Web-based 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

We use the following notation to describe the statistics or model parameters discussed in this study.

$k =$ number of sample times

$n_{\text{obs}} =$ the total number of individuals captured with no tags and treated as new individuals; when no recycling is present, n_{obs} is the number of unique individuals observed throughout the study

$p =$ 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 $j+1$. $j = 0, 1, ..., k-1$. b_0 is the expected fraction of individuals alive just prior to the first sample time.

$\upsilon =$ 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 $j+1$, $j = 0, 1, ..., k-1$.

$$b_j* = \begin{cases} b_0 & \text{if } j = 0 \\ b_j / \sum_{u=j}^{k-1} b_u & \text{if } j = 1, ..., k-1 \\ 1 & \text{if } j = k-1 \end{cases}$$

$B_j =$ net births; the number of individuals who enter the population after sample time j and survive to sample time $j+1$; $j = 0, 1, ..., k-1$. B_0 is the number of indiividuals 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 ϕ, p, and λ. 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; $j = 1, 2, ..., k$

$N_j =$ population size at time j. $\mathrm{E}(N_1|N) = B_0$, $\mathrm{E}(N_{j+1}|N) = (N_j - N_j p \upsilon)\phi + B_j$, which is the number of individuals that survive from time j minus the number lost on capture plus the number of births.

Complete Likelihood

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.

$$L = \binom{N}{n_{\text{obs}}} \left\{ \sum_{j=0}^{k-1} b_j(1-p)\chi_{(0,j+1,0)} \right\}^{(N-n_{\text{obs}})} \times \left\{ 1 - \sum_{j=0}^{k-1} b_j(1-p)\chi_{(0,j+1,0)} \right\}^{n_{\text{obs}}} \times$$

$$\binom{n_{\text{obs}}}{n_{\omega_1}, n_{\omega_2}, ..., n_{\omega_m}} \prod_{i=1}^{m} \left[\psi_{f_i} T_d \left\{ \prod_{j=f_i}^{l_i} p^{w*_{ij}} (1-p)^{(1-w*_{ij})} \right\} \left\{ \prod_{j=f_i}^{l_i-1} \phi \right\} \times \right.$$

$$\left. \prod_{d=1}^{2} \left\{ \left(\prod_{j=f_i}^{l_{id}-1} \lambda \right) \left(1 - \prod_{j=l_{id}}^{q_{id}-1} \lambda \right)^{I(l_{id} \neq l_i)} \right\} \times \chi_{f_i,l_i,nt_{l_i}} \right]^{n_{\omega_i}} \times$$

$$\left\{ 1 - \sum_{j=0}^{k-1} b_j(1-p)\chi_{(0,j+1,0)} \right\}^{-n_{\text{obs}}}$$

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

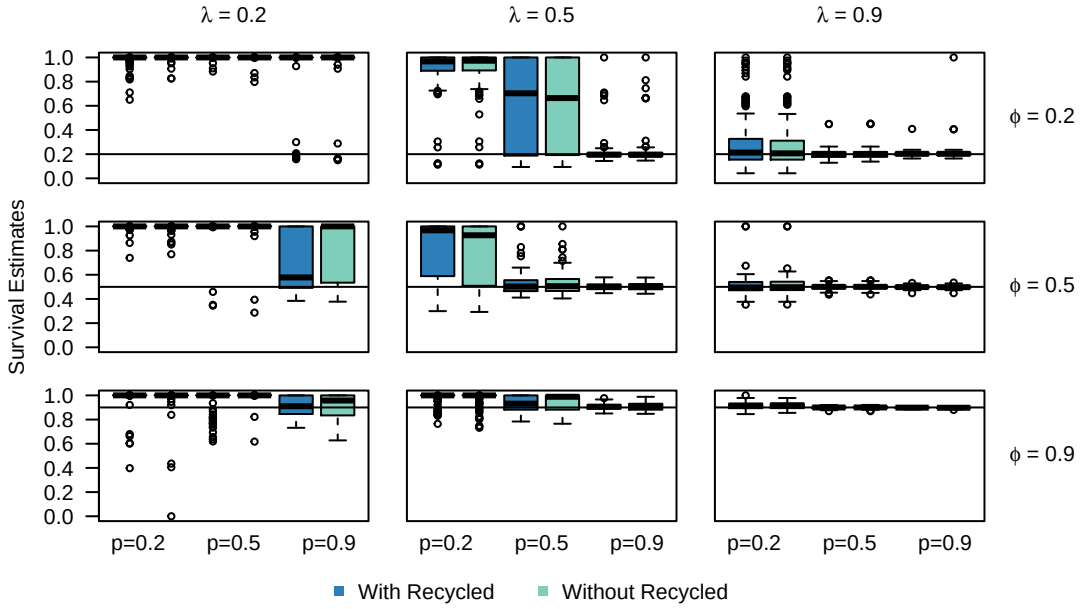
Web Table 2: Examples of the fraction of recycled individuals (number of recycled individuals captured / total number of individuals captured) at each sample occasion for a 7 occasion experiment with super-population size $N = 1000$ with 100% double-tagging.

	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
$\phi = 0.2, p = 0.9, \lambda = 0.2$	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

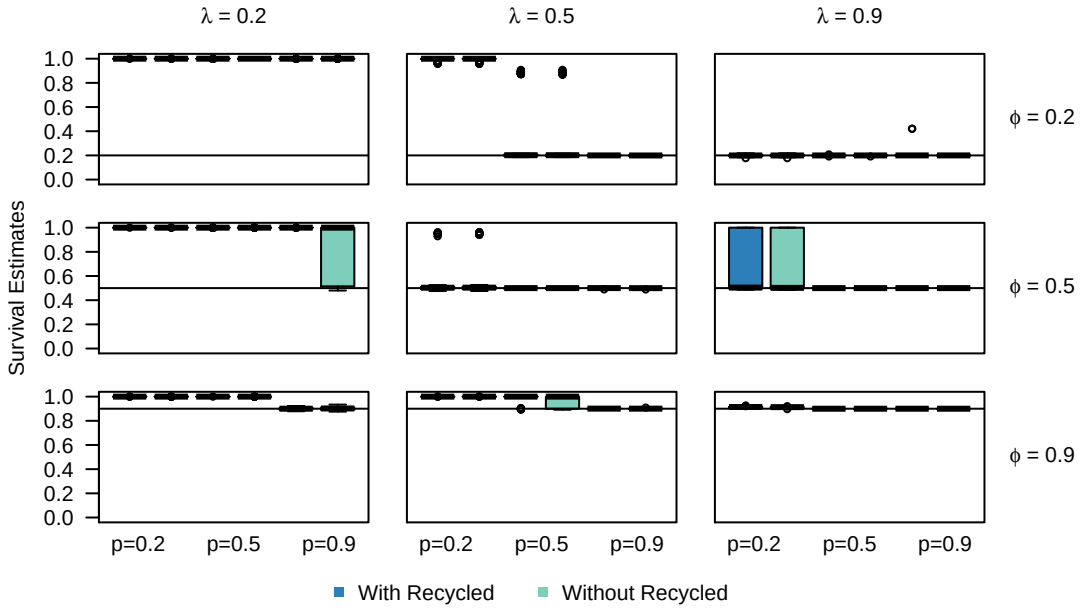
WEB TABLE 3: Examples of the fraction of recycled individuals (number of recycled individuals captured / total number of individuals captured) at each sample occasion for a 5 occasion experiment with super-population size $N = 1000$ with 100% double-tagging.

	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

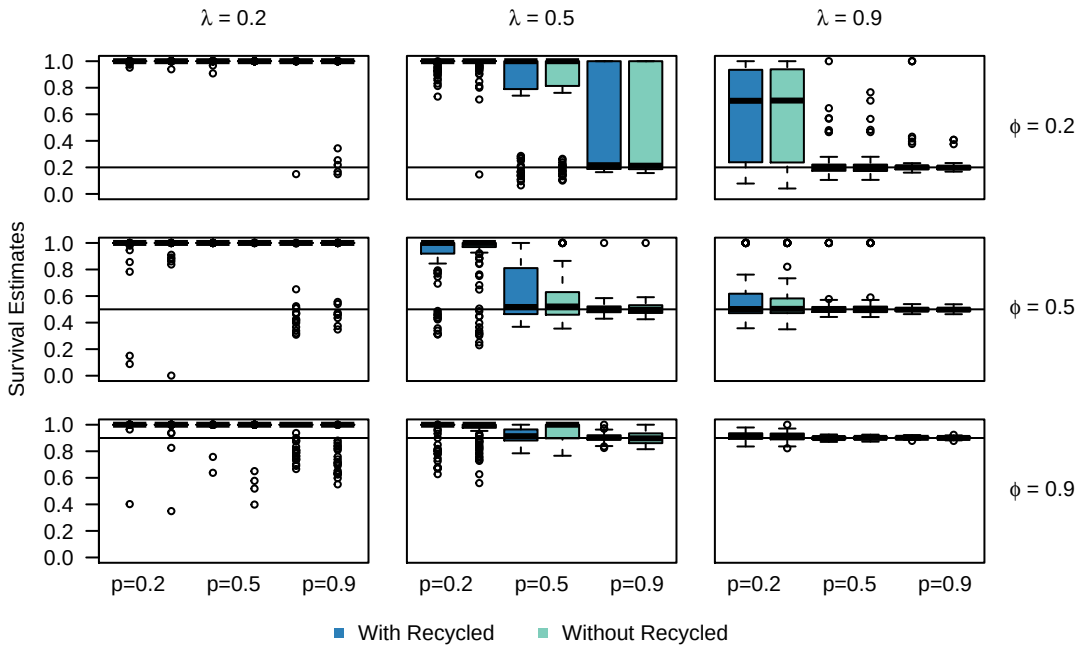
Survival Estimates



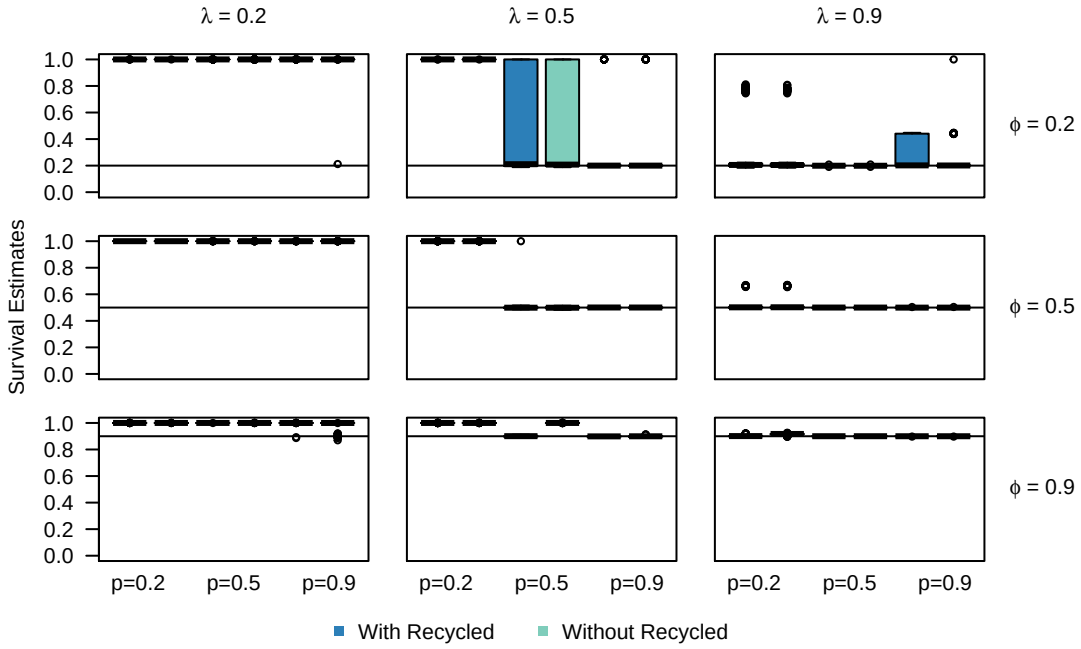
WEB FIGURE 1: Boxplots of survival estimates ($\hat{\phi}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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



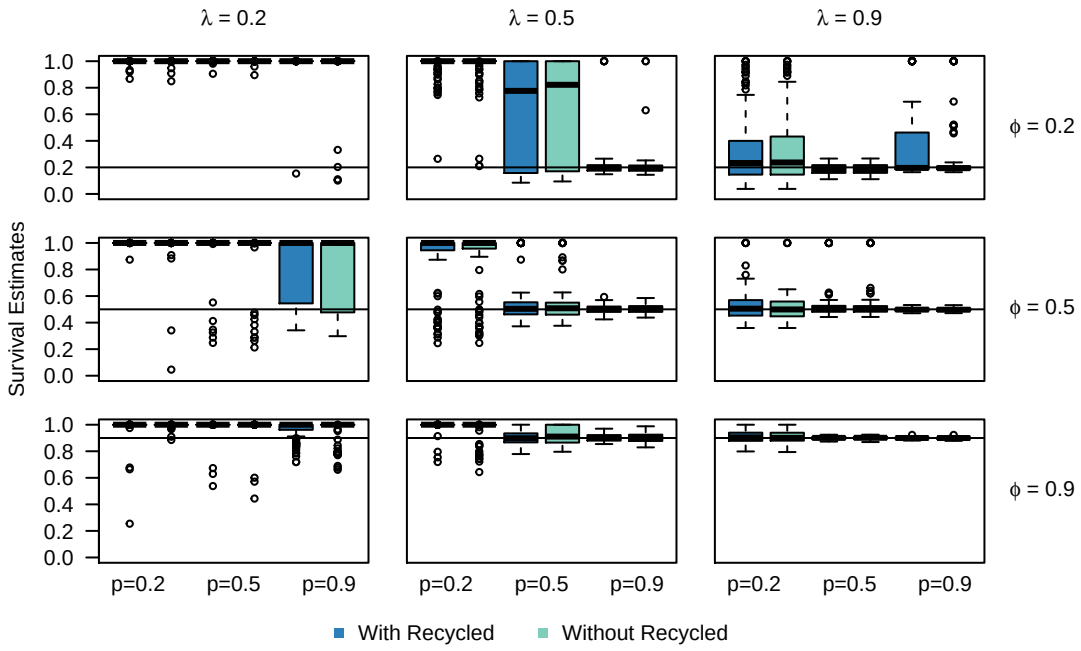
WEB FIGURE 2: Boxplots of survival estimates ($\hat{\phi}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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



