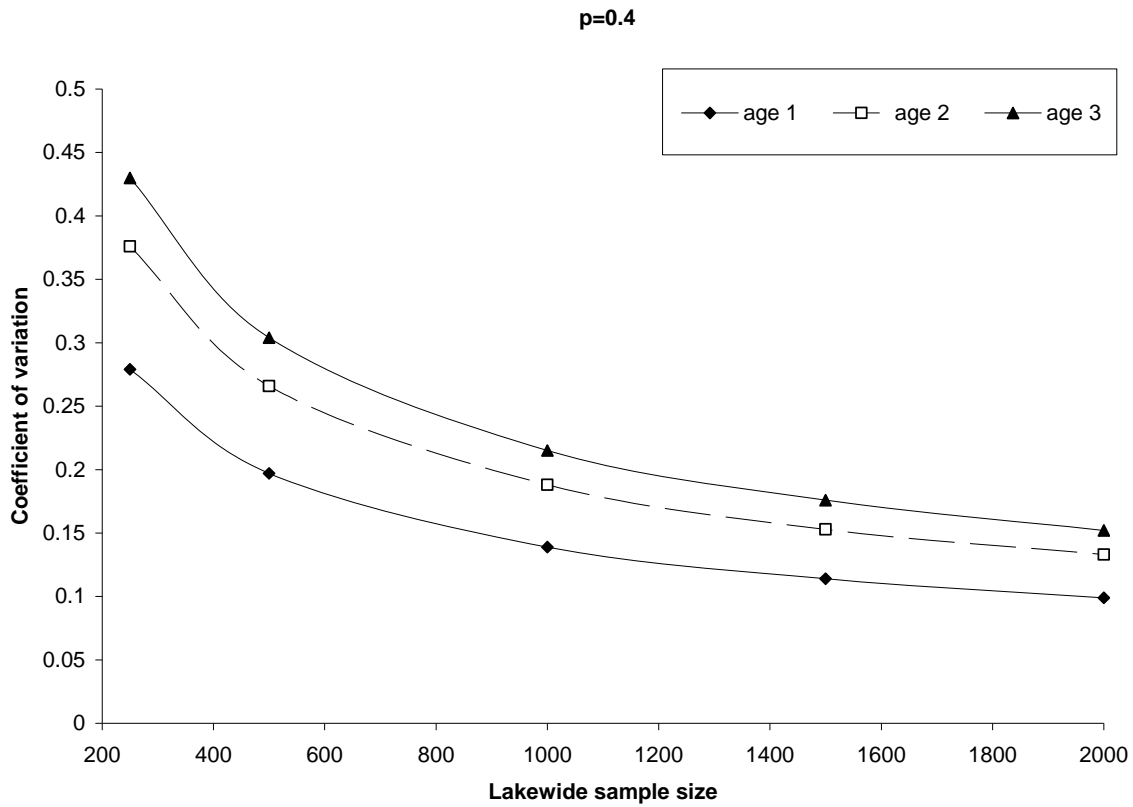


Figure 3e. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_1 and $p_w = 0.4$. The lake-wide sample size was divided evenly between the two length bins.

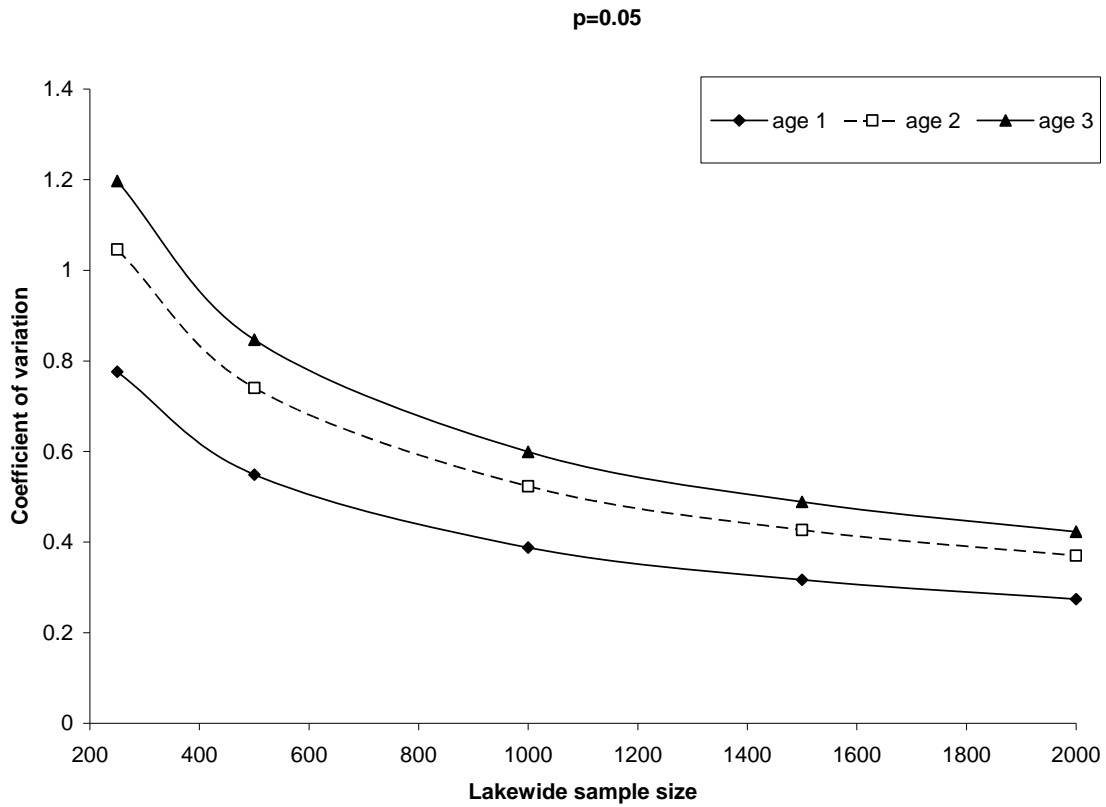


Figure 4a. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_2 and $p_w = 0.05$.

The lake-wide sample size was divided evenly between the two length bins.

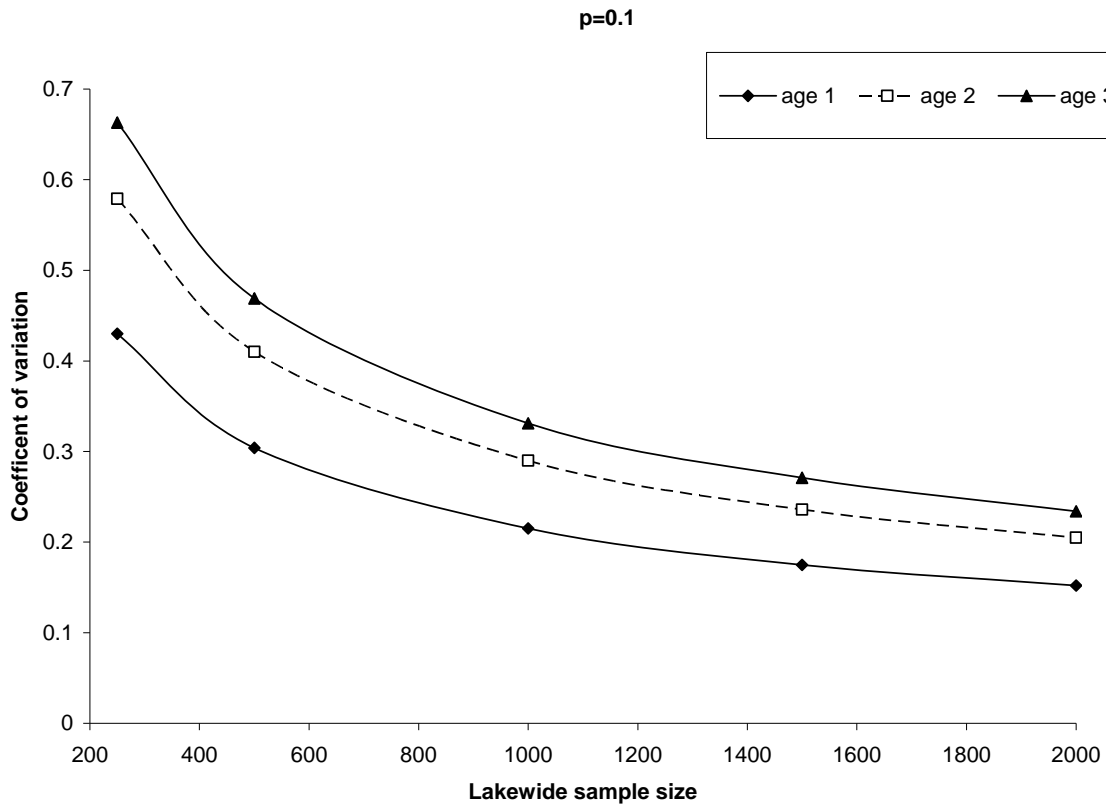


Figure 4b. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_2 and $p_w = 0.1$. The lake-wide sample size was divided evenly between the two length bins.

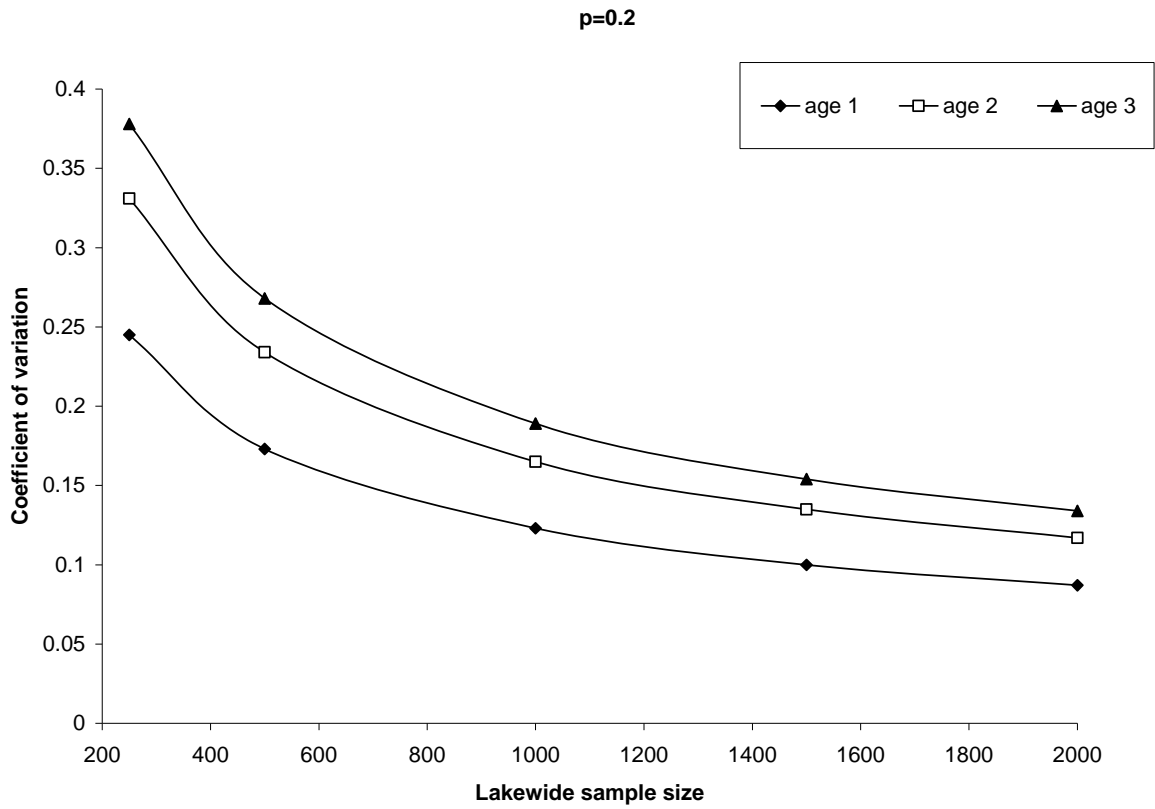


Figure 4c. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_2 and $p_w = 0.2$. The lake-wide sample size was divided evenly between the two length bins.

