

# Statistical review of the draft National Pateke Monitoring Guidelines

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# Statistical review of the draft National Pateke Monitoring Guidelines

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## ABSTRACT

This review provides guidance on the statistical precision to be expected in the proposed New Zealand national monitoring programme for pateke (brown teal, *Anas chlorotis*) for a range of sample sizes, including those suggested in the current draft. In estimating population size there appeared to be little gain from using more than the proposed four temporal replicates of the flock counts, and there is likely to be negligible loss in precision if this number is reduced to three. However, there may be relatively high levels of uncertainty in the estimates of population size, adult survival and juvenile survival if the proposed sample sizes (35 adults, 20 juveniles) are implemented. It is also difficult to predict whether sampling 20 nests and a mean of 1.5 ducklings per nest in order to estimate hatching rate and duckling survival will achieve a desirable level of precision, as this depends on the natural variation in these two rates between nests, estimates of which are not available. We have therefore considered a range of possibilities, in order to show the level of precision that might be attained. We have not considered what effects adjustments for rainfall or other environmental variables would have on the precision of the estimates; such adjustments might make the estimates less biased but also less precise.

Keywords: pateke, brown teal, *Anas chlorotis*, national monitoring guidelines, New Zealand, statistical precision, population estimates, sample size, survival estimates, nest sampling.

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# 1. Introduction

This report has been prepared as a result of discussions regarding the statistical aspects of the DOC draft guidelines (Pierce et al. 2003) for a national monitoring programme for pateke (brown teal, *Anas chlorotis*). We consider the protocols outlined in Sections 4.1–4.4 of that draft, which deal with flock counts, adult survival, hatching and duckling survival, and juvenile survival, respectively. We do not discuss field methods, issues regarding data entry and quality control, or other issues that appear not to be statistical. The details of our calculations are in Appendix 1.

## 2. Flock counts

### 2.1 USE TO ESTIMATE POPULATION SIZE

Flock counts (Section 4.1 of the draft) are to be made at a number of *sites* within each of the two main study *areas* (as well as control areas), with the focus being on the total count for that area. It has been proposed that  $n = 4$  total counts (temporal replicates) be made each year, and their mean, maximum and standard error (SE) be recorded. Our focus here is on the precision of the mean count *as an estimate of population size*. For simplicity of presentation, we do not distinguish between adult and juvenile counts.

It is important to note here that it is likely to be more meaningful to transform a measure of abundance to a logarithmic scale before statistical analysis. There are two reasons for this: one is to better satisfy the assumptions underlying standard statistical procedures; the other is to allow comparisons to be made in a relative rather than an absolute manner. In this context, for example, analysis on the log scale would lead us to focus on the percentage change in the flock count from one year to the next, rather than the change in the actual number of individuals. The use of a relative scale is linked to the idea of summarizing a trend by a growth rate.

The calculations used to assess precision involve estimating both sampling variation, i.e. between temporal replicate counts, and process variation, i.e. the scatter around a straight-line trend fitted to the *true* population size (on a log scale).

We have two estimates of sampling variation. The first is based on five replicate counts at Mimiwhangata Bay (about 50 km north of Whangarei, Northland) in 2002 (Mean = 140.6; SD = 5.2; CV = SD/Mean = 0.04). The second is based on four replicate counts at Whangapoua Beach (Great Barrier Island) in 2002 (Mean = 301.8; SD = 40.5; CV = SD/Mean = 0.13). In what follows, we have therefore assumed a CV for sampling variation of 0.1, slightly higher than the mean of these two estimates. Our estimate of the process variation CV is 0.16,

based on the counts at Whangapoua Beach during the period 1986–2001 (for the island-wide counts at Great Barrier I., the process CV was estimated as 0.08).