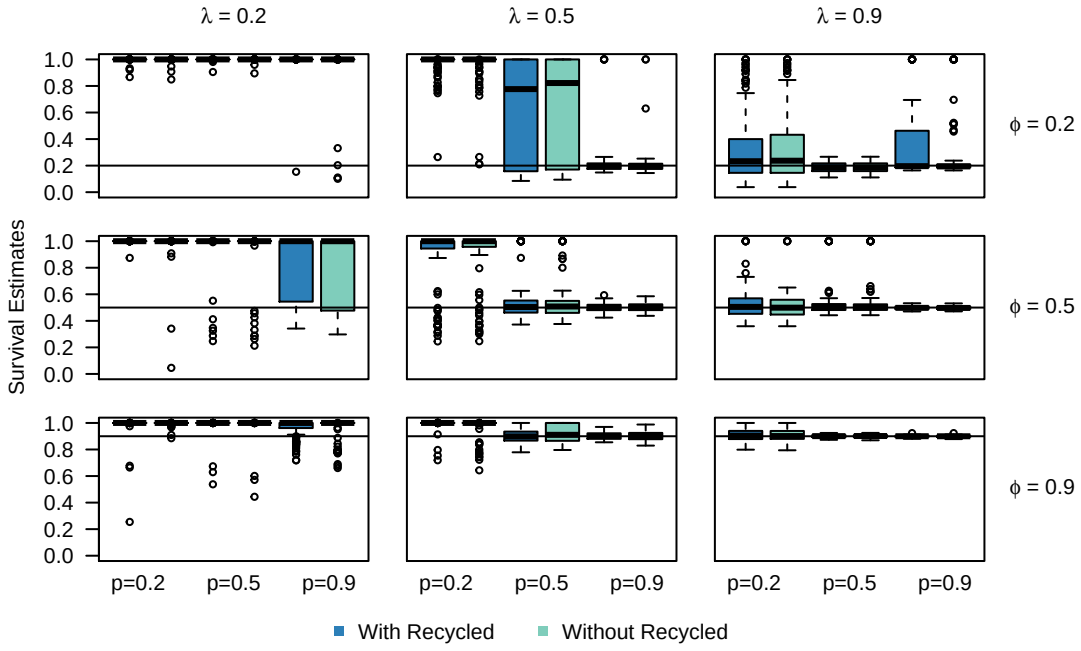
WEB FIGURE 3: Boxplots of survival estimates ($\hat{\phi}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 0.5$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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

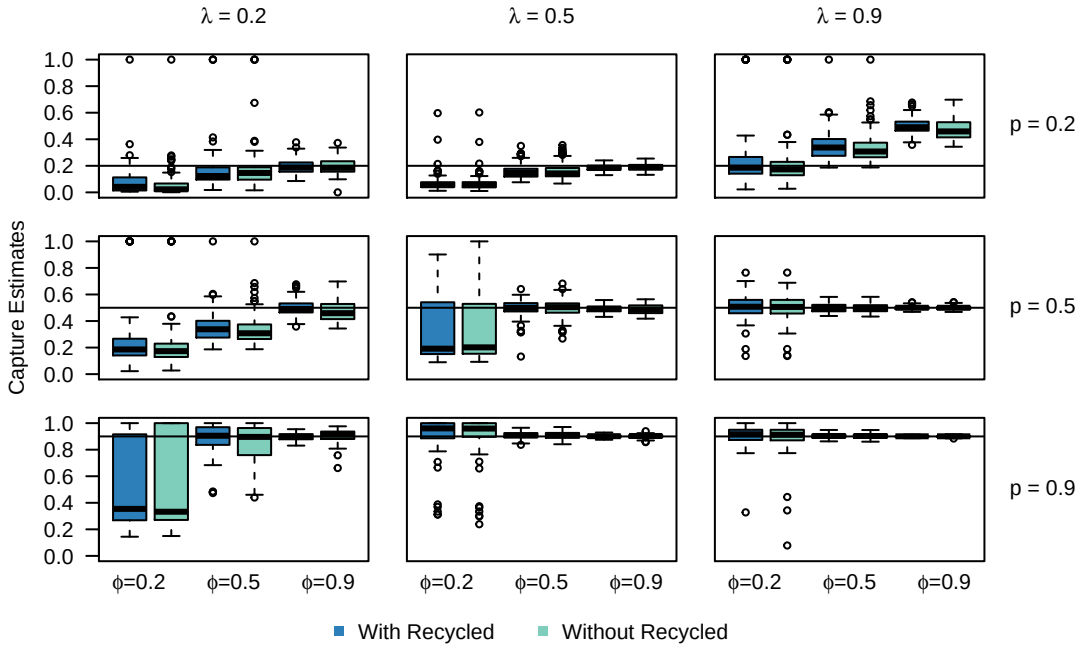


WEB FIGURE 5: Boxplots of survival estimates ($\hat{\phi}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 5 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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

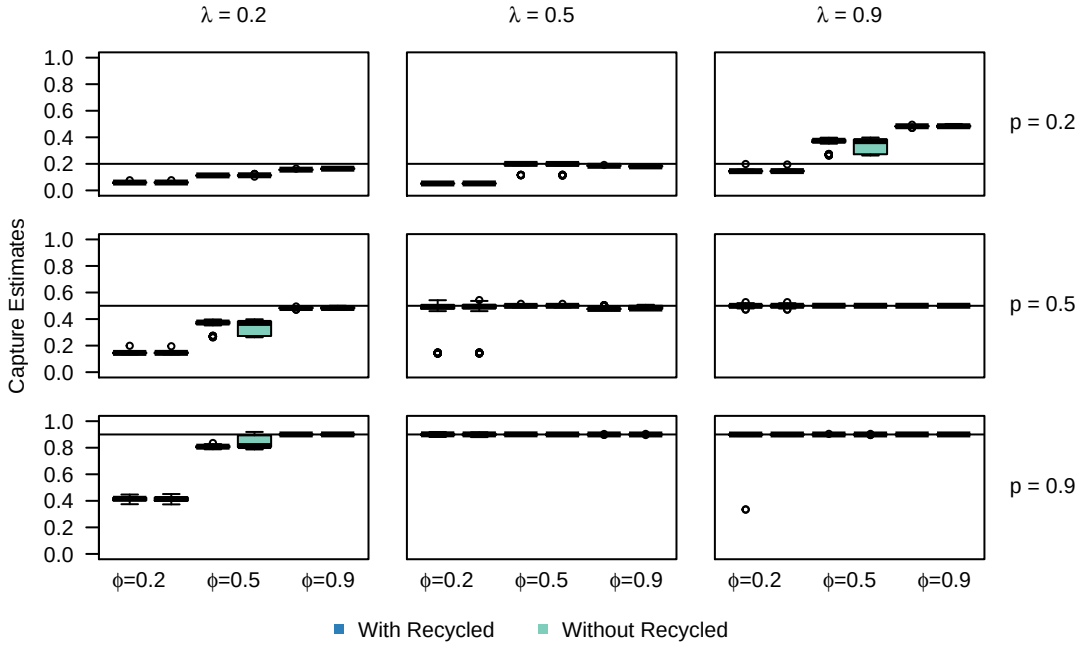


WEB FIGURE 6: Boxplots of survival estimates ($\hat{\phi}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 7 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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

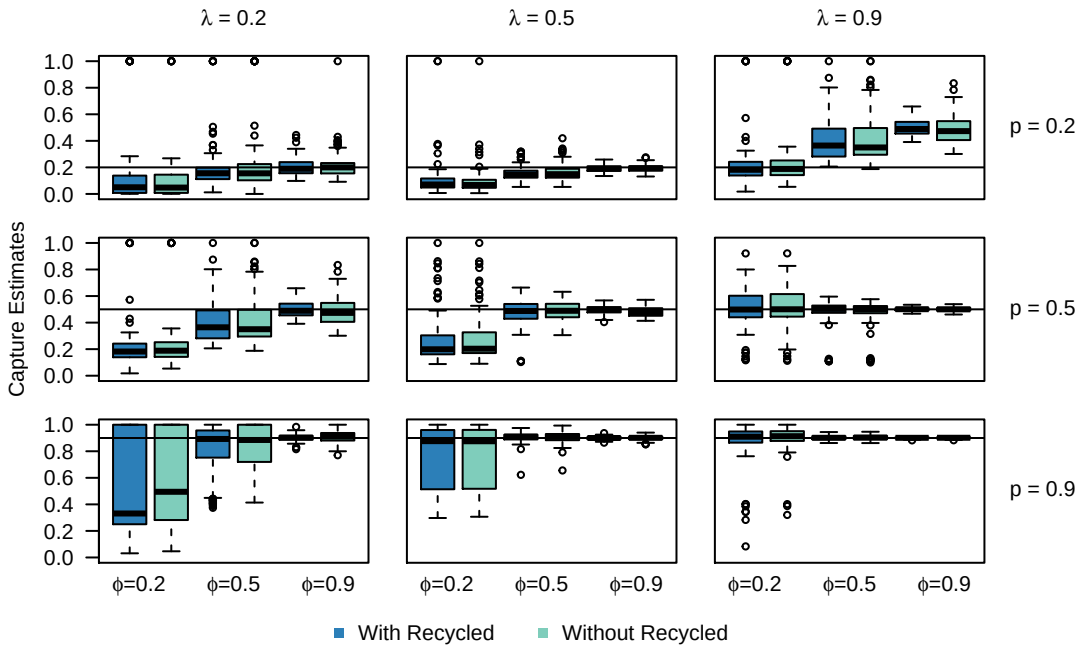
Capture Estimates



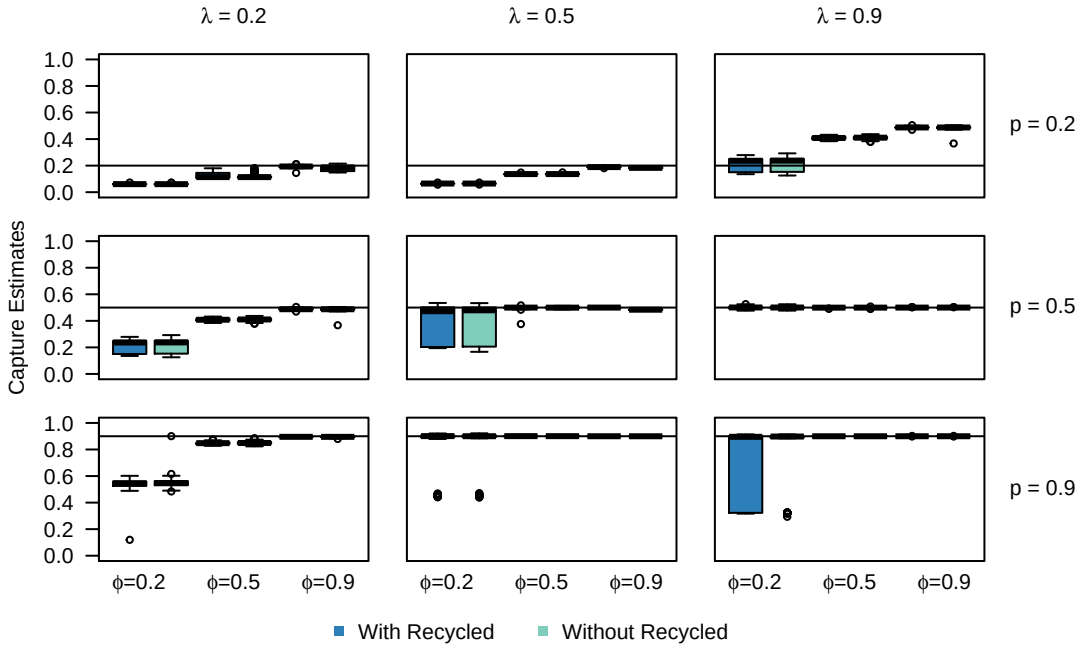
WEB FIGURE 7: Boxplots of capture estimates ($\hat{p}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention ($\lambda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



