Evaluation of Sampling Requirements to Answer Management Questions with Coded Wire Tagged Chinook Salmon Returns in Lake Michigan

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Introduction

As part of the Great Lakes mass marking program, beginning in 2011 all Chinook salmon stocked into lakes Michigan and Huron were to be implanted with coded wire tags (CWT) and to receive an adipose fin clip. The purpose of the marking program is to evaluate wild reproduction of Chinook salmon in the lakes, as well as to determine individual stocking site success, hatchery performance, intra- and inter-lake movement patterns, and contribution to the recreational fishery creel (S. Hansen, Wisconsin Department of Natural Resources, personal communication). In spring 2012, the Salmonid Working Group and the Lake Michigan Committee requested assistance from the Quantitative Fisheries Center (QFC) at Michigan State University to develop target sample size recommendations and sample collection protocols to help ensure statistically valid results can be gained from collections of tagged and wild fish. The Salmonid Working Group provided the following list of questions to the QFC that fishery managers were interested in exploring as part of the marking program:

- What is the contribution of Illinois, Indiana, Wisconsin, and Michigan origin Chinook salmon to their respective summer fisheries? Additionally, what are the contributions to the local and lake-wide summer fisheries of Chinook salmon stocked in specific state jurisdictions and management areas?
- Is there a difference in the contribution of Chinook salmon stocked at Waukegan, Diversey, and Jackson Harbor to the Illinois and lake-wide fishery?
- What are the return rates of Chinook salmon stocked by Illinois and other agencies to the fall spawning populations?
- What is the contribution of Lake Huron Chinook salmon to the Lake Michigan recreational fishery and vice versa?
- What is the rate of exchange between Lake Huron and Lake Michigan stockings sites?
- Is the current sampling design and target sample size at Michigan DNR weir index sites appropriate for biological data needs?

With regards to the last question, the specific biological data needs that managers were interested in were not specified, so I did not attempt to provide input on this question. The other questions are essentially variants of the same concept - namely, how large of a sample should be collected

to accurately estimate the proportional contribution of Chinook salmon from state-, location-, or hatchery-specific stocking events, as well as proportion wild, to a particular region of Lake Michigan, whether it be the whole lake or the recreational fishery operating in a specific jurisdictional area.

To answer the sample size questions, I referenced primary scientific literature pertaining to sample sizes for simultaneous estimation of confidence intervals for multinomial proportions. Numerous approaches exist for simultaneous estimation of confidence intervals for multinomial proportions, less has been published regarding target sample sizes to ensure a desired level of precision is achieved when estimating proportions. Several methods for determining sample sizes do exist and in this report I describe a fairly straightforward and conservative approach that can be used in a variety of situations. I begin the report by summarizing information provided in a Great Lakes Fishery Commission completion report entitled *Review of Procedures for Estimating Wild Production of Chinook Salmon through Marking Experiments: Evaluation of Needed Sampling of Marked Fish on Lake Michigan*, which was authored by Drs. Emily Szalai and James Bence from Michigan State University in the early 2000s (Szalai and Bence 2002). The Szalai and Bence (2002) report (hereafter referred to as the SB report) concerns estimating the proportion wild of Chinook salmon in Lake Michigan when stocked fish are marked with oxytetracyclene (OTC), which is different than estimating proportion wild using CWT tagging in that with the latter it is possible to determine proportion contributed from state- and location-specific stocking by way of unique tag codes. Despite this difference, many of the sampling issues discussed in the SB report are relevant to the CWT mass marking program. I then briefly review the multinomial distribution, including why I think this is the appropriate distribution for evaluating many of the questions that Lake Michigan fishery managers are interested in

answering. Lastly, I describe one approach for how sample sizes to achieve a desired level of absolute precision for multinomial proportions can be determined.

