Monitoring protocols for Hamilton's frogs *Leiopelma hamiltoni* on Stephens Island

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1. Introduction

This report provides recommendations for a sampling scheme for a mark-recapture study of Hamilton's frog *(Leiopelma hamiltoni)* on Stephens Island in the Marlborough Sounds.This is a threatened species, and monitoring is required for the next five years, with a view to ascertaining if the population is steady, increasing or decreasing.

Recommendations are given for appropriate numbers of trips per year and numbers of sampling nights per trip. Advice is also given about the sampling intensity and methods, the records to keep, and the appropriate statistical analyses to be used.

In the sections which follow, I have relied heavily on the previous studies by Newman (1990), Brown (1994) and Thomson (1996), and on Newman's 1996 report. Most of the following sections refer to the frogbank population: the frogpit population is discussed separately in Section 8.4.

2. Sampling methods

It is intended to run a mark-recapture study, in which frogs are captured, given individual marks, and returned to the population for subsequent recaptures and identification. For mark-recapture analysis to be possible, each frog must be marked at its first capture in a manner which will identify it at later captures. This will be achieved by a toe-clipping method, in which the particular combination of toe-clips will identify it unambiguously.

On the frogbank, the sampling will be clone under, and on a strip each side of, the boardwalk.The width of this strip should be fixed in advance: Newman's (1990) use of a 1 m strip looks appropriate, and staying with that width will make future results more easily compared with his work. I understand the strip will be kept clear of the *Muehlenbeckia* vines to maintain visibility and keep the sample numbers up.

I note that Thomson (1996) reported a strip of 1.5 m width being searched since 1990, but used Newman's search area estimate of 140 m^2, which was based on a 1 m strip. Her density estimates should be adjusted to allow for this.

3. Concomitant information

Although a basic Cormack Jolly-Seber mark-recapture analysis (see Section 5) does not use concomitant information like search effort and weather records,

it is still desirable to record these extra details. This is because other methods of mark-recapture analysis (e.g. Huggins 1989,1991; Otis *et al.* 1987; Pollock *et at.* 1984) often use these concomitant variables in the modelling, and it is sensible to retain the option of these possibly more appropriate models later. Also, if extremely bad luck with capture rates gives insufficient numbers for a reliable mark-recapture analysis, with weather and effort information available it will be possible to fall back on count data and search-effort Poisson models ("encounter sampling"), which are less powerful than mark-recapture methods but would still yield some information.

Accordingly, each night of sampling should have search effort and appropriate weather information recorded, as well as the captures. Newman (1990) found that presence/absence of rain during the search, humidity and light intensity were correlated with the numbers of frogs seen. Thomson (1990) found humidity, wind direction and wind speed were relevant.

Similarly, records of weight, snout-vent length, grid references, and whether found on rocks, vines, etc., are not strictly needed for the mark-recapture analysis, but will provide useful extra information - for example, weight and snout-vent length may help identify juveniles, thus giving some information about age structure.

4. Study design

The study will follow a plan in which a sequence of sampling sessions (or trips) will take place each year, within each of which there will be several successive nights of samples.

This samples-within-sessions method is called the robust design by Pollock (1982). To use the data for a Cormack Jolly-Seber analysis, information within each session is pooled to record which animals were captured at least once on that trip. The robust design is recommended because:

- The pooling within trips allows the capture probabilities to rise to levels acceptable for a Cormack Jolly-Seber analysis. One night's sampling would not be enough.

- Each session (trip) may be used to provide an estimate of the current population size based on closed population models, if enough captures occur. This gives information about trap response and heterogeneity of capture not available from the Cormack Jolly-Seber model.

- Once field workers have gone to the island it makes economic sense for them to stay several nights rather than one.

- Recent models by Kendall *et al.* (1995) fully exploit the information both within and between sessions, combining the closed and open population models. I do not yet have programmes available to do the estima-

tion, but will be working on them over the next year. Analysis using these new models should be available by the end of the study.

5. Methods of analysis

I recommend the Cormack Jolly-Seber model as appropriate for the frogbank data, supplemented by Kendall *et al.* (1995) models. These newer models will provide extra information about the population, although they are similar enough to the Cormack Jolly-Seber model to be unlikely to change the estimates much or provide more powerful tests.

