Two main variables influence the accuracy of different estimates of life-history and fishery parameters obtained from CWT or PBT data: 1) the number of tags (CWT-based or PBT-based) that are actually recovered, and 2) the accuracy with which those tags can be expanded to meaningful estimates of the expanded number of recoveries. The question of errors of estimation can be dissected by considering each of these factors.

**Number of Tag Recoveries**

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

However, changes in marking, tagging, and sampling rates may interact in complicated ways that are not always immediately obvious. 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 might reduce recoveries of tags from rare stocks and could also increase sampling costs with little benefit, and possibly create pressure to decrease sampling rates.

Optimizing a schedule of 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; however, in Appendix X, we begin to investigate the degree to which flexible changes to marking and tagging rates could increase recoveries of underrepresented release groups in visually-sampled fisheries from Alaska and California. Further exploration of the eon recovery rates to current levels ofmightalso .

**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 starting 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) Fish from which tissues are sampled in recovery areas or in the escapement may not yield scorable genotypes. This would render their tag-recoveries 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 unreadable CWTs or cases where CWTs are lost while attempting to extract them.

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 sufficiently powerful 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 fishery 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 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 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, though we describe the main points below.

In considering this uncertainty in PBT tagging rate, it is important to realize that even if the coded-wire tagging rate of smolts is known based on an exact 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 may be correlated with family. If the number of surviving adults per family is Poisson distributed with constant mean, then this correlation between family and survival is not an important factor; however salmon populations tend to exhibit overdispersion in family sizes making the effect of family-specific survival relevant to the question of uncertainty in the tagging rate. As shown in Appendix Y, so long as, there are at least ~100 parent pairs per release group, and ~96%+ of families are successfully genotyped, the additional variance in tagging rates introduced by variation in family size, though not negligible, is not dramatically larger (as a fraction of the true tagging rate) than the variance in adult tagging rate due to demographic stochasticity. However, the situation deteriorates somewhat dramatically when only a few families produce the release group, or when a much smaller fraction of families are successfully genotyped.

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 (as a general rule of thumb) with the square of the fraction of successfully genotyped individuals. Thus, if 95% of males and 95% of females are successfully genotyped, one expects only 90.2% of the families to have both parents genotyped. It 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 producing the fish in question. In applications of PBT in Idaho, broodstock genotyping success rates of XX% in Chinook and XX% in steelhead have been achieved over the last XX years, demonstrating that high genotyping success rates can be achieved.

The dependence of PBT tag rate variance on the number of parents producing the release group carries noteworthy ramifications given the current distribution of release group sizes. Because tagging a release group using PBT requires defining release groups 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 families. Table XX enumerates the release groups, broken down by the number of parents that would have produced them (assuming 3,800 smolts per Chinook female and 1,800 smolts per Coho female). A large fraction could be produced with fewer than 10 pairs of parents.

Tables are in attached csv files. Caption:

Table 1: Summary of tagged Chinook and Coho releases since brood year 2000 across all agencies. The No. releases column gives the number of families that would have been required to create both the tagged and untagged components of the release group if number of male and female parents were equal and each female averaged 3,800 (Chinook) or 1,800 (Coho) smolts surviving to the release stage. The column No. smolts gives the total number of smolts produced since 2000 in releases requiring number of familes in the range as given in No. familes. The column No. releases gives the number of actual release groups. The final two columns are percentages of the total smolts are release groups, respectively.