Relevant Aspects from the SB Report

Among the items discussed in the SB report that are relevant to the CWT mass marking program are the importance of accounting for marking error, sampling issues for inferring wild reproduction of the overall population when sampling is restricted to angler harvested fish, and sampling issues for inferring age-related differences in proportion wild when fish age is not known at time of capture. As noted in the SB report, the ability to accurately estimate the proportion of wild Chinook salmon depends critically on the ability to distinguish between stocked and wild fish. In the case of OTC marked fish, there existed the possibility that wild fish might be classified as stocked as a result of the appearance of fluorescence when examining vertebrae from wild produced fish and for stocked fish to be classified as wild as a result of degradation of OTC marks due to improper storage or other factors. In the case of the CWT mass marking program, the classification of wild fish as stocked fish seems highly unlikely, so the primary concerns are that stocked fish may shed their tags and that shedding rates might increase over time, which could result in age-related biases in the estimated proportion wild unless the estimates are corrected for shedding. Based on the 2011 CWT stocking database to which I had access, immediate tag retention for tagged fish was evaluated at some, but not all, release sites. It does not appear that there have been any attempts to rigorously evaluate long-term tag retention of CWT Chinook salmon (e.g., double tagging of some fish), although the adipose fin clipping of stocked individuals can provide general, but not state-, location-, or year-specific, information about long-term tag shedding. In studies conducted on other species,

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chronic CWT shedding does not appear to be a major issue (Dunning et al. 1990; Wallin and Van

Den Avyle 1994; Guy et al. 1996; Munro et al. 2003; Dorsey et al. 2004), so concerns about

shedding rates increasing as fish age may be unfounded.

Immediate CWT retention rates for stocking events where tag shedding was evaluated

based on the 2011 CWT stocking database ranged from 97.8% to greater than 99.9% (shedding

rates ranging from less than 0.1 to 2.2%). This level of tag loss is unlikely to have a large effect

on the accuracy of estimating the proportion of wild fish in the Chinook salmon population, but

it still would be a good idea to account for this shedding during estimation. Given that all fish

tagged with a CWT also receive an adipose-fin clip, it is still possible to distinguish between

wild and stocked individuals even if tags are shed. However, CWT shedding will result in

biases when it comes to estimating proportion contributed from state- or location-specific

stocking events. CWT shedding in effect will introduce an additional response category when

samples are collected from Lake Michigan (i.e., un-differentiable stocked individual). If

immediate CWT retention rates are available for each stocking event, then the corrected stocked

proportions can be easily adjusted. If immediate CWT retention rates are not available for each

stocking occurrence, then a weighted-average correction could be calculated based on stocking

events where shedding was evaluated and using the number of tagged fish for the stocking events

as the weighting factor.

Regarding the sampling issues for inferring wild reproduction in Chinook salmon, the SB

report discusses three possible objectives for Lake Michigan tagging/marking projects

1) Estimate the proportion wild in the Chinook salmon population

2) Estimate the proportion wild at age in the Chinook salmon population

3) Estimate the proportion wild at age in the Chinook salmon harvest

As noted in the SB report, the first two objectives are fundamentally different from the third objective in that they concern the lake-wide population rather than the recreational harvest. Meeting the first two objectives requires that sampling be representative of the at-large population. Fishery independent surveys for Chinook salmon are not widely conducted in the Great Lakes, so there is little choice but to rely on recreational fishery harvest for obtaining samples. As noted in the SB report, when samples of fish come from the recreational fishery, sampling needs to be conducted at a time when the population is well mixed to make inference to the proportion wild in the population. This assumption is necessary to ensure that samples from different locations can be combined as if they were samples from the same population. If the Chinook salmon population is divided into spatially distinct sub-populations consisting of different proportions of stocked and wild fish, the sampling design would need to be stratified by the location of the sub-populations. This would require knowing the spatial distribution of each sub-population and the relative sizes of the sub-populations. Since the SB report was completed, understanding of the spatial distribution of Chinook salmon has increased considerably as a result of research conducted by Adlerstein et al. (2008) and Williams (2012); however, knowledge of the spatial distribution of Chinook salmon from state- and location-specific stocking events is presently lacking. In the absence of such information, an assumption of a well-mixed population at certain times of the year is necessary for inferring to the lake-wide Chinook salmon population level.

