

The Effect of Recycled Individuals in the Jolly-Seber Model with Tag Loss

SUMMARY: In capture-recapture studies, recycled individuals occur when individuals lose all of their tags and are recaptured as though they were new individuals. Typically, the effect of these recycled individuals is assumed negligible. Through a simulation-based study, we examine the effect of recycled individuals on parameter estimates in the Jolly-Seber model with tag loss (Cowen and Schwarz, 2006) in double tagging experiments. With low tag-retention rates, high capture rates, and high survival rates, recycled individuals can produce overestimates of population size. These results are particularly noticeable in longer studies. We validate the simulation framework using long-term census data of elephant seals where we found population size estimates to be between 8 and 53% larger when recycled individuals were ignored. However, including recycled individuals did not affect estimates of capture, survival, and tag-retention probabilities.

KEY WORDS: Abundance; Capture-mark-recapture; Complete tag loss; Demography; Double-tagging; Elephant seal.

Introduction

Mark-recapture studies utilize statistical techniques to estimate population parameters. Over k sampling periods, individuals are captured, tagged with unique tags, released and potentially recaptured at subsequent sampling times. The Jolly-Seber model (Jolly, 1965; Seber, 1965) is used to model open populations since it can estimate parameters of interest such as population size and survival rates (Pollock et al., 1990). An important assumption of this model is that individuals never lose their tags. However, when this assumption is violated, serious bias can occur in the parameter and variance estimates (Arnason and Mills, 1981). Double-tagging, the placement of two tags on an individual, can be used to estimate tag retention rates. Double tagging studies have been used for a wide variety of species (for example cod: Björnsson et al. 2011, lobsters: Xu et al. 2014:, sea turtles: Bjørndal et al. 1996, elephant seals: Pistorius et al. 2000, black bears: Diefenbach and Alt 1998) to investigate probabilities of tag loss or tag shedding rates. Often a mixture of single- and double-tagged individuals is used for practical purposes. Cowen and Schwarz (2006) incorporated tag-loss by developing the Jolly-Seber tag-loss (JSTL) model for experiments where some fraction of individuals are double tagged. This model was further extended to account for heterogeneity in capture between groups (Xu et al., 2014). In the simplest form of the JSTL model, it is assumed that every individual present in the population at sampling occasion k has capture, survival, and tag retention probabilities that are homogeneous for all individuals in the population across all sampling occasions. However, these assumptions are rarely met and can induce significant bias in the parameter estimates (Schwarz and Costa, 2012).

Occasionally in mark-recapture experiments, previously captured individuals lose all of their tags (complete tag loss). These individuals are either recognized upon recapture (for example, through scarring or fin clipping), and not re-tagged, or if unrecognized, these individuals would be tagged again and treated as “new” individuals. Individuals who lose both tags and are recaptured and re-tagged are known as recycled individuals. For example, an individual

with the following tag history over three sampling occasions {11 01 00} was double tagged at time 1, lost a tag between times 1 and 2, and may have lost its last tag between sampling occasions 2 and 3 and then have been recaptured at sampling occasion 3 resulting in a new individual with capture history {00 00 11}. If the rate of tag loss is small, bias in the population estimate will also be small for the Peterson estimators (Seber and Felton, 1965). Typically in the Jolly-Seber and JSTL models, the effect of recycled individuals is assumed to be negligible. However, in situations where tag retention is low and survival and recapture probabilities are high it is suspected that recycled individuals will bias population size estimates upwards. The motivation for this study was to investigate the effect of recycled individuals on parameter estimates in the JSTL model through a simulation study and determine under which conditions researchers need to be concerned. This study is important as the assumption that the effect is negligible has not been fully tested and quantified, and most studies that rely on marking individuals typically experience tag loss. Thus, there is a need to account for recycled individuals given the desire for accurate and robust estimates for management and conservation purposes.

In order to determine whether the simulation framework provided a reasonable approximation to the real world, we analyzed the effects of recycled individuals in long-term census data of elephant seals (*Mirounga leonina*). For this particular population, seals could be identified even if they lost both tags given that they had a permanent brand (McMahon and White, 2009).

Methods

The Jolly-Seber Model with Tag Loss (JSTL)

Full development of the JSTL model is given by (Cowen and Schwarz, 2006) and summarized in the Online Supplement including a table of notation.