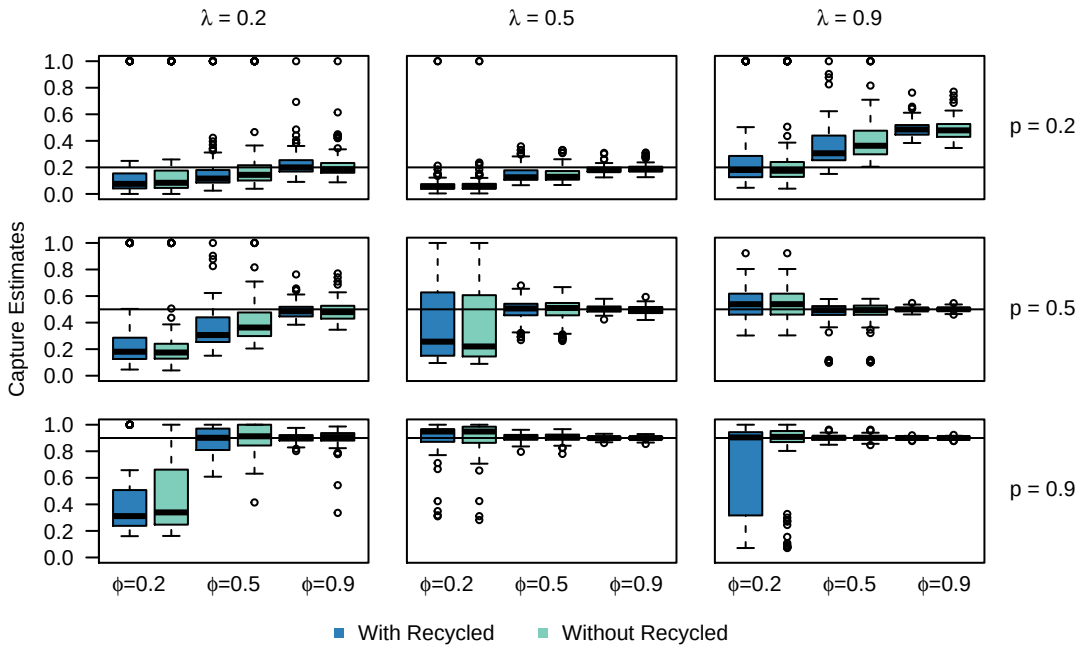
WEB FIGURE 8: Boxplots of capture estimates ($\hat{p}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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



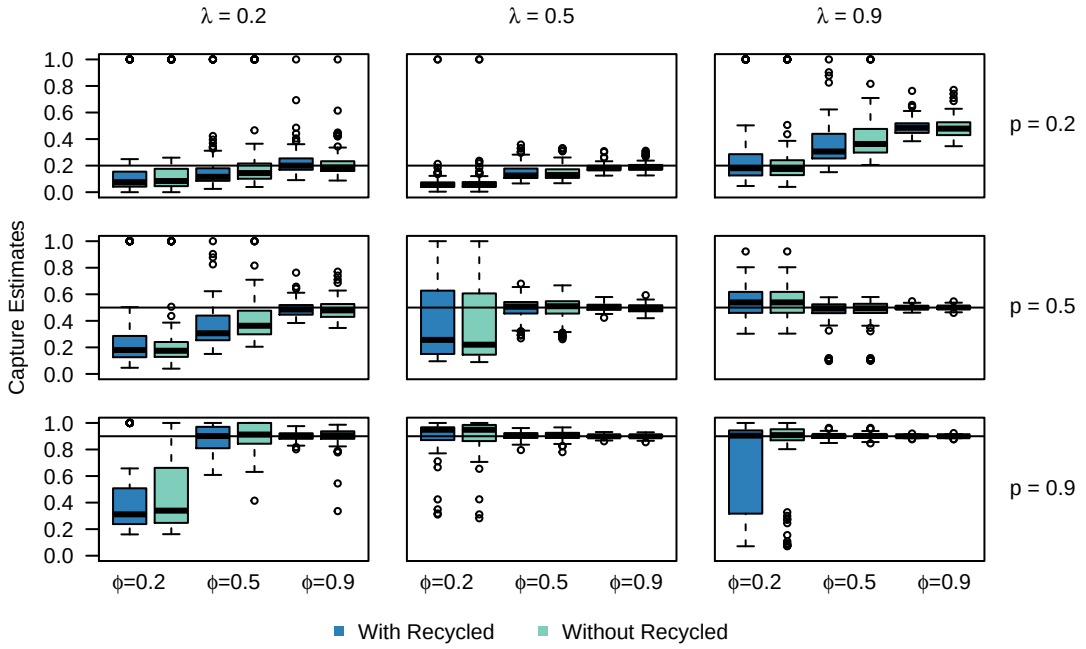
WEB FIGURE 9: Boxplots of capture estimates ($\hat{p}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 0.5$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention ($\lambda = 0.2, 0.5, 0.9$) 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.

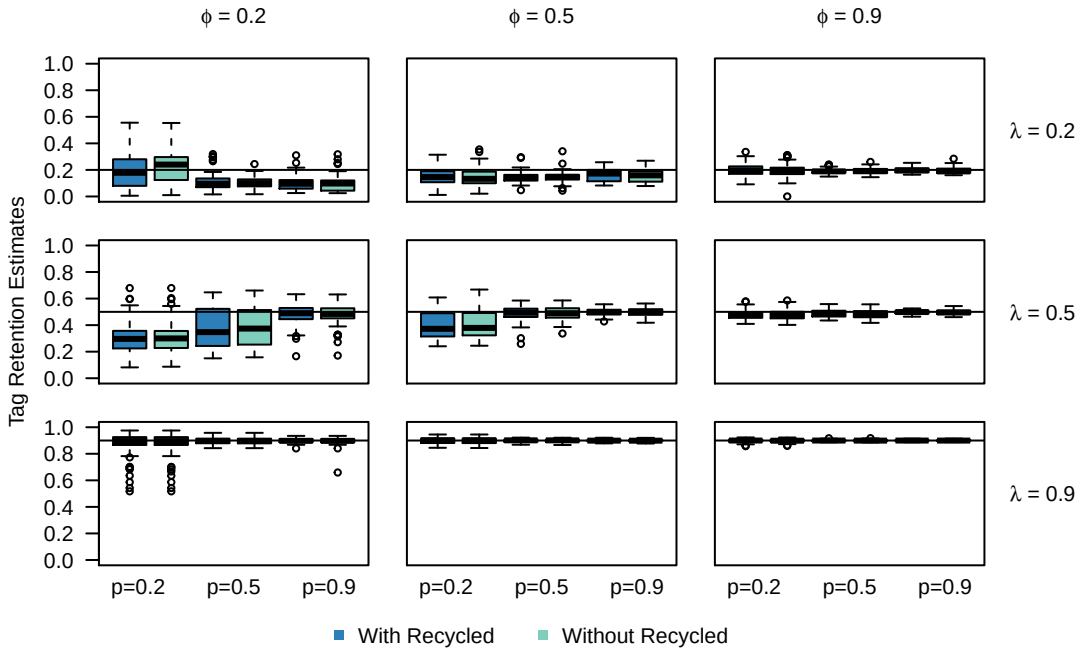


WEB FIGURE 11: Boxplots of capture estimates ($\hat{p}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 5 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention ($\lambda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

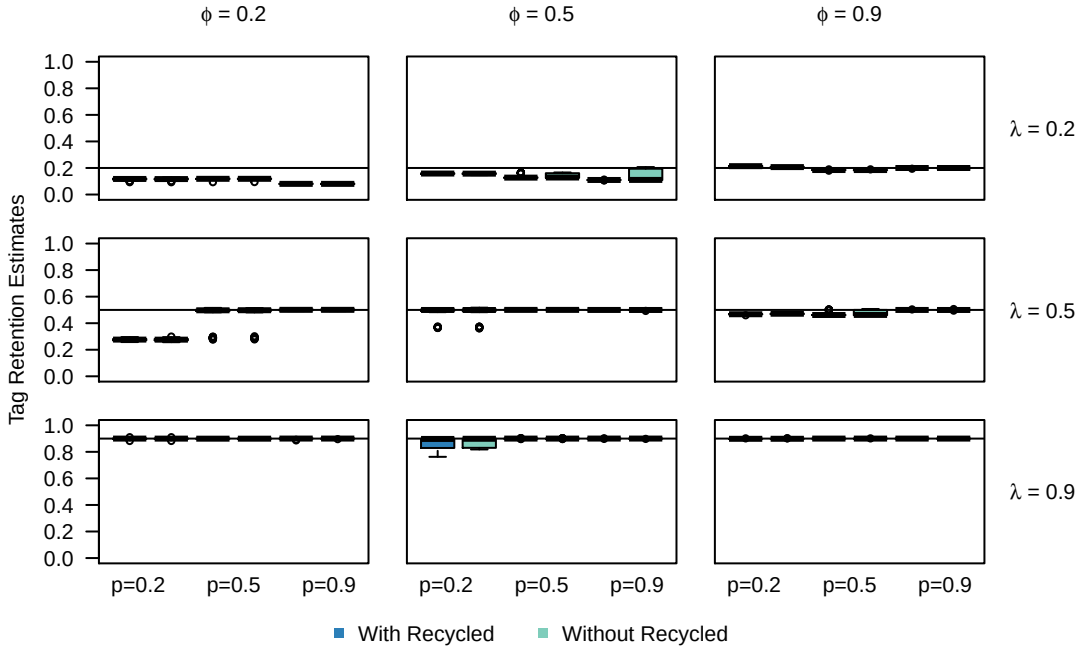


WEB FIGURE 12: Boxplots of capture estimates ($\hat{p}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 7 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention ($\lambda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

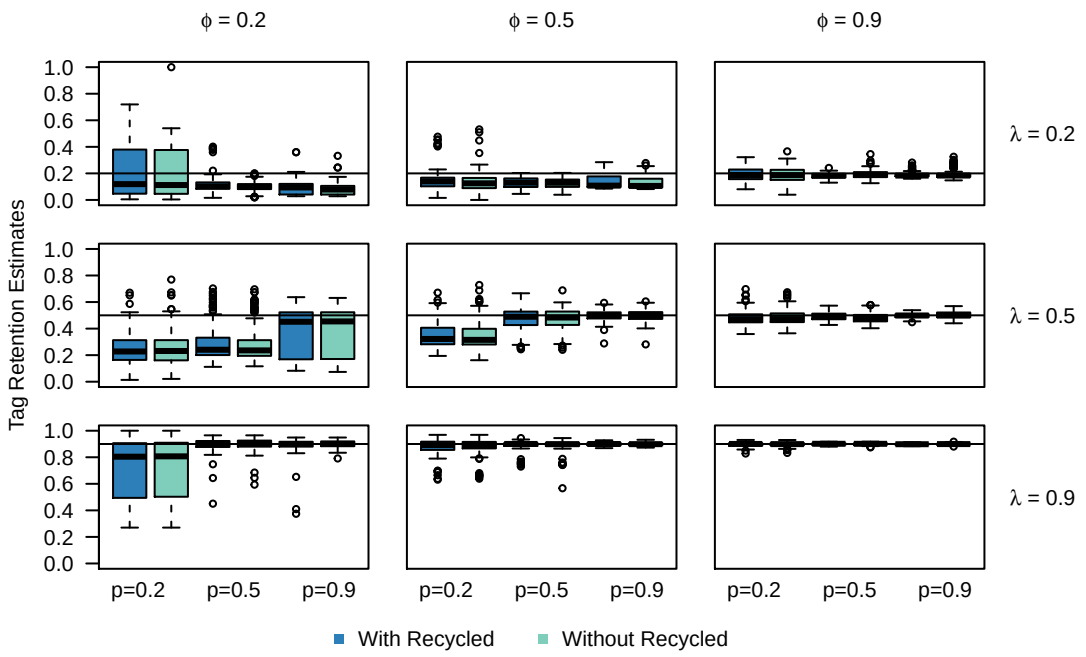
Tag Retention Estimates



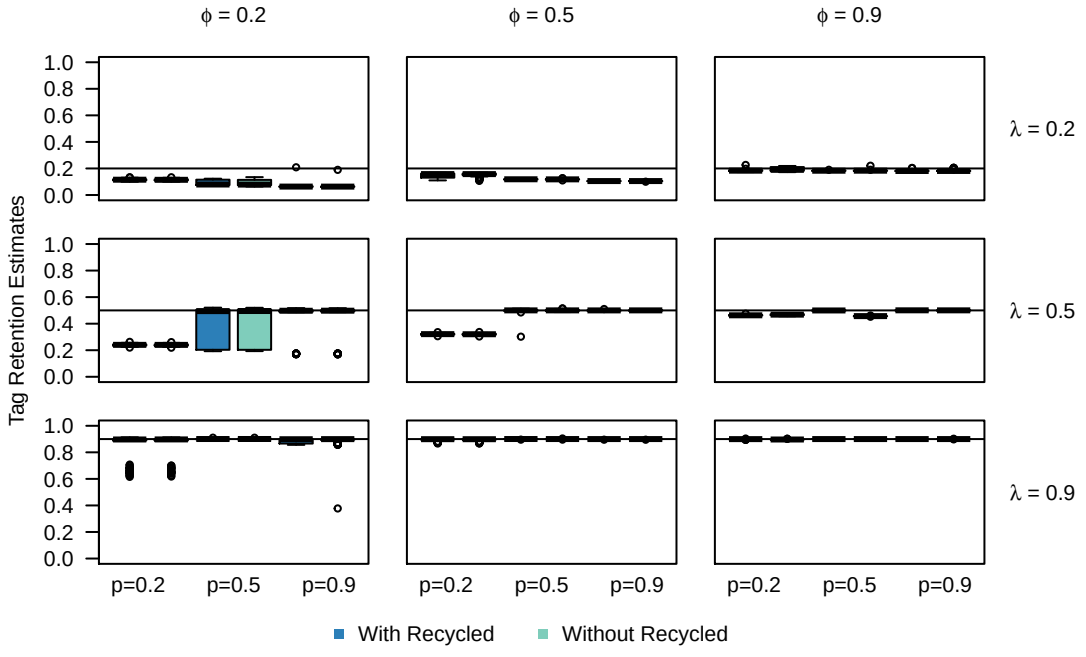
WEB FIGURE 13: Boxplots of tag retention estimates ($\hat{\lambda}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag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