The flock counts provide an index of population size only if the proportion of individuals from the population that are in the flock is the same for all flock sites, areas and years. This is unlikely to be the case. We therefore consider use of the total flock count ( $c$ ) to estimate the corresponding population size ( $N$ ) via the equation  $N = c/p$ , where  $p$  is the proportion of individuals from the population that are in the flocks counted. The proportion  $p$  can be estimated by the proportion of radio-tagged individuals that are in the flocks at the time of the counts (in what follows, we assume that  $p$  will be estimated in each year of monitoring). The precision of  $N$  depends upon the precision of the flock count and the uncertainty associated with estimating  $p$ . Figure 1 shows the precision (relative confidence limits) in estimating  $p$  using either  $t = 50$  or  $t = 100$  radio-tagged individuals. For example, if we have  $t = 50$  and  $p = 0.4$ , the confidence limits for  $p$  are between 0.65 and 1.35 of the estimate, i.e. between 0.26 ( $0.65 \times 0.4$ ) and 0.54 ( $1.35 \times 0.4$ ).

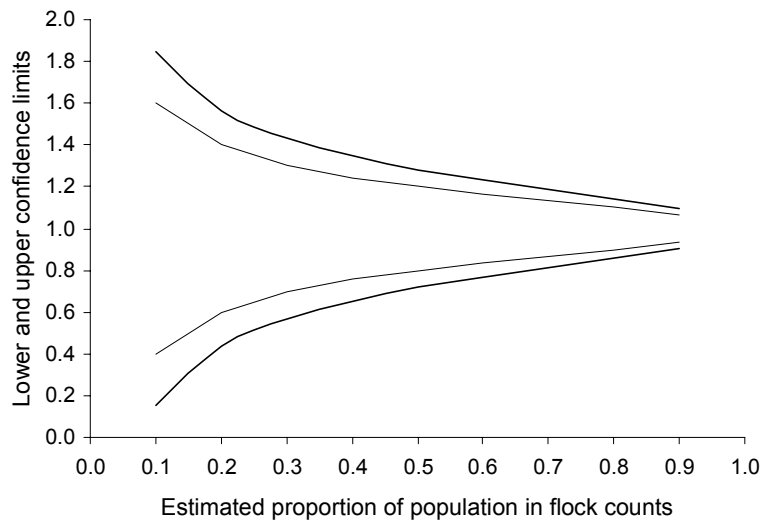


Figure 1. Relative confidence limits for the proportion of all individuals in the population that are also in the flock counts. The number of radio-tagged individuals is  $t = 50$  (thick, outer lines) and  $t = 100$  (fine, inner lines).

## 2.2 SIMPLE COMPARISON OF POPULATION SIZES

Figure 2 shows the precision (relative confidence limits) to be expected for a comparison of two estimated population sizes, based on  $t = 50$  radio-tagged individuals and  $n = 3$  or  $n = 4$ . For example, with  $n = 4$  and  $p = 0.5$ , we can expect the 95% confidence interval for the ratio of the two population sizes to be from 0.60 to 1.68 of the ratio. Suppose that for a particular area  $N$  increased by 50%, i.e. by a factor of 1.5. This factor is expected to have a 95% confidence interval from 0.90 ( $0.60 \times 1.5$ ) to 2.51 ( $1.68 \times 1.5$ ). We would therefore estimate that the ‘true’ change was somewhere between a decrease of 10% and an increase of 151%.