Many different models can be specified for the JSTL model where parameters are homogeneous or heterogeneous with respect to time or group. We consider the case of the JSTL model where capture, survival, and tag retention probabilities are constant over time (Cowen and Schwarz, 2006).

Assumptions of the JSTL model with constant survival, capture, and tag retention probabilities and time-varying entry probabilities are as follows:

- The effect of recycled individuals is negligible
- All individuals (marked and unmarked) are equally catchable, and that capture probabilities for all individuals are the same for all individuals at all sample times
- All individuals (marked and unmarked) have equal survival probabilities between all sample times
- All individuals have equal entry (birth or immigration) probabilities, but entry probabilities can vary between sample times
- All marked individuals have equal tag retention probabilities between all sample times
- For double-tagged individuals, tag loss is independent between tags
- There is independence across all individuals
- The sampling period is relatively short compared to the interval between sampling times

Likelihood and Estimation

The JSTL model is developed under the idea of a superpopulation (the number of individuals that will enter population at some point during the study) (Schwarz and Arnason, 1996) and this allows the likelihood to be formulated into three parts: 1) a model for the observed number of unique tag histories given the superpopulation size (L_1^A), 2) a model for the recaptures given the observed number of unique tag histories (L_1^B), and 3) a model for the number of individuals lost on capture (L_3). The third component L_3 , is typically used for

harvest or fisheries data when known deaths occur. In this study and in the elephant seal application, we assume there is no possibility of loss on capture, thus the third component of the likelihood simplifies to 1. The full likelihood is given by the product of the components of the likelihood ($L = L_1^A \times L_1^B$) and can be found in the Online Supplement.

Maximum likelihood parameter estimates are found using a Newton-Raphson type method. Estimated standard errors are computed using the delta theorem. Models were implemented using R software (R Core Team, 2014), and code can be obtained from the second author.

Experimental Design

To study the effect of recycled individuals on parameter estimates of this model, we conducted a simulation study. Data were simulated and analyzed using R 3.1.1 (R Core Team, 2014). Data sets varied both in super-population size, parameter values and percent double tagged. We generated data for the JSTL model with constant survival, capture, and tag retention probabilities for a double-tagging experiment. Super-population sizes of 1000 and 100 000 were considered in order to determine the effect that population size may have on the results. For the super-population size of 100 000, experiments with ten sampling occasions were considered. For the super-population size of 1000 we considered experiments with five, seven and ten sampling occasions in order to determine if the length of the study has any effect on the results. For each population size, we tested different proportions of double-tagged versus single-tagged individuals (0.5 and 1). Survival, capture, and tag retention probability parameters were varied in a 3^3 experimental design with low (0.2), medium (0.5) and high (0.9) values for each parameters. The entry rates were fixed to be $1/k$ at each of the sampling times. No individuals were lost on capture.

We considered the set of parameter values to be reasonable values that might be encountered in practice and also produce informative capture-recapture scenarios. Tag retention rates can vary by species, age of the tag, tag type, tag location, behaviour, season, and individual

quality (size of an animal for example in seals). For example, tag retention rates have ranged from 13% (Fogarty et al., 1980) to 95% (Gonzalez-Vicente et al., 2012) in lobsters. Other studies report tag retention rates of 65% male elephant seals (Pistorius et al., 2000) and 88% in Adelie penguins (Ainley and DeMaster, 1980). Mean retention of visible implant tags has been recorded as 32% in small rockpool fish (Griffiths, 2002). Turtles in particular experience high tag loss rates. For example Bellini et al. (1996) reports the probability of tag loss in hawksbill turtles as 0.57 and Bjorndal et al. (1996) observed the probability of tag loss in green nesting turtles to be as high as 0.38. Thus, we chose a wide range of tag loss parameter values to try to capture the diversity among published tag loss rates.

Simulation of Data

For all of the parameter combinations of super-population size ($N = 1000, 100\ 000$), fraction double-tagged $(0.5, 1)$, survival probability $(\phi = 0.2, 0.5, 0.9)$, capture probability $(p = 0.2, 0.5, 0.9)$ and tag retention probability $(\Lambda = 0.2, 0.5, 0.9)$, we generated 100 data sets where the simulated data met all the assumptions of the model.