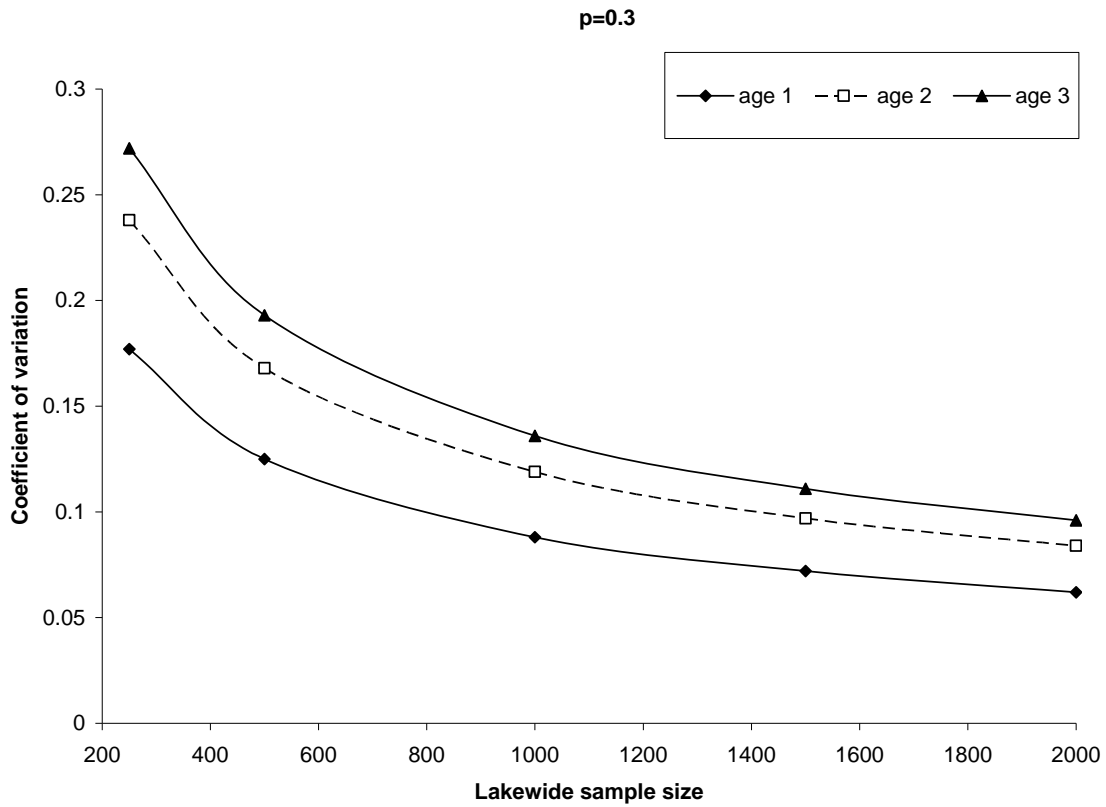


Figure 4d. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_2 and $p_w = 0.3$. The lake-wide sample size was divided evenly between the two length bins.

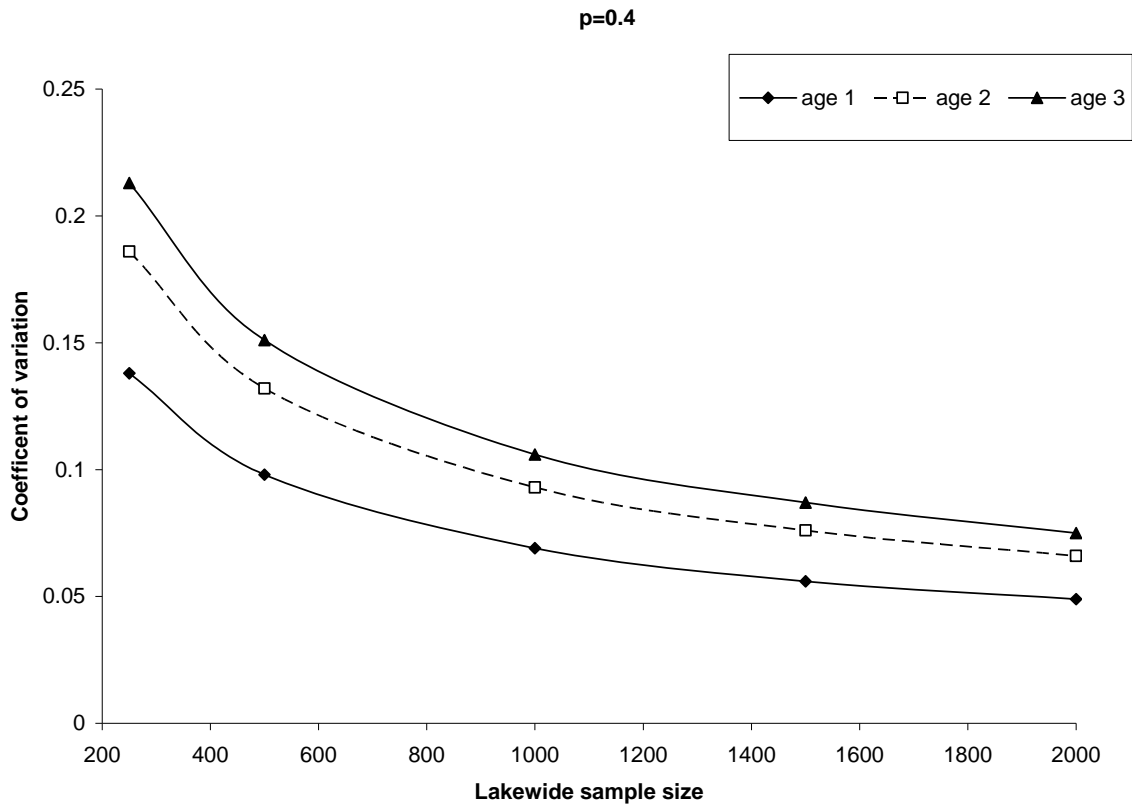


Figure 4e. Expected coefficient of variation for the estimated proportion wild at age using stratified random sampling for ages 1-3 with the classification error matrix T_2 and $p_w = 0.4$. The lake-wide sample size was divided evenly between the two length bins.

Table 3. Average boat harvest (in numbers) of chinook salmon (1985-2001) in the Wisconsin waters of Lake Michigan by statistical district and month from the creel database.

Month	Statistical District			
	WM3	WM4	WM5	WM6
March	7.2	2.4	30.5	2.3
April	14.5	4.7	61.1	4.6
May	39.3	197.8	1298.7	403.3
June	701.4	2474.9	2680.5	712.0
July	10640.4	12521.6	14111.1	3416.8
August	5564.6	9439.1	10980.5	2677.8
September	931.8	2003.1	3384.2	892.9
October	640.7	917.9	1626.5	334.3

Table 4. Average boat harvest (in numbers) of chinook salmon (1985-2001) in the Michigan waters of Lake Michigan by statistical district and month from the creel database.

Month	Statistical District							
	MM1	MM2	MM3	MM4	MM5	MM6	MM7	MM8
March	0	0	0	0	0	0	0	35.4
April	4.9	0	0	71.2	28.1	405.8	1948.1	2443.1
May	3.3	0	1.5	167.8	846.9	9226.0	10699.8	9606.9
June	39.3	5.0	49.2	44.7	1408.7	4577.8	3498.4	2293.8
July	1308.8	583.2	937.4	698.1	5466.7	15502.0	9245.4	5026.4
August	842.6	231.3	1907.3	1736.2	10872.1	28159.9	10929.1	8463.9
September	183.6	466.7	887.3	1435.9	1929.5	7644.0	4697.2	2733.5
October	21.8	45.1	29.2	254.4	116.5	453.5	175.8	69.8
November	0	0	0	0	10.3	5.3	0	0

Table 5. Average boat harvest (in numbers) of chinook salmon (1985-2001) in the Indiana and Illinois waters of Lake Michigan by month from the creel database.

Month	Illinois	Indiana
March	1.2	14.0
April	280.3	1026.5
May	937.7	1340.6
June	702	499.0
July	1620.6	897.1
August	2342.9	878.1
September	1333.6	1866.3
October	0	235.7
November	0	5.0

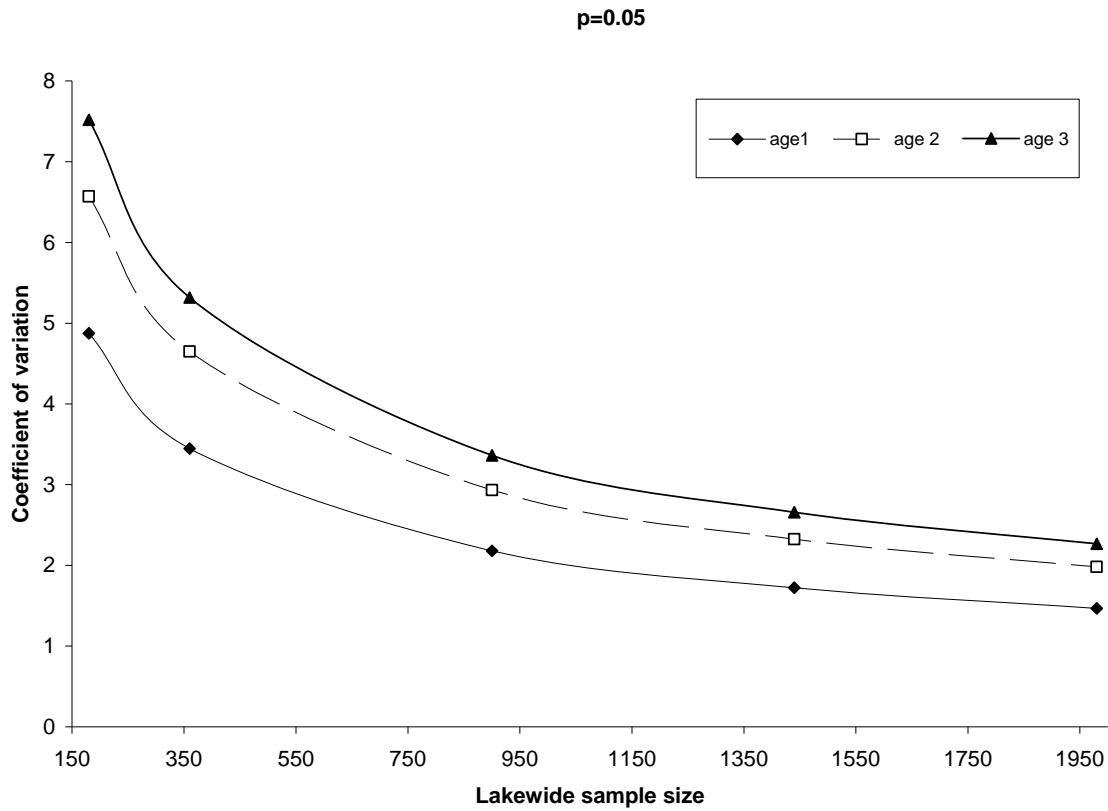


Figure 5a. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_1 and $p_w = 0.05$. The lake-wide sample size was divided evenly between each location, season and length class.

