

# Supplementary Materials for The Effect of Recycled Individuals in the Jolly-Seber Tag Loss Model

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## Web Appendix A: The Jolly-Seber Tag Loss Model

### Assumptions

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 time
- 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

### Notation

The following is a description of statistics and parameters used in the JSTL model where survival, capture, and tag retention probabilities are assumed to be constant across time.

*Statistics:*

- $k$  = number of sample times  
 $m$  = number of unique tag histories  
 $i$  = index for a tag history,  $i = 0, 1, 2, \dots, m$ .  $i = 0$  refers to the tag history of individuals never captured  
 $nt_j$  = the number of tags on individuals at sample time  $j$ ,  $j=1,2,\dots,k$ .  
 $n_j$  = total individuals captured at time  $j$   
 $n_{\text{obs}}$  = the total number of individuals captured with no tags and treated as new individuals; when no recycling is present,  $n_{\text{obs}}$  is the number of unique individuals observed throughout the study  
 $f_i$  = the first sample time where the individual with tag history  $i$  was captured  
 $l_i$  = the last sample time where the individual with tag history  $i$  was observed  
 $q_{id}$  = first sample time where tag  $d$  was known missing for the individual with capture history  $i$   
 $l_{id}$  = the last sample time where tag  $d$  is present on the individual with tag history  $i$ ,  $d = 1, 2$  for a double-tagging experiment  
 $\omega_i^*$  = capture history vector  $\omega_i^* = (\omega_{i1}^*, \omega_{i2}^*, \dots, \omega_{ik}^*)$ ,  $i=0,1,\dots,m$ , where
 
$$\omega_{ij}^* = \begin{cases} 1 & \text{if the individual with tag history } i \text{ captured for the first time at sample time } j. \\ 1 & \text{if the individual with tag history } i \text{ captured at sample time } f_i < j \text{ with at least} \\ & \text{one tag present.} \\ 0 & \text{if the individual with tag history } i \text{ not captured at sample time } j. \end{cases}$$
 $\omega_i$  = tag history vector  $\omega_i = (\omega_{i,1,1}, \omega_{i,1,2}, \omega_{i,2,1}, \omega_{i,2,2}, \dots, \omega_{i,k,1}, \omega_{i,k,2})$ ,  $i=0,1,\dots,m$ , where
 
$$\omega_{ijd} = \begin{cases} 1 & \text{if the individual with tag history } i \text{ captured and tag } d \text{ was present at sample time } j. \\ 0 & \text{if the individual with tag history } i \text{ captured and tag } d \text{ was not present at sample time } j. \\ 0 & \text{if the individual with tag history } i \text{ not captured at sample time } j. \end{cases}$$
 $n_{\omega_i}$  = number of  $\omega_i$  tag histories  
 $p$  = the probability that an individual is recaptured at a sample time given that the individual was alive at the previous sample time  
 $\phi$  = the probability that an individual survives and remain in the population between a sample time and the next sample time  
 $b_j$  = the probability that an individual enters the system between sample times  $j$  and  $j + 1$ .  $j = 0, 1, \dots, k - 1$ .  $b_0$  is the expected fraction of individuals alive just prior to the first sample time.  
 $v$  = the probability that an individual captured will be lost on capture  
 $T_d$  = the probability that an individual is marked with  $d$  tags. Note that the probability of marking with a single tag is one minus the probability of marking with a double tag:  $T_1 = 1 - T_2$   
 $\lambda$  = the probability that an individual captured will retain its tag between time periods given that it remains alive  
 $N$  = super-population size, the total number of individuals ever present in population and available for capture during the study

*Functions of Parameters:*

$b_{j*} =$  the expected fraction of the population remaining to enter the population that enters between sample times  $j$  and  $j + 1$ ,  $j = 0, 1, \dots, k - 1$ .  

$$b_{j*} = \begin{cases} b_0 & \text{if } j = 0 \\ b_j / \sum_{u=j}^{k-1} b_u & \text{if } j = 1, \dots, k - 1 \\ 1 & \text{if } j = k - 1 \end{cases}$$
  
 $B_j =$  net births; the number of individuals who enter the population after sample time  $j$  and survive to sample time  $j + 1$ ;  $j = 0, 1, \dots, k - 1$ .  $B_0$  is the number of individuals alive just before the first sample time. Note that  $E(B_j|N) = Nb_j$ .  
 $\chi_{(f_i, l_i, nt)} =$  the probability that the individual with capture history  $i$  is first seen at  $f_i$  and not seen after sample time  $l_i$ , with  $nt$  tags. This is a recursive function of  $\phi$ ,  $p$ , and  $\lambda$ . If  $f_i = 0$ , this indicates individuals not yet captured but alive at time  $l_i$ .  
 For individuals not yet captured:  

$$\chi_{(0, j, 0)} = \begin{cases} 1 - \phi + \phi(1 - p)\chi_{(0, j+1, 0)} & \text{if } j < k \\ 1 & \text{if } j = k \end{cases}$$
  
 For single tagged individuals:  

$$\chi_{(f_i, j, 1)} = \begin{cases} 1 - \phi + \phi(1 - p)\lambda\chi_{(f_i, j+1, 1)} + \phi(1 - \lambda) & \text{if } j < k \\ 1 & \text{if } j = k \end{cases}$$
  
 For double tagged individuals:  

$$\chi_{(f_i, j, 2)} = \begin{cases} 1 - \phi + \phi(1 - p)\lambda^2\chi_{(f_i, j+1, 2)} + \phi(1 - \lambda)^2 + 2\phi(1 - p)\lambda(1 - \lambda)\chi_{(f_i, j+1, 1)} & \text{if } j < k \\ 1 & \text{if } j = k \end{cases}$$
  
 $\psi_j =$  probability that an individual enters the population, is still alive and is not seen before time  $j$ ;  $j = 1, 2, \dots, k$   
 $N_j =$  population size at time  $j$ .  $E(N_1|N) = B_0$ ,  $E(N_{j+1}|N) = (N_j - N_j p v)\phi + B_j$ , which is the number of individuals that survive from time  $j$  minus the number lost on capture plus the number of births.

## Likelihood and Estimation

The likelihood of the JSTL model can be divided into three parts: the probability of observing  $n_{\text{obs}}$ , the number of tag histories, given the super-population size ( $L_1^A$ ), the probability of observing recaptures given the number of tag histories ( $L_1^B$ ), and the probability of observing the number of individuals lost on capture ( $L_3$ ).

The probability of observing  $n_{\text{obs}}$  capture histories is given by a binomial distribution conditional on the super-population size.

$$L_1^A = [n_{\text{obs}}|N] \sim \text{Binomial}(N, 1 - P_0), \text{ where}$$

$$P_0 \text{ is the probability of never being seen, given by } P_0 = \sum_{j=0}^{k-1} b_j(1 - p)\chi_{(0, j+1, 0)}.$$

The probability of observing each unique tag history  $\omega_i$  is modeled by a multinomial conditional upon being observed at least once.

$$L_1^B = [n_{\omega_i}|n_{\text{obs}}] \sim \text{Multinomial}(n_{\text{obs}}, \pi_{\omega_i}), \text{ where}$$

$$\pi_{\omega_i} = P_{\omega_i} / (1 - P_0) \text{ and}$$

$$P(\omega_i) = \psi_{f_i} T_d \left\{ \prod_{j=f_i}^{l_i} p^{w_{*ij}} (1 - p)^{(1 - w_{*ij})} \right\} \left\{ \phi^{l_i - 1 - f_i} \right\} \times \prod_{d=1}^2 \left\{ (\lambda^{l_{id} - 1 - f_i}) (1 - \lambda^{q_{id} - 1 - l_{id}})^{I(l_{id} \neq l_i)} \right\} \times \chi_{f_i, l_i, nt_{l_i}}$$

The third component  $L_3$  models the number of losses on capture as a binomial. In this study we assume there is no possibility of loss on capture, this third component of the likelihood simplifies to 1.

The complete likelihood for the Jolly-Seber tag loss model assuming no possibility of loss of capture and assuming homogeneous survival, capture, and tag retention probabilities is given below.

$$\begin{aligned}
L = & \binom{N}{n_{\text{obs}}} \left\{ \sum_{j=0}^{k-1} b_j (1-p) \chi_{(0,j+1,0)} \right\}^{(N-n_{\text{obs}})} \times \left\{ 1 - \sum_{j=0}^{k-1} b_j (1-p) \chi_{(0,j+1,0)} \right\}^{n_{\text{obs}}} \times \\
& \binom{n_{\text{obs}}}{n_{\omega_1}, n_{\omega_2}, \dots, n_{\omega_m}} \prod_{i=1}^m \left[ \psi_{f_i} T_d \left\{ \prod_{j=f_i}^{l_i} p^{w_{*ij}} (1-p)^{(1-w_{*ij})} \right\} \left\{ \prod_{j=f_i}^{l_i-1} \phi \right\} \times \right. \\
& \left. \prod_{d=1}^2 \left\{ \left( \prod_{j=f_i}^{l_{id}-1} \lambda \right) \left( 1 - \prod_{j=l_{id}}^{q_{id}-1} \lambda \right)^{I(l_{id} \neq l_i)} \right\} \times \chi_{f_i, l_i, nt_{l_i}} \right]^{n_{\omega_i}} \times \\
& \left\{ 1 - \sum_{j=0}^{k-1} b_j (1-p) \chi_{(0,j+1,0)} \right\}^{-n_{\text{obs}}}
\end{aligned}$$

## Recycled Individuals

WEB TABLE 1: Examples of the fraction of recycled individuals (number of recycled individuals captured / total number of individuals captured) at each sample occasion for a 10 occasion experiment with super-population size  $N = 1000$  with 100% double-tagging.

	Sampling Times									
	1	2	3	4	5	6	7	8	9	10
$\phi = 0.9, p = 0.9, \lambda = 0.2$	0.00	0.30	0.36	0.47	0.51	0.53	0.54	0.55	0.56	0.57
$\phi = 0.9, p = 0.9, \lambda = 0.5$	0.00	0.12	0.12	0.20	0.29	0.26	0.29	0.30	0.31	0.31
$\phi = 0.9, p = 0.9, \lambda = 0.9$	0.00	0.01	0.02	0.02	0.01	0.01	0.03	0.04	0.04	0.03
$\phi = 0.9, p = 0.5, \lambda = 0.2$	0.00	0.14	0.28	0.38	0.43	0.48	0.54	0.54	0.55	0.56
$\phi = 0.9, p = 0.5, \lambda = 0.5$	0.00	0.02	0.12	0.14	0.27	0.28	0.28	0.33	0.29	0.38
$\phi = 0.9, p = 0.5, \lambda = 0.9$	0.00	0.00	0.00	0.00	0.01	0.02	0.02	0.04	0.06	0.06
$\phi = 0.9, p = 0.2, \lambda = 0.2$	0.00	0.05	0.15	0.35	0.18	0.28	0.30	0.33	0.40	0.37
$\phi = 0.9, p = 0.2, \lambda = 0.5$	0.00	0.00	0.06	0.09	0.14	0.13	0.20	0.21	0.30	0.26
$\phi = 0.9, p = 0.2, \lambda = 0.9$	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.02	0.04	0.03
$\phi = 0.5, p = 0.9, \lambda = 0.2$	0.00	0.18	0.23	0.27	0.34	0.36	0.32	0.32	0.32	0.26
$\phi = 0.5, p = 0.9, \lambda = 0.5$	0.00	0.10	0.10	0.15	0.10	0.15	0.18	0.13	0.19	0.12
$\phi = 0.5, p = 0.9, \lambda = 0.9$	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.01	0.01
$\phi = 0.2, p = 0.9, \lambda = 0.2$	0.00	0.10	0.14	0.07	0.15	0.10	0.11	0.13	0.13	0.12
$\phi = 0.2, p = 0.9, \lambda = 0.5$	0.00	0.02	0.06	0.05	0.05	0.11	0.04	0.06	0.08	0.09
$\phi = 0.2, p = 0.9, \lambda = 0.9$	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
$\phi = 0.5, p = 0.5, \lambda = 0.5$	0.00	0.01	0.07	0.06	0.12	0.13	0.14	0.16	0.13	0.14

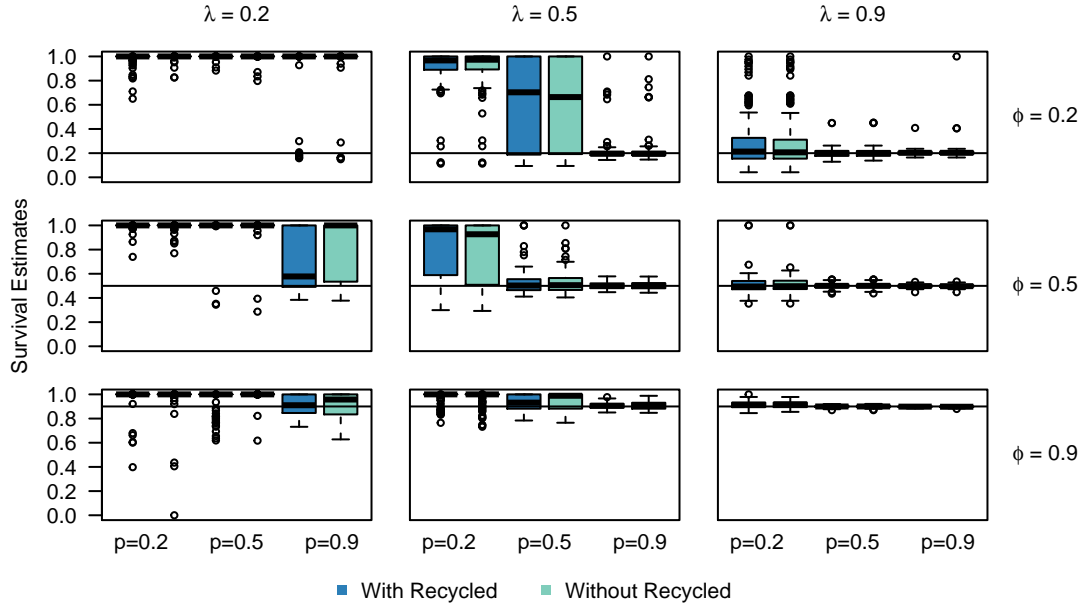
WEB TABLE 2: Examples of the fraction of recycled individuals (number of recycled individuals captured / total number of individuals captured) at each sample occasion for a 7 occasion experiment with super-population size  $N = 1000$  with 100% double-tagging.

