The accuracy of estimates of life-history and fishery parameters derived from CWT or PBT data depend on two principal factors: 1) the number of tags that are actually recovered, and 2) the accuracy with which those tags can be expanded into estimates of the total number of release group fish represented by those recoveries. We address the question of errors of estimation by evaluating each of these factors.

**Number of Tag Recoveries**

Ultimately, errors of estimation for a specific stock or release group are reduced as tag recoveries from that stock or release group are increased under either a CWT or PBT system. Tag recovery rates in turn are a function of the number of tags deployed and the sampling intensity. As per-fish tagging costs using PBT are lower than for CWTs, implementation of PBT would likely allow increased tagging rates for many stocks, which would reduce errors of estimation *if* sampling rates were held constant and the additional fish tagged were also marked such that they would be recovered in later sampling.

However, alterations in marking, tagging, and sampling rates may interact in complicated ways and have consequences that are not always immediately obvious. For example, increasing the tagging and marking rates on stocks that are only rarely encountered in subsequent sampling would increase the information available on such stocks with little increase in the overall burden on the sampling system, but increasing the tagging and marking rates on stocks that already make up a large number of recoveries could lead to substantially increased sampling costs with marginal information benefits for these larger stocks, and this might create financial pressure to reduce the overall sampling intensity and thus the tag recovery rate for small and rare stocks.

Optimization of the marking, tagging, and sampling rates would need to be done with careful consideration of individual stocks and the constraints on tagging, marking, and sampling each in the context of a larger coastwide sampling scheme. Fully addressing this issue is beyond the scope of this report. Exploration of the effects on recovery rates from changes to the current levels of marking, tagging, and sampling rates could be done using existing systems such as PlanIt! (Morishima et al. 2012).

**Uncertainty in Expansion Factors**

We note that the PBT + AWT “System 1” in section II.A would essentially duplicate the number of stock-specific tag recoveries of the current CWT system. This is a good reference point to consider the additional factors affecting errors of estimation between PBT and CWT. The qualitative differences between CWT and PBT as they affect errors of estimation are as follows:

1) PBT tagged fish from which tissues are sampled in fishery or escapement areas may not yield successful (scorable) genotypes, and thus render their release group of origin unknown. However the rate of genotyping failures can be quantified, and so long as the probability of such failure is not stock-dependent, can be dealt with using expansion factors the same way as is done for unreadable CWTs or cases where CWTs are lost while attempting to extract them from the fish.

2) Assignment of offspring to parents may be subject to either false positive errors (a sampled fish is assigned to a parent pair that is not its true parent pair) or false negative errors (a sampled fish has parents in the database, but is not assigned to them). With a sufficient number of genetic markers, such rates are typically low; however, there is a tradeoff: setting stringent assignment criteria in order to reduce the occurrence of false-positive errors will necessarily lead to a higher rate of false negative errors (Anderson & Garza 2006). Since there is no obvious way of correcting sample recovery estimates for false positive errors (since they are difficult to detect), it will usually be best to minimize them, and account for false negatives using expansion factors in the same manner that CWT tag loss is accounted for. Currently there is not a standardized way of estimating false negative rates in a particular fishery, though they can be predicted for a particular population using estimated genotyping error rates, the allele frequencies in the population, and knowledge of the degree of relatedness within the population. For PBT, it will be necessary to develop and agree upon a defensible method of estimating the false negative rate.

3) There is some uncertainty in the tagging rate achieved through PBT when not all parents are genotyped, due to the variance in family size. If mating pairs are unknown, there is additional uncertainty in the tagging rate because it is unknown how many matings the ungenotyped parent(s) participated in. Appendix Y addresses the first of these two issues in detail, but the main findings are summarized below.

When considering the uncertainty in the PBT tagging rate, it is important to realize that even in the case of a CWT release group, where the tag rate is estimated based on a count of tagged versus untagged individuals, the tagging fraction of *adults* may differ slightly from this tagging rate due to the stochastic nature of individual survival and the fact that it is unlikely that the *exact* proportions of tagged versus untagged individuals will survive to adulthood, even if there is no tagging effect on the probability of survival. With CWTs (and with PBT), the variance in the adult tagging rate varies inversely with the size of the release group. However, with PBT, the situation is more complex because survival to adulthood typically is correlated with family. Were the number of surviving adults per family to be Poisson distributed with constant mean, then this correlation between family and survival would not be an important factor. However, salmon populations tend to exhibit overdispersion in family size making the effect of family-specific survival relevant to the question of uncertainty in the tagging rate. Accordingly the use of PBT for tagging has the potential to increase the variance in the realized tagging rates.

The practical implications of this increased variance, however, must be evaluated in the context of the total variance of estimates obtained by sampling expansions. In many cases, the variance due to sampling only a small fraction of each release group far outweighs the additional variance from PBT-tagging rate variance.

Appendix Y describes simulations that document three main factors influencing the variance in the realized PBT tagging rate: 1) the variance in family size at the hatchery, which can be expressed as the ration of the effective number of spawners to the actual number; 2) the number of families used to produce the juveniles in the release group; 3) the fraction of families whose offspring are successfully tagged, which, in turn, is a function of the rate of successful genotyping;

as there are at least about 100 parent pairs per release group, and greater than 96% of the parent pairs are successfully genotyped, the additional variance in tagging rates introduced by variation in family size, although not negligible, is not dramatically larger (as a fraction of the true tagging rate) than the variance in the realized adult tagging rate due to demographic stochasticity. However, the situation deteriorates fairly dramatically when only a few parent pairs produce the release group, or when a much smaller fraction of the parent pairs are successfully genotyped.

The influence of the variance of the PBT tagging rate on expanded estimates of the total number of release group fish represented by tag recoveries, however, is dependent on the marking rate…

In this regard, it is important to recognize that, if parent *pairs* are required for parentage assignment, the fraction of families with both parents successfully genotyped decreases with the square of the fraction of successfully genotyped parents. Thus, if 95% of male parents and 95% of female parents are successfully genotyped, one expects only 90.2% of the families to have both parents genotyped. On the other hand, it POINT OUT EXTRA ADVANTAGE OF SINGLE PARENT---NOT LIKELY TO LOSE BOTH PARENTS. must also be stressed that if 100% of the parents are successfully genotyped, then there is no additional variance in the adult tagging rate due to variance in family size, regardless of the number of parents that produced the release group. In addition, the estimated tagging rate in the Idaho PBT programs over the last XX years averages XX% for Chinook and XX% for steelhead, demonstrating that high genotyping success rates can be achieved.

The dependence of the realized PBT tag rate variance on the number of parents producing the release group is important given the current distribution of release group sizes. Because tagging a release group using PBT requires defining the release group in terms of the parents that produced it, small release groups are subject to the PBT-tag rate variance incurred from using a small number of parent pairs. Table XX enumerates the coastwide number of release groups, brood year 2000 forward, according to the number of parents that would have produced them (assuming 3,800 released juveniles per Chinook female parent and 1,800 released juveniles per coho female parent). Approximately one-third of the release groups could have been produced with fewer than 10 parent pairs.

Tables are in attached csv files. Caption:

Table 1: Summary of coastwide CWT tagged Chinook and coho releases, brood year 2000 forward. The “No. families” column gives the number of families that would have been required to create both the tagged and untagged components of the release group if the number of male and female parents were equal and each female parent averaged 3,800 (Chinook) or 1,800 (coho) released juveniles. The column “No. juveniles released” gives the total number of juveniles released since brood year 2000. The column “No. release groups” gives the number of actual release groups. The final two columns are the percentages of the number of juveniles released and the number of release groups, respectively, across the family size categories.