The Cormack Jolly-Seber model, also known as the Jolly-Seber model, was developed by three authors, Cormack (1964), Jolly (1965) and Seber (1965). This is an open population model which allows for additions (births and immigration) and deletions (deaths and emigration) between sampling sessions. It makes the following assumptions:

- At the time of the i^{th} sampling session, all animals have the same probability p_i of capture. This implies that there is an assumption of no trap-response (trap-shyness or trap-happiness), and no difference of capture probability caused by age differences, sex differences, sampling area in relation to the frog's home range, etc. It does, however, allow for probability of capture to vary by time, which allows for weather effects.

- The population is closed within the time of each session.

- The probability of survival ϕ_i from sampling session i to $i + 1$ is the same for all individuals. Again, this does not allow for different survival rates due to age, sex, etc., but does allow for weather effects such as poor seasons.

- All individuals are marked uniquely at their first capture, and marks are adequate for identification on recapture.

- We also assume that all animals caught at the i^{th} sample are returned alive to the population - this is not strictly necessary for a Cormack-Jolly-Seber analysis, but I have assumed it for the power analyses in this report.

One possible failure of the Cormack Jolly-Seber assumptions might occur if there is a behavioural response to capture - e.g. shyness induced by the capturing and marking process. If this is short-term, as has been found for the Maud Island frogs (Bell & Pledger, in prep.), the Cormack Jolly-Seber analysis will be unaffected. This is because it essentially uses only the first capture of each frog within one session (probability p_i), and not subsequent captures within the session (probability $c_i < p_i$). However, long-term capture-shyness will cause the Cormack Jolly-Seber population estimates to overestimate the true population. Provided the robust sampling design is used, the recent meth-

ods of analysis by Kendall *et al.* (1995) will enable this to be allowed for in the model.

The Cormack Jolly-Seber estimates will also be biased if there is heterogeneity of capture, with some animals being more likely to be captured than others. This could be a behavioural effect, with bold and timid animals, or could be induced by the spatial effect of animals living at the edge of the sampling area having a lower probability of capture. Where there is heterogeneity of capture, the Cormack Jolly-Seber analysis will underestimate the true population size. However, as we will be comparing population estimates over time, the biases will approximately cancel, so that any trends in the population will still be detected.

The assumption of equal survival rates for all animals over any given time interval is often not a problem for such long-lived species as these frogs - they may spend much of their lives at a fairly constant survival rate before ageing sets in. There are goodness-of-fit tests available to check this assumption (Pollock *et al.* 1985). This longevity also ensures the population is approximately closed within each session.

6. A likelihood ratio test

The Cormack Jolly-Seber analysis is usually used to provide population estimates and their standard errors through time. A graph of these estimates and their confidence intervals versus time gives a visual impression of any possible trends in the population size, but since the estimates are correlated they may not be used in statistical tests, like simple linear regression, which require independent data.

To test for a trend versus a constant population, it is necessary to go back to the likelihood function for the original multinomial model. We may fit three models to the data:

- Model 1: Variable N. The population size N is assumed to vary through time. This model fits a different N for each session time, allowing for fluctuations. It is the model used for the Cormack Jolly-Seber estimates.

- Model 2: A linear trend in N. The population size is assumed to vary linearly through time. In this model, the population size is constrained to lie on a straight line $N = \alpha + \beta \times TIME$ where TIME might he measured say in months from the start of the study. Instead of fitting a different N at each time, there are two parameters to estimate, a and R and these fix the N estimates.A β estimate significantly below zero would indicate a declining population.

- Model 3: Constant N. The population is assumed to be constant. Only one parameter N is estimated.

Any two of these models may be compared by a (log) likelihood ratio test (analysis of deviance test). Of particular interest for an endangered population is the test of Model 2 (linear trend) versus Model 3 (constant population). This tests H_0: $\beta = 0$ (i.e., population is constant) versus H_1: $\beta \neq 0$ (a linear trend over time).

The test statistic is

χ^2 = Residual deviance under Model 3- Residual deviance under Model 2,

where the residual deviance of a model is 2 x (maximised log likelihood under the maximal model - maximised log likelihood under this model).