	Sampling Times						
	1	2	3	4	5	6	7
$\phi = 0.9, p = 0.9, \lambda = 0.2$	0.00	0.32	0.40	0.49	0.50	0.53	0.55
$\phi = 0.9, p = 0.9, \lambda = 0.5$	0.00	0.10	0.18	0.21	0.22	0.29	0.29
$\phi = 0.9, p = 0.9, \lambda = 0.9$	0.00	0.01	0.01	0.02	0.02	0.02	0.02
$\phi = 0.9, p = 0.5, \lambda = 0.2$	0.00	0.12	0.30	0.35	0.42	0.47	0.50
$\phi = 0.9, p = 0.5, \lambda = 0.5$	0.00	0.06	0.15	0.22	0.26	0.24	0.27
$\phi = 0.9, p = 0.5, \lambda = 0.9$	0.00	0.01	0.00	0.02	0.02	0.03	0.04
$\phi = 0.9, p = 0.2, \lambda = 0.2$	0.00	0.05	0.12	0.15	0.22	0.21	0.30
$\phi = 0.9, p = 0.2, \lambda = 0.5$	0.00	0.00	0.06	0.10	0.15	0.20	0.20
$\phi = 0.9, p = 0.2, \lambda = 0.9$	0.00	0.00	0.00	0.00	0.00	0.01	0.01
$\phi = 0.5, p = 0.9, \lambda = 0.2$	0.00	0.19	0.30	0.32	0.30	0.34	0.38
$\phi = 0.5, p = 0.9, \lambda = 0.5$	0.00	0.09	0.12	0.13	0.15	0.11	0.14
$\phi = 0.5, p = 0.9, \lambda = 0.9$	0.00	0.00	0.00	0.02	0.00	0.00	0.01
$\phi = 0.2, p = 0.9, \lambda = 0.2$	0.00	0.10	0.11	0.12	0.13	0.16	0.08
$\phi = 0.2, p = 0.9, \lambda = 0.5$	0.00	0.04	0.05	0.07	0.07	0.03	0.02
$\phi = 0.2, p = 0.9, \lambda = 0.9$	0.00	0.00	0.00	0.00	0.00	0.00	0.00
$\phi = 0.5, p = 0.5, \lambda = 0.5$	0.00	0.05	0.04	0.05	0.09	0.11	0.12

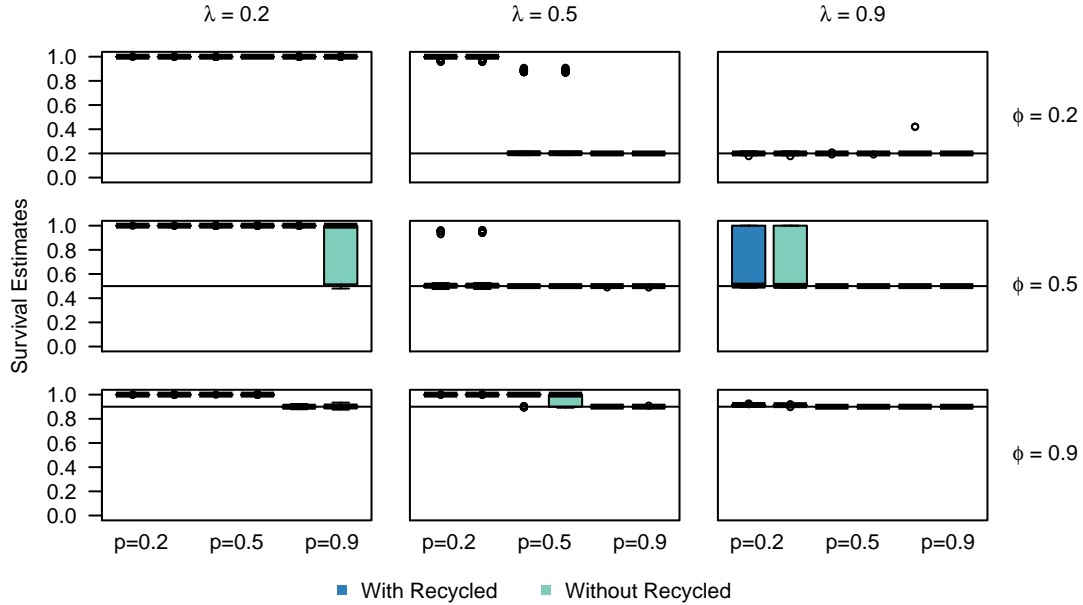
WEB TABLE 3: Examples of the fraction of recycled individuals (number of recycled individuals captured / total number of individuals captured) at each sample occasion for a 5 occasion experiment with super-population size  $N = 1000$  with 100% double-tagging.

	Sampling Times				
	1	2	3	4	5
$\phi = 0.9, p = 0.9, \lambda = 0.2$	0.00	0.29	0.34	0.45	0.52
$\phi = 0.9, p = 0.9, \lambda = 0.5$	0.00	0.08	0.22	0.23	0.28
$\phi = 0.9, p = 0.9, \lambda = 0.9$	0.00	0.01	0.01	0.02	0.02
$\phi = 0.9, p = 0.5, \lambda = 0.2$	0.00	0.14	0.27	0.33	0.38
$\phi = 0.9, p = 0.5, \lambda = 0.5$	0.00	0.05	0.13	0.18	0.25
$\phi = 0.9, p = 0.5, \lambda = 0.9$	0.00	0.00	0.01	0.01	0.02
$\phi = 0.9, p = 0.2, \lambda = 0.2$	0.00	0.06	0.15	0.16	0.29
$\phi = 0.9, p = 0.2, \lambda = 0.5$	0.00	0.03	0.06	0.08	0.12
$\phi = 0.9, p = 0.2, \lambda = 0.9$	0.00	0.00	0.00	0.01	0.01
$\phi = 0.5, p = 0.9, \lambda = 0.2$	0.00	0.14	0.25	0.30	0.33
$\phi = 0.5, p = 0.9, \lambda = 0.5$	0.00	0.05	0.13	0.10	0.15
$\phi = 0.5, p = 0.9, \lambda = 0.9$	0.00	0.00	0.01	0.01	0.00
$\phi = 0.2, p = 0.9, \lambda = 0.2$	0.00	0.11	0.10	0.13	0.12
$\phi = 0.2, p = 0.9, \lambda = 0.5$	0.00	0.02	0.03	0.05	0.04
$\phi = 0.2, p = 0.9, \lambda = 0.9$	0.00	0.00	0.00	0.00	0.00
$\phi = 0.5, p = 0.5, \lambda = 0.5$	0.00	0.03	0.09	0.10	0.12

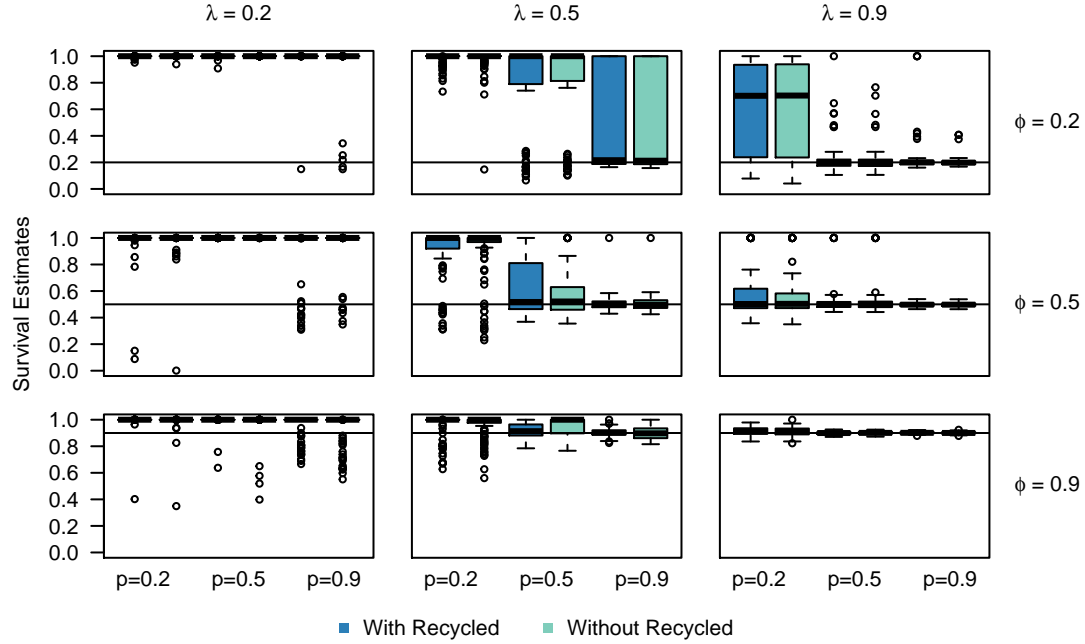
## Survival Estimates



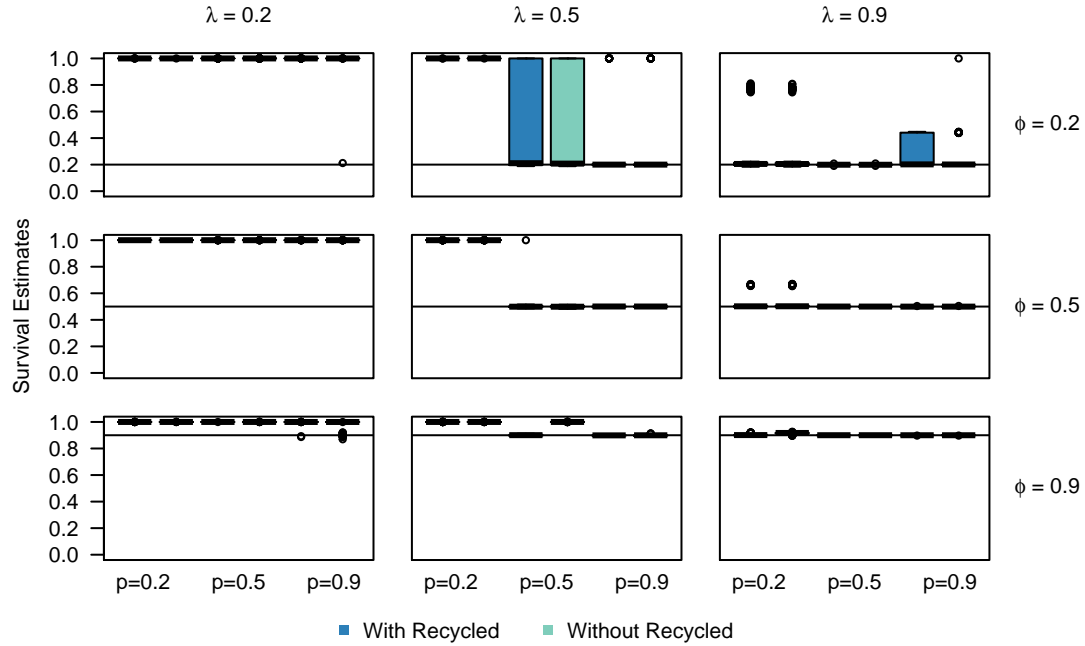
WEB FIGURE 1: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.



WEB FIGURE 2: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.

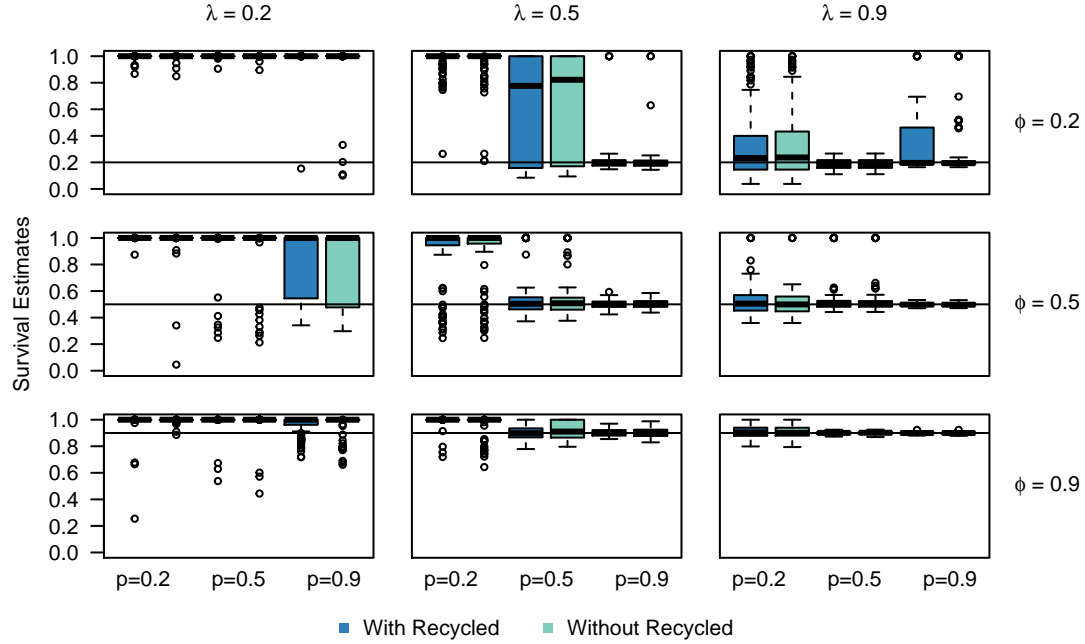


WEB FIGURE 3: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.

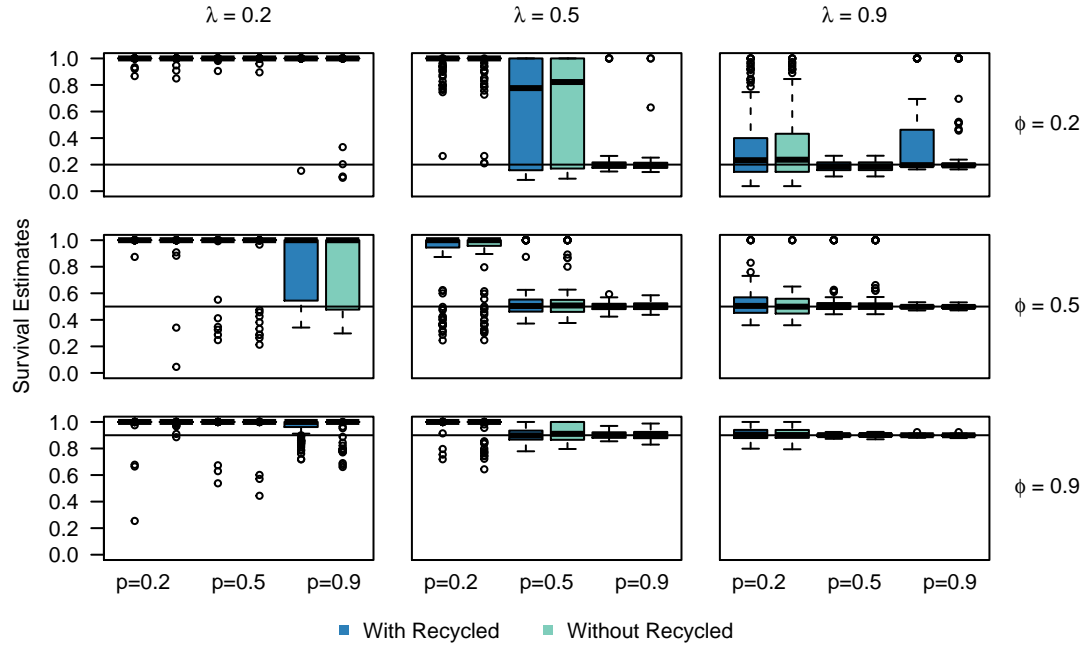


WEB FIGURE 4: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.