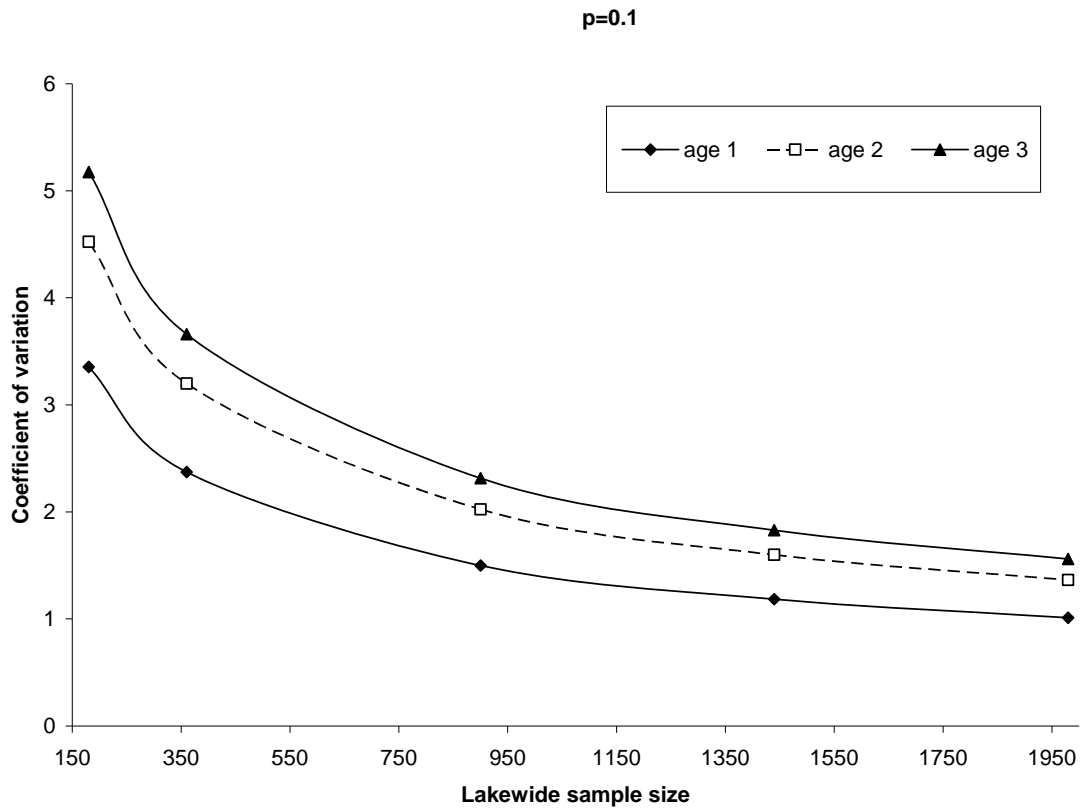


Figure 5b. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_1 and $p_w = 0.1$. The lake-wide sample size was divided evenly between each location, season and length class.

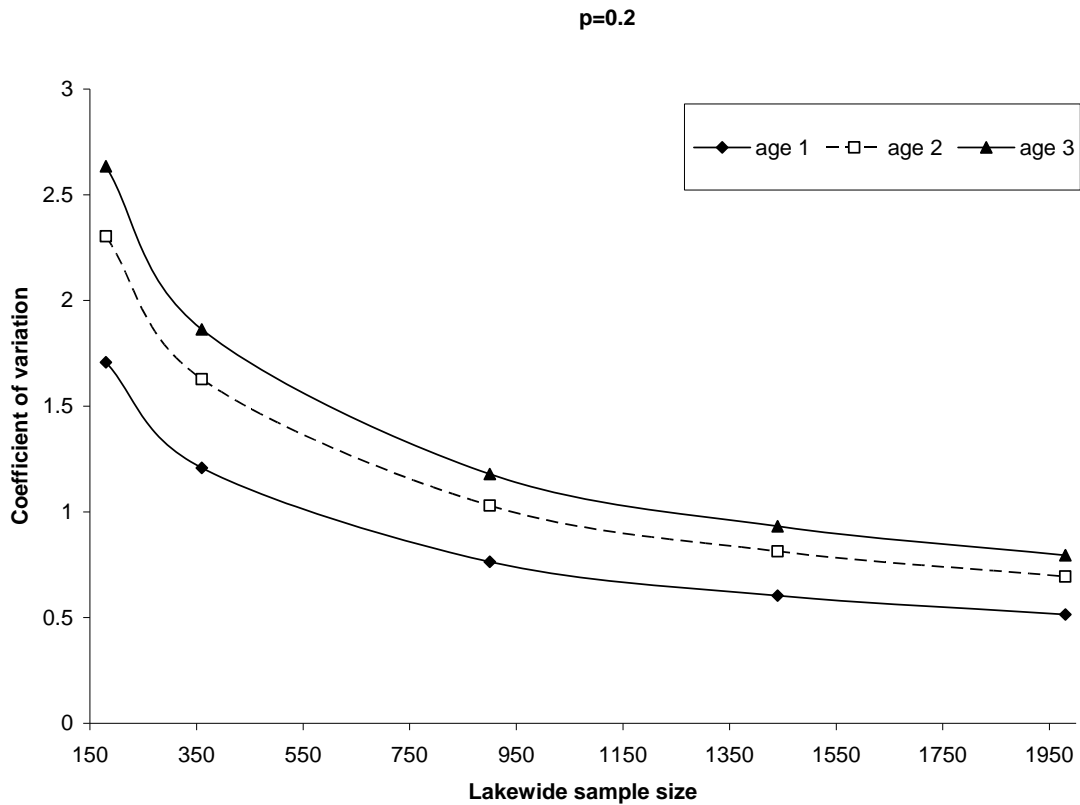


Figure 5c. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each loation in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_1 and $p_w = 0.2$. The lake-wide sample size was divided evenly between each location, season and length class.

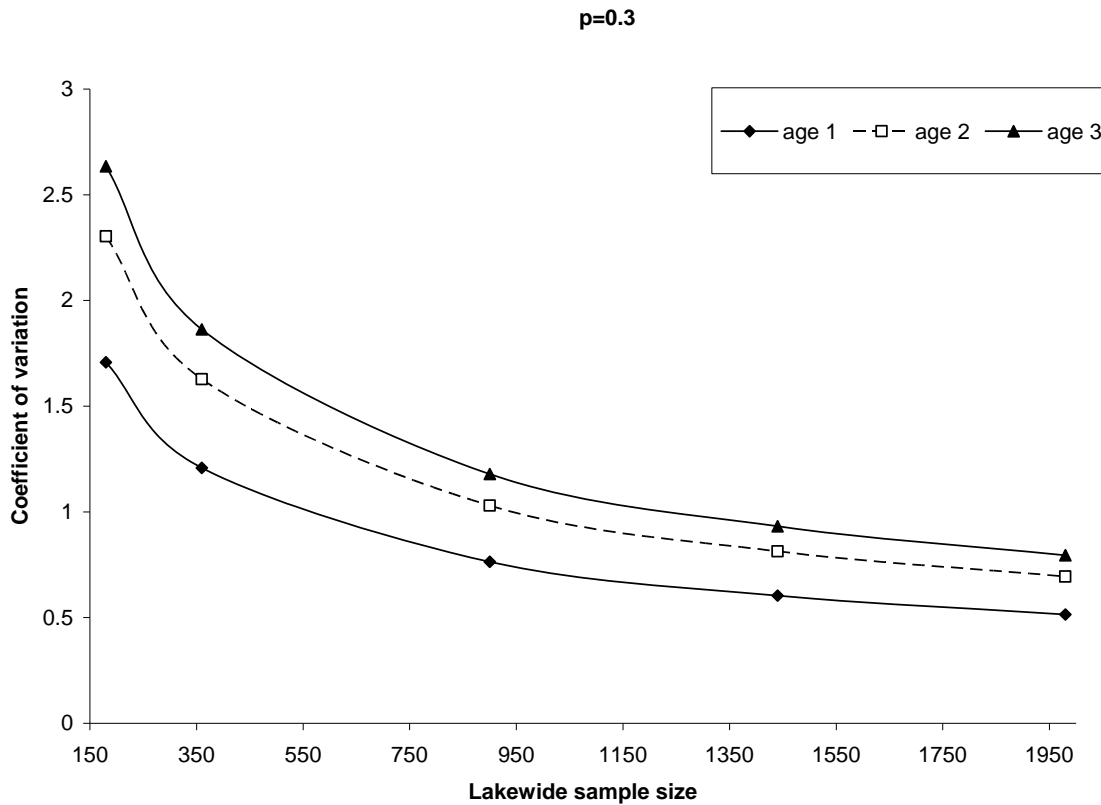


Figure 5d. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_1 and $p_w = 0.3$. The lake-wide sample size was divided evenly between each location, season and length class.

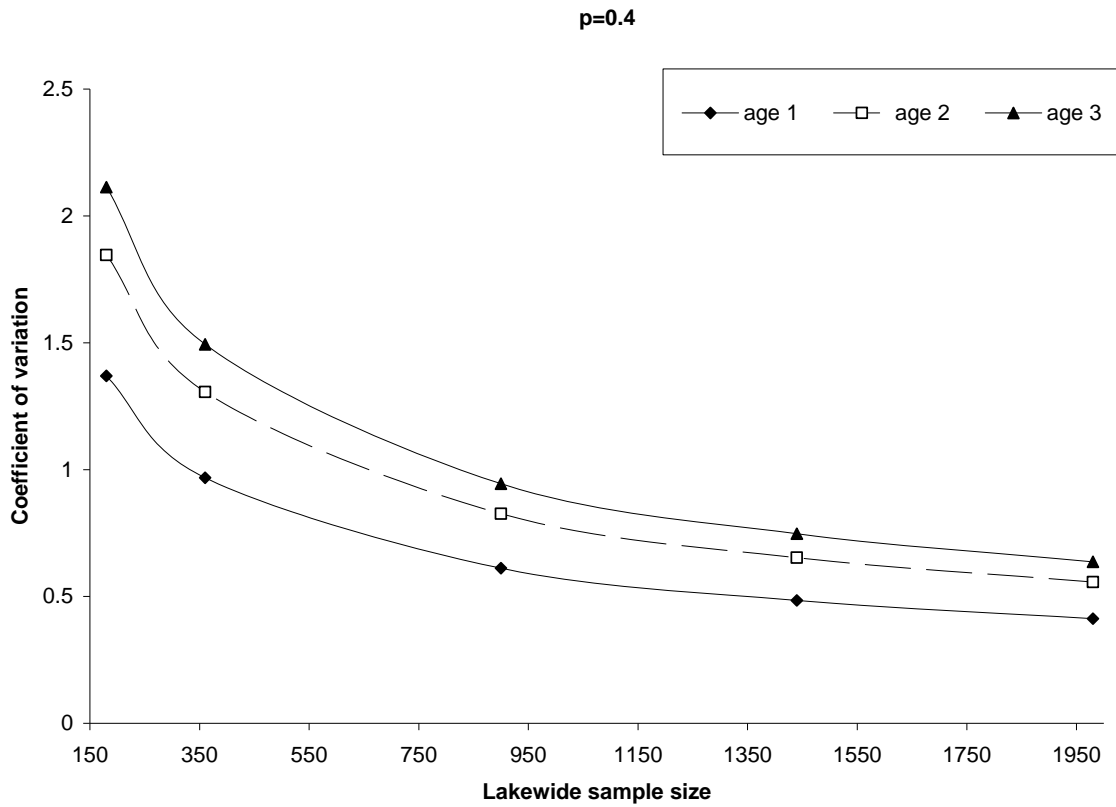


Figure 5e. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_1 and $p_w = 0.4$. The lake-wide sample size was divided evenly between each location, season and length class.