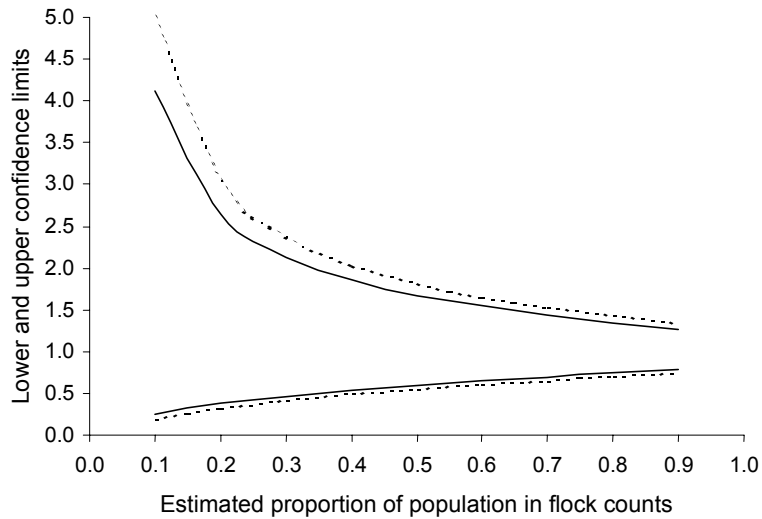


Figure 2. Precision attained for different proportions of individuals that are in the flock counts, in making a simple comparison between estimates of population sizes ( $t = 50$  and  $p$  the same for the two areas or years). The number of temporal replicate counts per year is  $n = 3$  (dashed line) or  $n = 4$  (solid line).

### 2.3 ESTIMATING TREND IN POPULATION SIZE

Figure 3 shows the precision (relative confidence limits) to be expected when estimating a trend in the population size at a particular area, with  $n = 4$ ,  $t = 50$  and  $p = 0.5$ . It is worth noting that the confidence limits for  $n = 3$  are almost identical to those shown, suggesting that little would be lost in reducing the number of temporal replicates each year to three.

As an example, after 5 years we can expect the 95% confidence interval for the trend to be from 0.80 to 1.25 of the trend. If the estimated trend is 1.3, for example, we expect the 95% confidence interval to be from 1.04 ( $0.80 \times 1.3$ ) to 1.62 ( $1.25 \times 1.3$ ). We would therefore state that the underlying trend was an increase of between 4% and 62%.

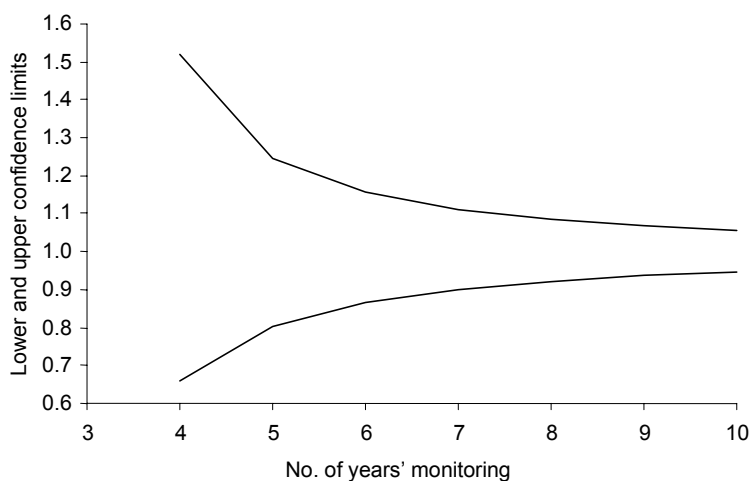


Figure 3. Precision attained for different years of monitoring, in estimating a trend in population size at a particular area ( $n = 4$ ,  $t = 50$  and  $p = 0.5$  in all years).



### 3. Adult survival

Under adult survival (Section 4.2), monitoring the proposed 35 adults is likely to make it difficult to determine whether adult survival is as high as 0.8. Figure 4 shows the precision (confidence limits) versus the number of individuals tagged. For example, if the true rate is 0.8 and we have 40 individuals tagged, we expect the 95% confidence limits to be  $0.80 \pm 0.13$ , i.e. from 0.67 to 0.93. When data are collected over a number of years, the precision of the estimate of mean annual survival over that period will depend on both the precision of each annual estimate and the variation in the true survival rates during that time. The best-case scenario would be one in which this latter variation was small, in which case the precision of the mean annual survival rate would be equivalent to that obtained for a single annual rate by tagging  $t \times k$  individuals, where  $t$  is the number of individuals tagged and  $k$  is the number of years. For example the precision of the mean estimate based on  $t = 40$  and  $k = 2$  would be equivalent to that for a single annual estimate based on tagging  $40 \times 2 = 80$  individuals. If there is a large amount of between-year variation in the true survival rates, the precision achieved for the estimate of the mean rate could be much less than this (and even less than for a single annual estimate).