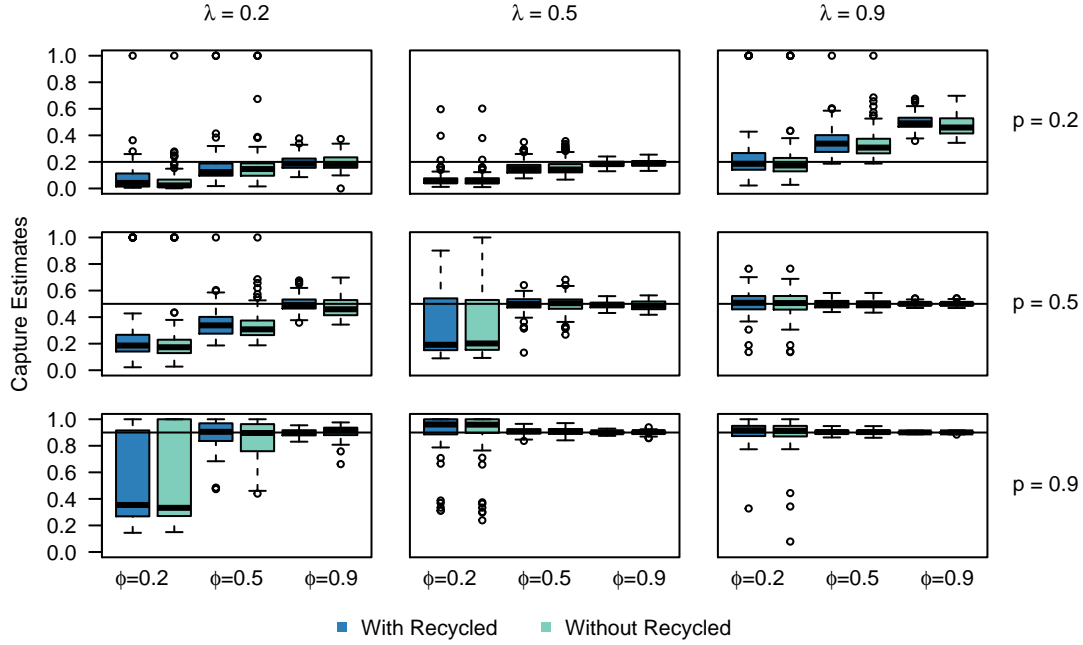


WEB FIGURE 5: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 5 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.

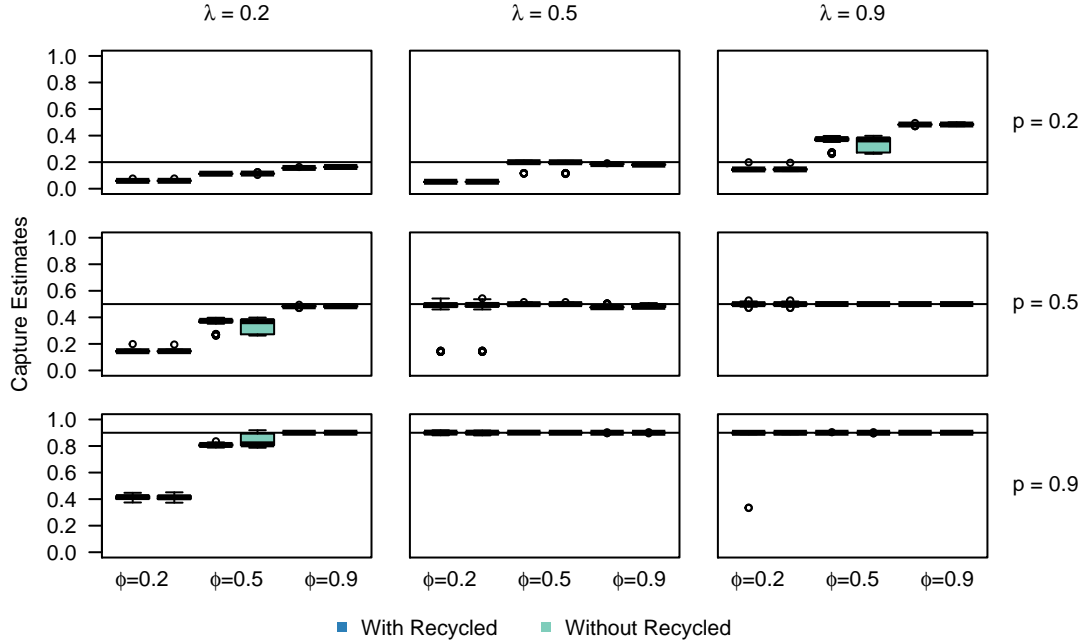


WEB FIGURE 6: Boxplots of survival estimates ( $\hat{\phi}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 7 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\phi$  used to simulate the data for each model.

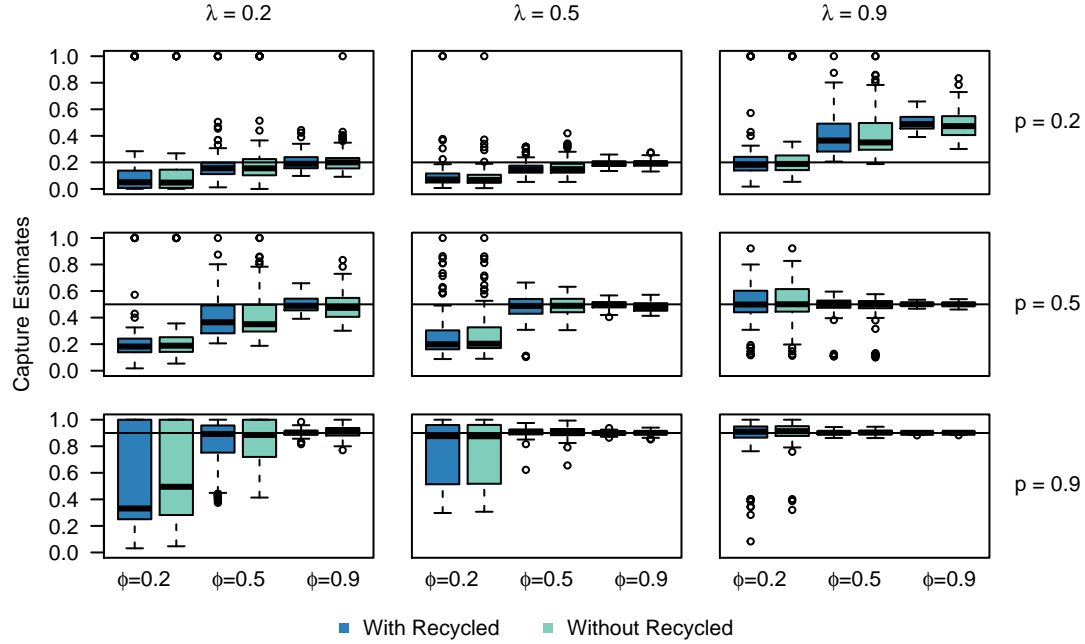
## Capture Estimates



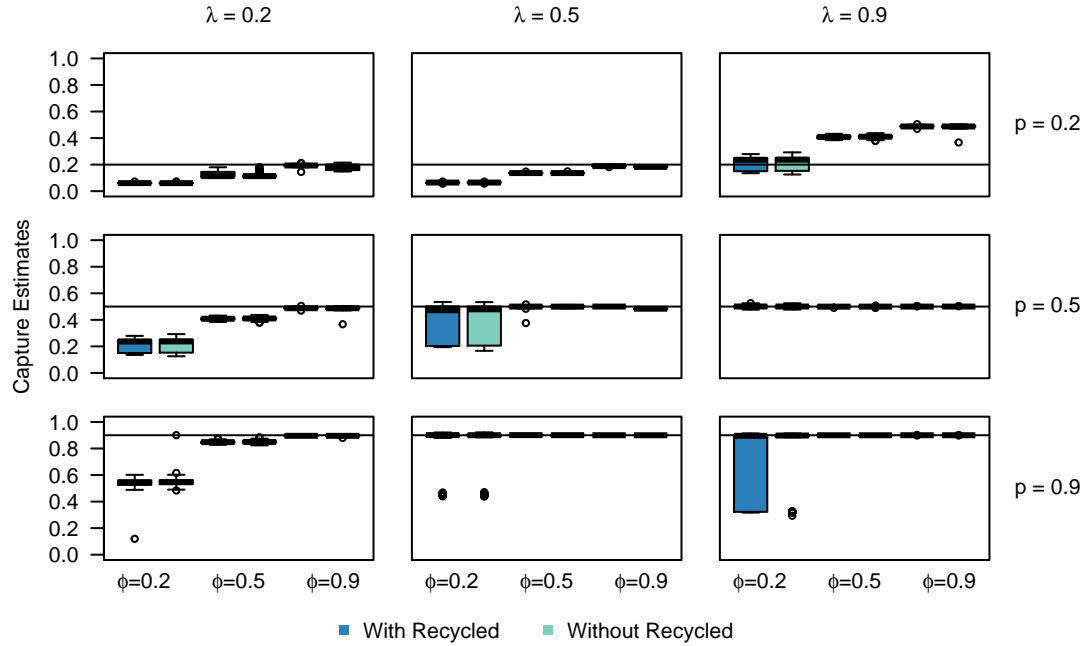
WEB FIGURE 7: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.



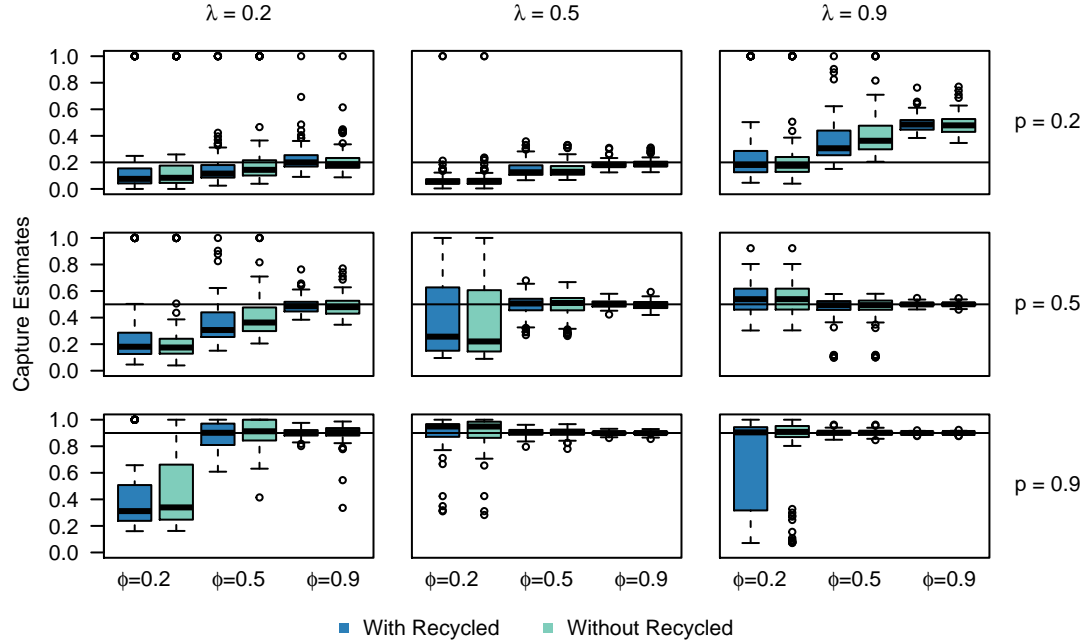
WEB FIGURE 8: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.



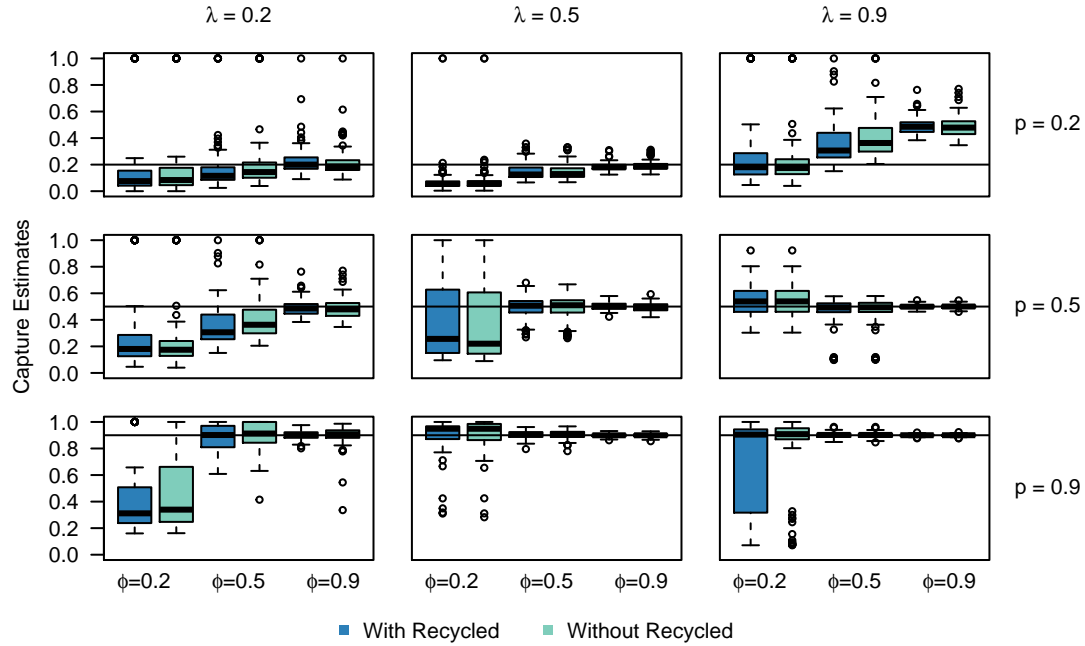
WEB FIGURE 9: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.



WEB FIGURE 10: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.