When a difference of deviances is taken, the maximal model part drops out. If H_0 is true, the distribution of the test statistic is χ^2_1, so the critical value for the test is taken from a χ^2 distribution on 1 degree of freedom.

The likelihood formula and an S+ programme for doing the test are in Appendix 1.

7. Power of the test

In planning a mark-recapture study, if preliminary estimates of population size, probability of capture and survival rates are available, the power to detect a trend in the population may be calculated for various sampling schemes. I have done this for some possible schemes.

The power of the test is the ability to detect departures from the null hypothesis - in this study, the probability of detecting a trend if in fact there is one. The power depends on the size of the trend (the actual value of the slope of the trend line), and on the chosen significance level at which the test will be run.

Using estimates from Newman (1990) and Thomson (1996), I have assumed that the population density will start at about 55/100 m^2, that the probability of capture per night will be about 0.1 (assuming autumn or winter sampling), and that the annual survival rate is about 0.9. I have tried various sampling schemes, various rates of decline of the population (as decline is of more concern than increase), and various significance levels for the test.

To calculate the power, I used the method detailed in Lebreton *et al.* (1992). For a population with the given sampling scheme and with the specified rate of decline, I calculated the expected Cormack Jolly-Seber counts (n, m, r, z). The test statistic is worked out for this population, and this gives the non-centrality parameter for the (distribution $\chi^2_1(\lambda)$ from which the test statistic comes. (If H_0 is true and there is really no decline, $\lambda = 0$. and the test statistic is from the null distribution, the central chi-squared χ^2_1.)

The power of the test is the probability of rejecting H_0. This is thus the probability that a random variable from the $\chi^2_1(\lambda)$ distribution exceeds a critical value from the central χ^2_1 distribution (e.g. 3.84 if using a 5% significance level). This is illustrated in Figure 1.

In the case that H_0 is true and there really is no change in the population, $\lambda = 0$ and the two distributions coincide, giving a power equal to a, the significance level chosen for the test. As the population trend becomes stronger, increases, the $\chi^2_1(\lambda)$ distribution moves to the right, and the power increases (towards a maximum of 1). Some power curves are shown in Figure 2.

The choice of an a-level should reflect the relative consequences of Type I and Type II errors, rejecting H_0 when it is true, and accepting it when it is false, respectively (Skalski and Robson 1992, pp21-22). Since an early warning of a possible decline in the population is of major importance here, a should be set fairly high, perhaps about 15% or 20%, to give more power to detect a decline. Skalski and Robson (1992) consider this reasonable for ecological studies.

Tables 1 and 2 in Appendices show some values of the power for various rates of decline in the population, for several sampling schemes and different significance levels. It is clear that the total number of successful sampling nights is of much more importance than the actual allocation of those nights into sessions and samples per session. It seems best to plan a certain number of trips per year, during autumn and winter, to keep the probability of capture acceptably high, and to be flexible if possible about how long the trip lasts. If there are good capture rates for the first few nights, with say 20 different animals seen over those nights (whether new or already seen on a previous trip), the trip could be concluded. However, if for example dry weather lowers the capture rate to below about 5 per night, a longer time would be needed to try to bring the number of different animals seen on this trip up to 20. Also, the exact spacing in time of the trips is not important, so if there is the possibility of delaying the trip until a long-term weather forecast indicates rain, this would be a good strategy.

It is possible to tie in this power analysis with a cost/benefit approach provided that rough estimates are available for the cost per trip (e.g. boat hire), the cost per person per trip (e.g. transport cost per individual), the cost per day (e.g. equipment usage), and the cost per person per day (wages food). With these estimates, one may either maximise statistical power for a fixed cost or minimise the cost for a fixed power (see e.g. Millard and Lettenmeier 1986).

8. Recommendations

8.1 SAMPLING DESIGN

- Number of trips: The proposal to make about four trips per year to the island seems good. These trips should be undertaken during autumn and winter, to help ensure adequate sample sizes. The number of trips could go above or below four without jeopardising the power to detect a population change. The exact timing of each trip is not crucial - they need not be evenly spaced. Some flexibility in planning the trips to coincide with wet weather would be useful.