The frequency of locating tagged individuals does not supply additional information regarding annual survival, i.e. there is no gain in precision of the estimated annual survival by increasing the frequency of locations from once to twice weekly. An appropriate level of effort should be determined by the goals related to determining cause of death.

It might be worthwhile to consider other approaches that could provide additional information on adult survival. One possibility would be to make greater use of individual colour bands. If it is feasible to band a greater number of birds, and individuals could be identified during flock counts or other sampling occasions, resightings may be used to augment the information

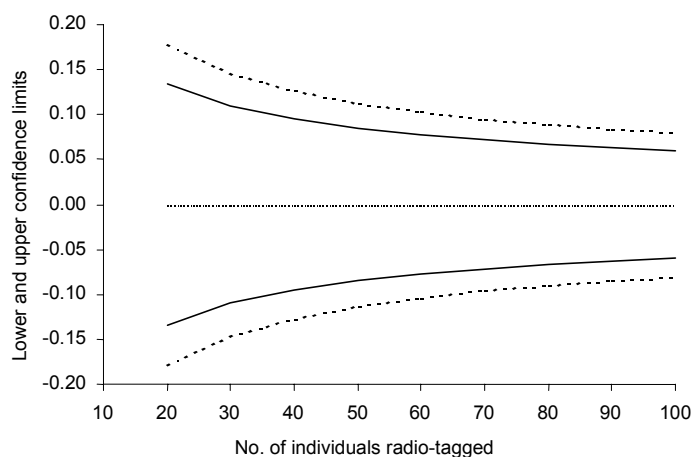


Figure 4. Precision attained for different numbers of individuals, in estimating adult survival rate. The confidence limits have been centred around zero, for ease of comparison. Two values for the survival rate are shown: 0.80 (dashed line) and 0.90 (solid line).

supplied by the radio locations. There are mark-recapture models that enable radio-telemetry and resighting data from uniquely marked individuals to be analysed simultaneously (e.g. Powell et al. 2000). Below, we outline how a likely study design may proceed, but suggest that a more thorough analysis of the situation is required before implementing such a study.

Each year a number of sampling occasions are conducted within a relatively short period of time, and at each sampling occasion a record is kept of the birds identified by colour band combinations. This is continued over multiple years, creating data collected over two time frames, within and between years. Such a design is often known as Pollock's robust design (see Pollock et al. 1990). The within-year sampling periods may be required, as some banded birds may not be identifiable in a given sample due to the bands not being visible or the bird being temporarily away from the sampling location. The resighting and telemetry data may then be combined in a single model, enabling improved estimation of survival and movement parameters.

## 4. Hatching and duckling survival

Under hatching and duckling survival (Section 4.3), there is one important statistical issue in estimating the rate at which eggs hatch and the survival rate to fledging. The sampling scheme proposed is a natural one in that the sample unit is a nest. However, as the unit of interest is an egg or duckling, this is a *cluster* sample, the nest (sample unit) constituting a cluster of units of interest. The impact of this is that the 'effective' sample size will be somewhere between the number of nests sampled and the number of eggs/ducklings sampled. If we can assume that the rate is the same for all nests, the sample size is the number of eggs/ducklings. It is unlikely that we wish to make that assumption. In predicting the precision associated with these two rates, we need to specify the likely amount of variation between nests. In the absence of data on this variation, we have chosen an arbitrarily high level (between-nest coefficient of variation in the true rate of 0.5) to illustrate the possibilities. In addition, given this variation, the expected precision will be least when the rate is close to 0.5, due to the properties of a binomial distribution. In the absence of information on the likely values for these two rates, we have therefore assumed both rates to be 0.5. More realistic values could be substituted into our calculations if they are available.