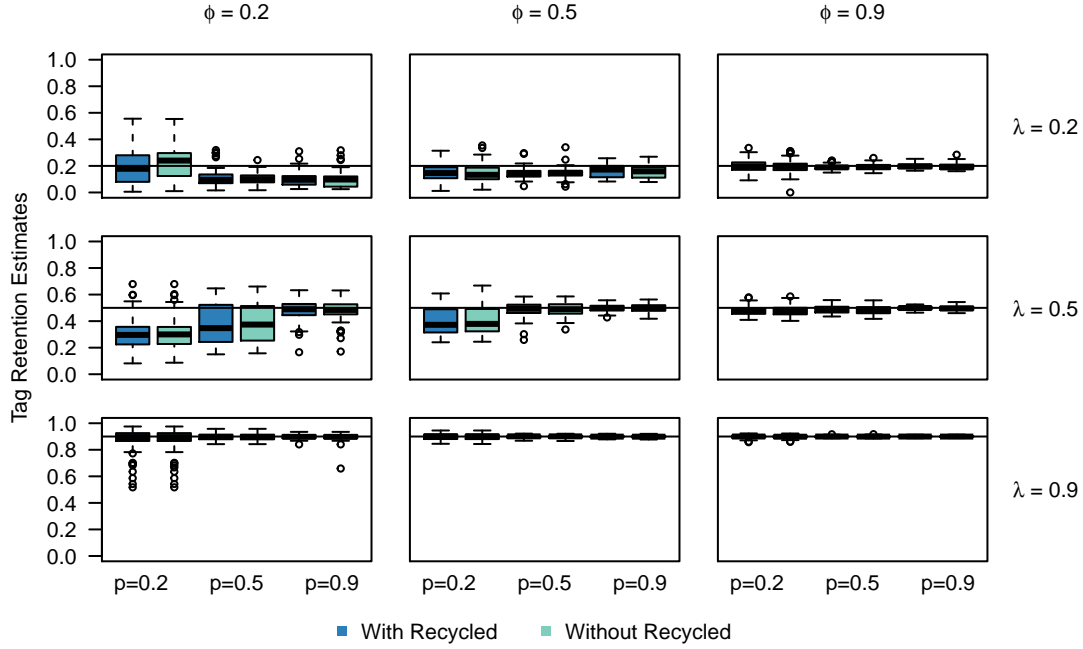


WEB FIGURE 11: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 5 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.

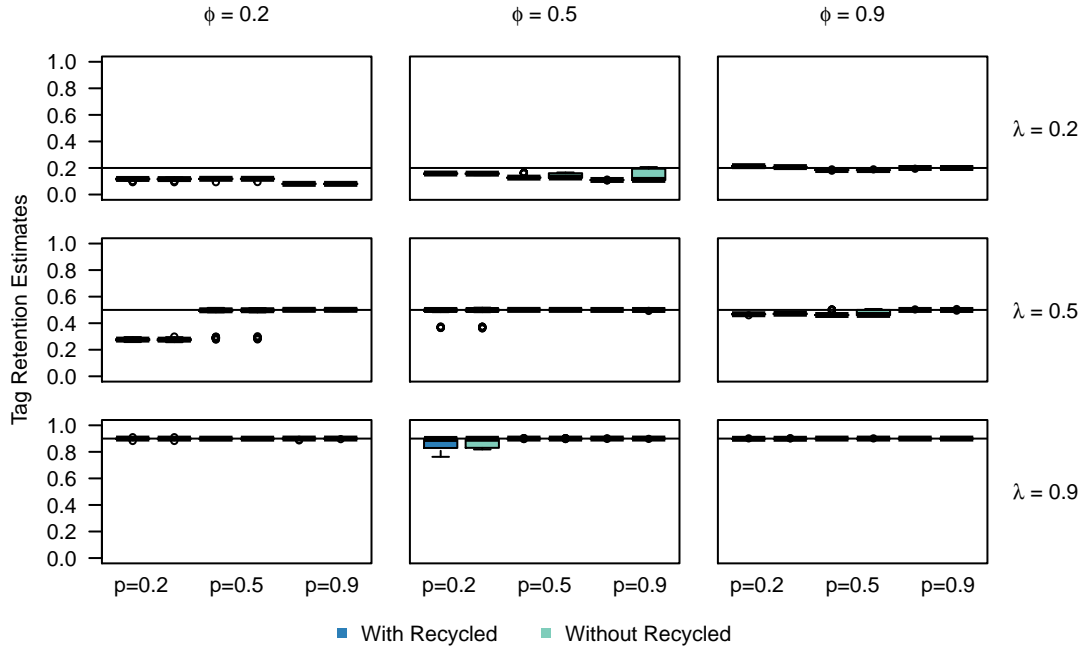


WEB FIGURE 12: Boxplots of capture estimates ( $\hat{p}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 7 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $p$  used to simulate the data for each model.

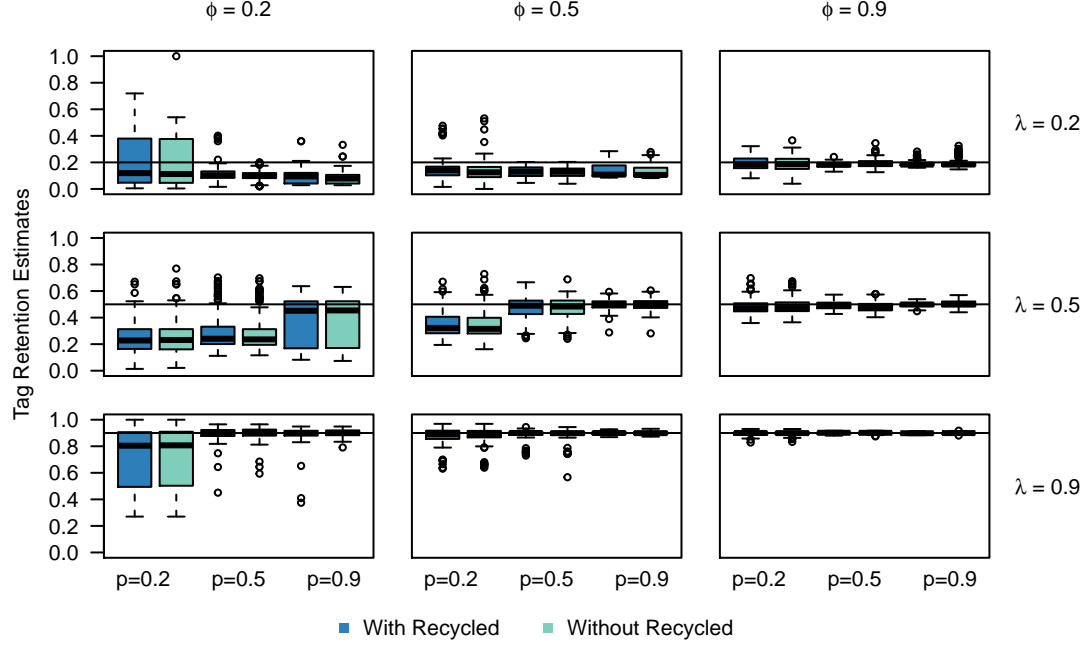
## Tag Retention Estimates



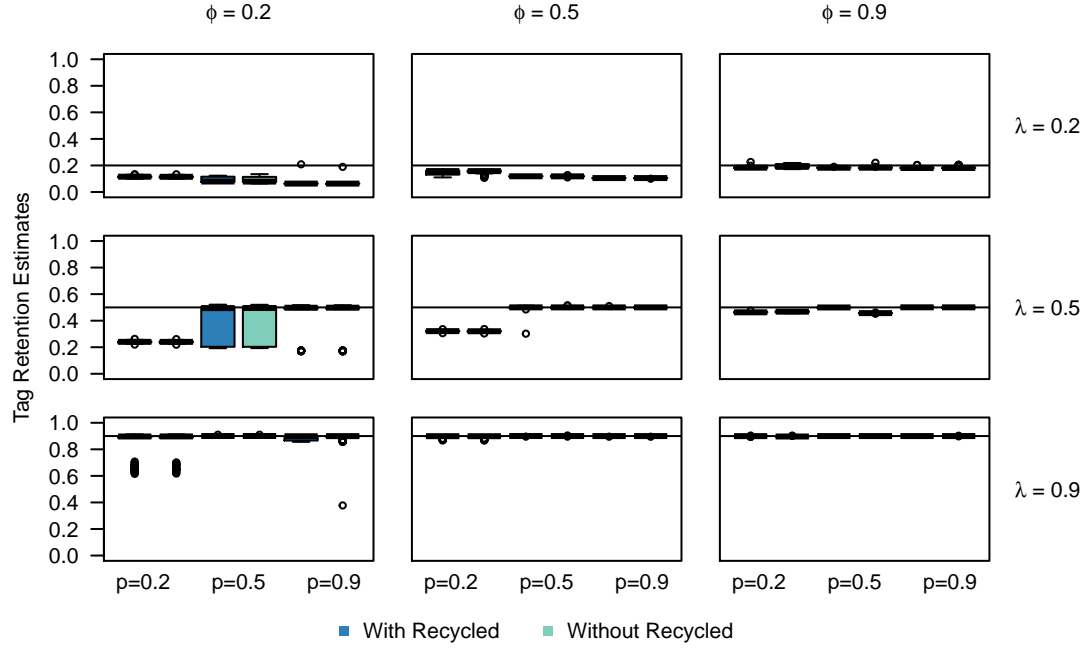
WEB FIGURE 13: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.



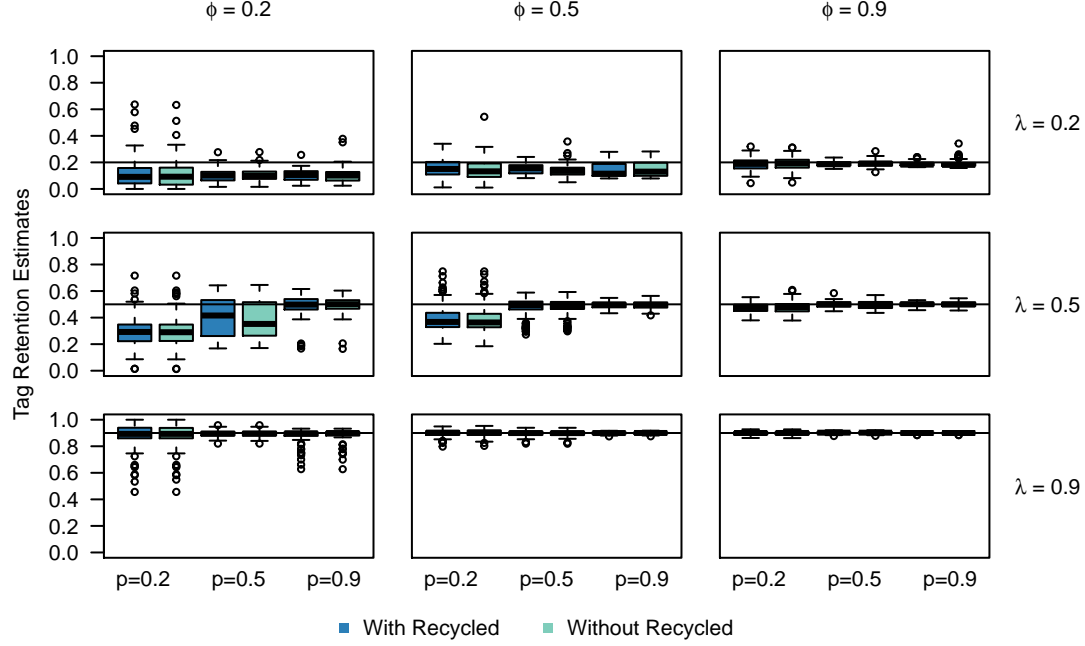
WEB FIGURE 14: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.



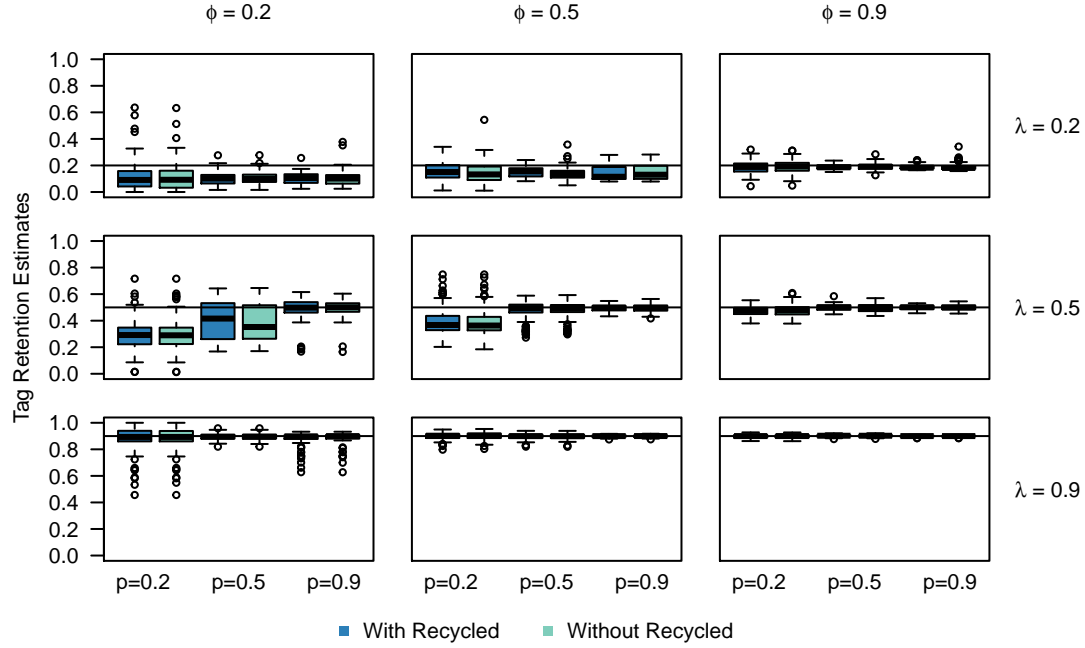
WEB FIGURE 15: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.



WEB FIGURE 16: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.