In the SB report, it was assumed that the Lake Michigan Chinook salmon population was well mixed during the month of July. There are likely some concerns as to whether an assumption of a well-mixed population in July can be supported. Hesse (1994) found differences in proportion wild of age-3 Chinook salmon for samples collected between May and September

at Ludington, Michigan and at Grand Haven, Michigan. Small sample sizes prevented rigorous testing of monthly differences in proportion wild (Hesse 1994). Williams (2012) recently found that proportion wild of age-1 Chinook salmon for samples collected between April and August were significantly greater in Michigan and Illinois jurisdictions than in Wisconsin jurisdictions, although once again monthly specific differences could not be evaluated. None of the other age classes assessed by Williams (2012) were found to significantly differ in terms of proportion wild. The degree of mixing of stocked fish from different states and stocking locations during different times of the year is a major unknown and I am not aware of any data source that might be used to assess this *a priori*. Even if it is assumed that the population is well mixed during a certain time of year, it is still nevertheless prudent to collect samples across a broad area so that large spatial differences in the proportion wild can be detected.

To estimate the proportion wild at age in the population, it is important to ensure that the sampling is designed to adequately sample all age classes of interest (i.e., stratified sampling). Unfortunately, at time of sampling, fish age is not known so it is typical for length bins to be used to separate ages. In the past, length bins of < 38 cm, 38 to 57, and > 57 cm have been used to distinguish between age-0, age-1, and age-2 and older Chinook salmon. In the SB report, it was assumed that age-2, age-3, and age-4 fish comprised 55, 42, and 3% of Chinook salmon > 57 cm. Thus, if data collection targeted 750 fish > 57 cm in length the expected sample size by age was approximately 413 age-2 fish, 315, age-3 fish, and 23 age-4 fish. Given that Chinook salmon growth rates have changed in recent years, different length bins and/or length bin age compositions should probably be developed and used for the CWT marking program.

When estimating the proportion wild at age in the harvest, the SB report indicated that sampling should be designed to account for differences in harvest between locations and seasons

around the lake. Specifically, it was recommended that sampling be stratified by location and season, in addition to length class, to ensure adequate samples were collected. In the SB report, six regions were used for stratification. The North region encompassed Michigan statistical districts MM2, MM3, and MM4. The Northeast region encompassed Michigan statistical districts MM5 and MM6. The Northwest region encompassed Wisconsin statistical districts WM3 and WM4. The Southeastern region encompassed Michigan statistical districts MM7 and MM8. The Southwestern region encompassed Wisconsin statistical districts WM5 and WM6. The Indiana-Illinois region encompassed all waters within the Illinois-Indiana jurisdictional boundaries. Seasons were categorized into early, mid, and late season. Early season encompassed Chinook salmon harvest prior to June 16. Mid season encompassed Chinook salmon harvest between June 16 and July 31. Late season encompassed Chinook salmon harvest after July 31. The same strata could be used for the CWT marking program, or the strata could be modified for finer (or broader) resolution.

    With stratified sampling, one important issue to consider is allocation of sampling effort (i.e., effort of head hunters in collecting specimens from recreational fishers). Without prior knowledge of population distribution, a logical choice is to allocate sampling effort equally across strata (e.g., evenly across 6 spatial strata, 3 seasonal strata, and 2 length strata). An alternative choice would be to allocate sampling to the strata in proportion to a prior estimate of each stratum's contribution to the total population being assessed. One reasonable basis for prior weighting would be the proportion of harvest. Based on creel survey reports from 1985 to 2000, the SB report presents the approximate proportion of total harvest that occurs in each season at each location (25% early season, 50% mid season, 25% late season) and in each spatial region (2% North, 33% Northeast, 17% Northwest, 27% Southeast, 16% Southwest, and 5%

Indiana/Illinois). If a choice is made to allocate sampling based on proportion of harvest, then the percentages established in the SB report should be updated.