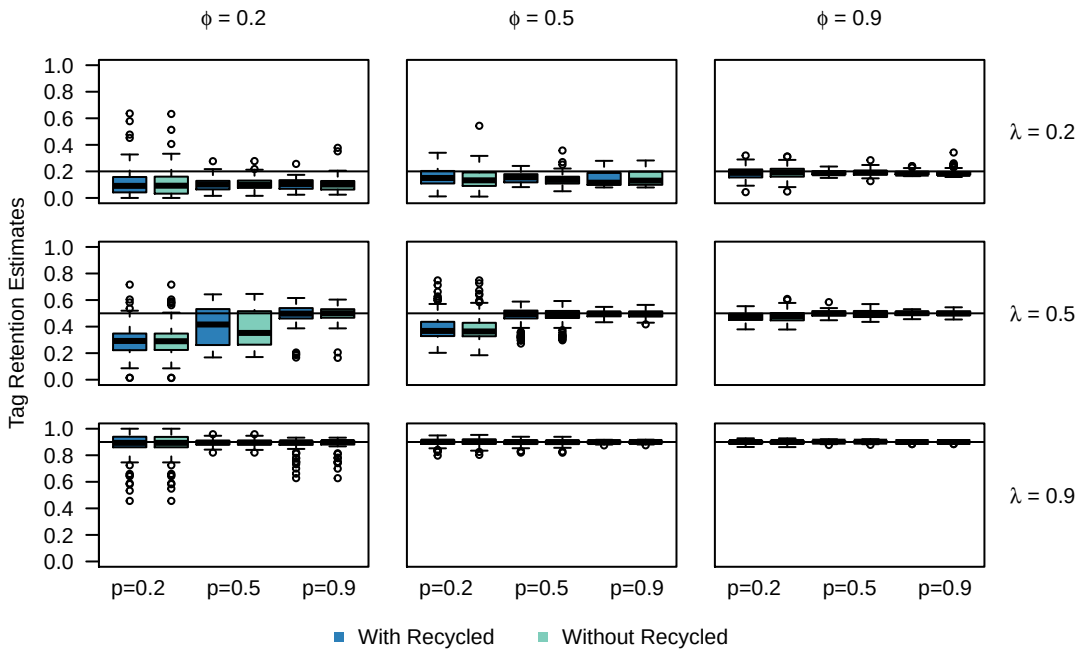
WEB FIGURE 14: Boxplots of tag retention estimates ($\hat{\lambda}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and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



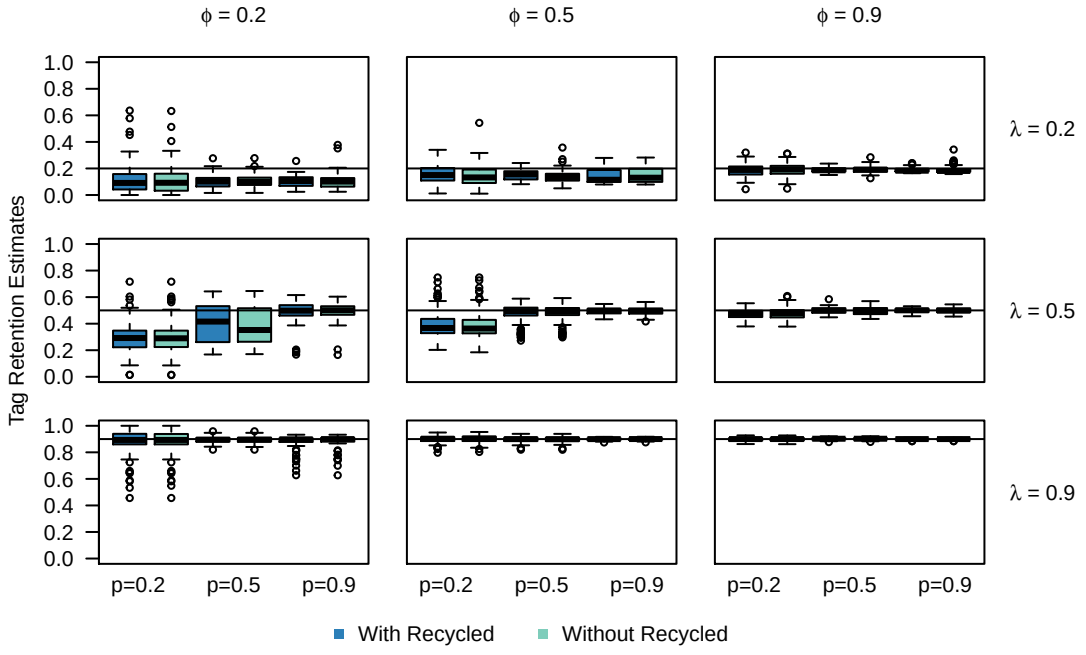
WEB FIGURE 15: Boxplots of tag retention estimates ($\hat{\lambda}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 0.5$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and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

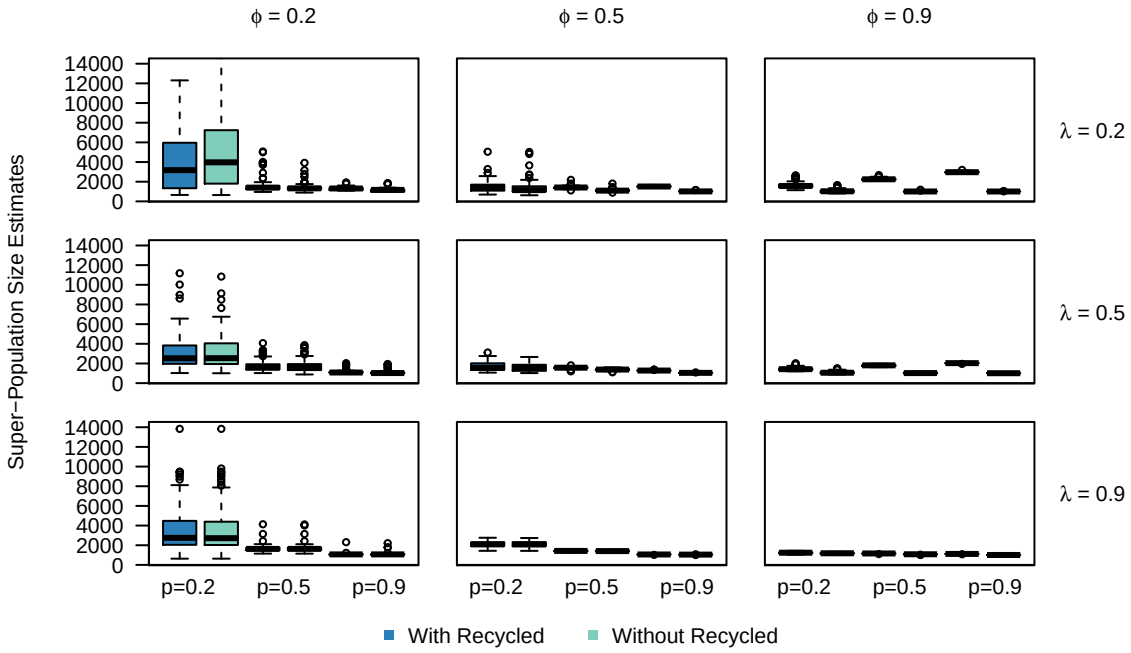


WEB FIGURE 17: Boxplots of tag retention estimates ($\hat{\lambda}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 5 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag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

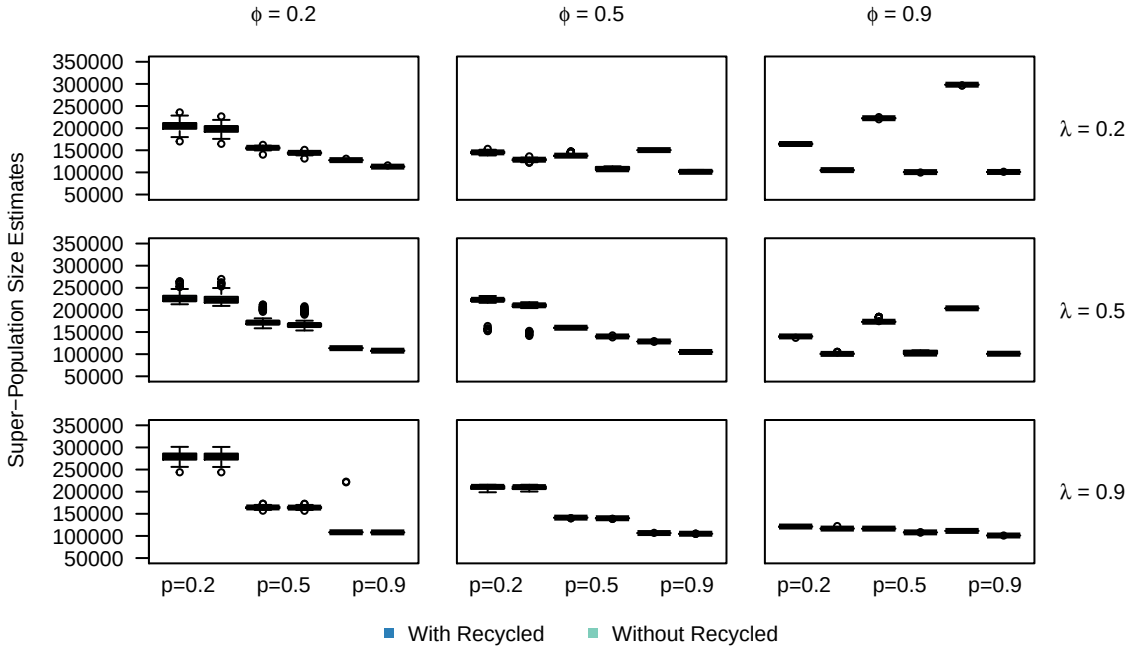


WEB FIGURE 18: Boxplots of tag retention estimates ($\hat{\lambda}$) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 7 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag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