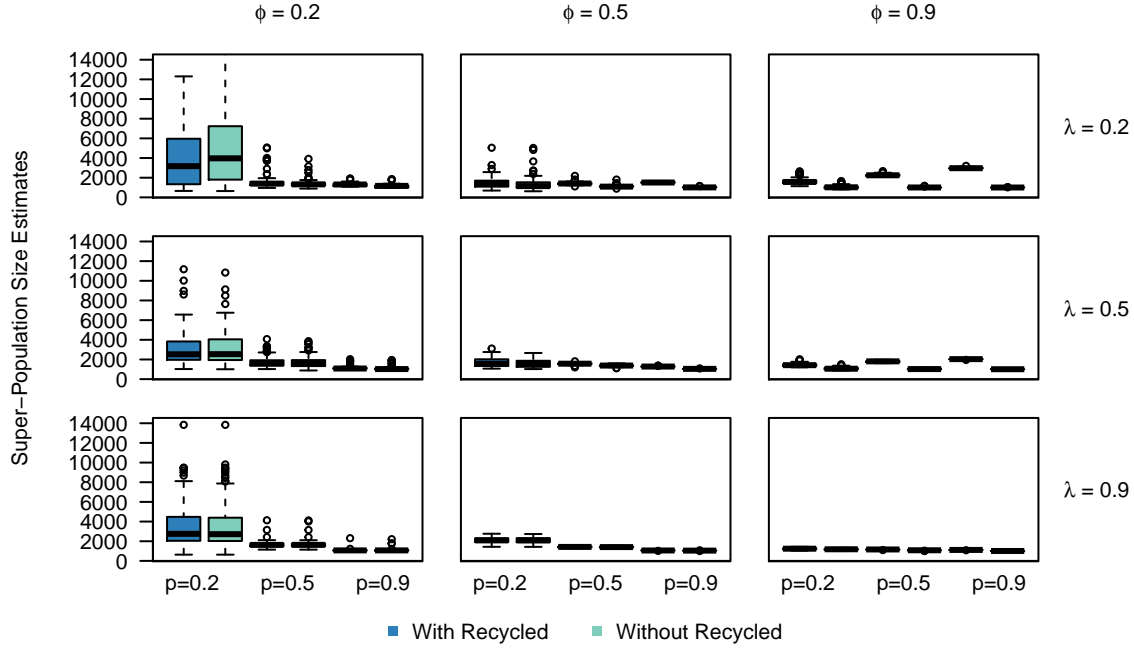


WEB FIGURE 17: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 5 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.

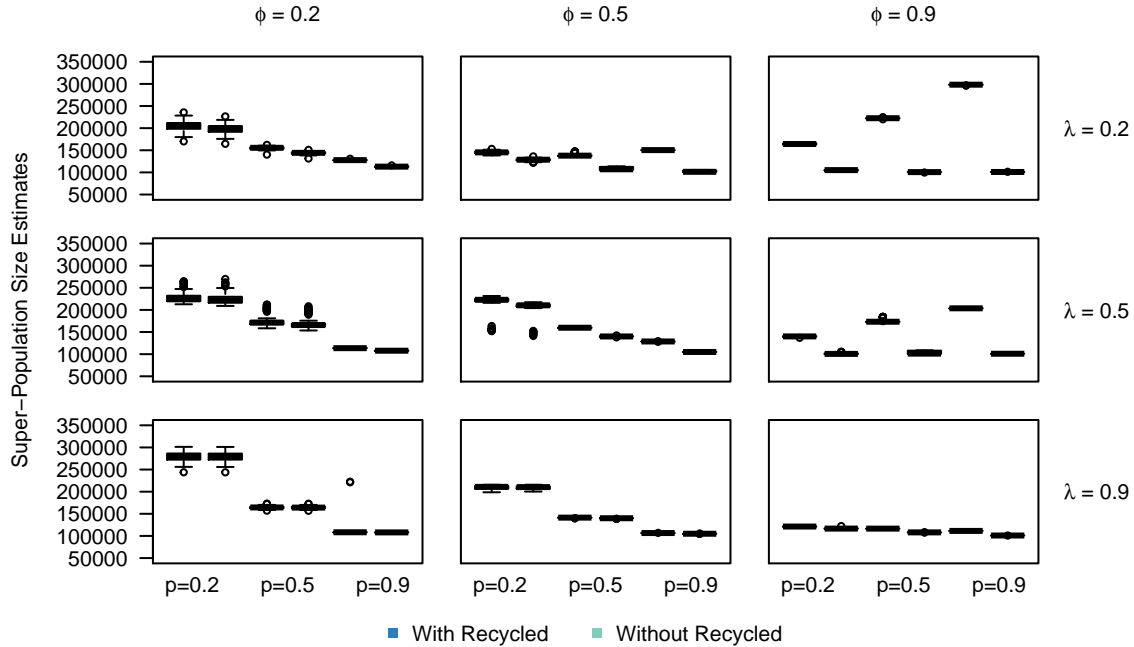


WEB FIGURE 18: Boxplots of tag retention estimates ( $\hat{\lambda}$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 7 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $\lambda$  used to simulate the data for each model.

## Super-Population Size Estimates

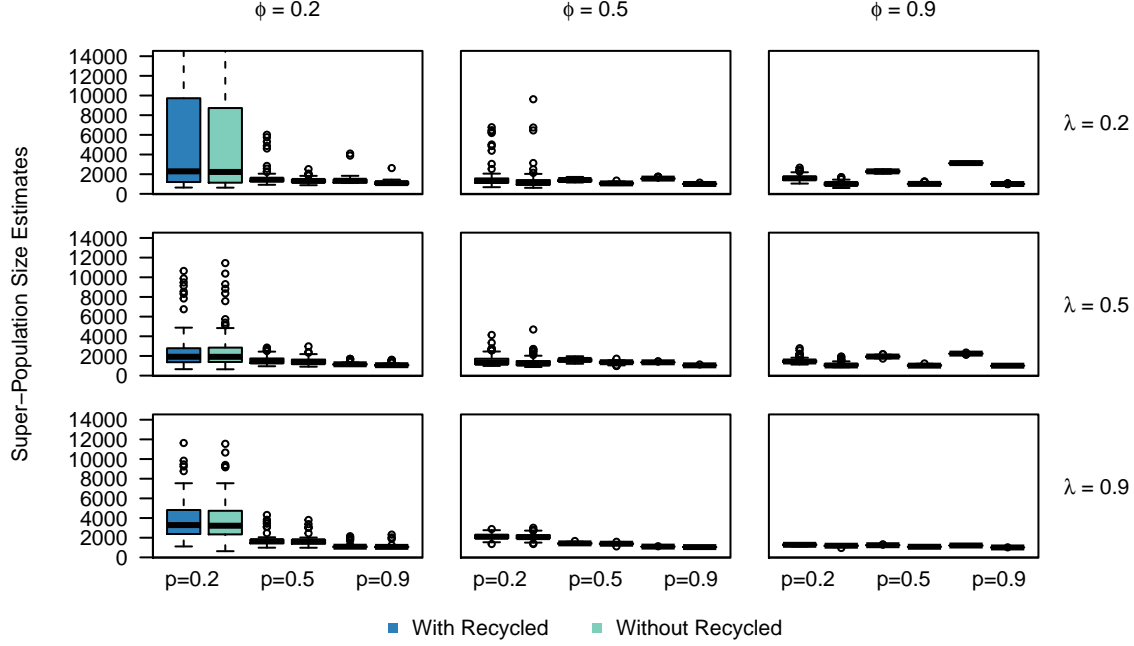


WEB FIGURE 19: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.

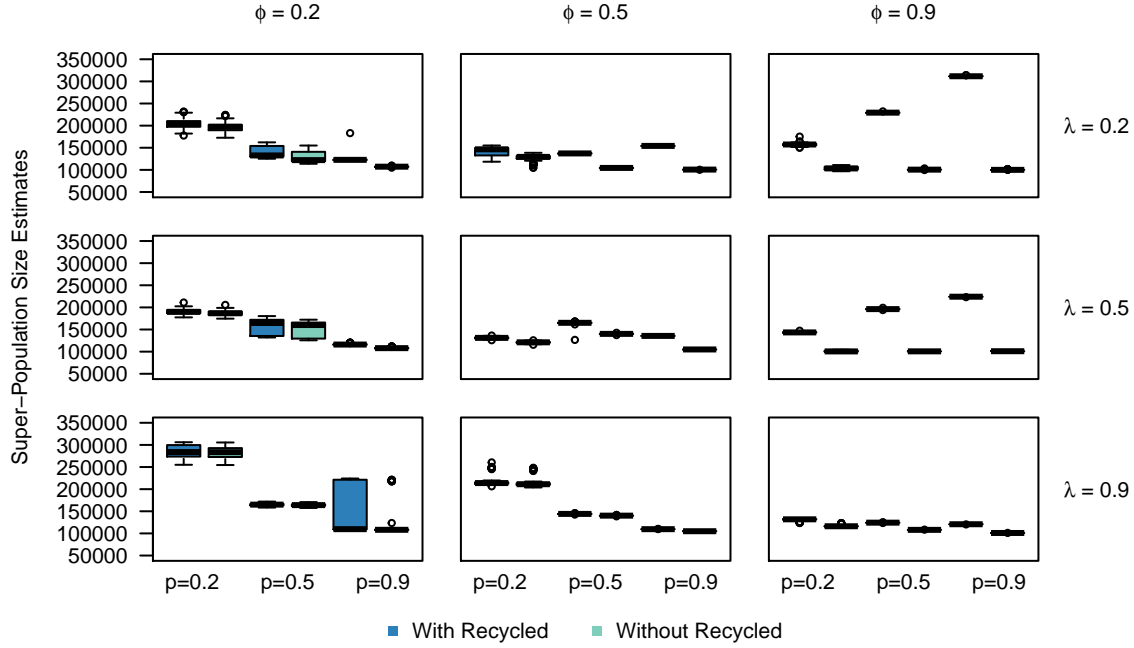


WEB FIGURE 20: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 1$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.

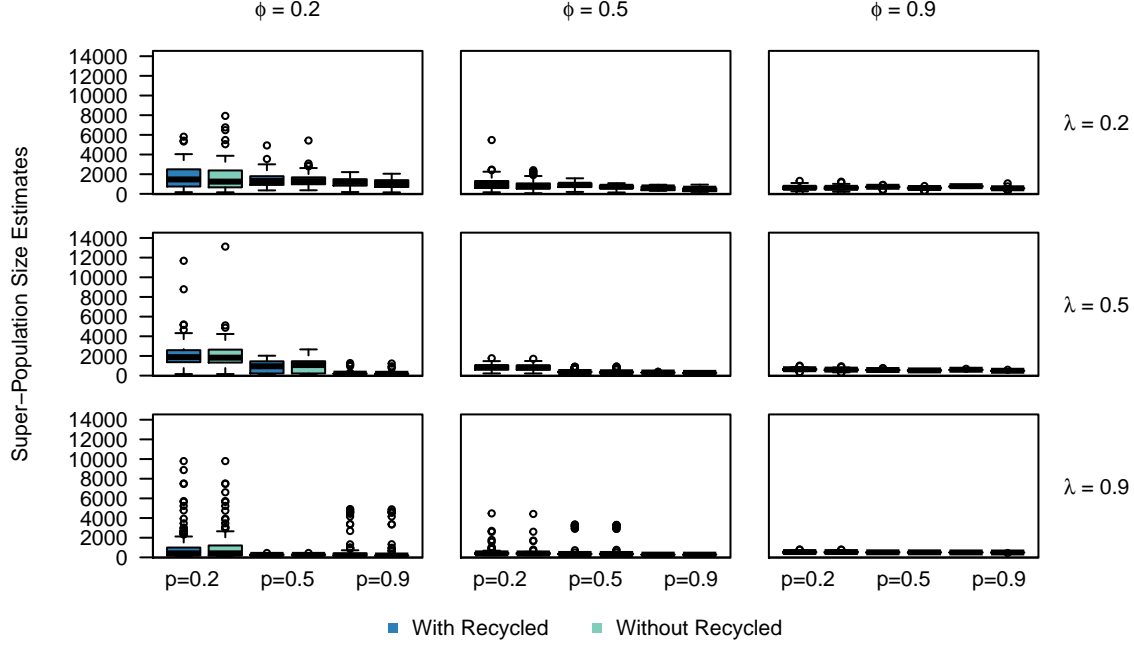




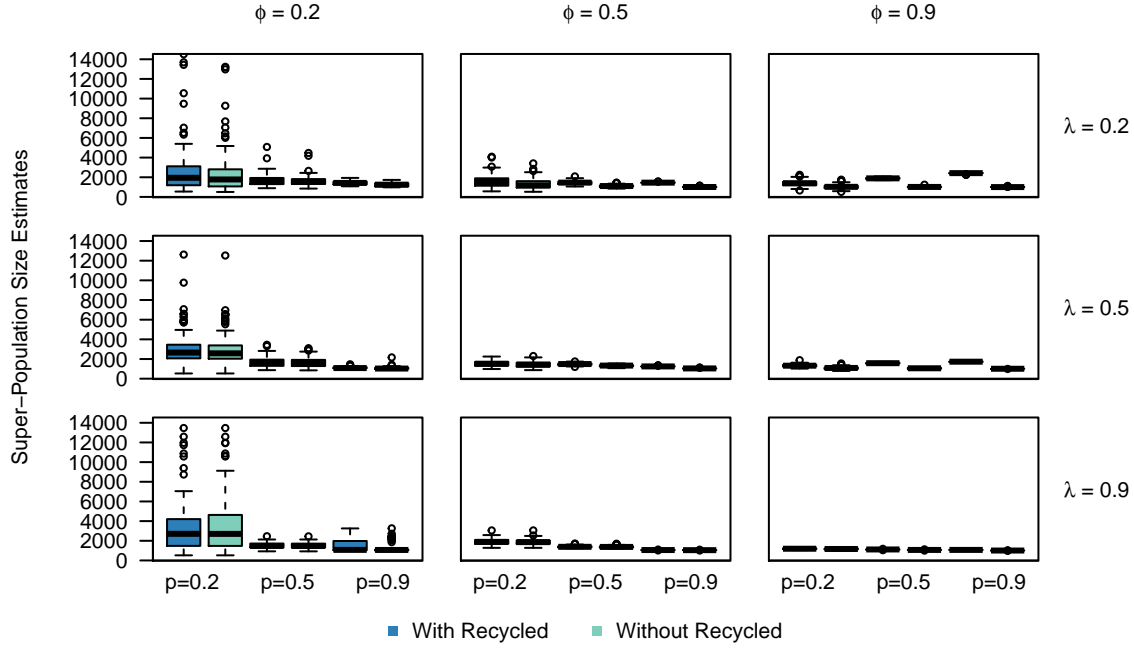
WEB FIGURE 21: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.



WEB FIGURE 22: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with  $T_2 = 0.5$  with 10 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.