For each individual, we simulated a capture history using the following algorithm:

1. Determine when the individual enters the population utilizing the entry probabilities.
2. For each time period after entry (until death or first capture) determine if the individual survives to that time period (with probability ϕ). If they are still alive, determine if they were first captured (with probability p). If they are captured, determine whether they are single or double-tagged.
3. For each time period after first capture (until death, loss of all tags or the end of the study) determine if the individual survives to that time period (with probability ϕ). Then if they are still alive, determine if they lose any of their tags (with probability $1 - \Lambda$). If they still have at least one of their tags, determine if they were recaptured

(with probability p). If they have lost all of their tags, consider them as a new individual entering the population at this time period.

By keeping track of all the recycled individuals, this algorithm provides us with two data sets: one that includes the recycled individuals (assumes individuals, who have lost their tags, are tagged again upon recapture and treated as new individuals) and one that doesn't include recycled individuals (assumes that individuals, who have lost their tags, can be recognized upon recapture and are not re-tagged). The JSTL model was fit to the 100 simulated data sets twice (once with and once without recycled individuals). We assumed that any difference between the two analyses was due entirely to the recycled individuals.

Evaluation Criteria

To evaluate the resulting parameter estimates from each of the simulations, we looked at several criteria including: average parameter estimate, relative bias of the estimates, the average standard error of the parameter estimates, the standard deviation of the parameter estimates, and root mean squared error (RMSE) of the parameter estimates.

Given that the \hat{p}_i 's are the parameter estimates from each of the 100 simulations, we calculated:

- the mean parameter estimate as $\hat{p} = \frac{1}{100} \sum_{i=1}^{100} \hat{p}_i$
- average standard error of the parameter estimate as $SE(\hat{p}) = \frac{1}{100} \sum_{i=1}^{100} SE(\hat{p}_i)$.
- the standard deviation of the parameter estimates as $SD(\hat{p}) = \sqrt{\frac{1}{99} \sum_{i=1}^{100} (\hat{p}_i - \hat{p})^2}$.
- the RMSE of the parameter estimates as $RMSE = \sqrt{\frac{1}{100} \sum_{i=1}^{100} (\hat{p}_i - p)^2} \approx \sqrt{\hat{SD}^2 + \hat{Bias}^2}$.

We compared the average parameter estimates to the true parameter values using relative bias. We calculated the relative bias of the estimators as $(\hat{p}) = (\hat{p} - p)/p$, where \hat{p} is the average parameter estimate calculated from the 100 simulations and p is the true value of the parameter. We also compared the relative bias from the analysis with the recycled

individuals to the relative bias from the analysis without the recycled individuals. We calculated the difference in the two relative biases and consider this to be the relative bias that was contributed entirely by the recycled individuals being tagged as “new” individuals.

Simulation Results

The relative bias of the survival estimates are biased for some parameter combinations of survival, capture, and tag retention probabilities. As an example, box plots of survival estimates for data with super-population size $N=1000$ and 100% double tagging are provided (Figure 1). Box plots of survival estimates for other super-population sizes and double-tagging rates are provided in the Online Supplement (Figures A1-A4). Although there is bias in the survival estimates for several of the parameter combinations, the bias is similar between the analysis with and the analysis without the recycled individuals included for both super-population sizes ($N = 1000$ and 100000) and for both double-tagging rates ($T_2 = 0.5, 1$). In fact, the differences in relative bias due to recycled individuals for the parameters ϕ , p and Λ is small (<0.01) for all 108 parameter combinations considered. In general, the SE, SD and RMSE of the estimates of ϕ , p and Λ are similar for both the analysis with and without recycled individuals for the parameter combinations considered. It seems that, in general, the treatment of recycled individuals has little effect, if any, on the accuracy of the JSTL estimators for survival, capture, and tag-retention probabilities. Box plots of capture and tag retention estimates for all models can also be found in the Online Supplement (Figures A5-A12).

Results are similar for both the super-population sizes of 1000 and 100000 for all parameter combinations of survival, capture, and tag retention probabilities. There is slightly more bias due to recycled individuals for parameter combinations where the probability of double tagging (T_2) was only 0.5, compared to the parameter combinations where all individuals were double tagged. As an example, relative bias of the parameters are presented for the

parameter combination where $\phi = 0.9, p = 0.9$ and $\Lambda = 0.2$ for both the analysis with and without recycled individuals for varying population size and double-tagging probabilities (Table 1).