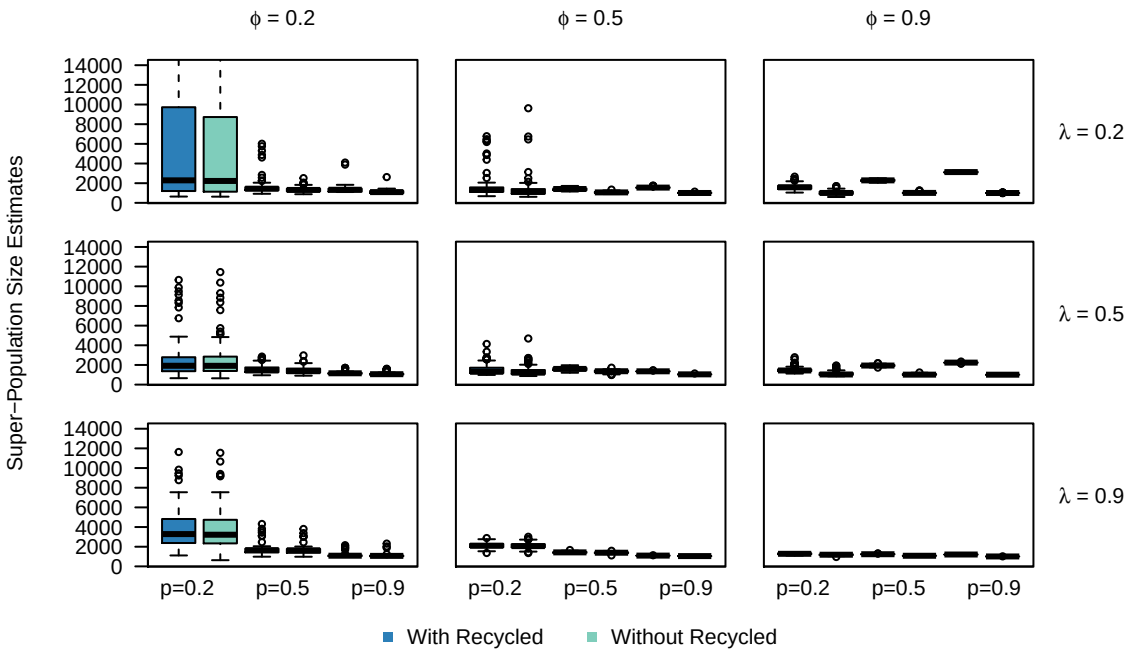
Super-Population Size Estimates



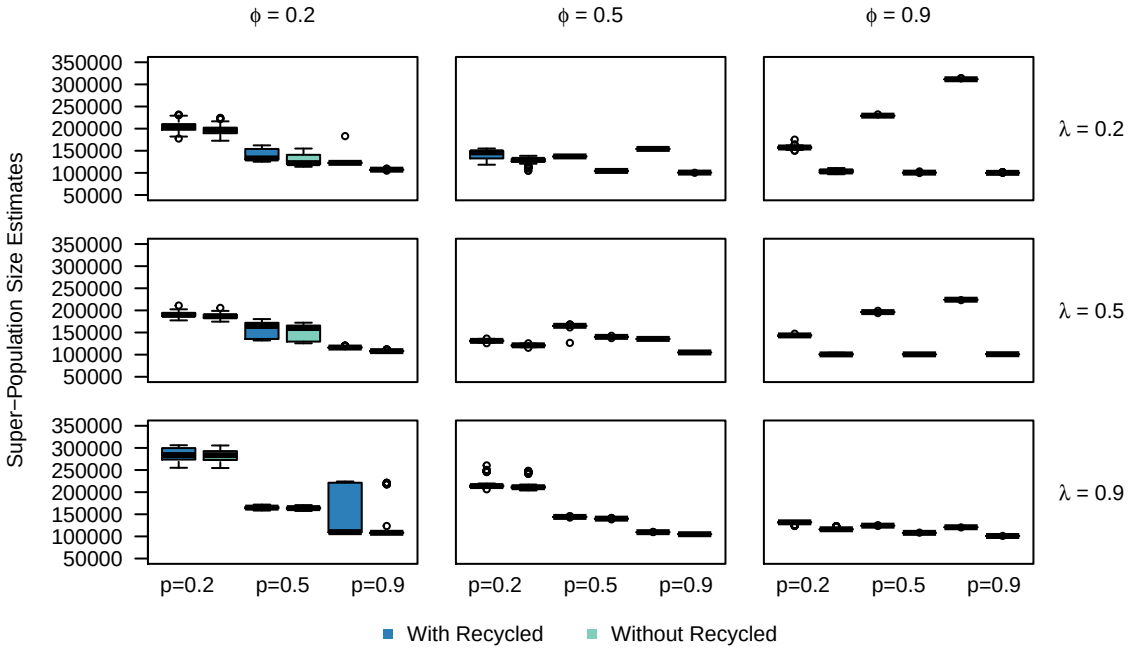
WEB FIGURE 19: Boxplots of super-population size estimates (N) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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



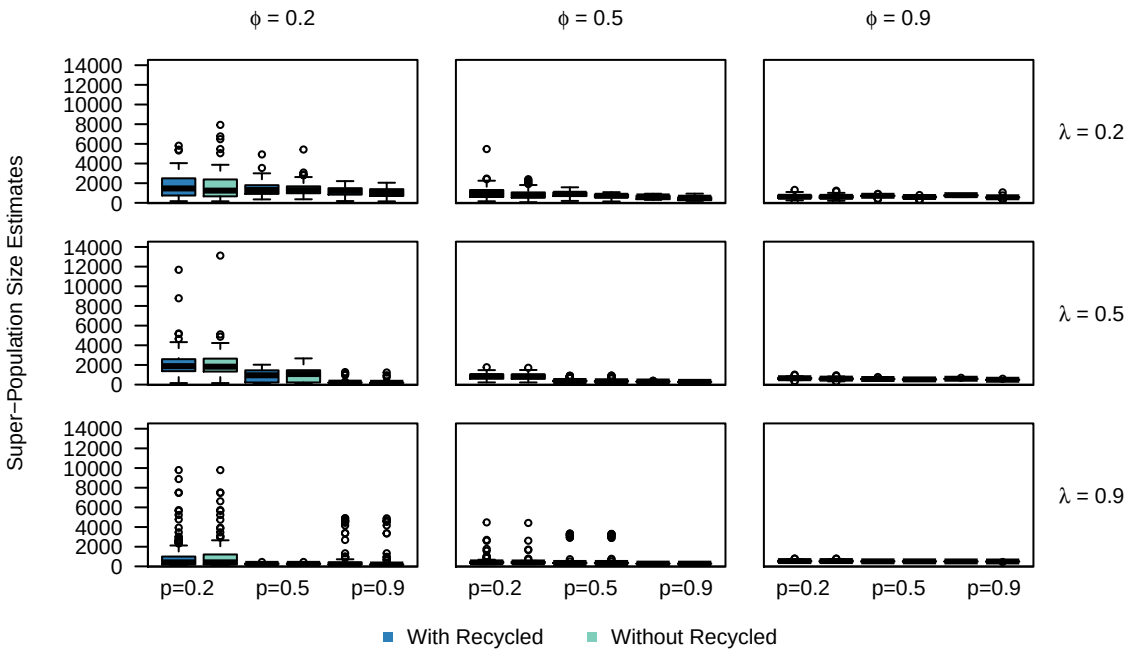
WEB FIGURE 20: Boxplots of super-population size estimates (N) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 100000 with $T_2 = 1$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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



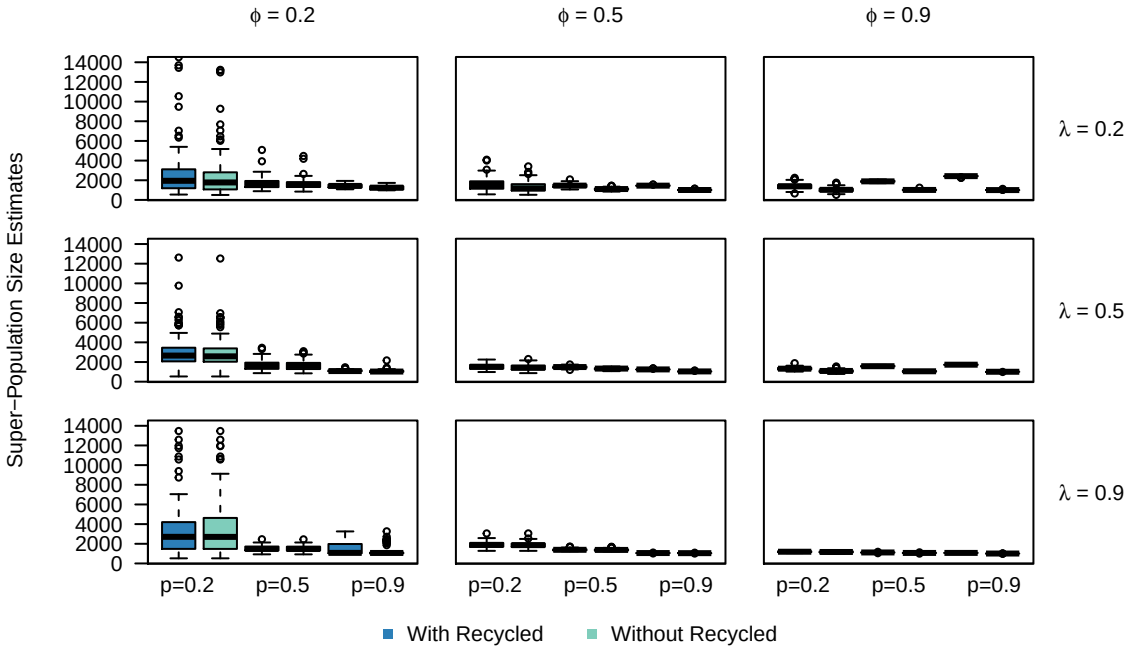
WEB FIGURE 21: Boxplots of super-population size estimates (N) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 0.5$ with 10 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention ($\lambda = 0.2, 0.5, 0.9$) 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.

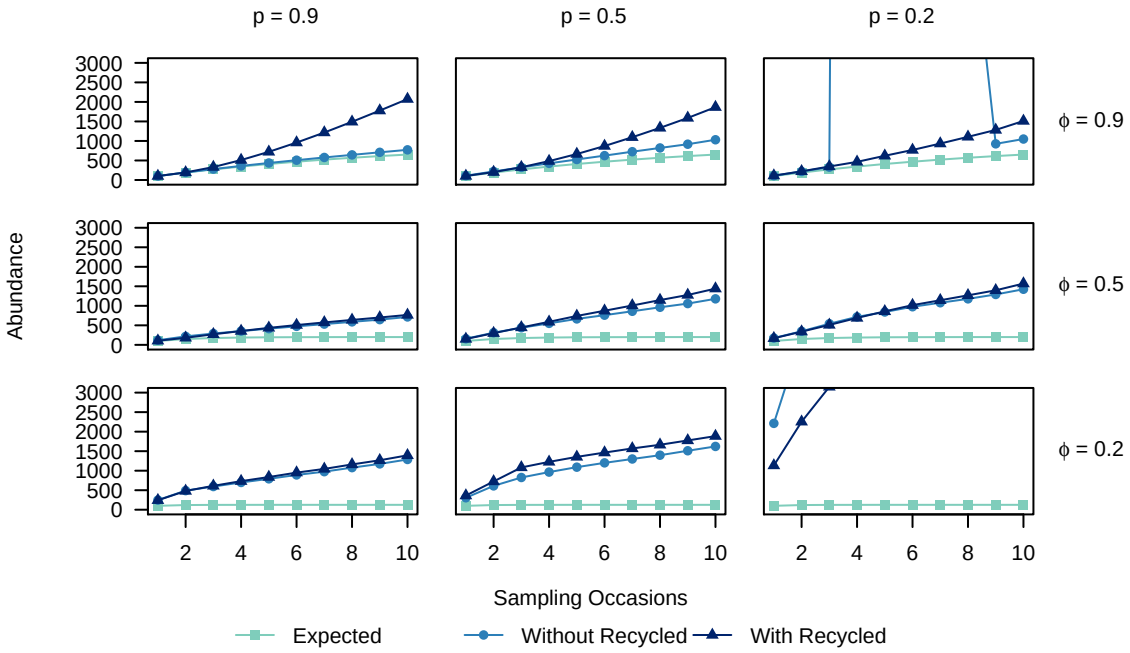


WEB FIGURE 23: Boxplots of super-population size estimates (N) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 5 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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

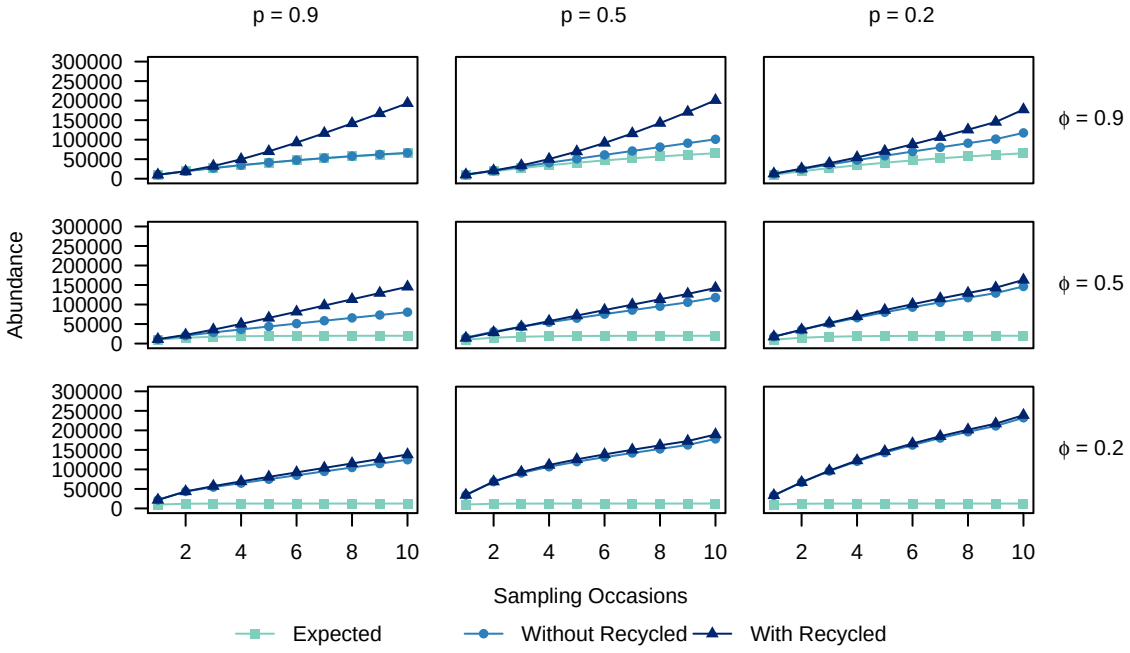


WEB FIGURE 24: Boxplots of super-population size estimates (N) of 100 simulated datasets analyzed with and without the effect of recycled individuals for population size 1000 with $T_2 = 1$ for 7 time periods for varying survival ($\phi = 0.2, 0.5, 0.9$), capture ($p = 0.2, 0.5, 0.9$), and tag retention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