Figure 5 shows the precision (confidence limits) to be expected in the estimate of hatching rate versus number of nests, when the number of eggs per nest has a mean of 6 and the hatching rate is 0.5. There are two levels of variation between nests shown, zero and high, giving the extremes to be expected in practice. Figure 6 shows the equivalent results for survival to fledging, assuming a mean of two ducklings to be observed per nest.

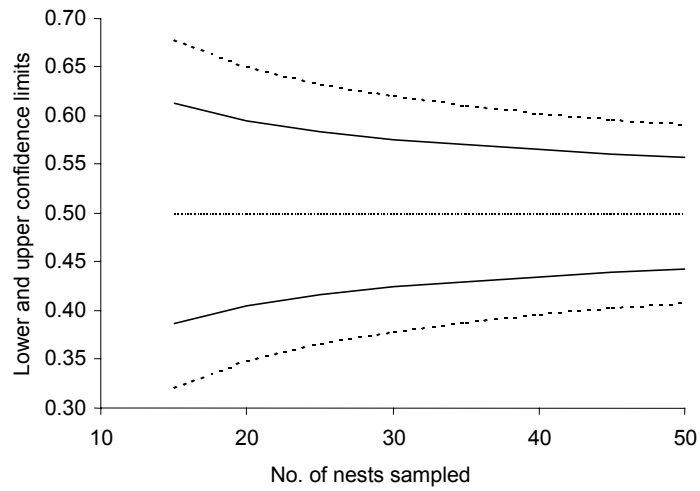


Figure 5. Precision attained for different numbers of nests sampled, in estimating hatching rate (mean of six eggs per nest). Two levels of *between-nest* variation are shown: none (solid line) and high (dashed line).

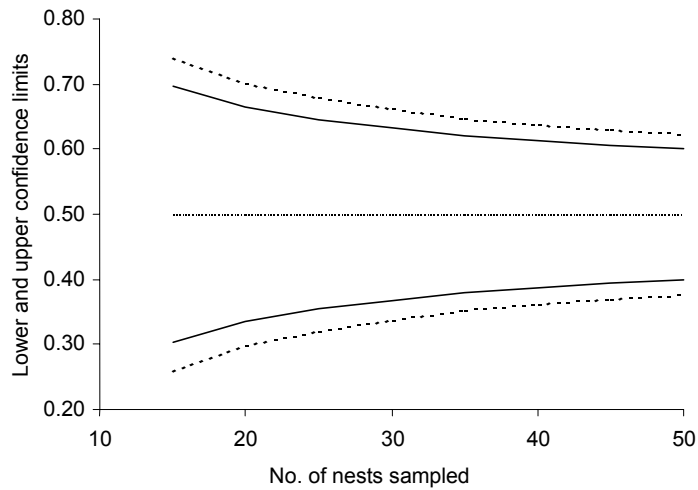


Figure 6. Precision attained for different numbers of nests sampled, in estimating survival rate to fledging (mean of two ducklings sampled per nest). Two levels of *between-nest* variation are shown: none (solid line) and high (dashed line).

Note that we assume that the sampling will be as close to random as possible, possibly stratified according to any variables (e.g. habitat type) that may affect the rates.

## 5. Juvenile survival

With juvenile survival (Section 4.4), the comments on sample size for adult survival are also relevant. Monitoring only 20 juveniles would result in a large degree of uncertainty in the estimated survival rate (Fig. 4), although it may be

adequate to indicate catastrophic losses to the population (say survival less than 0.4). Similarly, if the radio-tagged juveniles are used to provide information on dispersal patterns, the proposed sample size would be insufficient to accurately assess what proportion is dispersing from the main study area. However, they may at least give some indication as to where dispersing juveniles go, which could be useful for planning future studies or monitoring programmes.