The SB report concluded with a series of recommendations for the OTC marking program. Many of these recommendations are valid for the CWT mass marking program as well, although the wording of the recommendations requires some modification.

1) Tag shedding is important to acknowledge in the mass marking program. Failure to account for shedding may result in biases in the proportion of wild fish or biases in the proportion contributed from state- or location-specific stocking events.

2) Sampling of CWT fish to estimate the proportion wild and proportion contributed from state- or location-specific stocking to the harvest should be concentrated at locations where large numbers of Chinook salmon are harvested. This can be accomplished by targeting tournaments or sampling at locations during times that are known to produce large harvests.

3) Sampling efforts directed at estimating wild contributions should be concentrated on estimating the proportion wild at age. Sampling only to estimate overall proportion wild does not provide information on how year class strength changes temporally, which is perhaps the key uncertainty regarding Chinook salmon population dynamics.

4) Samples for determining proportion wild or proportion contributed from state or location-specific stocking at the population level should be taken from different locations from around the lake so that patterns in the proportions across the lake can be examined.

Review of the Multinomial Distribution

The multinomial distribution is a generalization of the binomial distribution. Whereas the binomial distribution is assumed to consist of n independent repetitions where the outcome of a repetition can be only one of two possible categories, the outcome for a multinomial distribution can be one of k possible categories. In early OTC studies conducted on Lake Michigan Chinook salmon, the binomial distribution was an appropriate distribution for analyses as there were only two possible outcomes when fish were collected from the lake: stocked or wild. In the case of the CWT mass marking program, the outcomes for sampling fish from the lake can take on of several possible variants depending on the scale of inference. At the finest scale, the outcomes could consist of all tag batch codes that have been released in the lake in addition to wild produced fish, Lake Huron stocked fish, and un-differentiable stocked fish (i.e., fish with adipose fin clips but no recoverable tag). In 2011, 19 unique batch codes were used to mark Chinook salmon released into Lake Michigan: 3 unique codes were used by Illinois, 3 unique codes were used by Indiana, 3 unique codes were used by Michigan, and 10 unique codes were used by Wisconsin. In 2012, another 19 unique batch codes were used to mark Chinook salmon: 3 unique codes were used by Illinois, 3 unique codes were used by Indiana, 3 unique codes were used by Michigan, and 10 unique codes were used by Wisconsin. At a broader scale, the outcomes of sampling fish from Lake Michigan could be considered to consist of the states from which stocked fish were planted (Michigan, Wisconsin, Illinois, and Indiana) in addition to wild produced fish, Lake Huron stocked fish, and un-differentiable stocked fish. At the broadest scale, the outcomes of sampling fish from Lake Michigan that fishery managers would be interested in categorizing would be Lake Michigan stocked fish, Lake Huron stocked fish, un-differentiable stocked fish, and wild fish. Most of the questions posed to the QFC by the

Salmonid Working Group included some mention of state- or location-specific contributions, rather than just stocked versus wild contributions, so it would seem that there is greater interest in categorizing outcomes at fine rather than broad scales.