- Number of nights per trip: Within each trip, there will be a number of sampling nights. If there are 5 or more frogs captured each night, 5 nights per trip should be enough to ensure a respectable power of about 0.8 to detect a population density drop of 1 per year, from 55/100 m^2 at the start to 50/100 m^2 at the end of the study, if the significance level α is set at 15%. The power is higher for a larger drop in population. The main criterion for the number of nights per trip is that about 20 different animals (excluding recaptures within that trip) should be seen. This level of sampling could be achieved by choosing the trips to coincide with wet weather, by taking several searchers, or by waiting and continuing sampling until the numbers of captures build up to the desirable level. Power is lost as the number of captures drops. Different trips may have different numbers of nights: it is not necessary to have the numbers of nights balanced.A minimum of three nights is needed to exploit fully the chance of optional extra analyses using closed population models.

- Number of searchers: The number of searchers employed is important only insofar as it may increase the number of frogs seen and so improve the power of the statistical analyses. Any searchers would need to be fully trained so as to spot the frogs successfully. If an unobservant searcher were regularly put on one section of the boardwalk, frogs in that area would have lower probability of capture, thus introducing undesirable heterogeneity of capture.

- Area to search: If time is running short for a sample, do not search only part of the length of the boardwalk. This also would introduce heterogeneity of capture. It would be better to do a quick search of all the area. This would lower the probability of capture that night for all the frogs equally, thus retaining the homogeneity of capture rate required by the Cormack Jolly-Sober model.

- Frog handling: The frog must be marked on its first capture (unless it is already identifiable from natural toe loss or previous toe clips by Brown 1994). The toeclip code given should avoid those already used by Brown.

8.2 DATA TO RECORD

Each night:

- Date of sample.
- Weather information: Whether or not rain fell, humidity, light intensity, and also (if possible) wind direction, wind speed and temperature.
- Search effort information:The number of searchers, and number of minutes spent by each in actual search time (excluding handling time).

Each capture or recapture

- Date of capture.
- Toeclip code of frog (either the existing toeclip or the one just given).
- Weight, measurements (e.g. snout-vent length). Presumably these need not be recorded if the frog has already been seen on this trip.
- Grid reference, whether found on vines, rocks, etc.
- Any other information, e.g. scars, etc.

8.3 STATISTICAL ANALYSIS

At the end of the study (and also part way through, if desired), use the Cormack-Jolly-Seber likelihood ratio test to test for a trend versus a constant population. The usual Cormack Jolly-Seber estimates of population and survival and their confidence intervals should also be calculated and graphed against time.

On the way through the study, for trips with sufficient data, closed population estimates of Otis et al. (1975) will give progress reports on how the population is faring. However, these are unlikely to have narrow enough confidence bounds for any firm conclusions to be reached.

8.4 THE FROGPIT

All the previous discussion has centred on the frogbank population, which is large enough for statistical testing to be done. In the frogpit, although searching and toeclipping will yield interesting information, there will be no chance of a conclusive statistical analysis (unless there is a population explosion in the next year or so). During these few years, the data will provide descriptive measures only, but there is a possibility of its being usefully incorporated into later studies.

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10. Appendices

10.1 FORMULAE AND PROGRAMMES

Likelihood Formula

The likelihood formula for the Cormack-Jolly-Seber model is:

$$\prod_{i=1}^{K}\binom{U_i}{u_i} p_i^{u_i} q_i^{U_i-u_i} \cdot \frac{\prod_{i=1}^{K} u_i!}{\prod_h x_h!} \prod_{i=1}^{K-1}\left(\chi_i^{n_i-r_i}(\phi_i q_{i+1})^{z_{i+1}}(\phi_i p_{i+1})^{m_{i+1}}\right)$$

(Seber 1973 p.198), where

K = number of sampling sessions

U_i = number of unmarked animals in population at time i

u_i = number of unmarked animals caught in i^{th} session

p_i = probability of capture in i^{th} session

q_i 1 - p_i

χ_i = probability an animal caught at i is not seen again

ϕ_i = probability an animal alive at i survives until $i+1$

x_h = number of animals with capture history h, where h indexes the observed capture histories.