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# Appendix 1

## METHODS USED IN ASSESSING PRECISION

We present here the methods used for the precision calculations in this report, separately for each figure.

*Figure 1, p. 7*

The relative precision of  $p$  is calculated using the formula for the standard error of a binomial random variable, giving relative confidence limits of:

$$1 \pm 2 \sqrt{\frac{1-p}{tp}}$$

where  $t$  is the number of radio-tagged individuals.

*Figure 2, p. 8*

The relative precision of a comparison of two estimated population sizes is calculated using the formula

$$\exp\left(\pm t_{2(n-1)} \sqrt{2 \ln(1 + CV_N^2)}\right)$$

where  $t_{2(n-1)}$  is the 5% critical value for a  $t$ -distribution with  $2(n-1)$  degrees of freedom ( $n$  = number of temporal replicate counts) and  $CV_N$  is the coefficient of variation (= SE/Estimate) of estimated population size (assumed to be the same for each of the two estimates being compared). The value of  $CV_N$  is calculated using:

$$CV_N^2 = CV_c^2 + CV_p^2$$

where  $CV_c$  and  $CV_p$  are the coefficients of variation for  $c$  and  $p$  respectively. These are given by:

$$CV_c = \frac{CV_s}{\sqrt{n}} \text{ and } CV_p = \sqrt{\frac{1-p}{tp}}$$

where  $CV_s = SD/Mean$  is the relative sampling variation (between temporal replicate counts), estimated to be 0.10.

*Figure 3, p. 8*

The relative precision of an estimated trend in population size is calculated using the formula:

$$\exp\left(\pm t_{k-2} \sqrt{\frac{\ln(1 + CV_N^2) + \ln(1 + CV_{pV}^2)}{k(k+1)(k-1)/12}}\right)$$

where  $t_{k-2}$  is the 5% critical value for a  $t$ -distribution with  $k-2$  degrees of freedom,  $k$  is the number of years of monitoring,  $CV_N$  is the coefficient of variation of estimated population size (assumed to be the same for each year of monitoring), as given above for Fig. 2, and  $CV_{pV}$  is the relative process variation, estimated to be 0.16.

*Figure 4, p. 9*

The precision of the adult survival rate  $s$  is calculated using the formula for the standard error of a binomial random variable, i.e. as:

$$s \pm 2 \sqrt{\frac{s(1-s)}{ts}}$$

where  $t$  is the number of tagged individuals.

*Figure 5, p. 11*

The precision of the hatching rate  $h$  is calculated using the formula:

$$h \pm t_{n_1-1} \sqrt{\frac{h^2 CV_h^2}{n_1} + \frac{h(1-h)}{n_1 n_2}}$$

where  $t_{n_1-1}$  is the 5% critical value for a  $t$ -distribution with  $n_1 - 1$  degrees of freedom,  $n_1$  is the number of nests sampled,  $n_2$  is the *mean* number of eggs per nest and  $CV_h$  is relative variation between nests in the true hatching rate, assumed to be either 0 or 0.5 (representing an expected upper bound).

*Figure 6, p. 11*

The relative precision of fledging rate  $f$  is calculated as for hatching rate, i.e. using the formula:

$$f \pm t_{n_1-1} \sqrt{\frac{f^2 CV_f^2}{n_1} + \frac{f(1-f)}{n_1 n_2}}$$

where  $t_{n_1-1}$  is the 5% critical value for a  $t$ -distribution with  $n_1 - 1$  degrees of freedom,  $n_1$  is the number of nests sampled,  $n_2$  is the *mean* number of fledglings per nest and  $CV_f$  is relative variation between nests in the true fledging rate, assumed to be either 0 or 0.5 (representing an expected upper bound).