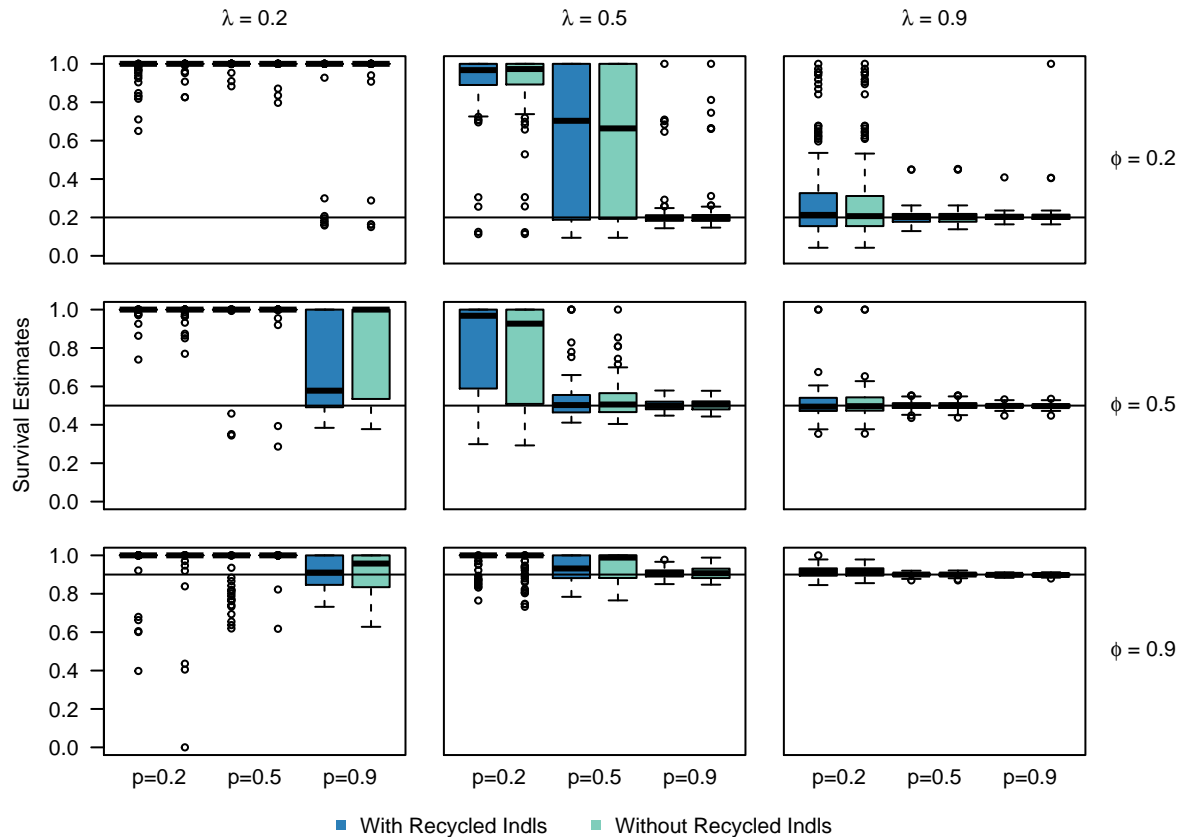


FIGURE 1: *Survival probability estimates for simulated data with super-population size $N = 1000$ with 100% double-tagging for different tag retention probabilities ($\Lambda = 0.2, 0.5, 0.9$), survival probabilities ($\phi = 0.2, 0.5, 0.9$), and different capture probabilities ($p = 0.2, 0.5, 0.9$) using the JSTL model from a ten-sample-time study. Box plots of the estimates of ϕ for the model analyzed with and without the recycled individuals are provided. The black line indicates the true value of ϕ used to simulate the data for each model.*

TABLE 1: *The mean relative bias of the parameters from the model analyzed*

with (R) and without (R') the recycled individuals for data with high survival probability ($\phi = 0.9$), high capture probability ($p = 0.9$), and low tag retention ($\Lambda = 0.2$) for different super-populations sizes ($N = 1000, 100000$) and different tag retention probabilities ($T_2 = 0.5, 1$) using the JSTL model from a ten-sample-time study.