The number in the population at time i is $U_i + M_i$, where M_i is the number of marked animals alive in the population at time i. Estimates of the unknown terms in the likelihood equation are found by maximising the likelihood, and the further estimates are $\hat{M}_i = m_i/\hat{p}_i$ and $\hat{N}_i = \hat{U}_i + \hat{M}_i$.

For Model 2, N_i is constrained to be $\alpha + \beta \times T$, where T is time in months from the start of the study.

For Model 3, N_i is constrained to be a constant, N.

S+ Likelihood Calculations for Model 2

This S+- programme does the log likelihood calculations for M odel 2 (linear trend):

```
# Log likelihood functions for JS model, linear trend in N.
# This function differs from the true log likelihood by a constant
# which will cancel when comparisons of models are done.
```

```
# INPUTS:

# K      = number of sessions.
# u.vect = K-vector of number of new captures in each sample.
# n.vect = K-vector of numbers captured in the samples.
# m.vect = K-vector of numbers already marked and captured
#          in the samples.
# r.vect = K-vector of numbers in sample i which will be
#          recaptured.
# z.vect = K-vector of z counts.
# times.vect = vector of times of samples (e.g. months from
#              start of study).

# UNKNOWN PARAMETERS:

# alpha = intercept of N line.
# beta = slope of N line.
# p.vect = K-vector of probabilities of capture.
# phi.vect = (K-1)-vector of survival probabilities.

# CREATE THE LIKELIHOOD FUNCTION:

ll.jslin <- function(alpha,beta,p.vect,phi.vect)

   if (min(p.vect)>O) U.vect <- alpha +
                     beta*times.vect - m.vect/p.vect else
      U.vect <- alpha + beta*times.vect - m.vect
   chi.vect <- rep(O,K)              # Calculate chi vector
   chi.vect[K] <- 1
   for (j in (K-1):1)
      chi.vect[j] <- 1-phi.vect[j]+phi.vect[j]*
                     (1-p.vect[j+1])*chi.vect[j+l]
   if ((min(U.vect-u.vect)>=0)&(min(p.vect)>O)&
       (max(p.vect)<l)&(min(phi.vect)>O)&(max(phi.vect)<l))

      loglik <- 0
      for (i in 1:K)

         loglik <- loglik + lgamma(U.vect[i]+1) -
                   lgamma(U.vect[i]-u.vect[i]+1) +
                   n.vect[i]*log(p.vect[i]) +
                   (U. vect [i] -u. vect [i] +z . vect [i] )
                   log(1-p.vect[i]) +
                   (n.vect[i]-r.vect[i])*log(chi.vect[i])

      for (i in 1:(K-1))
         loglik <- loglik+(z.vect[i+l]+m.vect[i+l])*
```

```
                    log(phi.vect[i])
      } else loglik <- -1000000
   loglik


# TO DO THE OPTIMISATION:

jslin.fit <- ms(" -11.jslin(alpha,beta,p.vect,phi.vect),start =
                   list(alpha=mean(n.vect)+50,beta=0,
                   p.vect=rep(0.5,K),phi.vect=rep(0.8,K-1)))
\end[verbatim}

\subsection*{S+ Likelihood Calculations for Model 3}

This is the programme for Model 3 (constant N):

\begin{verbatim}
# Log likelihood functions for JS model with N constrained
# to be constant.
# This function differs from the true log likelihood by a constant
# which will cancel when comparisons of models are done.

# INPUTS:

# K      = number of sessions.
# u.vect = K-vector of number of new captures in each sample.
# n.vect = K-vector of numbers captured in the samples.
# m.vect = K-vector of numbers already marked and captured
#          in the samples.
# r.vect = K-vector of numbers in sample i which will be recaptured.
# z.vect = K-vector of z counts.

# UNKNOWN PARAMETERS:

# N = constant number in population.
# p.vect = K-vector of probabilities of capture.
# phi.vect = (K-1)-vector of survival probabilities.

# CREATE THE LIKELIHOOD FUNCTION:

ll.jsconst <- function(N,p.vect,phi.vect)

   if (min(p.vect)>O) U.vect <- N - m.vect/p.vect else
      U.vect <- N - m.vect
   chi.vect <- rep(O,K)                  # Calculate chi vector
   chi.vect[K] <- 1
   for (j in (K-1):1)
```

```
      chi.vect[j] <- 1-phi.vect[j]+phi.vect[j]*
                     (1-p.vect [j+l])*chi .vect [j+l]
   if ((N>=0)&(min(U.vect-u.vect)>=0)&(min(p.vect)>O)&
       (max(p.vect)<l)&(min(phi.vect)>O)&(max(phi.vect)<1))

      loglik <- 0
      for (i in 1:K)

         loglik <- loglik + lgamma(U.vect[i]+1) -
                   lgamma(U.vect[i]-u.vect[i]+1) +
                   n.vect[i]*log(p.vect[i]) +
                   (U.vect[i]-u.vect[i]+z.vect[i])*
                   log(1-p.vect[i]) +
                   (n. vect [i]-r. vect [i]) *log(chi . vect [i] )

      for (i in 1:(K-1))
         loglik <- loglik+(z.vect[i+l]+m.vect[i+l])*
                   log(phi.vect[i])
      } else loglik <- -1000000
   loglik


# TO DO THE OPTIMISATION:

jsconst.fit <- ms(" -ll.jsconst(N,p.vect,phi.vect),start =
               list(N=max(n.vect)+50,
               p.vect=rep(0.5,K),phi.vect=rep(0.8,K-1)))
```