With n independent repetitions and $i=1\ldots k$ possible outcomes, the multinomial distribution gives the probability of observing a particular combination of categories in a sample where the probability of observing the i-th category is equal to p_i and the total number of occurrences of a particular category is denoted as x_i. Each p_i is assumed to be greater than or equal to 0.0, less than 1.0, and the sum of all the p_is is assumed to equal 1.0 (i.e., the categories are mutually exclusive and exhaustive). The expected number of occurrences of a particular category is $E(x_i) = np_i$. The variance associated with a particular category is $Var(x_i) = np_i(1.0-p_i)$, while the covariance between the i-th and j-th categories is $Cov(x_i,x_j) = -np_i(p_j)$. The covariance between two categories is necessarily negative because for a fixed number of repetitions an increase in one category necessitates a decrease in another category. For the multinomial distribution, the sample proportions x_i/n are the unbiased estimates of the population proportions for each category. The variances of the sample proportions are simply $Var(\hat{p}_i) = p_i(1.0-p_i)/n$, while the covariance of two sample proportions is $Cov(\hat{p}_i, \hat{p}_j) = -(p_ip_j)/n$. The presented formulas for the variances and covariances do not include a finite population correction factor because sample sizes from the CWT mass marking program should be large enough that the correction factor would have negligible influence. Also, as noted by Cochran (1977), although it is common practice for the variances of sample proportions to be denoted as $Var(\hat{p}_i) = p_i(1.0-p_i)/n$, this is a biased estimate. An unbiased estimate is $Var(\hat{p}_i) = p_i(1.0-p_i)/(n-1)$, although this seems to be rarely used in practice. The bias of $p_i(1.0-p_i)/n$ decreases as sample size increases.

As previously stated, my interpretation of most of the questions posed to the QFC is that

fishery managers are interested in using collections of fish from Lake Michigan to estimate the

proportion wild or proportion contributed from state- or location-specific stocking to the

Chinook salmon population or fishery harvest, thus the desire is to make inferences regarding the

p_is. Some possible comparisons that managers may be interested in making include testing

whether estimated p_is differ from known values (e.g, testing whether the proportions contributed

from state-specific stocking estimated for the lake-wide population differ from the stocking

proportions) or in testing differences in the p_is for particular outcomes (e.g., differences in

proportion contributed among the Waukegan, Diversey, and Jackson Harbor stocking locations).

Alternatively, fishery managers may simply be interested in estimating the uncertainty associated

with particular p_is (i.e., generative confidence intervals associated with the estimated p_is). Each

of these can be accomplished under an assumption that the data are multinomially distributed,

although in most cases the underlying methods make use of a normal approximation to the

multinomial distribution. To test whether an estimated proportion is different from an assumed

level (H0: $p_i = p_0$ versus H1: pi $\neq p_0$), the following test statistic can be used

$$Z = \frac{\hat{p}_i - p_0}{\sqrt{\frac{p_0(1.0 - p_0)}{n}}}.$$

This test statistic would then get compared to a standard normal curve at a particular Type-I error

rate (α) for deciding whether the null hypothesis could be accepted or rejected. Alternatively, the

test could be based on a Student's t-distribution with degrees of freedom equal to 1 less than the

total sample size. I presented the formula as a standard normal distribution as I anticipated that

the collected sample sizes through the CWT marking program would be large enough to be able

to assume a standard normal distribution. To test differences in the p_is for two particular

outcomes ((H0: $p_i - p_j = 0$ versus H1: $p_i - p_j \neq 0$), the following test statistic can be used

$$Z = \frac{\hat{p}_i - \hat{p}_j}{\sqrt{\dfrac{\hat{p}_i(1.0 - \hat{p}_i)}{n} + \dfrac{\hat{p}_j(1.0 - \hat{p}_j)}{n} + 2\dfrac{\hat{p}_i\hat{p}_j}{n}}},$$

which again would get compared to a standard normal curve at a particular Type-I error rate for

deciding whether the null hypothesis could be accepted or rejected. For constructing confidence

intervals around proportion estimates, there are several methods that can be used. The simplest

approach is to construct asymptotic (Wald) confidence intervals as

$$\hat{p}_i \pm Z_{1-\alpha/2}\sqrt{\frac{\hat{p}_i(1.0 - \hat{p}_i)}{n}} \ .$$

where $Z_{1-\alpha/2}$ is the upper $\alpha/2$ point of the standard normal distribution. Alternative methods

include Agresti-Coull, Clopper-Pearson, Jeffreys, and Wilson score intervals. When multiple

tests of proportions or confidence intervals are calculated, appropriate corrections should be used

to protect the experiment-wise Type-I error rate (e.g., Bonferroni corrections). Alternatively,

simultaneous approaches for estimating confidence intervals for proportion estimates or testing

differences in proportions can be used. For background on simultaneous approaches for

estimating confidence intervals for multinomial proportions of testing differences in proportions,

see Goodman (1965), Fitzpatrick and Scott (1987), Sison and Glaz (1995), Kwong (1998), Glaz

and Sison (1999), Piegorsch and Richwine (2001), and Cai and Krishnamoorthy (2006).