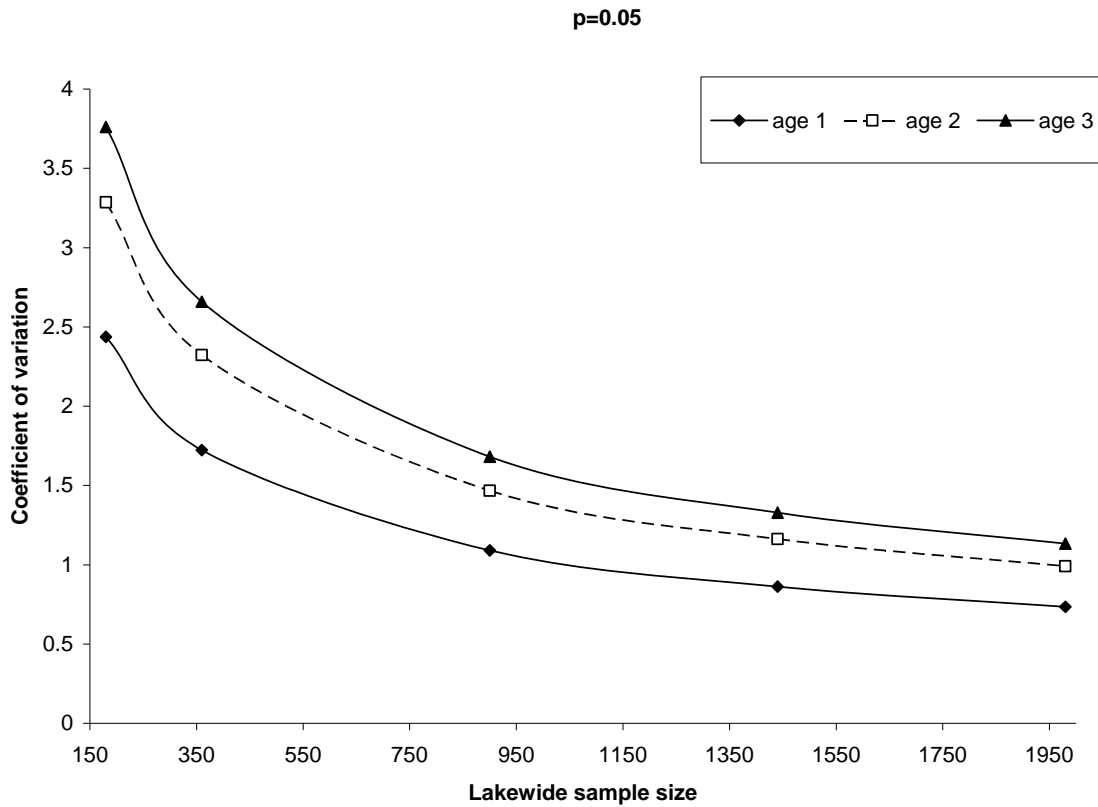


Figure 6a. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_2 and $p_w = 0.05$. The lake-wide sample size was divided evenly between each location, season and length class.

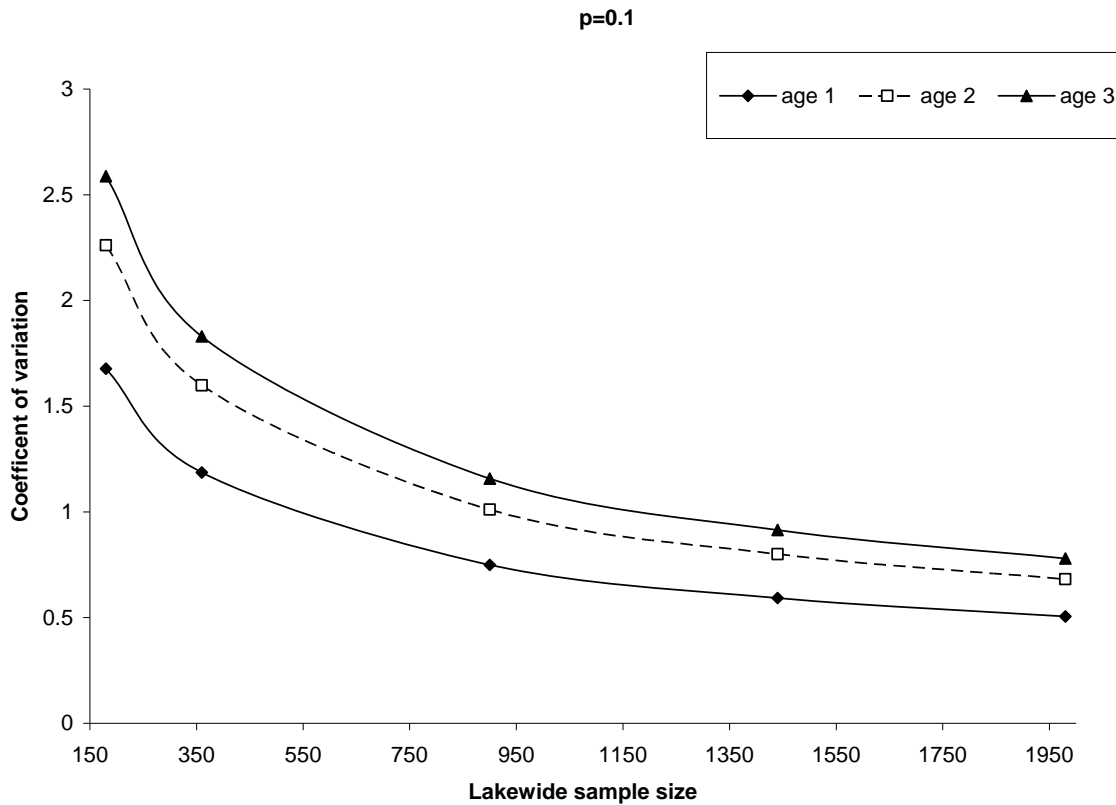


Figure 6b. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_2 and $p_w = 0.1$. The lake-wide sample size was divided evenly between each location, season and length class.

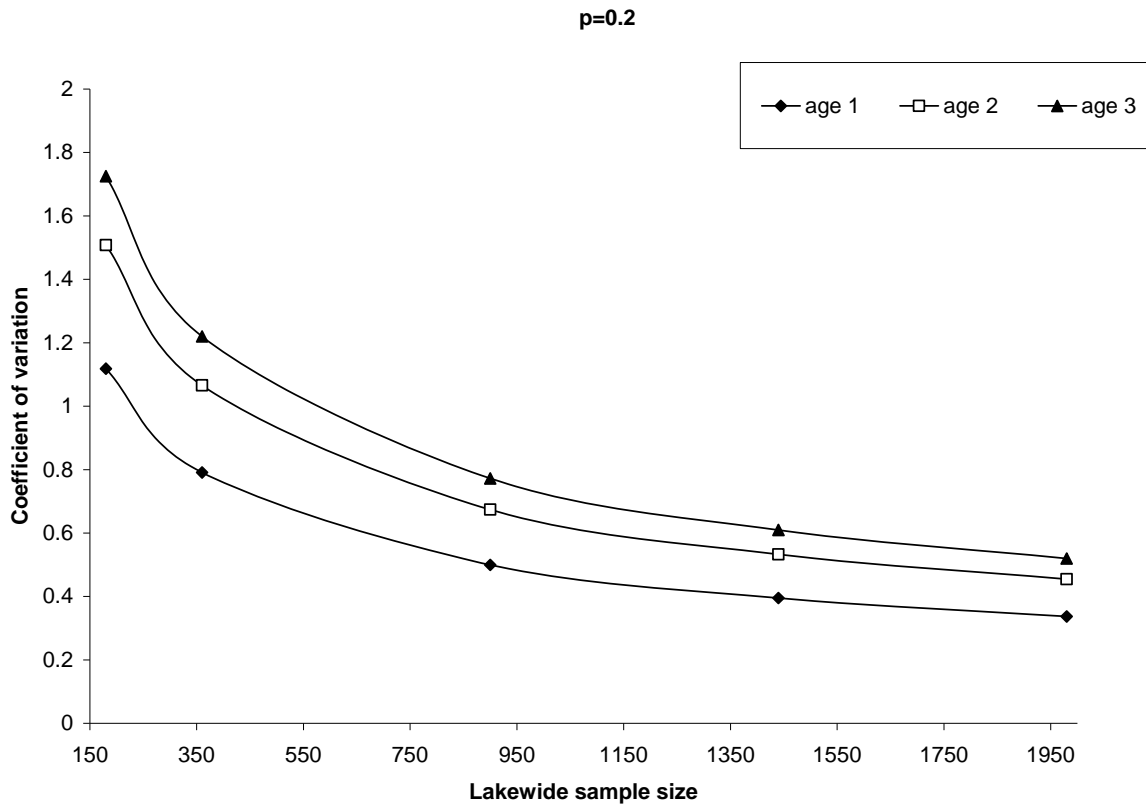


Figure 6c. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_2 and $p_w = 0.2$. The lake-wide sample size was divided evenly between each location, season and length class.

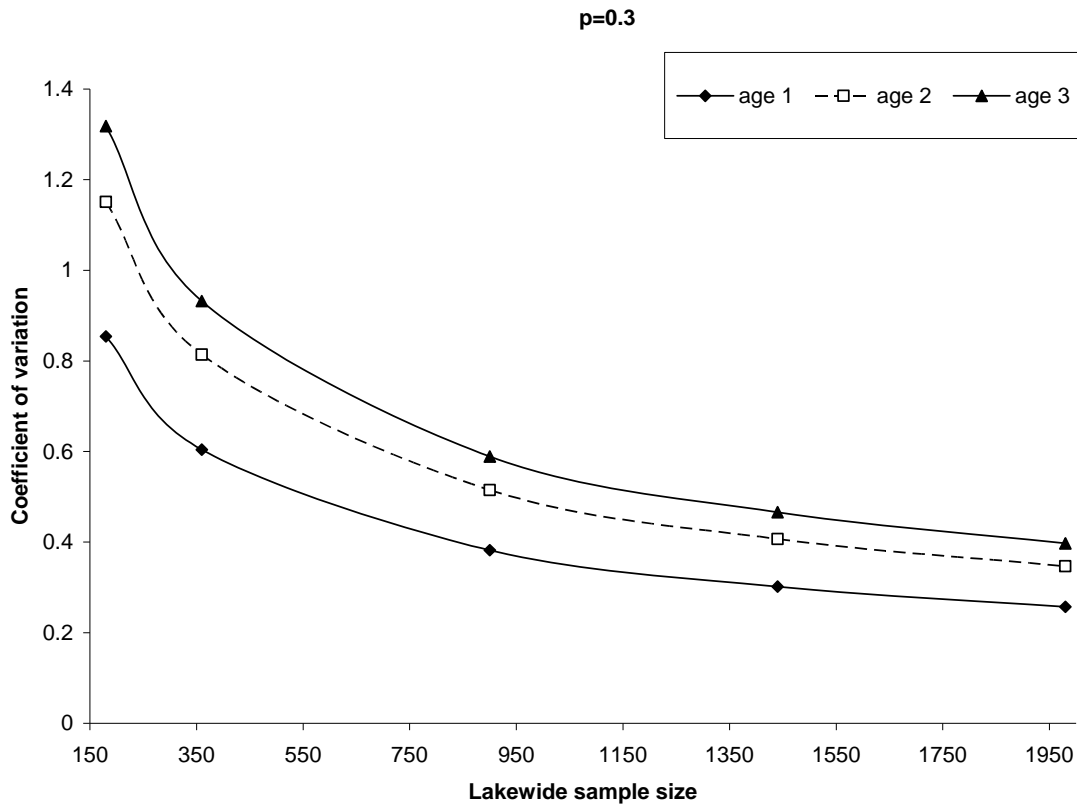


Figure 6d. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_2 and $p_w = 0.3$. The lake-wide sample size was divided evenly between each location, season and length class.