S-}- Power Calculations

The programme used for the power calculations follows.

```
# Commands for finding power, using expected counts.

# Initialise with

# sig = sig level at which test is to be run (O.OS,O.l,etc.)
# phi = annual survival rate
# pcapt = prob. capt. on one night
# nyears = number of years of study
# sampy = number of samples per year
# Nstart = starting value of N
# sess.list = vector of numbers of sessions per year
 # dec.list = vector of amount of decrease
```

```
sig <- 0.25
phi <- 0.9
pcapt <- 0.1
nyears <- 5
sampy <- 20
Nstart <- 77   # This is for the 140 sq.m. area, not 100 sq.m.
sess.list <- c(4)
dec.list <- seq(0,4,0.2) # Density loss per year
power.mat <- matrix(rep(0,length(sess.list)*length(dec.list)),
                    length(sess.list),length(dec.list))

for (sl in 1:length(sess.list)) # nsess = no. sessions per year

   nsess <- sess.list[sl]
   nsamp <- round(sampy/nsess)
   if (nsess==1) times.vect <- c(6,18,30,42,54)
      # June sampling
   if (nsess==2) times.vect <- c(4,7,16,19,28,31,40,43,52,55)
      # Apr,Jul
   if (nsess==3) times.vect <-
      c(4,6,8,16,18,20,28,30,32,40,42,44,52,54,56)
      # Apr,Jun,Aug
   if (nsess==4) times.vect <-
    c(3,5,6,8,15,17,18,20,27,29,30,32,39,41,42,44,51,53,54,56)
      #Mar,May,Jun,Aug
   if (nsess==6) times.vect <- c(3:8,15:20,27:32,39:44,51:56)
      #Mar:Aug
   K <- nyears*nsess
   # Between-session survival rates
   phi.vect <- rep(0,(K-1))
   for (j in 1:(K-1))
      phi.vect[j] <- phi**((times.vect[j+l]-times.vect[j])/12)
   # Prob   at least one capture per session.
   probcapt <- 1 - (1-pcapt)**nsamp
   # Vector of prob. capt. values
   p.vect <- rep(probcapt,K)
   # Calculate chi vector (prob. an animal caught at i is not
   # seen again).
   chi.vect <- rep(0,K)
   chi.vect[K] <- 1
   for (j in (K-1):1) chi.vect[j] <-
      1-phi.vect[j]+phi.vect[j]*(1-p.vect[j+l])*chi.vect[j+l]
   for (dl in 1:length(dec.list))

      decrease <- dec.list[dl]     # Decrease by end of 5 years
      # Construct vector of N values
      beta <- -7*decrease/60          # beta is slope of N line
```

```
# and has been adjusted for the 140 sq.m.
N.vect <- Nstart + beta*times.vect
# Find psi vector (prob. animal caught at i was not seen
# before).
psi.vect <- rep(O,K)
for (j in 2:K) psi.vect[j] <- psi.vect[j-1]*
                              N.vect [j-1] /N.vect [j]
# Calculate lambda vector.
lambda.vect <- rep(O,K)
lambda.vect[l] <- 1
for (j in 2:K) lambda.vect[j] <-
   1-psi.vect[j]+psi.vect[j]*(1-p.vect[j-1])*
   lambda.vect [j-1]
# Expected counts
U.vect <- lambda.vect*N.vect
n.vect <- p.vect*N.vect
u.vect <- lambda.vect*n.vect
m.vect <- (1-lambda.vect)*n.vect
r.vect <- (1-chi.vect)*n.vect
z.vect <- (1-lambda.vect)*(1-chi.vect)*
          (1-p.vect)*N.vect
# Find lls under linear model and constant model.
Min <- ll.jslin(Nstart,beta,p.vect,phi.vect)
llconst <- ll.jsconst(mean(N.vect),p.vect,phi.vect)
# Find change in deviance
dev.change <- 2*(lllin - llconst)
# Calculate power, store in matrix.
crit.val <- gchisq((1-sig),l)
power.mat[sl,dl] <- 1 - pchisq(crit.val,l,dev.change)
```