As noted earlier, the categories used to summarize collections of Chinook salmon can

range from fine scale (all possible tag codes) to broad scale (by lake). When estimating

proportions at broad scales, the estimated proportions can be considered to consist of linear

combinations of the category probabilities at the finest possible scale. In some cases, fishery

managers may be interested in summarizing the outcomes in a number of different ways (i.e., calculating many linear combinations of the fine scale categories). When calculating many linear combinations of multinomial proportions, the Bonferroni correction can be overly conservative for determining confidence intervals and there are other approaches that can be used to protect the experiment-wise error rate of the intervals (Johnson and Wichern 1992). How these methods perform relative to Bonferroni corrected confidence intervals ultimately depend on the number of linear combinations that are considered (see Brenden et al. 2008)

Sample Sizes to Achieve a Desired Level of Precision for Multinomial Proportions

Estimating sampling sizes to achieve a desired level of precision for any parameter estimate oftentimes can be difficult because the sample sizes may depend on an unknown parameter value. For example, when determining sample sizes for proportions from a binomially distributed random variable, necessary sample sizes depend on the outcome probabilities. For this reason, sample size requirements sometimes are presented graphically as there is not a necessarily concise approach for presenting the information. For example, in the SB report, sample size requirements for estimating proportion wild and proportion stocked for the Lake Michigan Chinook salmon population was presented in a series of graphs where proportion wild ranged from 0.05 to 0.4 and with different levels of desired relative precision. In the case of sample sizes to achieve a desired level of precision for multinomial proportions, concisely presenting the information is made even more difficult as a consequence of the potentially large number of possible outcomes. As a result, sample size requirements are often based on a worst-case scenario, which generally occurs when some of the proportions being considered are equal

and the rest are zero. An analogous situation is occasionally used when setting sample size targets for proportions from a binomial random variable. The formula for determining same sizes for binomial proportions is

$$n = \frac{Z^2_{1-\alpha/2}\, p(1.0-p)}{d^2},$$

where d is the desired level of absolute precision (the standard error) around the estimated proportions. For example, if it was believed that the probability of success for some event was 0.3 and researchers wanted to collect a sample size large enough such that there was a 95% probability that the estimated p was between 0.30 ± 0.05, than a sample size of 323 should be targeted. It should be noted that n is at a maximum when $p = 0.5$. Thus if there is little information to suggest beforehand what actual proportions are for a binomial random variable, sample size determinations will be calculated assuming $p = 0.5$ to err on the side of conservatism. See the final paragraph for discussion regarding the distinction between absolute and relative precision.

Thompson (1987, 1992) presents a table for determining sample sizes for simultaneously estimating the proportions of a multinomial random variable within a desired level of absolute precision and at a given significance level under the worst possible case. Part of the table is reproduced below, including situations where sample sizes are calculated when it is desired that proportions are within 0.01, 0.025, or 0.05 of their true values. To find the target sample size, one just needs to select a probability level (α) and the desired absolute precision level (d). As an example, if it is desired that there is a 95% probability that all proportions are within 0.025 of the true proportions, than a sample size of 2,038 should be collected. If it is desired that there is a 95% probability that all proportions are within 0.05 of the true proportions, than a sample size of 510 should be collected. If it is desired that there is a 95% probability that all proportions are

within 0.01 of the true proportions, than a sample size of 12,736 should be collected. Again, it

should be noted that this is for the worst possible scenario; when it comes to calculating actual

confidence intervals around proportion estimates, the actual confidence interval may be

considerably smaller for a particular sample size.