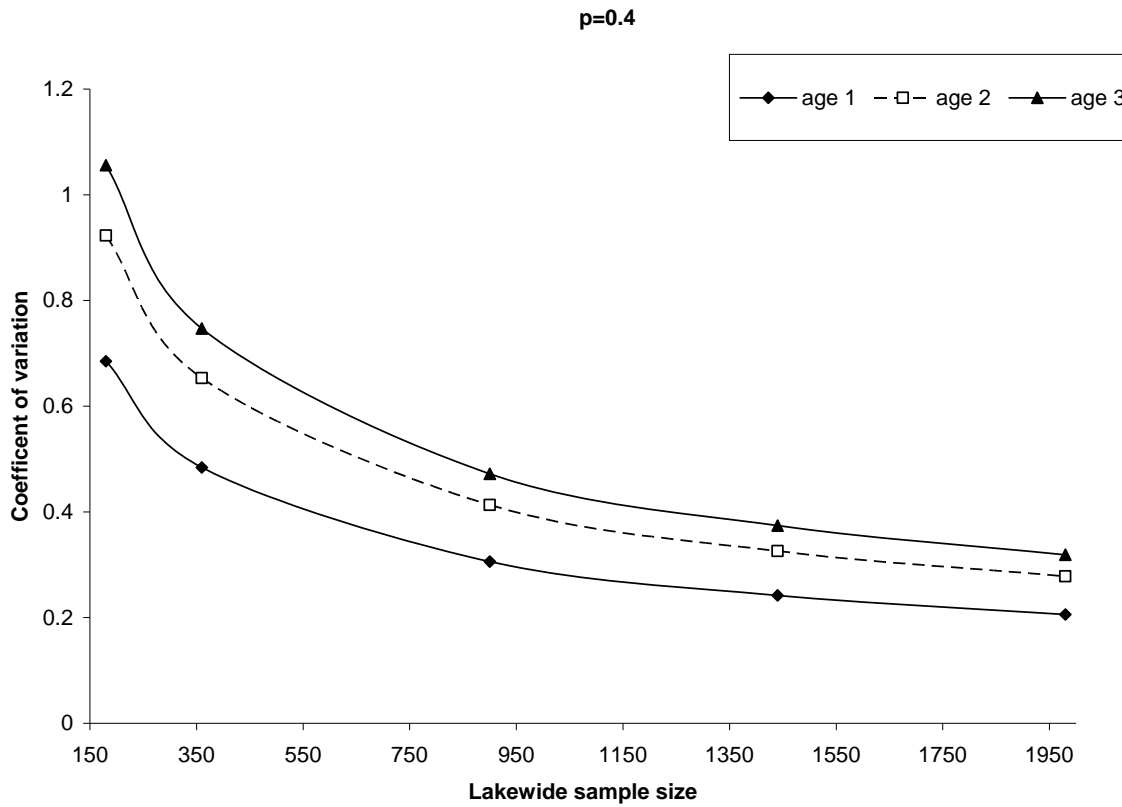


Figure 6e. Expected coefficient of variation for the estimated proportion wild at age in the harvest at each location in each season using stratified random sampling (location, season and length class) for ages 1-3 with the classification error matrix T_2 and $p_w = 0.4$. The lake-wide sample size was divided evenly between each location, season and length class.

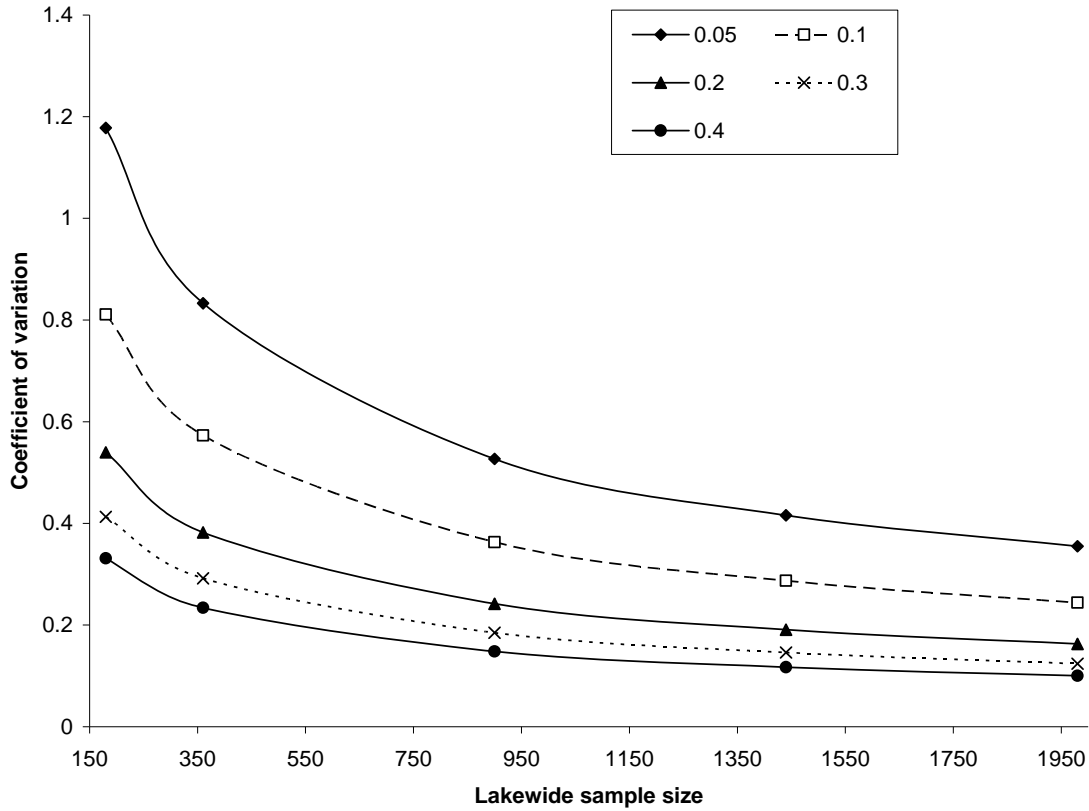


Figure 7a. Expected coefficient of variation of the estimate proportion wild in the harvest (averaged across locations, seasons and age class) for a variety of true proportions wild using stratified random sampling with the classification error matrix, T_1 . The lake-wide sample size was divided evenly between each location, season and length class.

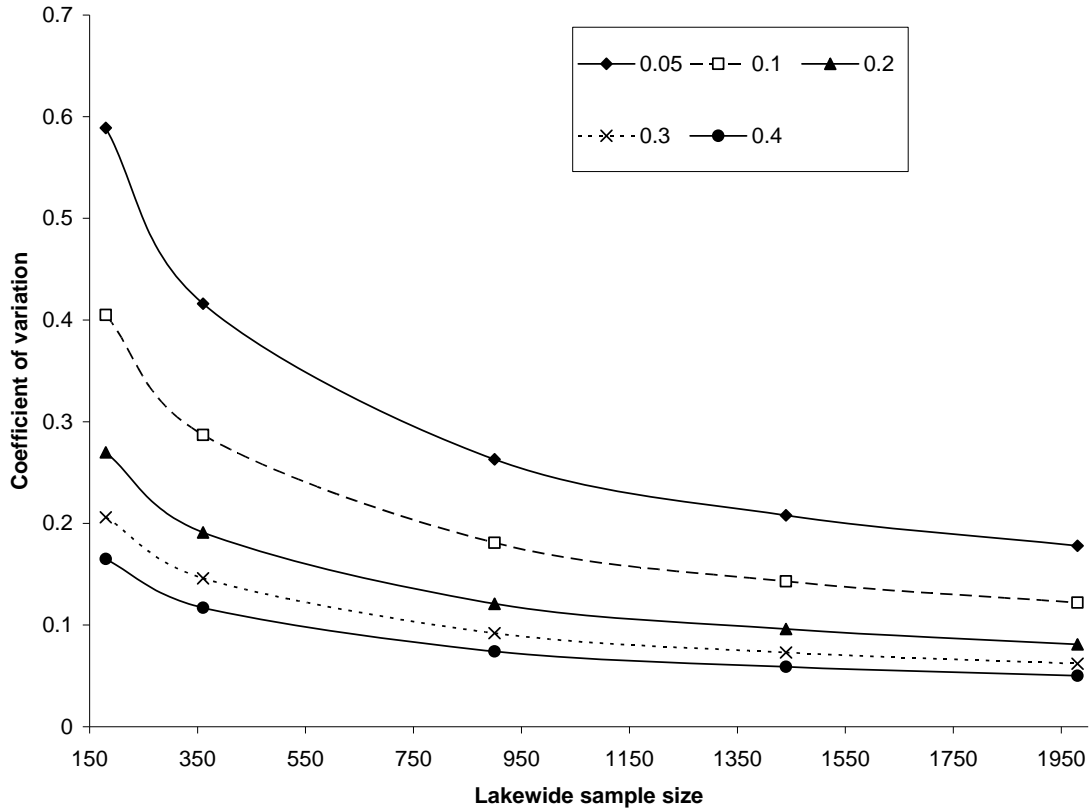


Figure 7b. Expected coefficient of variation of the estimate proportion wild in the harvest (averaged across locations, seasons and age class) for a variety of true proportions wild using stratified random sampling with the classification error matrix, T_2 . The lake-wide sample size was divided evenly between each location, season and length class.

Appendix A:

Lake Michigan Chinook Salmon OTC Marking Project: Guide to Sample Size Calculations Program (MarkN)

This program calculates the expected standard error and coefficient of variation for the estimated proportion wild (p) for a variety of sampling schemes and sample sizes. It also is capable of calculating the power for a test if the estimated p is significantly different then some specified constant. The program is run in SAS using the IML procedure.

There are three main sampling schemes implemented in this program. The first is a simple random sample of the population when it is well mixed. This type of sampling protocol allows for inference about the proportion of wild fish that are in the population. It does not provide information about the proportion wild at age or about the proportion wild in the harvest. In this sampling protocol, the program calculates the expected standard error and coefficient of variation for the estimated proportion wild in the populations for a variety of sample sizes. In order to be able to make these calculations, the true proportion wild in the population must be specified. The user can change both the sample sizes and true proportions wild used in these calculations. To change the sample sizes, the user simply changes the values in *samplesizes* (Line 7). The user can specify as many sample sizes as they desire and the numbers must be separated by commas when entered. The user can also change the values of the true proportion wild in the population. This can be done by simply changing the values in *truep* (Line 5). Again, the user can specify as many proportions as desired. The values entered must be greater than zero and less than one and should be separated by commas. This program also calculates the power of the statistical test with $\alpha=0.05$:

$$H_0 : p = p_{test}$$

$$H_A : p \neq p_{test}$$

where p is the proportion wild in the population and p_{test} is a specified constant. The user can change the value of p_{test} used by changing the value of *testp* (Line 10). The output of the

program for this sampling protocol includes a matrix of standard deviations, coefficients of variation and power for the specified sample sizes (in rows) and true proportions (in columns).