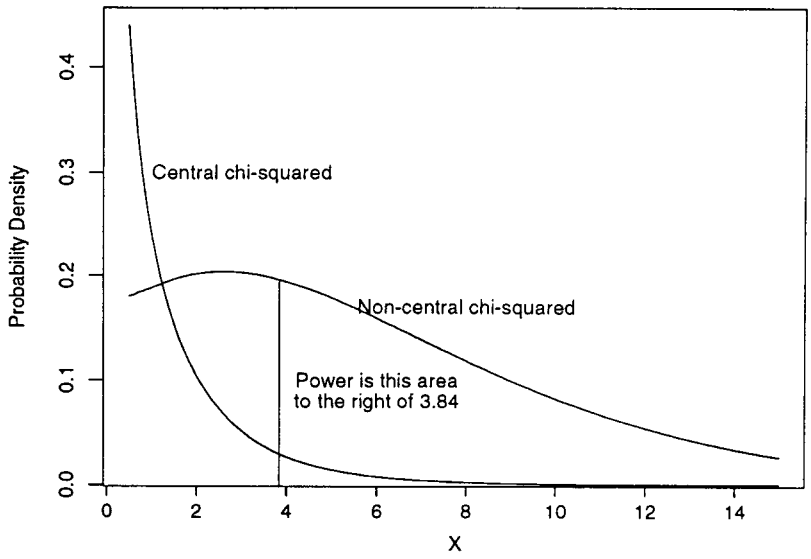

Figure 1. THE POWER OF THE TEST IS THE AREA UNDER THE NON-CENTRAL χ^2 DISTRIBUTION TO THE RIGHT OF THE CRITICAL VALUE DETERMINED BY THE CENTRAL DISTRIBUTION. IF α=0.05, THE CRITICAL VALUE IS 3.84.