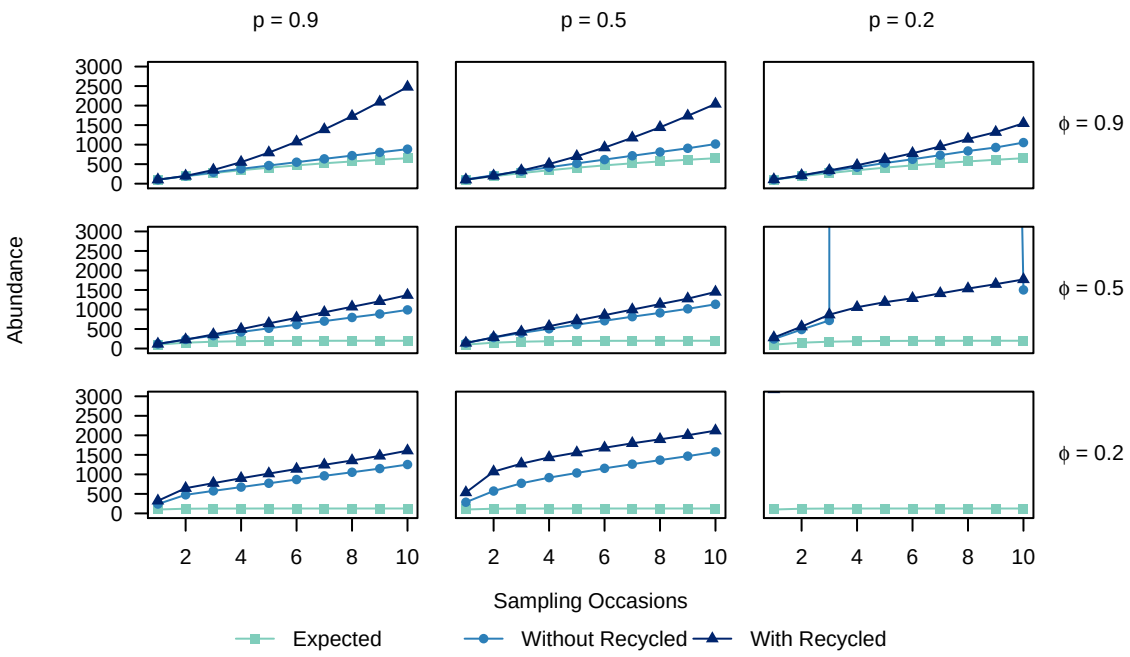
Abundance Estimates



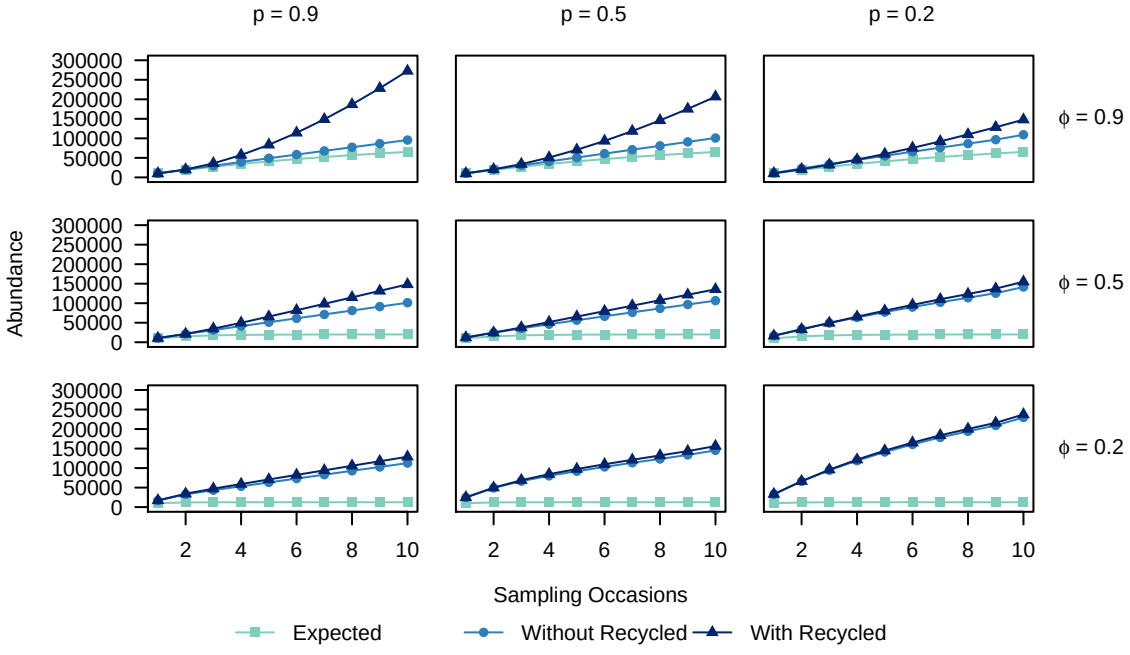
WEB FIGURE 25: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 10 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$) and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



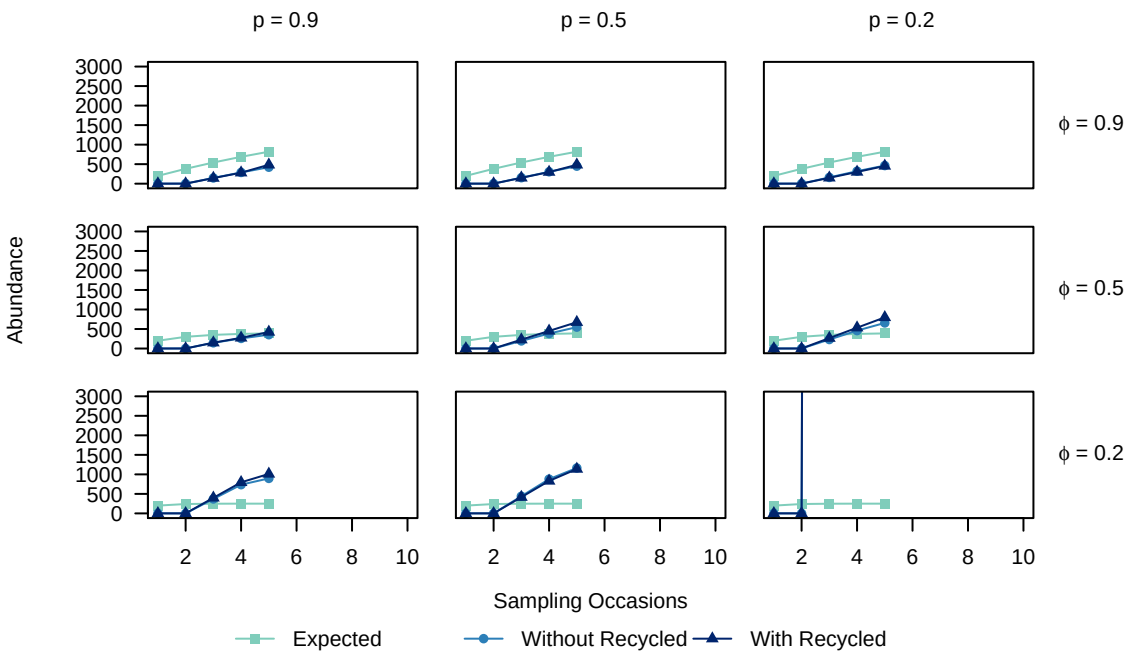
WEB FIGURE 26: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 100000$ with $T_2 = 1$ with 10 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



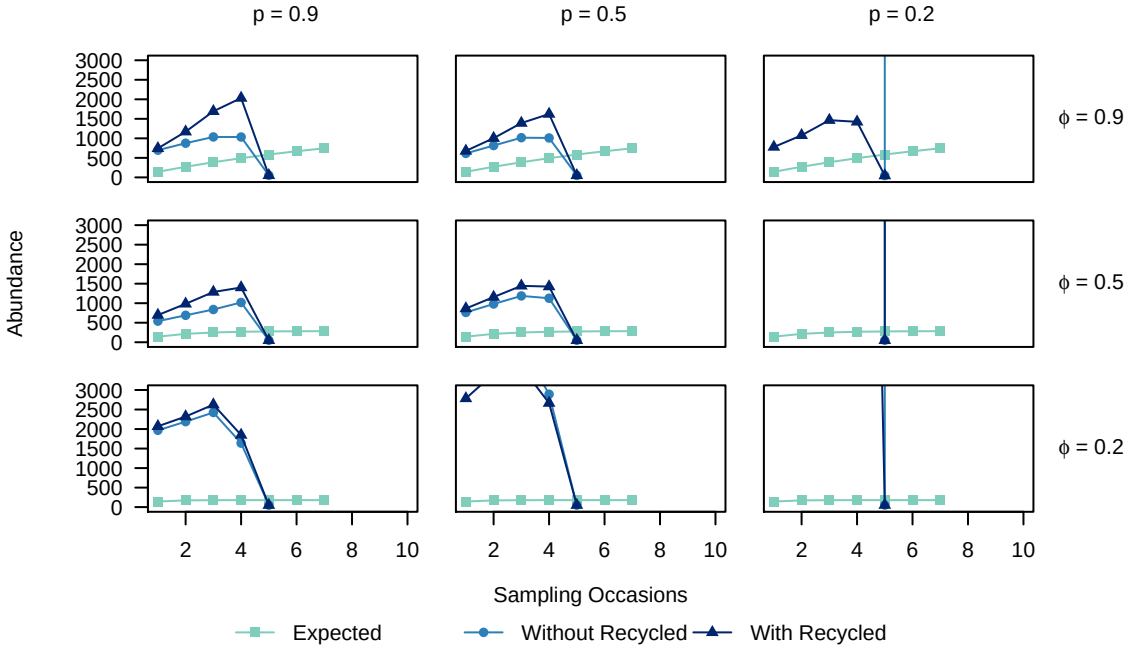
WEB FIGURE 27: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 0.5$ with 10 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



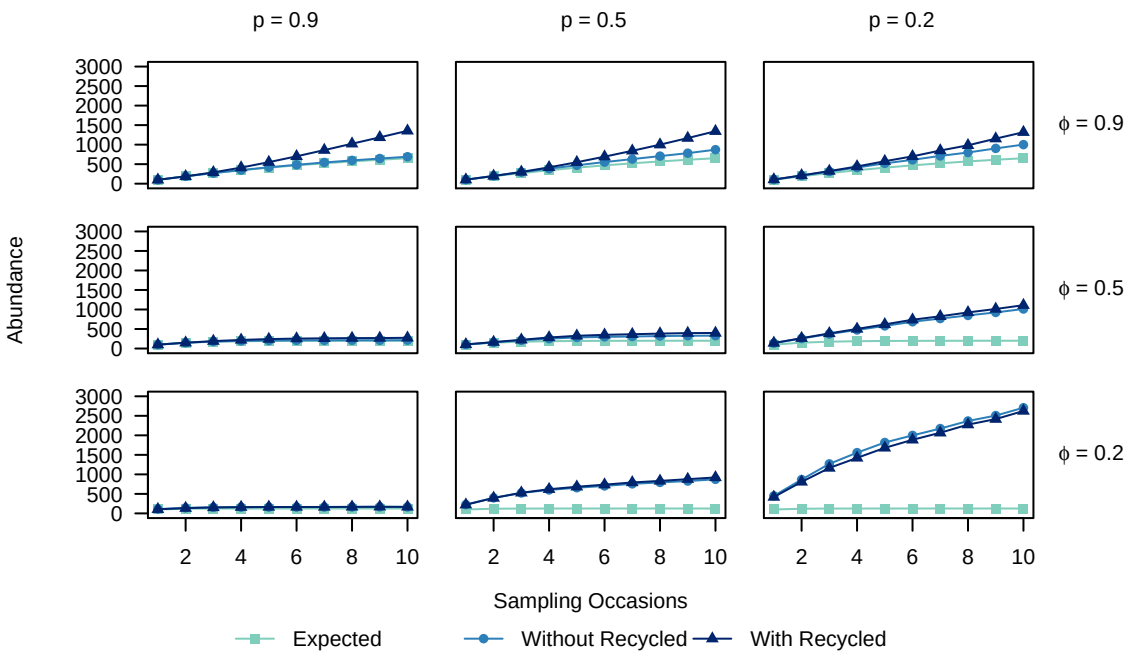
WEB FIGURE 28: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 100000$ with $T_2 = 0.5$ with 10 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



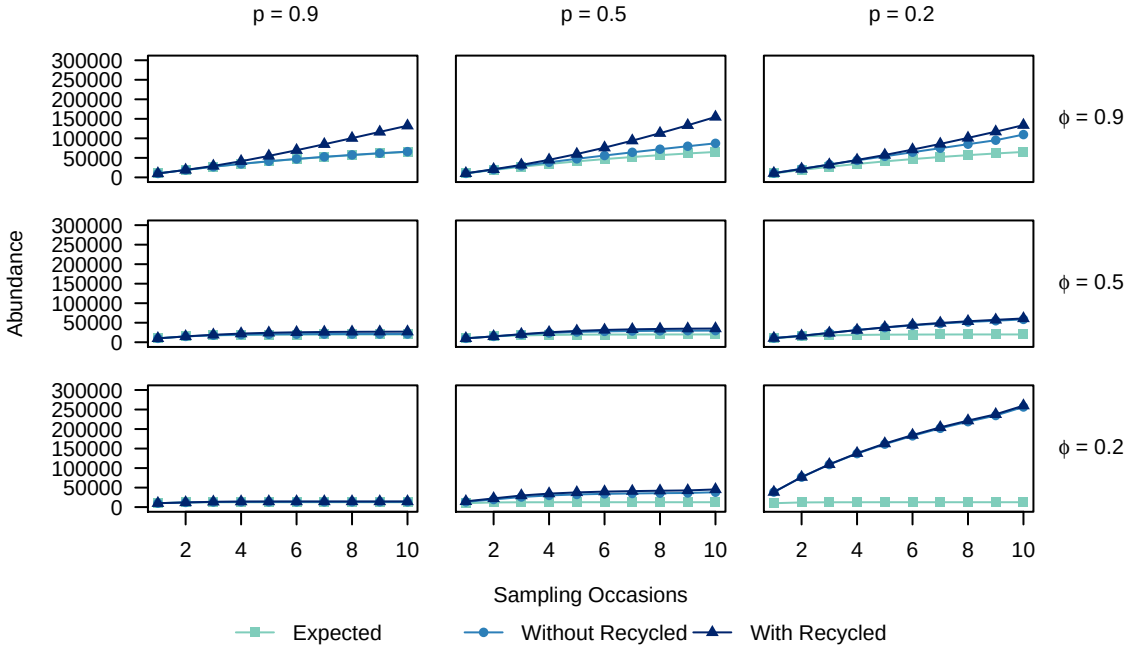
WEB FIGURE 29: Mean abundance estimates (N_j's) for each sample time ($k = 5$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 5 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$) and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