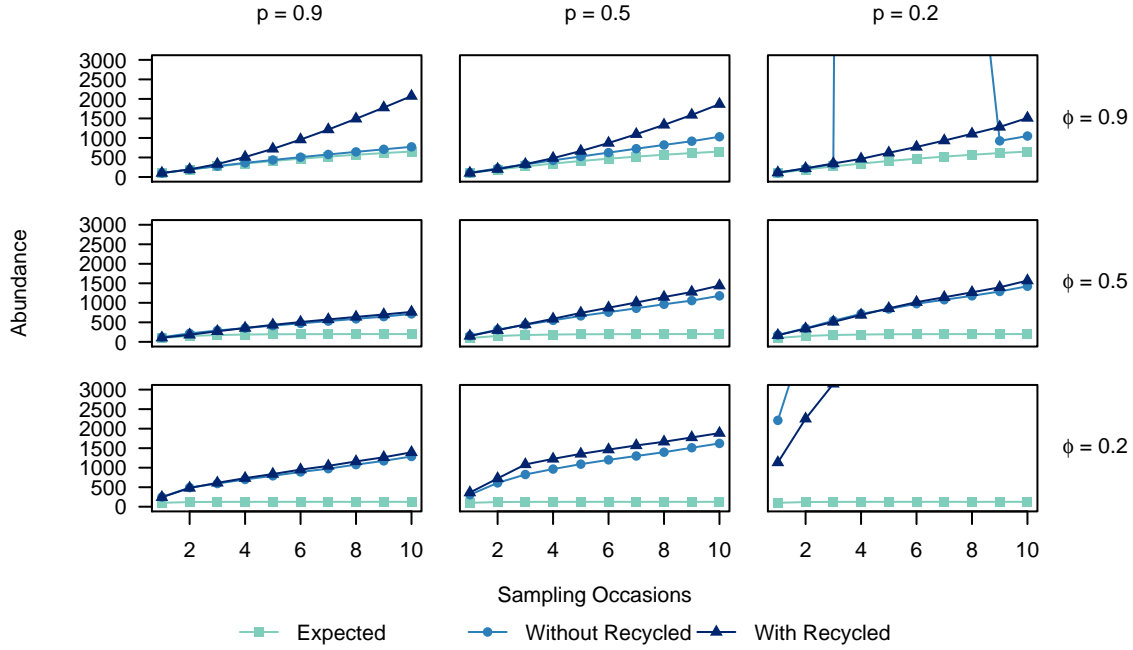


WEB FIGURE 23: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 5 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.

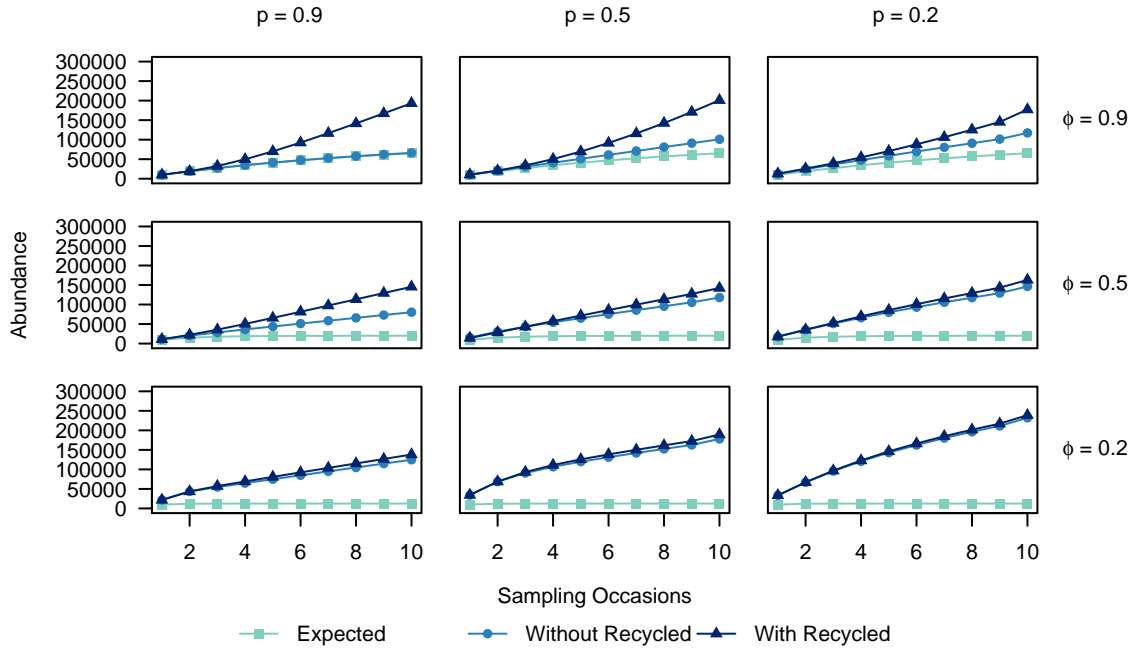


WEB FIGURE 24: Boxplots of super-population size estimates ( $N$ ) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with  $T_2 = 1$  for 7 time periods for varying survival ( $\phi = 0.2, 0.5, 0.9$ ), capture ( $p = 0.2, 0.5, 0.9$ ), and tag retention ( $\lambda = 0.2, 0.5, 0.9$ ) probabilities. The black line indicates the true value of  $N$  used to simulate the data for each model.

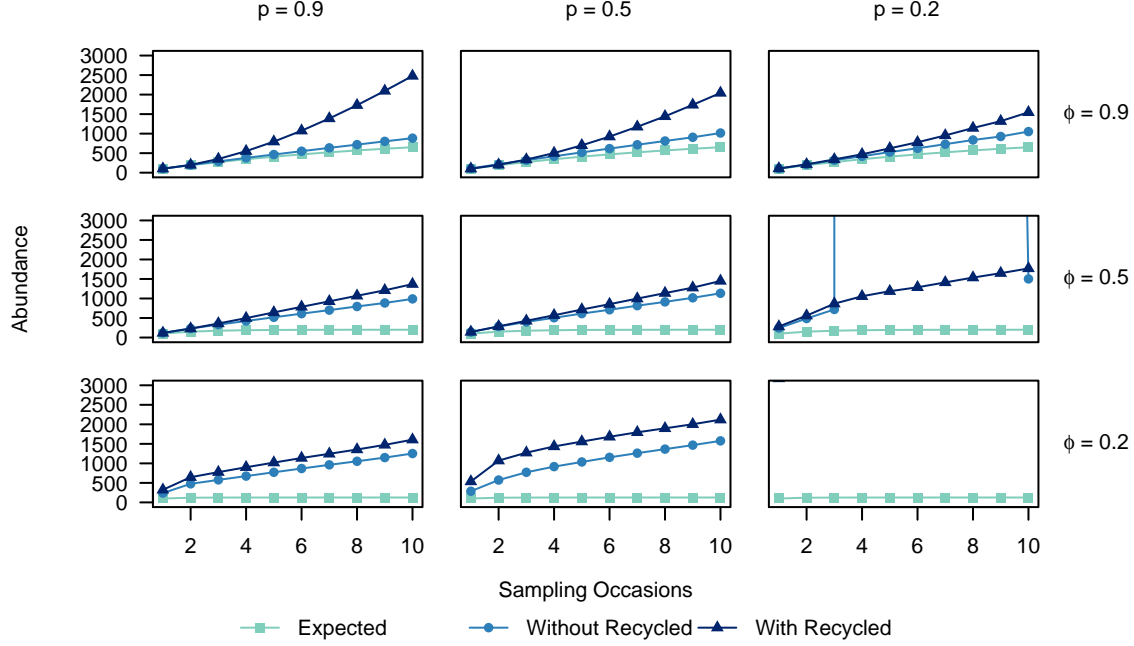
## Abundance Estimates



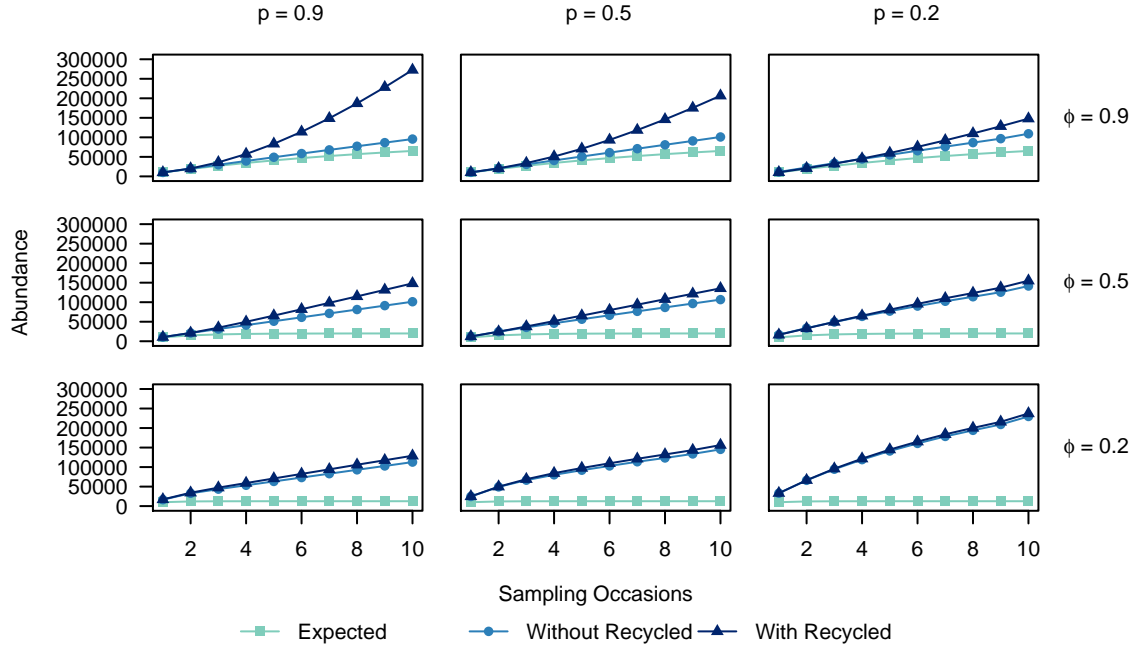
WEB FIGURE 25: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 10 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



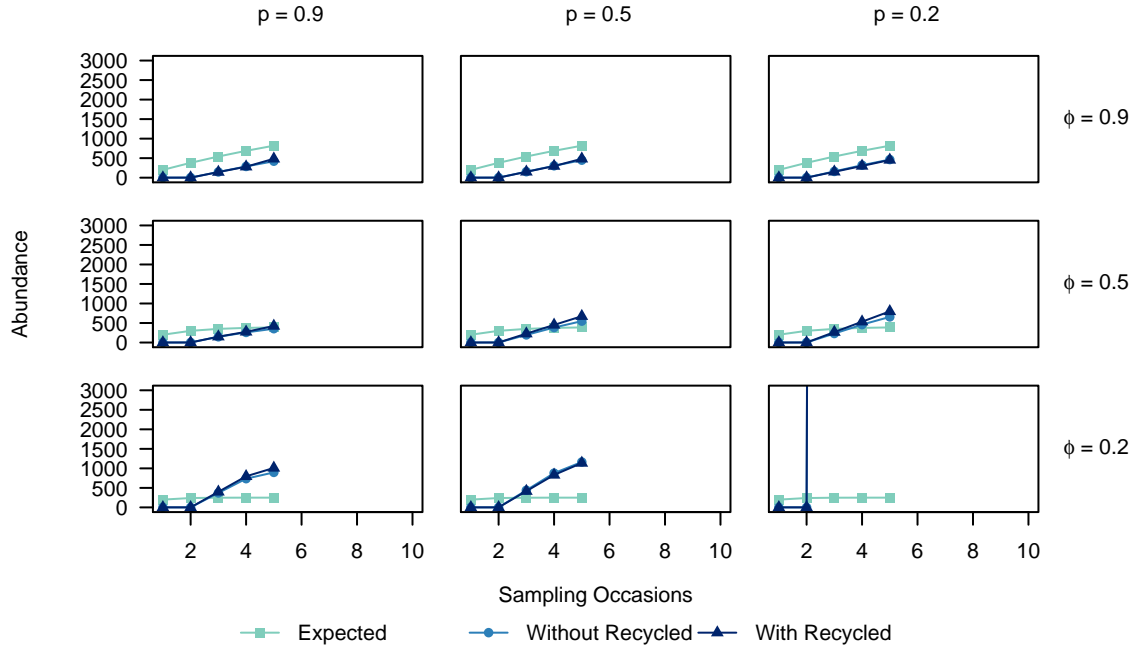
WEB FIGURE 26: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 1$  with 10 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



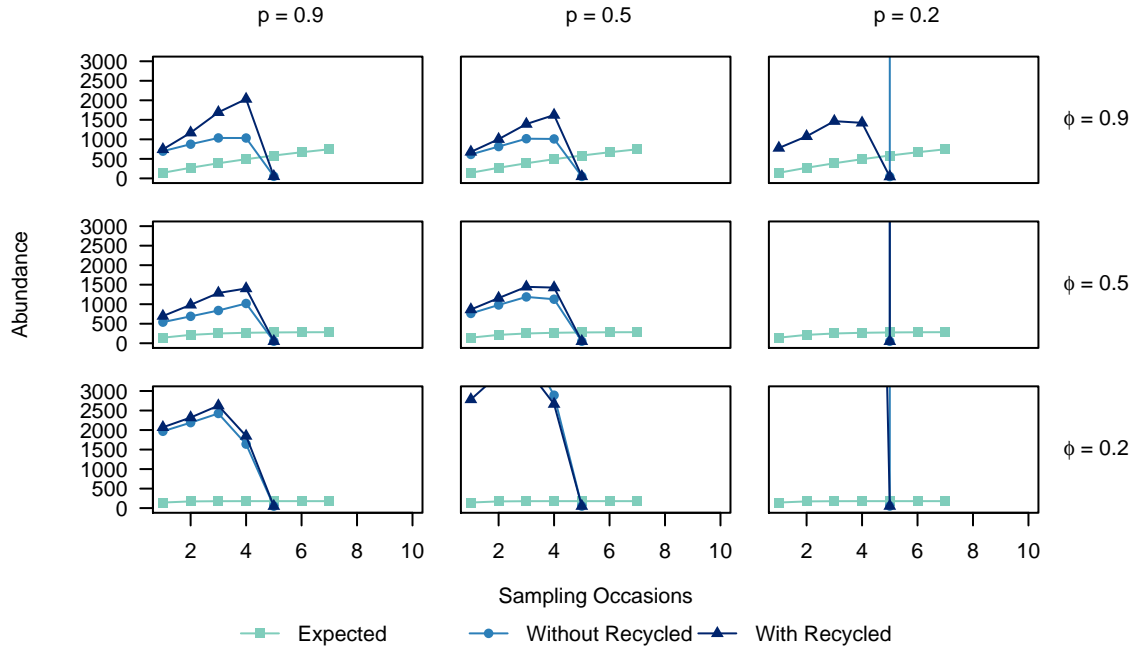
WEB FIGURE 27: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 0.5$  with 10 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