The second sampling protocol implemented in the program uses a stratified random sample by length class of chinook salmon. It is assumed that the samples are taken randomly within the length classes at a time when the population is well mixed. This sampling protocol provides estimates of proportion wild in the population by age, along with estimates of the proportion wild in the total population. It does not provide any inferences on the proportion wild in the harvest. The program uses two of the three length classes defined in the diet protocol (38-57 cm, and greater than 58 cm in total length). The user specifies the sample size for each length class in the matrix *samplesize_lthclass* (Line 38). The matrix has 2 rows each one corresponding to a length class. The number of columns can be changed by the user to test any number of sample sizes. An example matrix is shown below.

```
{100 200 500 1000,  
 100 200 500 1000}
```

In this matrix, the first column represents a sampling protocol where 100 chinook are sampled from each length class. When the values are entered in the matrix, the numbers within each row are separated by spaces and the rows are separated by commas. The program assumes that the true proportion wild is the same for each age class. The values for the true proportion wild in the population are adjusted as before (on Line 5) as is constant for the hypothesis testing (on Line 10). The sample sizes within each length class are then converted to sample sizes for each age class (ages 1 - 4) by applying an inverse age length key (size distribution at age). The inverse age length key can be altered by the user by changing *agelengthkey* on Lines 44-47. In order to calculate the standard deviations, coefficients of variation and power for the proportion wild in the total population, the user must specify the age composition of the population. These values can be changes on Line 49, *propatage_pop*.

The program then outputs matrices of the standard deviations, coefficients of variation and powers for the proportion wild at age for each true proportion wild specified by the user.

The rows represent each age class and the columns the total sample sizes (summed across length classes). It also outputs the matrices of the standard deviations, coefficients of variation and powers for the proportion wild in the population. The rows represent the different values of true proportion wild specified and the columns the total sample sizes.

The final sampling protocol allows for inference on the proportion of wild fish in the harvest rather than the population. For this reason, the sampling is stratified by location, season and length class. The number of locations and seasons can be specified by the user by changing the values of *num_loc* (Line 102) and *num_seasons* (Line 103). The user can specify the true proportion wild in the harvest by changing *truep_har* (Line 98). The sample in each location and season is again stratified by length class, however since age-0 chinook are not caught in the harvest, there are only 2 potential length classes. The sample size per length class is entered similarly to above in *samplesize_lthclass_har* (Lines 104-105). Again, the user can change the inverse age length key for the harvest by changing *agelengthkey_har* (Lines 107-110). The model currently assumes that the inverse age length key and proportion wild for the harvest is the same for all seasons and locations. In order to calculate the proportion wild in each season at each location, the user needs to specify the proportion at age in the harvest. This is currently assumed to be constant across locations and seasons and can be changed by changing *propatage_har* (Line 120). To calculate the proportion wild at each location across all seasons, the user can specify the proportion of the harvest caught in each season. It can currently be different in each location and can be changed by the user by changing *propharbyseason* (Lines 122-127). Each row represents a location. To calculate the proportion wild in the harvest across all locations, the user needs to specify the proportion of harvest that occurs in each locations. These values are specified by the user in Line 129, *propharbyloc*.

The program first outputs the standard deviations, coefficients of variation, and power for the proportion wild at age in each season and location for each true proportion wild in the harvest specified by the user. The results are output as a matrix (for each *p*) with the rows representing age classes and the columns the total sample size for each location in each season

(again summed across length classes). Next, the standard deviations, coefficients of variation, and powers for the proportion wild in the harvest for each location and season is displayed as a matrix with the rows representing the true proportion in the harvest and the columns total sample size in each location and season. Then, the standard deviations, coefficients of variation, and powers for the proportion wild in the harvest for each location across all seasons is displayed as a matrix with the rows representing the true proportion in the harvest and the columns total sample size in each location and season. Finally, the standard deviations, coefficients of variation, and powers for the proportion wild in the harvest across all locations and seasons is displayed as a matrix with the rows representing the true proportion in the harvest and the columns total sample size in each location and season.

The final section of the program evaluates the effects of misclassification on the estimate of p and its variability. The user can specify the misclassification rates of wild and stock fish on lines 227-228 in the matrix T. Again, the elements in each row should be separated by spaces and commas should separate each row. The error rates are entered into the matrix as follows:

T={classification rate of wild fish as unmarked classification rate of wild fish as marked,
classification rate stocked fish as unmarked classification rate of stocked fish as marked }

The program then uses this classification matrix to determine the expected estimate of the proportion wild in the population if misclassification is ignored. It also computes the expected standard deviation, coefficient of variation, and power for the hypothesis test for the cases where misclassification is ignored. It also calculates the same statistics for the case where the estimates are corrected for the misclassification rates, assuming that the misclassification rates are known.

```

1  proc iml; /* Appendix B. MarkN SAS program */
2  *random sampling not stratified by length class or area;
3  * Assuming all unmarked fish are wild;
4  truep={0.05,0.1,0.2,0.3,0.4};
5  trueq =1-truep;
6  samplesizes={250,500,750,1000,1500,2000};
7  sample=char(samplesizes);
8  pval=char(truep);
9  testp=0.3;
10 location=truep-testp;
11 n=nrow(samplesizes);
12 p=nrow(truep);
13 var=truep#trueq;
14 cv=j(n,p,1);
15 sd=j(n,p,1);
16 power=j(n,p,1);
17 cutoff=j(n,p,1);
18 do i=1 to n by 1;
19     do j=1 to p by 1;
20         sd[i,j]=sqrt((var[j]/samplesizes[i]));
21         cv[i,j]=sd[i,j]/truep[j];
22         cutoff[i,j]=1.96*sd[i,j];
23         power[i,j]=1-
24 cdf('Normal',cutoff[i,j],location[j],sd[i,j])+cdf('Normal', -
25 cutoff[i,j],location[j],sd[i,j]);
26     end;
27 end;
28 print "Random sampling P wild in pop";
29 print "Standard Deviation of estimated proportion wild (Sample Size X true
30 p)";
31 print sd [rowname=sample][colname=pval];
32 print "CV of estimated proportion wild (Sample Size X true p)";
33 print cv [rowname=sample][colname=pval];
34 print "Power of z test of true p vs " testp "(Sample Size X true p)";
35 print power [rowname=sample][colname=pval];
36 *adding in stratification into two length classes 38-57 cm (age1), and >58 cm
37 (age 2+);
38 samplesize_lthclass={125 250 500 750 1000,
39                      125 250 500 750 1000};
40 ageclasses={1,2,3,4};
41 totsamplesize={1 1}*samplesize_lthclass;
42 totsample=char(totsamplesize);
43 age=char(ageclasses);
44 agelengthkey = { 1 0,
45                  0 0.55,
46                  0 0.42,
47                  0 0.03};
48 samplebyage=agelengthkey*samplesize_lthclass;
49 propatage_pop={0.43 0.31 0.22 0.04};
50 print "Stratifying sample by lth class";
51 print "Sample Size by age class (Age class by Total Sample Size)";
52 print samplebyage [rowname=age][colname=totsample];
53 m=ncol(samplesize_lthclass);
54 o=nrow(agelengthkey);
55 cv=j(o,m,1);
56 sd=j(o,m,1);
57 power=j(o,m,1);
58 power_pop=j(p,m,1);
59 cutoff_pop=j(p,m,1);
60 cutoff=j(o,m,1);

```

```

61 pop_sd=j(p,m,1);
62 pop_cv=j(p,m,1);
63 print "SD,CV, Power (Age class x Total Sample Size) for p at age in population
64 for each true proportion wild in population
65 Testing versus p=" testp;
66 do k=1 to p by 1;
67   do i=1 to m by 1;
68     do j=1 to o by 1;
69       sd[j,i]=sqrt((var[k]/samplebyage[j,i]));
70       cv[j,i]=sd[j,i]/truep[k];
71       cutoff[j,i]=1.96*sd[j,i];
72       power[j,i]=1-
73 cdf('Normal',cutoff[j,i],location[k],sd[j,i])+cdf('Normal', -
74 cutoff[j,i],location[k],sd[j,i]);
75     end;
76   end;
77   pnow=truep[k];
78   print "True p" pnow ;
79   print sd [rowname=age][colname=totsample];
80   print cv [rowname=age][colname=totsample];
81   print power [rowname=age][colname=totsample];
82   pop_sd[k,]=sqrt((propatage_pop##2*sd##2));
83   pop_cv[k,]=pop_sd[k,]/truep[k];
84   do i=1 to m by 1;
85     cutoff_pop[k,i]=1.96*pop_sd[k,i];
86     power_pop[k,i]=1-
87 cdf('Normal',cutoff_pop[k,i],location[k],pop_sd[k,i])+cdf('Normal', -
88 cutoff_pop[k,i],location[k],pop_sd[k,i]);
89   end;
90 end;
91 print " SD, CV and Power (True p X Total Sample size) for total pop p wild
92   Testing versus p=" testp;
93 print pop_sd [rowname=pval] [colname=totsample];
94 print pop_cv [rowname=pval] [colname=totsample];
95 print power_pop [rowname=pval] [colname=totsample];
96 /*now calc. prop wild in harvest, stratifying by season,location,
97 and length class (only 2 - don't catch age 0)*/
98 truep_har={0.05,0.1,0.2,0.3,0.4};
99 pval_har=char(truep_har);
100 trueq_har =1-truep_har;
101 var_har=truep_har#trueq_har;
102 num_loc=6;
103 num_seasons=3;
104 samplesize_lthclass_har={5 10 25 40 55,
105                           5 10 25 40 55}; *this is sample size at by lth
106 class for each location in each season;
107 agelengthkey_har={1 0,
108                   0 0.55,
109                   0 0.42,
110                   0 0.03}; *assuming same for each location;
111 ageclass_har={1,2,3,4};
112 age_har=char(ageclass_har);
113 totsamplesize_har={1 1}*samplesize_lthclass_har;
114 totsample_har=char(totsamplesize_har);
115 samplebyage_har=agelengthkey_har*samplesize_lthclass_har;
116 print "Stratifying sample by season, location and lth class for harvest p";
117 print "Sample size by age (Age class x Total sample size) at each location in
118 each season";
119 print samplebyage_har [rowname=age_har] [colname=totsample_har];
120 propatage_har={0.25 0.39 0.31 0.05}; *assuming same age comp of harvest over
121 seasons and locations;