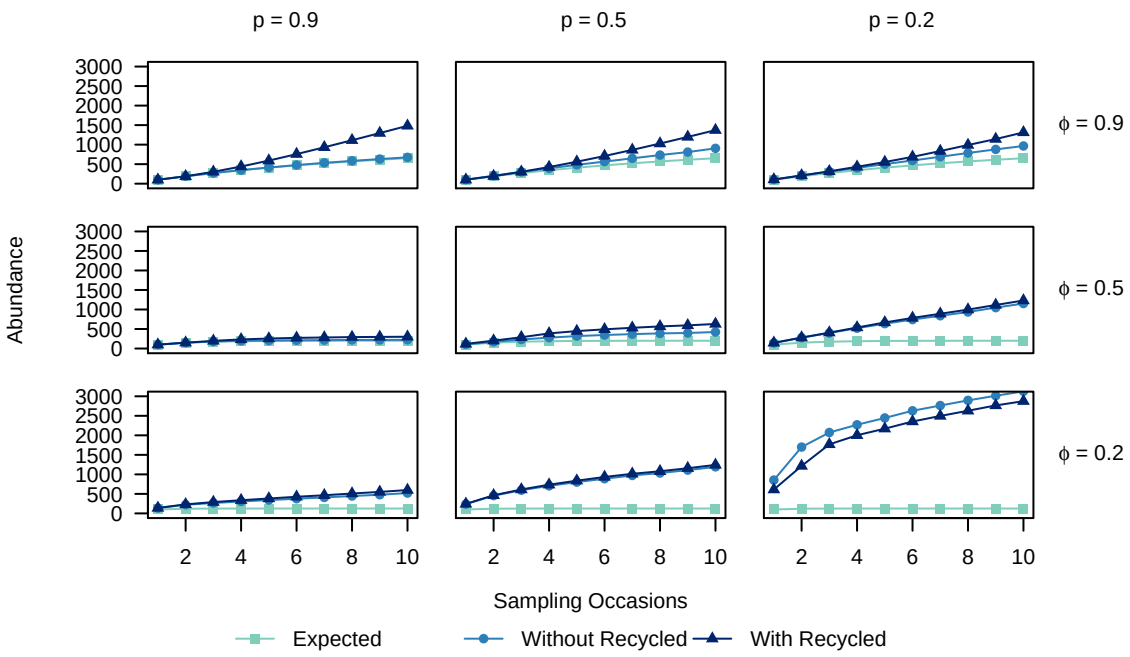
WEB FIGURE 30: Mean abundance estimates (N_j's) for each sample time ($k = 7$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 7 time periods for low tag retention ($\lambda = 0.2$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$) and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



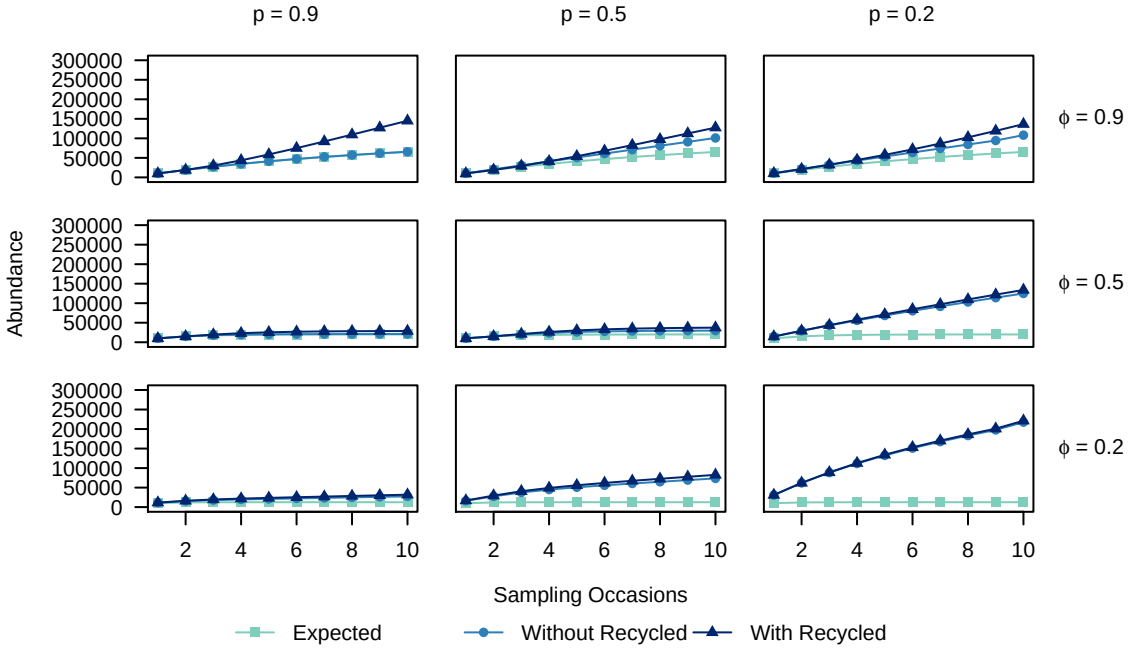
WEB FIGURE 31: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 10 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



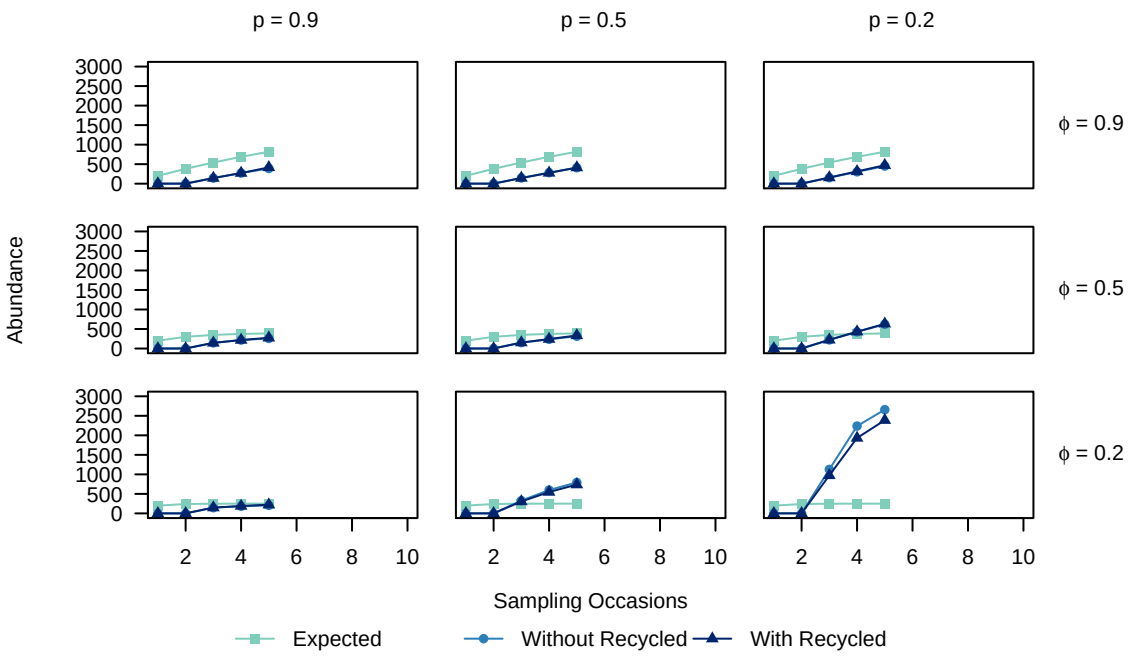
WEB FIGURE 32: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 100000$ with $T_2 = 1$ with 10 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



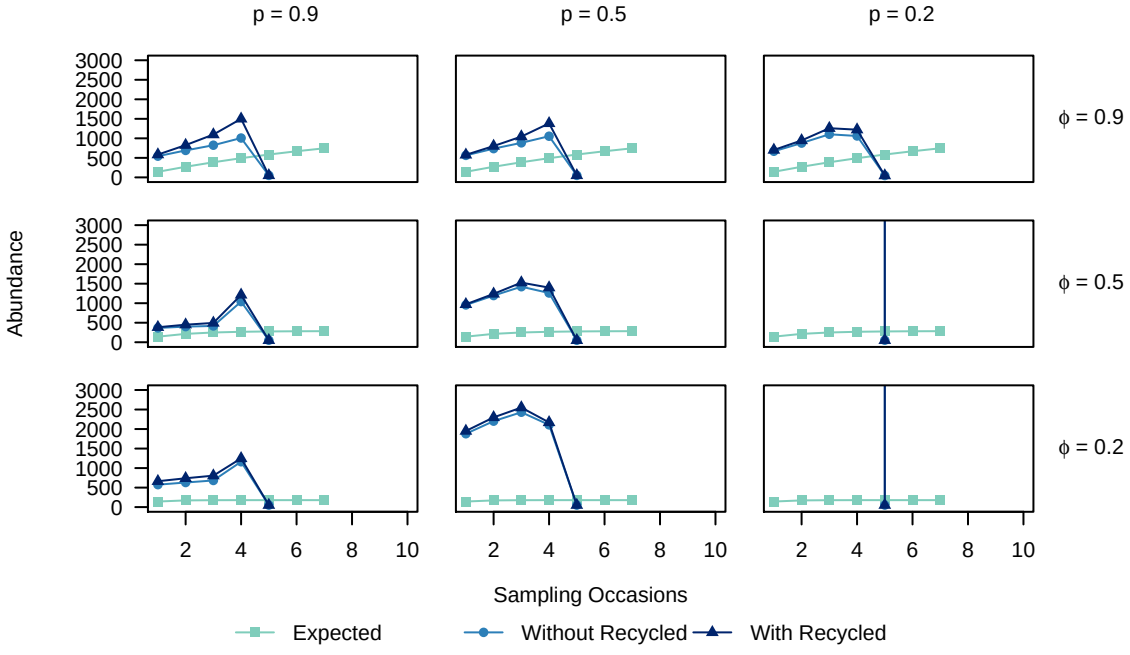
WEB FIGURE 33: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 0.5$ with 10 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



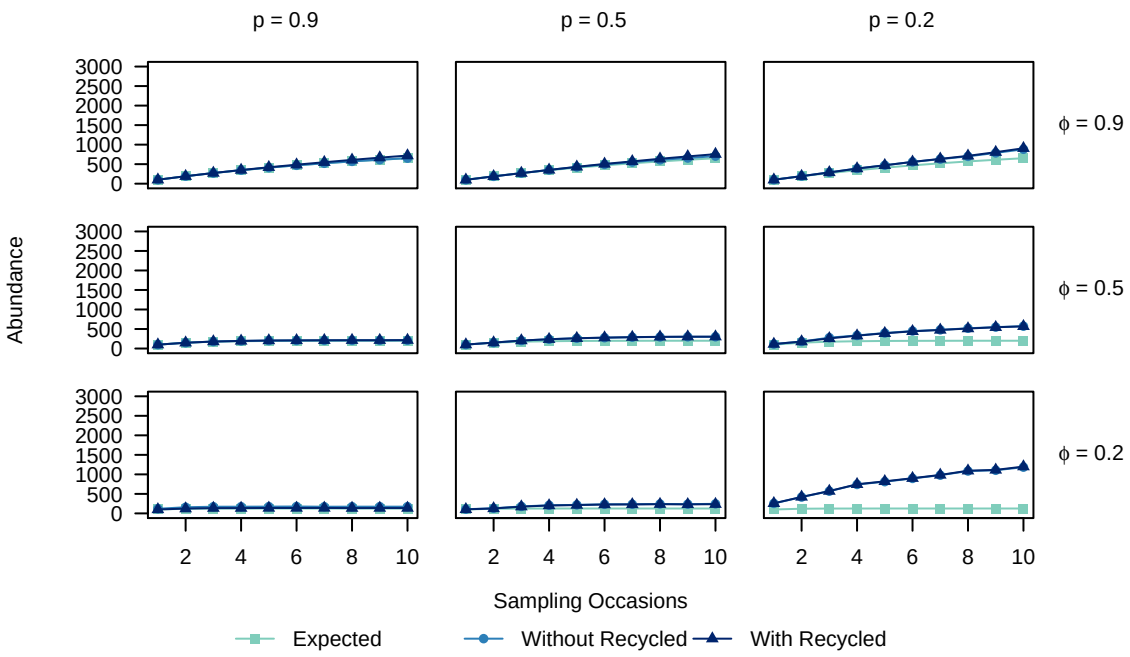
WEB FIGURE 34: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 100000$ with $T_2 = 0.5$ with 10 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5,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