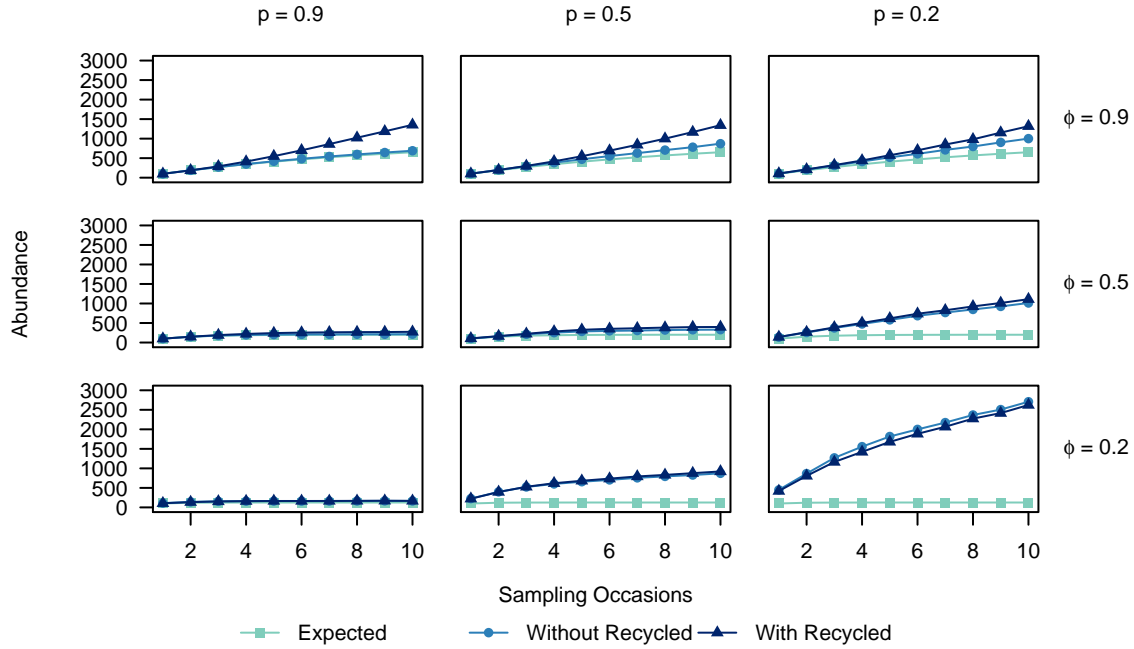
WEB FIGURE 28: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 0.5$  with 10 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



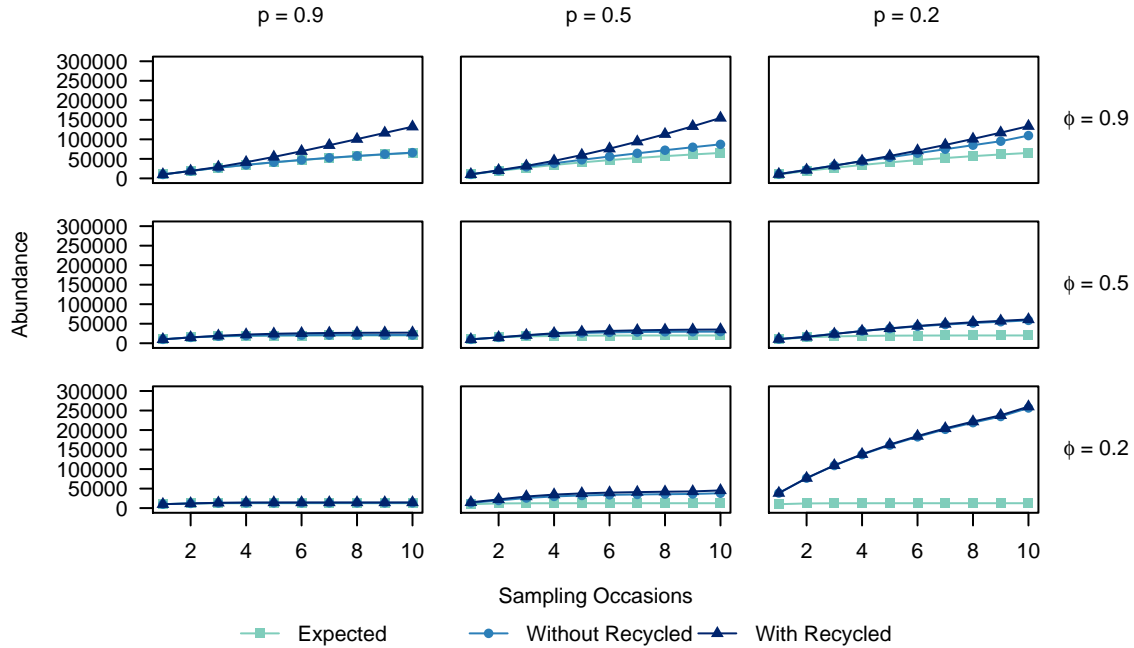
WEB FIGURE 29: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 5$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 5 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



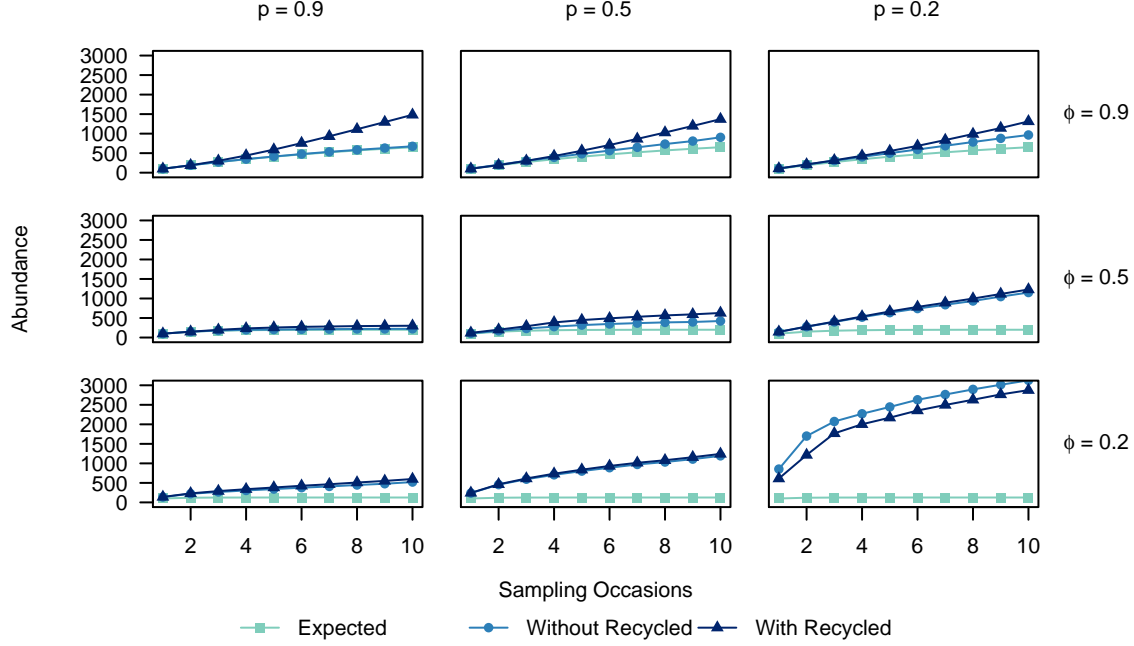
WEB FIGURE 30: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 7$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 7 time periods for low tag retention ( $\lambda = 0.2$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



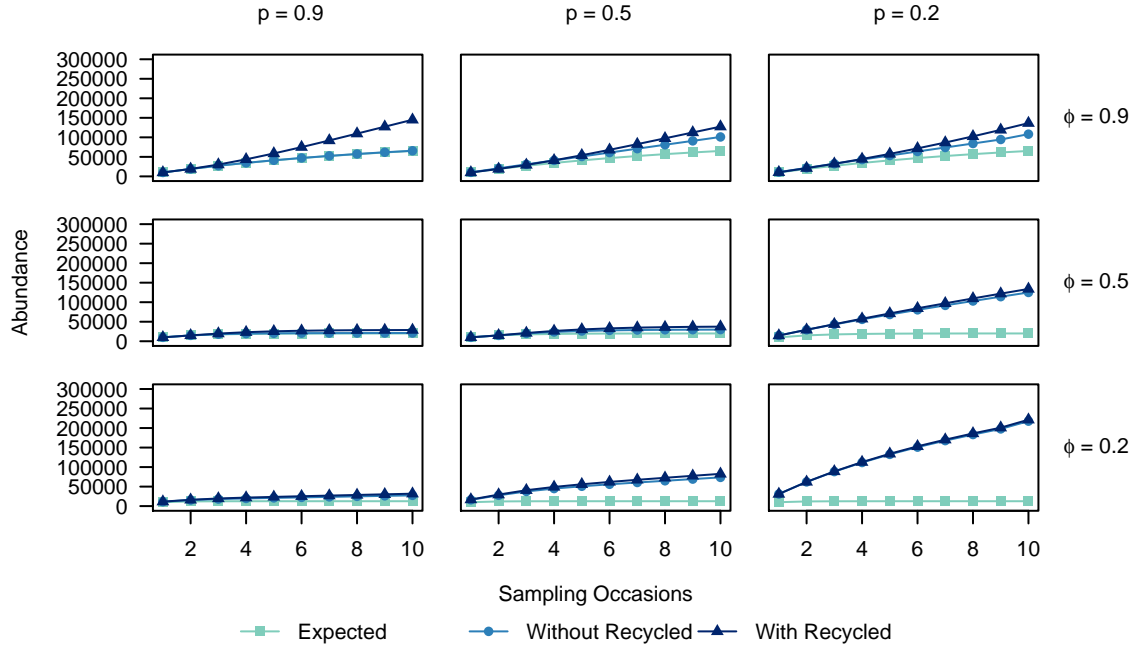
WEB FIGURE 31: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 10 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



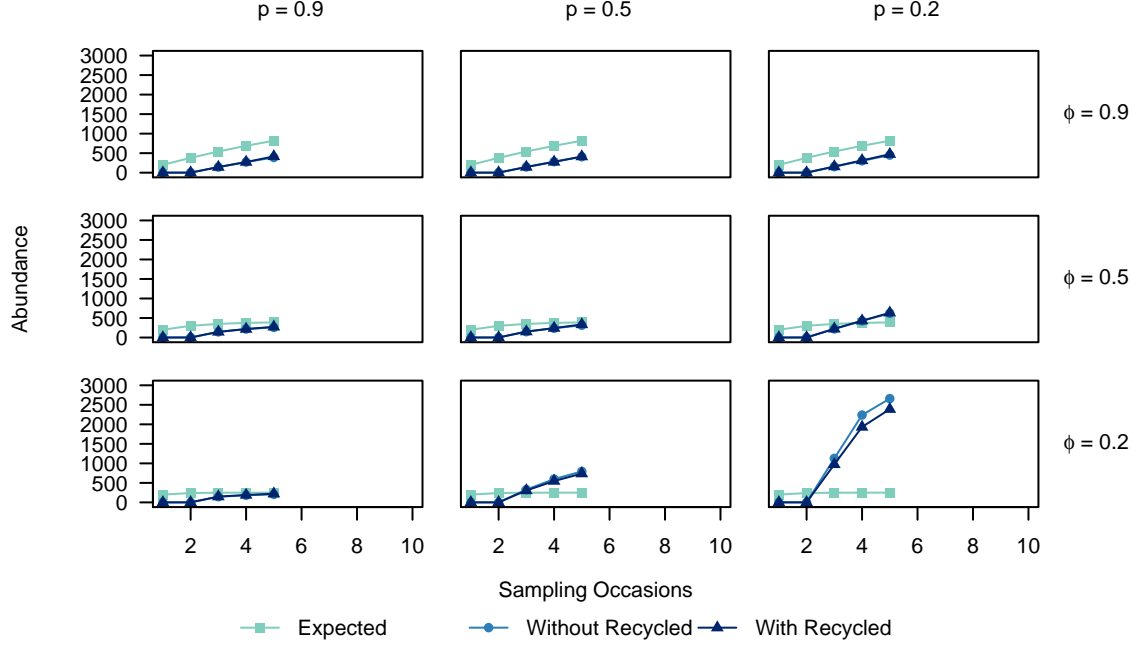
WEB FIGURE 32: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 1$  with 10 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



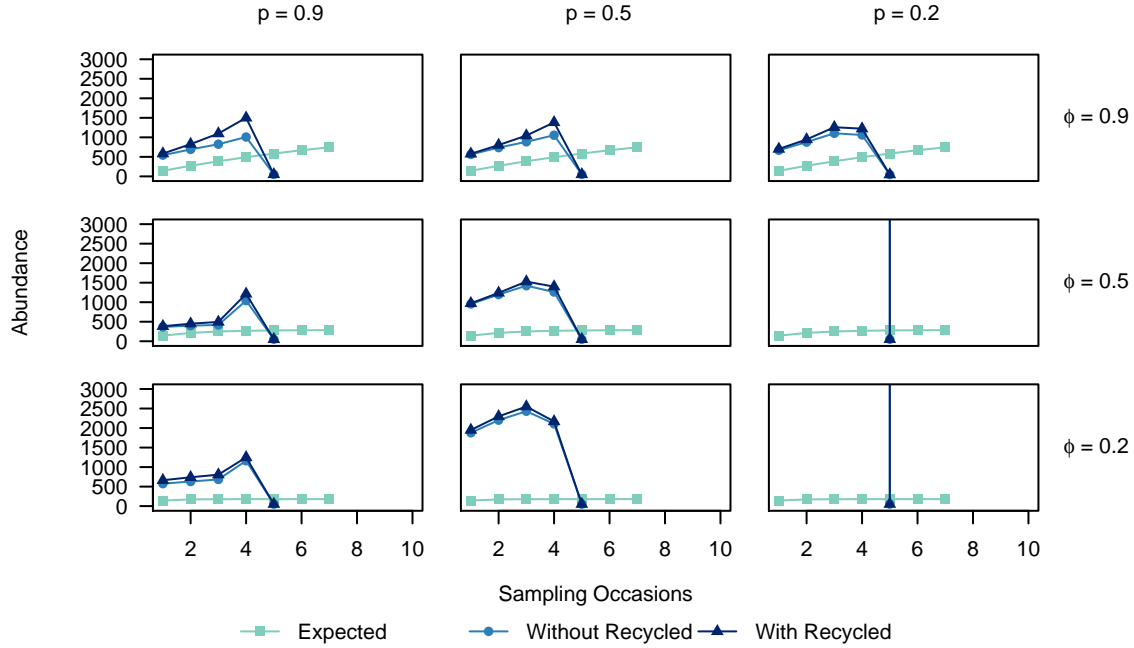
WEB FIGURE 33: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 0.5$  with 10 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



WEB FIGURE 34: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 0.5$  with 10 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).