	Population Size (N) and Proportion Double Tagged (T_2)							
	N=1000				N=100000			
	$T_2 = 1$		$T_2 = 0.5$		$T_2 = 1$		$T_2 = 0.5$	
	R	R'	R	R'	R	R'	R	R'
ϕ	0.00	0.00	0.06	0.05	0.00	0.00	0.11	0.10
p	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Λ	0.00	0.00	0.00	0.00	0.00	0.00	-0.09	-0.08
N	1.98	0.00	2.13	0.00	1.98	0.00	2.12	0.00

The estimate of super-population size (\hat{N}) is computed as $\hat{N} = n_{\text{obs}}/(1 - \hat{P}_0)$, where \hat{P}_0 is the estimated probability of never being seen. In the scenarios where many recycled individuals were recaptured and considered as “new” individuals, the number of observed individuals, n_{obs} , is larger than it should be and thus, \hat{N} is biased upwards. This bias is corrected in the analysis without the recycled individuals considered. The relative bias in the super-population size (\hat{N}) due to recycled individuals is highest in the scenario with high survival rates ($\phi = 0.9$), high capture rates ($p = 0.9$) and low tag retention rates ($\Lambda = 0.2$), as predicted (Figure 2, Table 1). The relative bias is small for all scenarios where tag retention was high, but relative bias increases as tag retention decreases. The relative bias in \hat{N} decreases as capture probability decreases, but recycled individuals appear to still have some effect on the estimates even when capture probabilities are low ($p = 0.2$). The relative bias in \hat{N} is high for scenarios where survival probability is high, and decreases as survival probability decreases. In all scenarios where survival probability is low ($\phi = 0.2$) individuals are unlikely to survive long enough to be able to be tagged, lose tag(s) and be recaptured as “new” individuals. When survival probability is low, the relative bias due to the recycled individuals is small (less than

0.15) and hence not shown in Figure 2. SE, SD, and RMSE of \hat{N} varies, but remains similar between the analyses with and without recycled individuals included, across all scenarios.

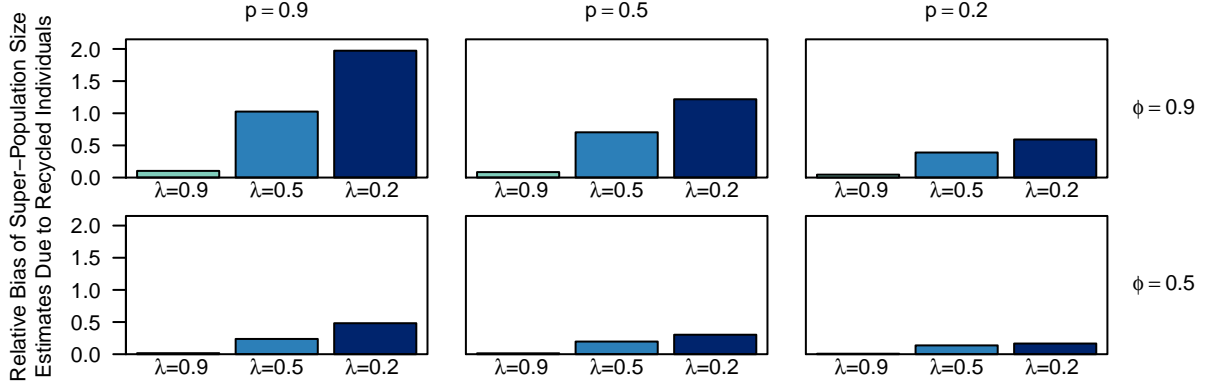


FIGURE 2: The difference in mean relative bias of the super-population estimate (\hat{N}) between the model analyzed with and without the recycled individuals for data with super-population size $N = 100000$ with 100% double-tagging for different tag retention probabilities ($\Lambda = 0.2, 0.5, 0.9$), survival probabilities ($\phi = 0.2, 0.5, 0.9$), and capture probabilities ($p = 0.2, 0.5, 0.9$) using the JSTL model from a ten-sample-time study.