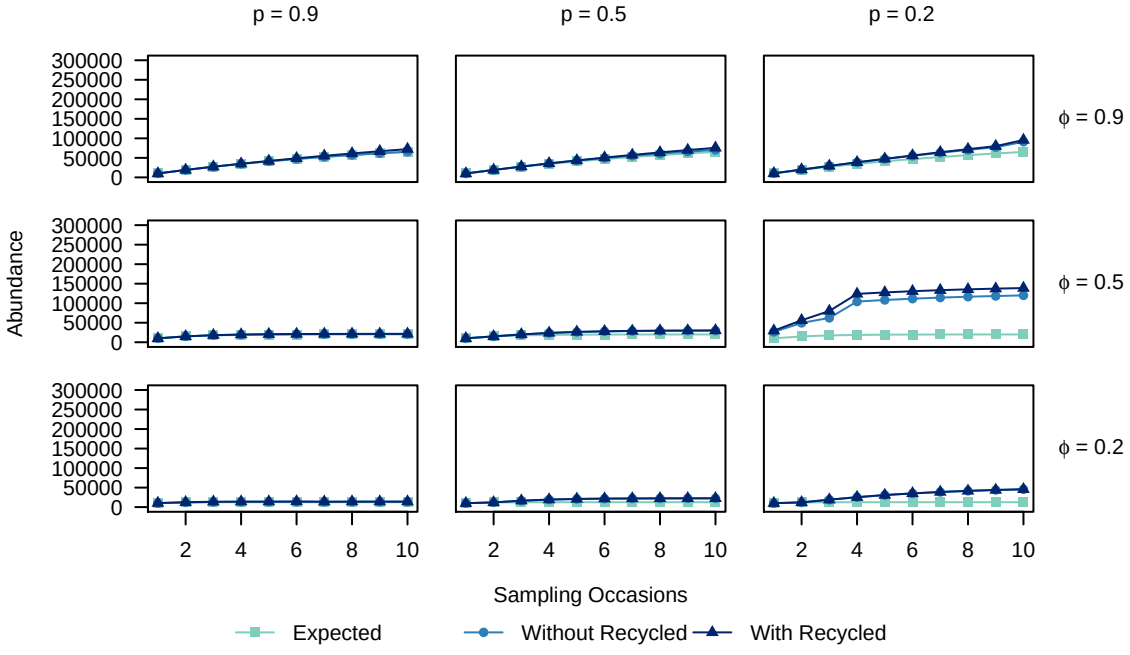
WEB FIGURE 35: Mean abundance estimates (N_j's) for each sample time ($k = 5$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 5 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



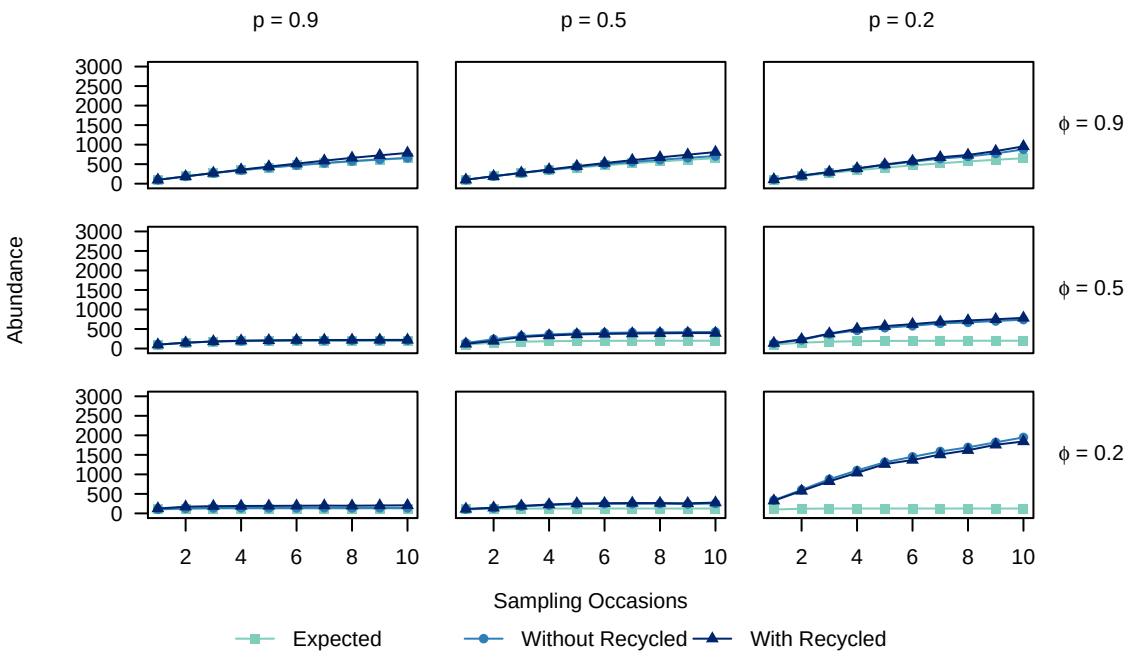
WEB FIGURE 36: Mean abundance estimates (N_j's) for each sample time ($k = 7$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 7 time periods for medium tag retention ($\lambda = 0.5$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



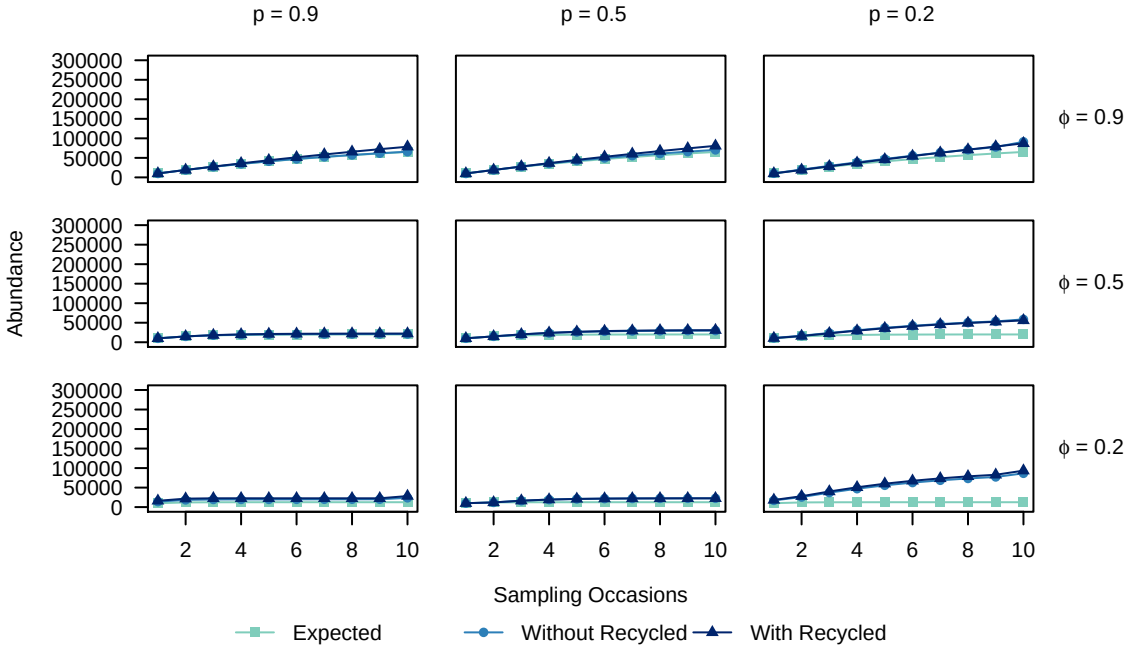
WEB FIGURE 37: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 1$ with 10 time periods for high tag retention ($\lambda = 0.9$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



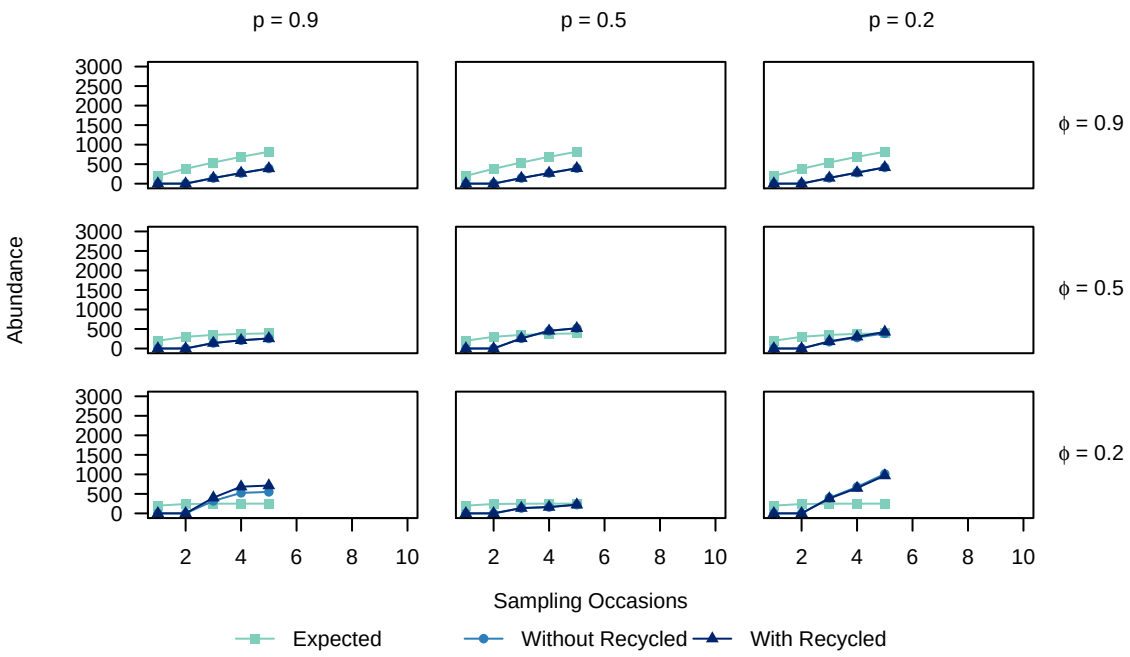
WEB FIGURE 38: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 100000$ with $T_2 = 1$ with 10 time periods for high tag retention ($\lambda = 0.9$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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



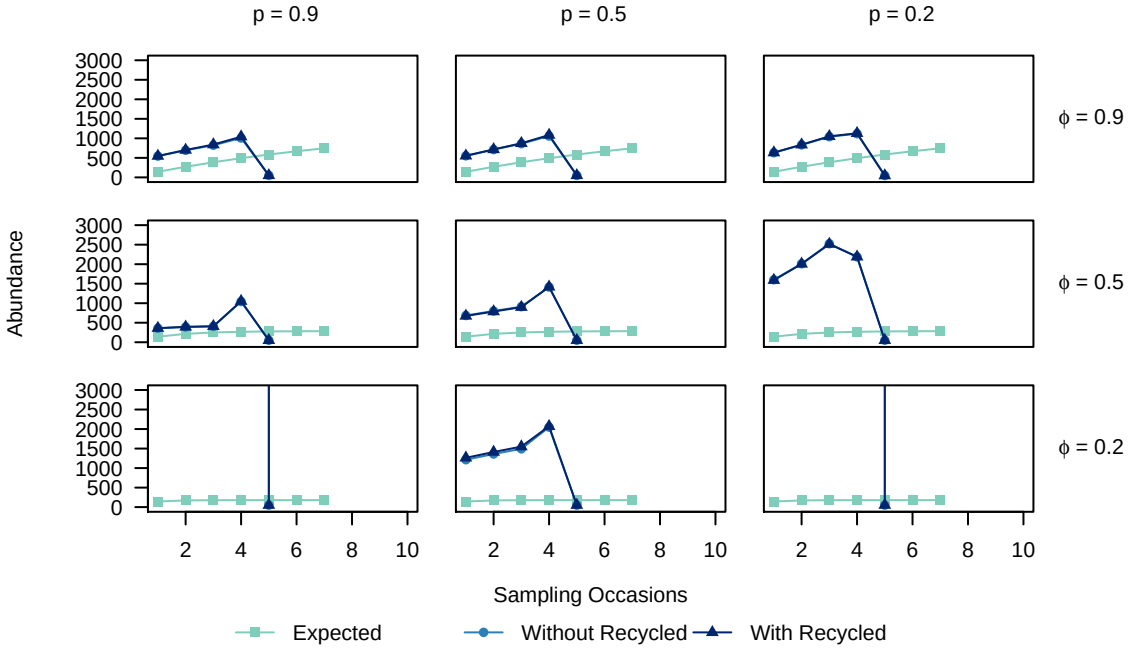
WEB FIGURE 39: Mean abundance estimates (N_j's) for each sample time ($k = 10$) between analysis with and without recycled individuals with population size $N = 1000$ with $T_2 = 0.5$ with 10 time periods for high tag retention ($\lambda = 0.9$), varying survival probabilities ($\phi = 0.2, 0.5, 0.9$)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