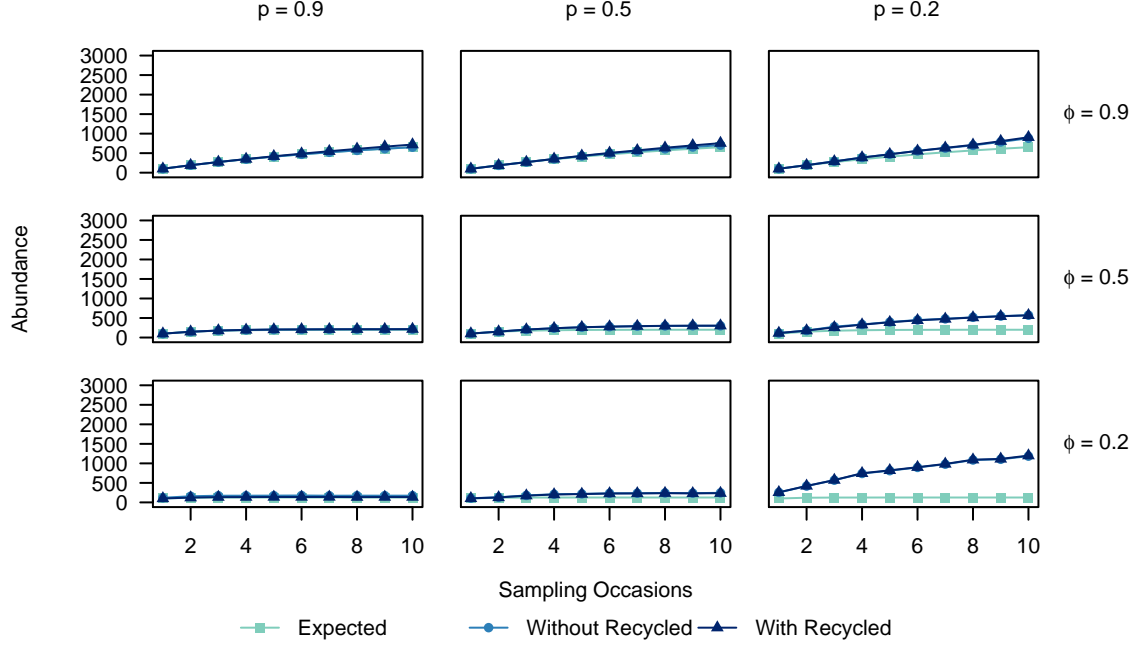


WEB FIGURE 35: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 5$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 5 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).

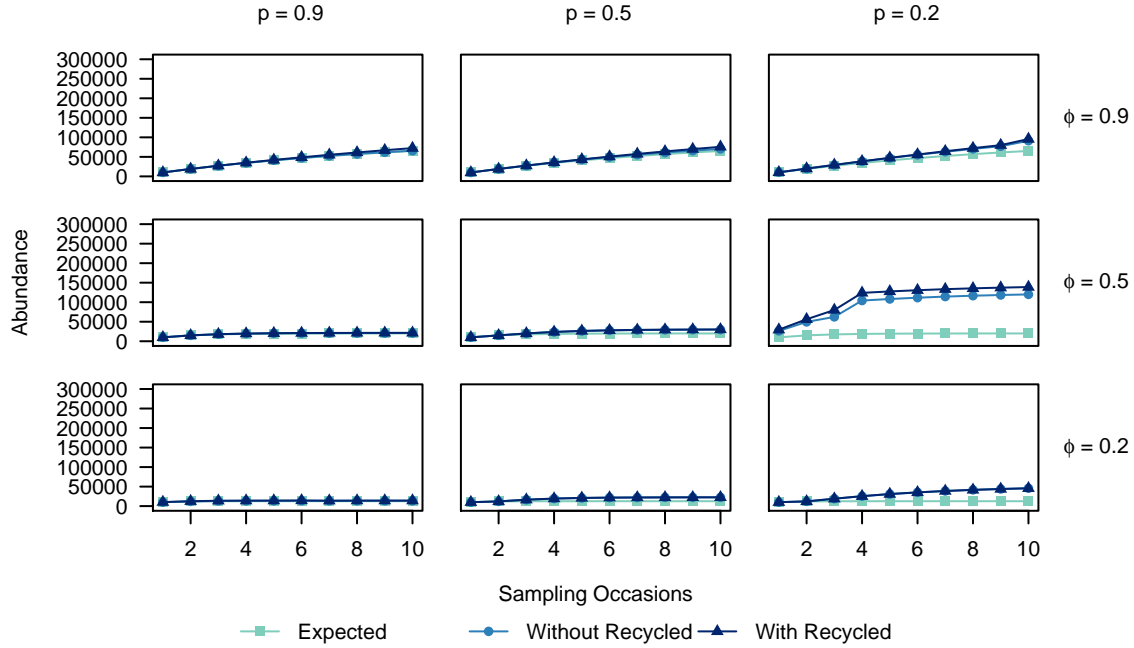


WEB FIGURE 36: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 7$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 7 time periods for medium tag retention ( $\lambda = 0.5$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).

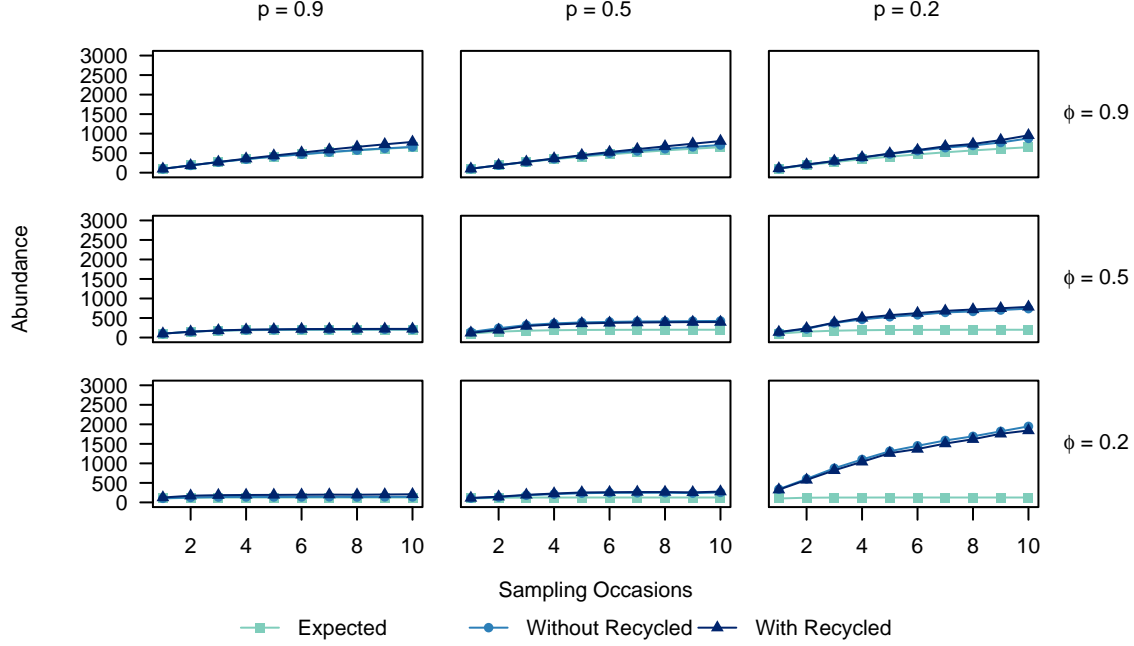




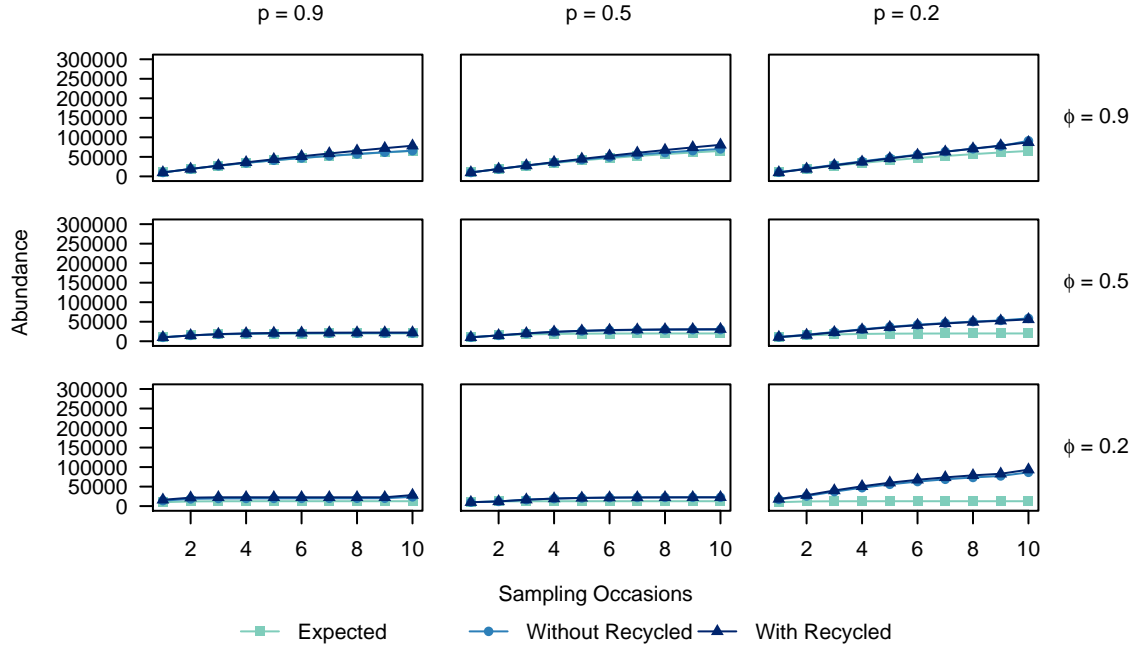
WEB FIGURE 37: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 10 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



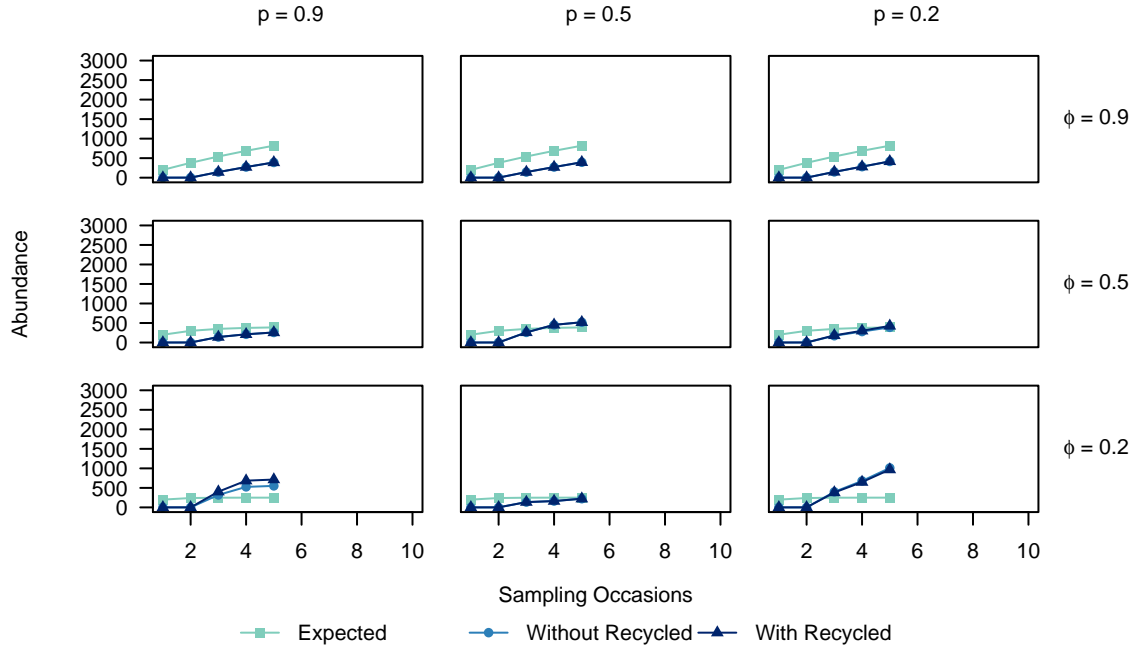
WEB FIGURE 38: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 1$  with 10 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



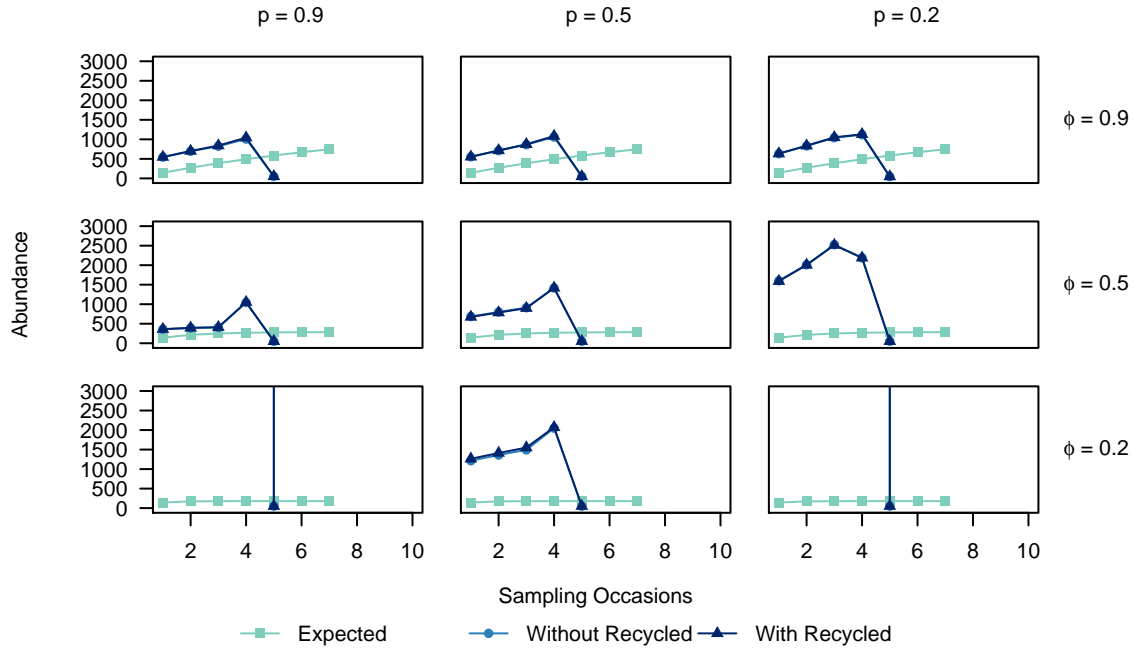
WEB FIGURE 39: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 0.5$  with 10 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



WEB FIGURE 40: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 10$ ) between analysis with and without recycled individuals with population size  $N = 100000$  with  $T_2 = 0.5$  with 10 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



WEB FIGURE 41: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 5$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 5 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).



WEB FIGURE 42: Mean abundance estimates ( $N_j$ 's) for each sample time ( $k = 7$ ) between analysis with and without recycled individuals with population size  $N = 1000$  with  $T_2 = 1$  with 5 time periods for high tag retention ( $\lambda = 0.9$ ), varying survival probabilities ( $\phi = 0.2, 0.5, 0.9$ ) and varying capture probabilities ( $p = 0.2, 0.5, 0.9$ ).