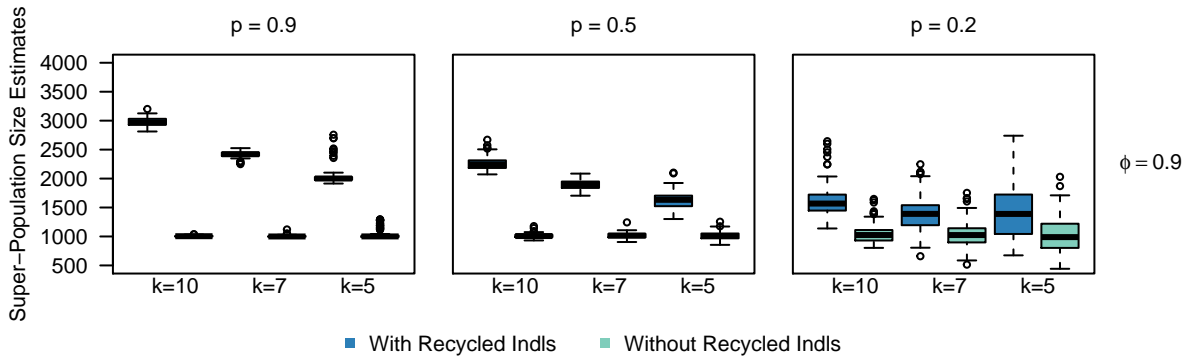


FIGURE 3: Box plots of the estimates of N for the model analyzed with and without the recycled individuals for data with super-population size $N = 1000$ with 100% double-tagging for different capture probabilities ($p = 0.2, 0.5, 0.9$),

and constant survival ($\phi = 0.9$) and tag retention ($\Lambda = 0.2$) probabilities using the JSTL model from experiments with $k = 10, 7$, and 5 sample-times.

There is more bias in \hat{N} due to recycled individuals in longer experiments (Figure 3). With a larger number of sampling occasions, there is more time for individuals to be captured and tagged, lose their tags, and survive to be recaptured (be recycled). In shorter studies, there are fewer numbers of recycled individuals and thus the bias in \hat{N} due to recycled individuals is lower although not unnoticeable in the worst case scenarios (low tag retention, high survival and high capture probabilities). Box plots of super-population size (N) for all scenarios are available in the Online Supplement (Figures A19-A24).

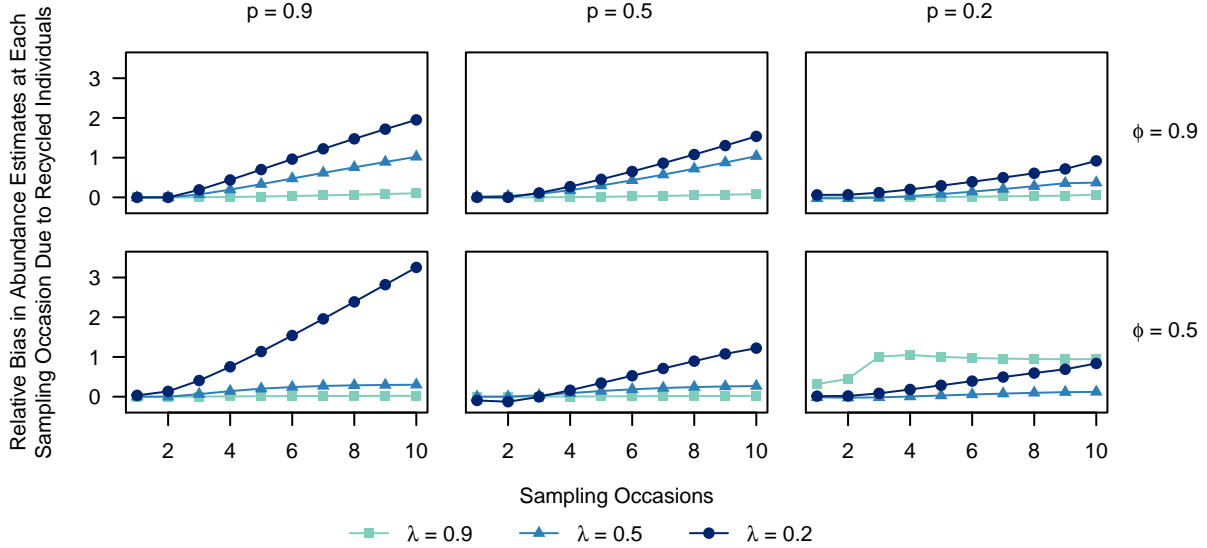


FIGURE 4: The difference in mean relative bias of the abundance estimates at each time period (\hat{N}_j) between the model analyzed with and without the recycled individuals for data with super-population size $N=100\ 000$ with 100% double-tagging for different tag retention probabilities ($\Lambda = 0.2, 0.5, 0.9$), survival probabilities ($\phi = 0.2, 0.5, 0.9$), and different capture probabilities ($p = 0.2, 0.5, 0.9$) using the JSTL model from a ten-sample-time study. Note that lines are added between the points to emphasize the difference in values; no models were fit to generate these lines.