```

```

122  propharbyseason={0.25 0.5 0.25,
123                    0.25 0.5 0.25,
124                    0.25 0.5 0.25,
125                    0.25 0.5 0.25,
126                    0.25 0.5 0.25,
127                    0.25 0.5 0.25}; *prop of harvest in each location
128  by season;
129  propharbyloc={0.02 0.33 0.17 0.27 0.16 0.05}; * prop of harvest across all
130  seasons in each location(N NE NW SE SW IN/IL);
131  m=ncol(samplesize_lthclass_har);
132  o=nrow(agelengthkey_har);
133  p=nrow(truep_har);
134  cv=j(o,m,1);
135  sd=j(o,m,1);
136  power=j(o,m,1);
137  cutoff=j(o,m,1);
138  cutoff_harsl=j(p,m,1);
139  power_harsl=j(p,m,1);
140  harsl_sd=j(p,m,1);
141  harsl_cv=j(p,m,1);
142  harl_sd=j(p,m,0);
143  harl_cv=j(p,m,1);
144  wsum2=j(p,m,0);
145  har_sd=j(p,m,0);
146  har_cv=j(p,m,1);
147  power_harl=j(p,m,2);
148  cutoff_harl=j(p,m,4);
149  cutoff_har=j(p,m,4);
150  power_har=j(p,m,2);
151  location_har=truep_har-testp;
152  print "SD, CV, and Power (Age class x Total sample size) for p at age",;
153  print "for each true p in harvest-same across all locations and seasons",;
154  print "Testing versus p=" testp;
155  do k=1 to p by 1;
156    do i=1 to m by 1;
157      do j=1 to o by 1;
158        sd[j,i]=sqrt((var_har[k]/samplebyage_har[j,i]));
159        cv[j,i]=sd[j,i]/truep_har[k];
160        cutoff[j,i]=1.96*sd[j,i];
161        power[j,i]=1-
162  cdf('Normal',cutoff[j,i],location[k],sd[j,i])+cdf('Normal', -
163  cutoff[j,i],location[k],sd[j,i]);
164      end;
165    end;
166    pnow=truep_har[k];
167    print "True p" pnow ;
168    print sd [rowname=age_har] [colname=totsample_har];
169    print cv [rowname=age_har] [colname=totsample_har];
170    print power [rowname=age_har] [colname=totsample_har];
171    harsl_sd[k,]=sqrt((propatage_har##2*sd##2));
172    harsl_cv[k,]=harsl_sd[k,]/truep_har[k];
173    do i=1 to m by 1;
174      cutoff_harsl[k,i]=1.96*harsl_sd[k,i];
175      power_harsl[k,i]=1-
176  cdf('Normal',cutoff_harsl[k,i],location_har[k],harsl_sd[k,i])+cdf('Normal', -
177  cutoff_harsl[k,i],location_har[k],harsl_sd[k,i]);
178    end;
179  end;
180  print "SD, CV, Power (True p x Total sample size) of p wild in harvest",;
181  print "for each season and location - same across all locations and seasons",;
182  print "Testing versus p=" testp;

```

```

183 print harsl_sd [rowname=pval_har] [colname=totsample_har];
184 print harsl_cv [rowname=pval_har] [colname=totsample_har];
185 print power_harsl [rowname=pval_har] [colname=totsample_har];
186 print "SD, CV, Power (True p x Total sample size) of p wild in harvest",;
187 print "by location across seasons",;
188 print "Testing versus p=" testp;
189 do k=1 to num_loc by 1;
190     wsum=j(p,m,0);
191     do l=1 to num_seasons by 1;
192         wsum=wsum+(propharbyseason[k,l]##2*harsl_sd##2);
193     end;
194     harl_sd=sqrt(wsum);
195     do i = 1 to p by 1;
196         harl_cv[i,]=harl_sd[i,]/truep_har[i];
197         do j=1 to m by 1;
198             cutoff_harl[i,j]=1.96*harl_sd[i,j];
199             power_harl[i,j]=1-
200 cdf('Normal',cutoff_harl[i,j],location_har[i],harl_sd[i,j])+cdf('Normal', -
201 cutoff_harl[i,j],location_har[i],harl_sd[i,j]);
202         end;
203     end;
204     print "Location" k;
205     print harl_sd [rowname=pval_har] [colname=totsample_har];
206     print harl_cv [rowname=pval_har] [colname=totsample_har];
207     print power_harl [rowname=pval_har] [colname=totsample_har];
208     wsum2=wsum+(propharbyloc[k]##2*harl_sd##2);
209 end;
210 har_sd=sqrt(wsum2);
211 do i=1 to p by 1;
212     har_cv[i,]=har_sd[i,]/truep_har[i];
213     do j=1 to m by 1;
214         cutoff_har[i,j]=1.96*har_sd[i,j];
215         power_har[i,j]=1-
216 cdf('Normal',cutoff_har[i,j],location_har[i],har_sd[i,j])+cdf('Normal', -
217 cutoff_har[i,j],location_har[i],har_sd[i,j]);
218     end;
219 end;
220 print " SD, CV, Power (True p x Total Sample Size) for p wild in harvest",;
221 print "across all locations",;
222 print "Testing versus p=" testp;
223 print har_sd [rowname=pval_har] [colname=totsample_har];
224 print har_cv [rowname=pval_har] [colname=totsample_har];
225 print power_har [rowname=pval_har] [colname=totsample_har];
226 * Now incorporating marking error (not all unmarked fish are wild);
227 T={0.9 0.1,
228     0.1 0.9}; *this is the marking error matrix;
229 * Simple Random sampling;
230 true_pop=j(p,2,1);
231 true_pop[,1] = truep;
232 true_pop[,2]=trueq;
233 prop_marked=t(T*t(true_pop));
234 marked={'Unmarked', 'Marked'};
235 Tinv=inv(T);
236 print "Random sampling P wild in pop with marking error";
237 print "Estimate proportion stocked and wild in population";
238 print " for each true p without correcting for marking error";
239 print prop_marked[rowname=pval][colname=marked];
240 location=prop_marked[,1]-testp;
241 location_corrected=truep-testp;
242 n=nrow(samplesizes);
243 p=nrow(truep);

```

```

244 var=prop_marked[,1]#prop_marked[,2];
245 cv=j(n,p,1);
246 cv_corrected=j(n,p,1);
247 sd=j(n,p,1);
248 sd_corrected=j(n,p,1);
249 power=j(n,p,1);
250 power_corrected=j(n,p,1);
251 cutoff=j(n,p,1);
252 cutoff_corrected=j(n,p,1);
253 do i=1 to n by 1;
254     do j=1 to p by 1;
255         sd[i,j]=sqrt((var[j]/samplesizes[i]));
256
257 sd_corrected[i,j]=sqrt(Tinv[1,1]**2*sd[i,j]**2+Tinv[1,2]**2*sd[i,j]**2-
258 2*Tinv[1,1]*Tinv[1,2]*sd[i,j]**2);
259     cv[i,j]=sd[i,j]/prop_marked[j,2];
260     cv_corrected[i,j]=sd_corrected[i,j]/truep[j];
261     cutoff[i,j]=1.96*sd[i,j];
262     cutoff_corrected[i,j]=1.96*sd_corrected[i,j];
263     power[i,j]=1-
264 cdf('Normal',cutoff[i,j],location[j],sd[i,j])+cdf('Normal', -
265 cutoff[i,j],location[j],sd[i,j]);
266     power_corrected[i,j]=1-
267 cdf('Normal',cutoff_corrected[i,j],location_corrected[j],sd_corrected[i,j])+cd
268 f('Normal', -cutoff_corrected[i,j],location_corrected[j],sd_corrected[i,j]);
269     end;
270 end;
271 print "Standard Deviation of estimated proportion wild (Sample Size X true
272 p)";
273 print "Not corrected for marking error";
274 print sd [rowname=sample][colname=pval];
275 print " Corrected for marking error";
276 print sd_corrected [rowname=sample][colname=pval];
277 print "CV of estimated proportion wild (Sample Size X true p)";
278 print "Not corrected for marking error";
279 print cv [rowname=sample][colname=pval];
280 print " Corrected for marking error";
281 print cv_corrected[rowname=sample][colname=pval];
282 print "Power of z test of true p vs " testp "(Sample Size X true p)";
283 print "Not corrected for marking error";
284 print power [rowname=sample][colname=pval];
285 print " Corrected for marking error";
286 print power_corrected [rowname=sample][colname=pval];
287 * Now adding in stratification by length class;
288 print "Stratifying sample by lth class with marking error";
289 m=ncol(samplesize_lthclass);
290 o=nrow(agelengthkey);
291 cv=j(o,m,1);
292 cv_corrected=j(o,m,1);
293 sd=j(o,m,1);
294 sd_corrected=j(o,m,1);
295 power=j(o,m,1);
296 power_corrected=j(o,m,1);
297 power_pop=j(p,m,1);
298 power_pop_corrected=j(p,m,1);
299 cutoff_pop=j(p,m,1);
300 cutoff_pop_corrected=j(p,m,1);
301 cutoff=j(o,m,1);
302 cutoff_corrected=j(o,m,1);
303 pop_sd=j(p,m,1);
304 pop_sd_corrected=j(p,m,1);

```

```

305 pop_cv=j(p,m,1);
306 pop_cv_corrected=j(p,m,1);
307 print "SD,CV, Power (Age class x Total Sample Size) for p at age in population
308 for each true proportion wild in population
309 Testing versus p=" testp;
310 do k=1 to p by 1;
311   do i=1 to m by 1;
312     do j=1 to o by 1;
313       sd[j,i]=sqrt((var[k]/samplebyage[j,i]));
314       sd_corrected[j,i]=sqrt(sd[j,i]**2*Tinv[1,2]**2
315 +sd[j,i]**2*Tinv[1,1]**2-2*Tinv[1,1]*Tinv[1,2]*sd[j,i]**2);
316       cv[j,i]=sd[j,i]/prop_marked[k,2];
317       cv_corrected[j,i]=sd_corrected[j,i]/truep[k];
318       cutoff[j,i]=1.96*sd[j,i];
319       cutoff_corrected[j,i]=1.96*sd_corrected[j,i];
320       power[j,i]=1-
321 cdf('Normal',cutoff[j,i],location[k],sd[j,i])+cdf('Normal', -
322 cutoff[j,i],location[k],sd[j,i]);
323       power_corrected[j,i]=1-
324 cdf('Normal',cutoff_corrected[j,i],location_corrected[k],sd_corrected[j,i])+cd
325 f('Normal', -cutoff_corrected[j,i],location_corrected[k],sd_corrected[j,i]);
326     end;
327   end;
328   pnow=truep[k];
329   print "True p" pnow ;
330   print "Uncorrected for marking error";
331   print sd [rowname=age][colname=totsample];
332   print "Corrected for marking error";
333   print sd_corrected [rowname=age][colname=totsample];
334   print "Uncorrected for marking error";
335   print cv [rowname=age][colname=totsample];
336   print "Corrected for marking error";
337   print cv_corrected [rowname=age][colname=totsample];
338   print "Uncorrected for marking error";
339   print power [rowname=age][colname=totsample];
340   print "Corrected for marking error";
341   print power_corrected[rowname=age][colname=totsample];
342   pop_sd[k,]=sqrt((propatage_pop##2*sd##2));
343   pop_sd_corrected[k,]=sqrt((propatage_pop##2*sd_corrected##2));
344   pop_cv[k,]=pop_sd[k,]/prop_marked[k,2];
345   pop_cv_corrected[k,]=pop_sd_corrected[k,]/truep[k];
346   do i=1 to m by 1;
347     cutoff_pop[k,i]=1.96*pop_sd[k,i];
348     cutoff_pop_corrected[k,i]=1.96*pop_sd_corrected[k,i];
349     power_pop[k,i]=1-
350 cdf('Normal',cutoff_pop[k,i],location[k],pop_sd[k,i])+cdf('Normal', -
351 cutoff_pop[k,i],location[k],pop_sd[k,i]);
352     power_pop_corrected[k,i]=1-
353 cdf('Normal',cutoff_pop_corrected[k,i],location_corrected[k],pop_sd_corrected[
354 k,i])+cdf('Normal', -
355 cutoff_pop_corrected[k,i],location_corrected[k],pop_sd_corrected[k,i]);
356   end;
357 end;
358 print " SD, CV and Power (True p X Total Sample size) for total pop p wild
359 Testing versus p=" testp;
360 print "Uncorrected for marking error";
361 print pop_sd [rowname=pval] [colname=totsample];
362 print " Corrected for marking error";
363 print pop_sd_corrected [rowname=pval] [colname=totsample];
364 print "Uncorrected for marking error";
365 print pop_cv [rowname=pval] [colname=totsample];