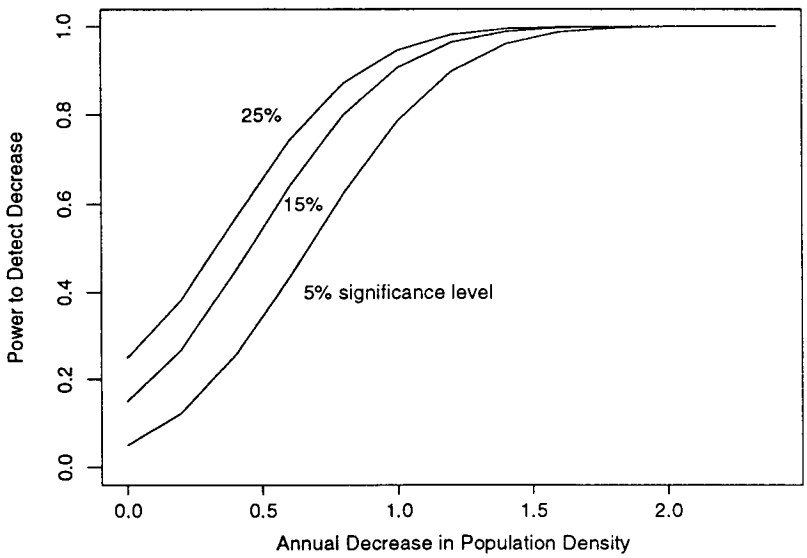

Figure 2. THE POWER TO DETECT A DECLINE IN POPULATION DENSITY, ASSUMING A STARTING DENSITY OF $55/100\text{m}^2$, PROBABILITY OF CAPTURE 0.1 PER NIGHT, WITH FOUR SESSIONS EACH OF FIVE NIGHTS PER YEAR

Table 1. Powers for 12 Nights' Sampling per Year

Significance level of test	Number of Trips	Number of nights per trip	Annual Decline in Population Density per 100rn 2				
			0	1	2	3	4
0.05	1	12	.0.5	.426	.916	.999	1.000
	2	6	.05	.418	. 911	.999	1.000
	3	4	.0.5	.416	. 911	. 999	1.000
	4	3	.05	.41.5	.910	. 999	1.000
	6	2	.0.5	.41.5	.910	. 999	1.000
0.10	1	12	. 10	.5.52	.955	1.000	1.000
	2	6	. 10	.543	.952	1.000	1.000
	3	4	. 10	.541	.952	1.000	1.000
	4	3	. 10	.540	.951	1.000	1.000
	6	2	. 10	.540	.951	1.000	1.000
0.15	1	12	.1.5	.632	.971	1.000	1.000
	2	6	.1.5	.623	.969	1.000	1.000
	3	4	.15	.622	.969	1.000	1.000
	4	3	.15	.621	.969	1.000	1.000
	6	2	.15	.611	.969	1.000	1.000
0.20	1	12	.20	.690	.980	1.000	1.000
	2	6	.20	.652	.979	1.000	1.000
	3	4	.20	.681	.979	1.000	1.000
	4	3	.20	.650	.9 78	1.000	1.000
	6	2	.20	.680	.978	1.000	1.000
0.25	1	12	.25	.73.5	.986	1.000	1.000
	2	6	.25	.728	.985	1.000	1.000
	3	4	.25	.727	.984	1.000	1.000
	4	3	. 25	.726	.95-1	1.000	1.000
	6	2	. 2.5	.726	.984	1.000	1.000

Table 2: Powers for 24 Nights' Sampling per Year

Significance level of test	Number of Trips	Number of nights per trip	Annual Decline in Population Density per 100m 2				
			0	1	2	3	4
0.05	1	24	. 05	1.000	1.000	1.000	1.000
	2	12	.05	.905	1.000	1.000	1.000
	3	8	.05	.900	1.000	1.000	1.000
	4	6	.05	.897	1.000	1.000	1.000
	6	4	.05	.897	1.000	1.000	1.000
0.10	1	24	.10	1.000	1.000	1.000	1.000
	2	12	.10	.948	1.000	1.000	1.000
	3	8	.10	.945	1.000	1.000	1.000
	4	6	.10	.943	1.000	1.000	1.000
	6	4	. 10	.943	1.000	1.000	1.000
0.15	1	24	. 15	1.000	1.000	1.000	1.000
	2	12	. 15	.967	1.000	1.000	1.000
	3	8	. 15	.964	1.000	1.000	1.000
	4	6	. 15	.963	1.000	1.000	1.000
	6	4	. 15	.963	1.000	1.000	1.000
0.20	1	24	.20	1.000	1.000	1.000	1.000
	2	12	.20	. 977	1.000	1.000	1.000
	3	8	.20	.975	1.000	1.000	1.000
	4	6	.20	.974	1.000	1.000	1.000
	6	4	.20	.974	1.000	1.000	1.000
0.25	1	24	.25	1.000	1.000	1.000	1.000
	2	12	.25	.983	1.000	1.000	1.000
	3	8	.25	.982	1.000	1.000	1.000
	4	6	.25	.981	1.000	1.000	1.000
	6	4	.25	.981	1.000	1.000	1.000