In general, the bias due to recycled individuals in the \hat{N}_j 's follows a similar pattern to the bias due to recycled individuals in \hat{N} , with relative bias in the \hat{N}_j 's increasing as tag retention decreases, survival increases, and capture probability increases (Figure 4). For all scenarios, the relative bias in the estimates of abundance at each sample time j is smaller for earlier sampling occasions and larger for later sampling occasions. Since the estimates of the population sizes at each time j are computed iteratively as $\hat{N}_{j+1} = \hat{\phi}(\hat{N}_j) + \hat{b}_j(\hat{N})$, any bias in the earlier abundance estimates is magnified in the later sampling occasions abundance estimates. The scenario with $\phi = 0.5$, $p = 0.9$, and $\Lambda = 0.2$ appears to have very high relative bias in the abundance estimates in later sampling occasions (>3 for \hat{N}_{10}), which is caused by a combination of more upward bias in the survival probability estimates for the analysis with recycled individuals than without (Figure A14) as well as upward bias in the super-population size estimates. Plots of the mean abundance estimates for all scenarios are available in the Online Supplement (Figures A17-A28).

Case Study: Elephant Seals

To validate the simulation framework, we analyzed data from a long-term mark-recapture study of elephant seals on Macquarie Island. The data used for the case study consists of 7 years between 1993 and 2000. Elephant seal pups were marked with two tags in the inter-digital webbing of their hind flippers and were given a permanent hot-iron branding with a unique identifier on their flank (McMahon et al., 2009). This permanent branding allowed for individual elephant seals to be identified even if they lost both tags. Thus, recycled individuals could be easily identified.

We considered two analyzes of the data:

1. We assumed that recycled individuals could not be recognized upon recapture (ignoring branding) and were re-tagged as if they are new individuals. This scenario simulates analysis ignoring the effects of recycled individuals.

2. Recycled individuals were recognized upon recapture (by branding) and were re-tagged with new tags identical to their lost tags.

For the elephant seal data, there were several differences in parameter estimates of the JSTL model when recycled individuals were included compared to when recycled individuals were excluded. For this analysis, we used the same model as the simulation study where capture, survival and tag retention rates were held constant.

As expected, the super-population size estimate for the analysis which included the recycled individuals ($\hat{N} = 8985$) is 30% larger than the estimate in the analysis which excluded recycled individuals ($\hat{N} = 6949$) who were recognized upon recapture. This relationship also holds true for the abundance estimates at each time period (Table 2). The bias in the abundance estimates increases as time goes on, again validating the results of our simulation study.

Similar to the simulations, there is not much difference in the estimates of survival and capture probabilities between the analysis with and without recycled individuals. For comparison to the previous simulations, we note that tag retention probability for the elephant seals was estimated to be ≈ 0.8 (high). Standard error estimates are also higher when recycled individuals are included in the analysis. The same pattern is seen in the simulation studies (see Web Appendix A).

TABLE 2 *Estimates of survival probability (ϕ), capture probability (p), and super-population size (N) for the elephant seal data analyzed with and without the recycled individuals. Standard errors are presented for survival and capture probabilities.*

	With Recycled		Without Recycled	
Parameter	Estimate	SE	Estimate	SE
ϕ	0.759	0.006	0.744	0.006
p	0.682	0.006	0.741	0.006
Λ	0.792	0.005	0.799	0.005
N_{1994}	1740	48	1601	36
N_{1995}	1859	41	1717	40
N_{1996}	2515	46	2264	42
N_{1997}	3179	50	2727	43
N_{1998}	3793	54	2965	48
N_{1999}	4300	59	3229	46
N_{2000}	4973	65	3238	50