```

```

366 print " Corrected for marking error";
367 print pop_cv_corrected [rowname=pval] [colname=totsample];
368 print "Uncorrected for marking error";
369 print power_pop [rowname=pval] [colname=totsample];
370 print " Corrected for marking error";
371 print power_pop_corrected [rowname=pval] [colname=totsample];
372 /*now calc. prop wild in harvest, stratifying by season,location,
373 and length class (only 2 - don't catch age 0)*/
374 print "Stratifying sample by season, location and lth class for harvest p";
375 print "with marking error ";
376 true_har=j(p,2,1);
377 true_har[,1] = truep_har;
378 true_har[,2]=trueq_har;
379 prop_marked_har=t(T*t(true_har));
380 est_har=t(Tinv*t(prop_marked_har));
381 marked={'Unmarked', 'Marked'};
382 print "Estimate proportion stocked and wild in harvest";
383 print " for each true p without correcting for marking error";
384 print prop_marked_har[rowname=pval][colname=marked];
385 m=ncol(samplesize_lthclass_har);
386 o=nrow(agelengthkey_har);
387 p=nrow(truep_har);
388 cv=j(o,m,1);
389 cv_corrected=j(o,m,1);
390 sd=j(o,m,1);
391 sd_corrected=j(o,m,1);
392 power=j(o,m,1);
393 power_corrected=j(o,m,1);
394 cutoff=j(o,m,1);
395 cutoff_corrected=j(o,m,1);
396 cutoff_harsl=j(p,m,1);
397 cutoff_harsl_corrected=j(p,m,1);
398 power_harsl=j(p,m,1);
399 harsl_sd=j(p,m,0);
400 harsl_cv=j(p,m,1);
401 harl_sd=j(p,m,0);
402 harl_cv=j(p,m,1);
403 power_harsl_corrected=j(p,m,1);
404 harsl_sd_corrected=j(p,m,0);
405 harsl_cv_corrected=j(p,m,1);
406 harl_sd_corrected=j(p,m,0);
407 harl_cv_corrected=j(p,m,1);
408 har_sd=j(p,m,0);
409 har_cv=j(p,m,1);
410 wsum2=j(p,m,0);
411 wsum2_corrected=j(p,m,0);
412 power_harl=j(p,m,2);
413 cutoff_harl=j(p,m,4);
414 cutoff_har=j(p,m,4);
415 power_har=j(p,m,2);
416 location_har=prop_marked_har[,2]-testp;
417 har_sd_corrected=j(p,m,0);
418 har_cv_corrected=j(p,m,1);
419 power_harl_corrected=j(p,m,2);
420 cutoff_harl_corrected=j(p,m,4);
421 cutoff_har_corrected=j(p,m,4);
422 power_har_corrected=j(p,m,2);
423 location_har_corrected=truep_har-testp;
424 print "SD, CV, and Power (Age class x Total sample size) for p at age",;
425 print "for each true p in harvest-same across all locations and seasons",;
426 print "Testing versus p=" testp;

```

```

427 do k=1 to p by 1;
428   do i=1 to m by 1;
429     do j=1 to o by 1;
430       sd[j,i]=sqrt((var_har[k]/samplebyage_har[j,i]));
431
432 sd_corrected[j,i]=sqrt(Tinv[1,2]**2*sd[j,i]**2+Tinv[1,1]**2*sd[j,i]**2-
433 2*Tinv[1,1]*Tinv[1,2]*sd[j,i]**2);
434   cv[j,i]=sd[j,i]/prop_marked_har[k,2];
435   cv_corrected[j,i]=sd_corrected[j,i]/truep_har[k];
436   cutoff[j,i]=1.96*sd[j,i];
437   cutoff_corrected[j,i]=1.96*sd_corrected[j,i];
438   power[j,i]=1-
439 cdf('Normal',cutoff[j,i],location[k],sd[j,i])+cdf('Normal', -
440 cutoff[j,i],location[k],sd[j,i]);
441   power_corrected[j,i]=1-
442 cdf('Normal',cutoff_corrected[j,i],location_corrected[k],sd_corrected[j,i])+cd
443 f('Normal', -cutoff_corrected[j,i],location_corrected[k],sd_corrected[j,i]);
444   end;
445   end;
446   pnow=truep_har[k];
447   print "True p" pnow ;
448   print "Uncorrected for marking error";
449   print sd [rowname=age_har] [colname=totsample_har];
450   print cv [rowname=age_har] [colname=totsample_har];
451   print power [rowname=age_har] [colname=totsample_har];
452   print "Corrected for marking error";
453   print sd_corrected [rowname=age_har] [colname=totsample_har];
454   print cv_corrected [rowname=age_har] [colname=totsample_har];
455   print power_corrected [rowname=age_har] [colname=totsample_har];
456   harsl_sd[k,]=sqrt((propatage_har##2*sd##2));
457   harsl_cv[k,]=harsl_sd[k,]/prop_marked_har[k,2];
458   harsl_sd_corrected[k,]=sqrt((propatage_har##2*sd_corrected##2));
459   harsl_cv_corrected[k,]=harsl_sd_corrected[k,]/truep_har[k];
460   do i=1 to m by 1;
461     cutoff_harsl[k,i]=1.96*harsl_sd[k,i];
462     power_harsl[k,i]=1-
463 cdf('Normal',cutoff_harsl[k,i],location_har[k],harsl_sd[k,i])+cdf('Normal', -
464 cutoff_harsl[k,i],location_har[k],harsl_sd[k,i]);
465     cutoff_harsl_corrected[k,i]=1.96*harsl_sd_corrected[k,i];
466     power_harsl_corrected[k,i]=1-
467 cdf('Normal',cutoff_harsl_corrected[k,i],location_har_corrected[k],harsl_sd_co
468 rrected[k,i])+cdf('Normal', -
469 cutoff_harsl_corrected[k,i],location_har_corrected[k],harsl_sd_corrected[k,i])
470 ;
471   end;
472   end;
473 end;
474 print "SD, CV, Power (True p x Total sample size) of p wild in harvest",;
475 print "for each season and location - same across all locations and seasons",;
476 print "Testing versus p=" testp;
477 print "Uncorreated for marking error";
478 print harsl_sd [rowname=pval_har] [colname=totsample_har];
479 print harsl_cv [rowname=pval_har] [colname=totsample_har];
480 print power_harsl [rowname=pval_har] [colname=totsample_har];
481 Print "Corrected for marking error";
482 print harsl_sd_corrected [rowname=pval_har] [colname=totsample_har];
483 print harsl_cv_corrected [rowname=pval_har] [colname=totsample_har];
484 print power_harsl_corrected [rowname=pval_har] [colname=totsample_har];
485 print "SD, CV, Power (True p x Total sample size) of p wild in harvest",;
486 print "by location across seasons",;
487 print "Testing versus p=" testp;

```

```

488 do k=1 to num_loc by 1;
489   wsum=j(p,m,0);
490   wsum_corrected=j(p,m,0);
491   do l=1 to num_seasons by 1;
492     wsum=wsum+(propharbyseason[k,l]##2*harsl_sd##2);
493     wsum_corrected=wsum_corrected
494 +(propharbyseason[k,l]##2*harsl_sd_corrected##2);
495   end;
496   harl_sd=sqrt(wsum);
497   harl_sd_corrected=sqrt(wsum_corrected);
498   do i = 1 to p by 1;
499     harl_cv[i,]=harl_sd[i,]/prop_marked_har[i,2];
500     harl_cv_corrected[i,]=harl_sd_corrected[i,]/truep_har[i];
501     do j=1 to m by 1;
502       cutoff_harl[i,j]=1.96*harl_sd[i,j];
503       power_harl[i,j]=1-
504 cdf('Normal',cutoff_harl[i,j],location_har[i],harl_sd[i,j])+cdf('Normal', -
505 cutoff_harl[i,j],location_har[i],harl_sd[i,j]);
506       cutoff_harl_corrected[i,j]=1.96*harl_sd_corrected[i,j];
507       power_harl_corrected[i,j]=1-
508 cdf('Normal',cutoff_harl_corrected[i,j],location_har_corrected[i],harl_sd_corr
509 ected[i,j])+cdf('Normal', -
510 cutoff_harl_corrected[i,j],location_har_corrected[i],harl_sd_corrected[i,j]);
511     end;
512   end;
513   print "Location" k;
514   print "Uncorrected for marking error";
515   print harl_sd [rowname=pval_har] [colname=totsample_har];
516   print harl_cv [rowname=pval_har] [colname=totsample_har];
517   print power_harl [rowname=pval_har] [colname=totsample_har];
518   print "Corrected for marking error";
519   print harl_sd_corrected [rowname=pval_har] [colname=totsample_har];
520   print harl_cv_corrected [rowname=pval_har] [colname=totsample_har];
521   print power_harl_corrected [rowname=pval_har] [colname=totsample_har];
522   wsum2=wsum2+(propharbyloc[k]##2*harl_sd##2);
523   wsum2_corrected=wsum2_corrected+(propharbyloc[k]##2*harl_sd_corrected##2);
524 end;
525 har_sd=sqrt(wsum2);
526 har_sd_corrected=sqrt(wsum2_corrected);
527 do i=1 to p by 1;
528   har_cv[i,]=har_sd[i,]/prop_marked_har[i,2];
529   har_cv_corrected[i,]=har_sd_corrected[i,]/truep_har[i];
530   do j=1 to m by 1;
531     cutoff_har[i,j]=1.96*har_sd[i,j];
532     power_har[i,j]=1-
533 cdf('Normal',cutoff_har[i,j],location_har[i],har_sd[i,j])+cdf('Normal', -
534 cutoff_har[i,j],location_har[i],har_sd[i,j]);
535     cutoff_har_corrected[i,j]=1.96*har_sd_corrected[i,j];
536     power_har_corrected[i,j]=1-
537 cdf('Normal',cutoff_har_corrected[i,j],location_har_corrected[i],har_sd_correc
538 ted[i,j])+cdf('Normal', -
539 cutoff_har_corrected[i,j],location_har_corrected[i],har_sd_corrected[i,j]);
540   end;
541 end;
542 print " SD, CV, Power (True p x Total Sample Size) for p wild in harvest",;
543 print "across all locations",;
544 print "Testing versus p=" testp;
545 print " Uncorrected for marking error";
546 print har_sd [rowname=pval_har] [colname=totsample_har];
547 print har_cv [rowname=pval_har] [colname=totsample_har];
548 print power_har [rowname=pval_har] [colname=totsample_har];

```

```
549 print "Corrected for marking error";
550 print har_sd_corrected [rowname=pval_har] [colname=totsample_har];
551 print har_cv_corrected [rowname=pval_har] [colname=totsample_har];
552 print power_har_corrected [rowname=pval_har] [colname=totsample_har];
553 quit;
```