Table 1. Table for determining sample sizes for simultaneously estimating multinomial proportions within a desired absolute precision level *(d)* at a 1- α probability level.

α	d^2n	*m*	*d*=0.01	*d*=0.025	*d*=0.05
0.30	0.60123	3	6,013	962	241
0.20	0.74739	3	7,474	1,196	299
0.10	1.00635	3	10,064	1,610	403
0.05	1.27359	3	12,736	2,038	510
0.025	1.55963	2	15,597	2,495	624
0.02	1.65872	2	16,588	2,654	664
0.01	1.96986	2	19,699	3,152	788
0.005	2.28514	2	22,852	3,656	915

Note: Worst possible case occurs when the population proportions are $1/m$ for *m* of the *k* possible categories. See Thompson (1987) and Fitzpatrick and Scott (1987) for additional information regarding the determination of the worst-possible cases for determining sample sizes for multinomial proportions.

In my mind, the main advantage of using the above table for determining target sample

sizes for the mass marking program is that the specified targets are somewhat independent of the

question. In other words, it does not matter if the question is directed at determining proportions

contributed by state-specific stocking events or proportion contributed from location-specific

stocking events (or some combination of both) as the target sample size will meet the desired

precision level for any number of categories. The sampling frame scope also does not matter in

terms of determining target sample sizes. If fishery managers are interested in determining a

target sample size for determining proportions contributed by state- or location-specific stocking to the recreational fishery operating within Illinois jurisdictional boundaries within 0.025 of the true values at a 0.95 probability level, the target sample size would be no different than if the goal was to determine proportions contributed by state- or location-specific stocking to the lake-wide recreational fishery. Rather, the difficulty is ensuring a representative sample has been collected for inferring to the lake-wide recreational fishery.

When using OTC marking to infer proportion wild of Chinook salmon in Lake Michigan, to a large extent collected sample sizes were restricted by the time required to process samples. Tail sections of collected fish needed to be removed, vertebrae removed and cleaned, and then the vertebrae examined under a stereo microscope. This limited the number of samples that could be examined in a given year to 2000 (Szalai and Bence 2002). Presumably, the processing of samples for the presence of CWT tags will be considerably more efficient and sample sizes will primarily be restricted on the number of personnel (i.e., head hunters) that can be employed to collect samples from anglers. Given the desire to answer questions pertaining to proportions contributed by state- and location-specific stocking events to state- and lake-wide- recreational fisheries, a coordinated conversation regarding target precision levels and availability of personnel should be had among the Salmonid Working Group for how efforts will be allocated.

As a concluding comment and something that may need to be discussed in the future, the target sample sizes generated from Table 1 above is based on the use of absolute precision across the all the outcome categories. For example, if an absolute precision of 0.05 is used to set target sample sizes, then the level of precision is the same regardless of whether the estimated proportion is 0.02, 0.5, or 0.9. An alternative strategy would be to use relative precision (i.e., the coefficient of variation). For example, if a relative precision for multinomial proportions was set

at 10%, the for an outcome with an estimated probability of being observed equal to 0.2, the target absolute precision level would be 0.18 to 0.22 (0.20±(0.1×0.2)), while the outcome with an estimated probability of being observed equal to 0.7 the target precision level would be 0.63 to 0.77 (0.70±(0.1×0.7)).   From the questions submitted to the QFC and in follow-up conversations with cooperators in the Lake Michigan mass marking program, it's unclear if relative or absolute precision should be used in setting target sample sizes. I used absolute precision as the basis for this report as most of the research studies that I have encountered regarding sample size targets for multinomially distributed data also were based on absolute precision. Basing target sample sizes on the idea of relative precision may be considerably more difficult as defining a worst-case scenario may not be possible. As a result, sample size recommendations would need to be context dependent and would have to assume some specific outcome probabilities.

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