Discussion

Through both a simulation study and an elephant seal case study, we examined the effect of recycled individuals on parameter estimates from the Jolly-Seber tag loss model. In an attempt to emulate the many different real life scenarios researchers may face, we simulated over many different values of survival probability, capture probability, tag-retention probability, population size, study length, and proportion double tagged. While these scenarios do not cover all possible realistic mark-recapture experiments, our simulations are sufficient to show that the JSTL abundance estimates can be substantially biased by recycled individuals, especially when tag-retention is low combined with high survival, high capture rates, or both. This effect is especially noticeable in longer experiments. These results brings context to the assumption that the effect of recycled individuals is negligible in mark-recapture models. However, we show that in general, recycled individuals have little effect on the accuracy of the survival, capture, and tag-retention probability estimates and that for short-term studies,

the effects are reduced.

For longer term studies when survival and capture probabilities are low, the bias in abundance estimates associated with recycled individuals is smaller. These are characteristics that might be associated with small, endangered, or decreasing populations.

It is not surprising that survival estimates are not biased upwards when recycled individuals are ignored. Survival estimates are essentially a relative measure of how many individuals are around now versus the previous time step. Thus the bias in numerator and denominator essentially cancels out (i.e. $\hat{\phi}_j = \hat{N}_j / \hat{N}_{j-1}$).

Although the case study of elephant seals validated some of the results from the simulation study (recycled individuals bias abundance estimates upwards), some caution must be taken when comparing simulation studies to the real world. There are many parameters that may differ or be uncertain, such as entry probabilities, that may influence the results. Simplifications of the individuals in the simulation studies may not take into account the complexities that arise in real life scenarios.

Although our study provides some evidence that recycled individuals have an effect on estimators of the JSTL model in particular situations, there is room for improvement in our approach and questions remain for future work. We only examined three levels of survival, capture, and tag-retention probabilities (Low=0.2, Medium=0.5 and High=0.9) which was intended to simulate across a variety of scenarios that may exist in real life. Future work could examine levels of survival, capture, or tag retention for scenarios of interest for particular populations or could simulate across more levels to try to get a better sense of the relationship between the parameters and the effect of recycled individuals. Additionally, future work could examine the effect of recycled individuals in situations where survival, capture or tag-retention probabilities are thought to be time-varying.

For researchers interested in conducting and analyzing mark-recapture studies, unsurprisingly we stress the importance of using tags with high retention rates, especially in situations

where survival and capture rates are suspected to be high. As long as tag-retention is high, the JSTL estimator of population size is not affected by recycled individuals. In situations where it is possible to recognize if an individual has been captured previously (by scarring, marking, etc), excluding these recycled individuals from the analysis can improve accuracy of the abundance estimates. Permanent marking should be used where possible. If researchers are only interested in the survival rates, they do not need to be concerned with the effect of recycled individuals regardless of the study's tag-retention rates.

Developing a model to incorporate recycled individuals is a similar problem to that of incorporating misidentification of individuals. Schwarz and Stobo (1999) developed a model to deal with tag-misreads in an open population capture-recapture setting. However most of the misidentification literature focusses on genetic or photographic identification errors. Here multiple identities can be assigned to the same individual leading to overestimates in population size if misidentification is ignored (Yoshizaki et al., 2011). This is the same result that we see when recycled individuals are ignored. Link et al. (2010) introduced the notion of using a latent multinomial to model the latent capture histories for a closed population model. Others have extended Link et al.'s model to deal with multiple non-invasive marks (Bonner and Holmberg, 2013; McClintock et al., 2013), heterogeneity in parameters (McClintock et al., 2014) and open populations (Bonner and Holmberg, 2013). These latent multinomial models could be extended to include misidentification produced by complete tag loss.

Finally, the JSTL model we looked at did not include a component for loss on capture (when for example a fishery harvest occurs). It would be interesting for future work to include loss on capture to determine if recycled individuals are still problematic under this scenario. There remains a great deal more to study including testing some of the many assumptions that capture-mark-recapture analyses rely on, many of which we know are violated in the real world. Increasing computation power and a larger community applying themselves to these problems has the potential to answer and inform researchers and managers in a meaningful way, especially in terms of how we use imperfect observations to estimate vital rates (survival

and fecundity). Having more robust estimates of vital rates is especially important if we are to manage efficiently an ever increasing list of endangered species.

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