Power analysis
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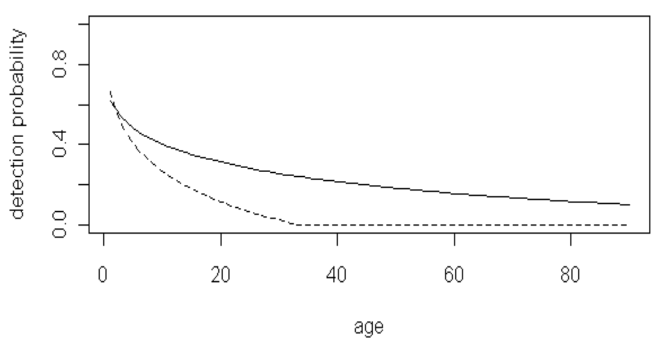
Purpose:
Perform power analysis to understand how many carcasses need to be tracked in a QAQC sampling framework in order to evaluate the aggregate detection probability function. (Definition: Aggregate detection probability function is *D(t) = probability that the evidence of a carcass persists and is detected, given a search occurs at t days after fatality*).

Specific objectives: Determine:
I) the precision of estimating the aggregate detection probability function based on a sample size of 50, 75, 100, 200, or 1000 fresh carcasses.
II) the number of carcasses needed to achieve standard errors within a precision of ±5%, ±10%, or ±20% of the detection estimate, i.e. CV=0.05, 0.10, or 0.20.
III) the probability of statistically detecting differences in the aggregate detection probability rate compared to the Smallwood (2007) model.

Method: All analyses are performed via simulation.

Population model: Data were simulated using the general model $D(t) = R(t) \times p(t)$, where $R(t) = a_{rem} + b_{rem} \log(t+1)$ and $p(t) = \exp(a_{det} + b_{det}\, t) / (1+\exp(a_{det} + b_{det}\, t))$. We've seen this model structure before. Smallwood (2007) estimates of $R(t)$ and p corresponds to this very same model when a_{rem}=121.86, b_{rem}=-34.54, a_{det}=1.1, and b_{det} =0. Note that the parameters a_{det} = 1.1 and b_{det} = 0 prescribe $p(t)$ to a constant p=0.75. Later, in my P207 document, I reported some results of simulations based on a somewhat different hypothetical model, sharing the same structure, but having a shallower decay curve for $R(t)$ and a lower and slightly decaying function for $p(t)$ (a_{rem} =115, b_{rem} = -20, a_{det} = 0.5, and b_{det} = -0.01).

Figure 1. Detection probability curves based on Smallwood (2007) estimates (dashed line) and P207 hypothetical population detection dynamics (solid line).



For comparison, I generated simulations using both the Smallwood and the P207 models of population detection dynamics. We can loosely think of these two simulation models as representing two different population demographies. The following analyses attempts to shed light on the ability (precision and power) of a QAQC style of survey to estimate the probability detection function, given either of these two demographies.

Variations of QAQC:

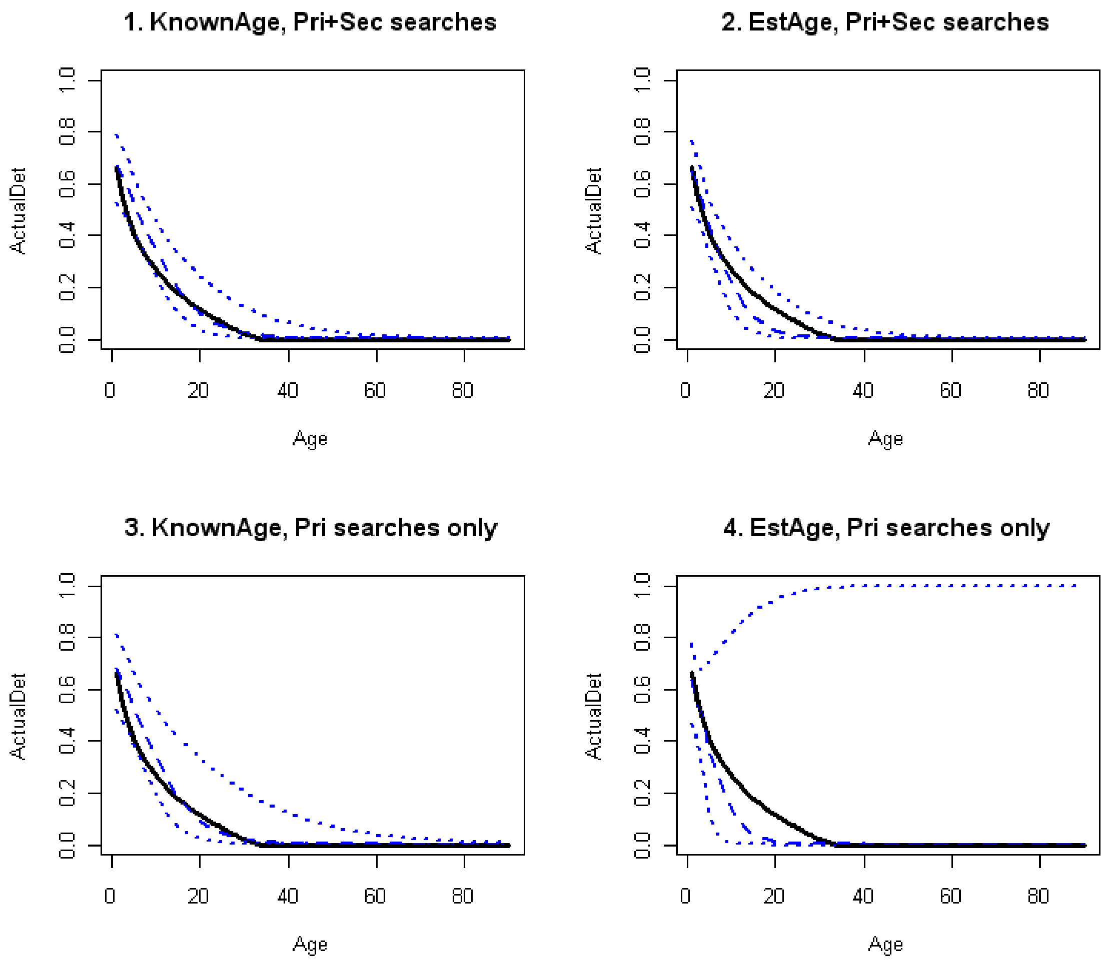
In P207, I simulated multiple versions of QAQC style of data based on different assumptions about survey technique. These models vary by the amount of knowledge about the age of trial carcasses (known vs. estimated), and the intensity of searches used to collect detection data (primary + secondary vs. just primary surveys). Further details about these differences are described in P207. Models based on all four permutations of these assumptions were applied to the simulations in this document.

Detection models below are based on a logistic regression of detection success regressed on carcass age for simulated detection data assuming each trial carcass is left out for a 90-day period after its deposit. Although in P207 there were other variants of the simulations, such as performing the logistic regressing against a log-transformation of age or leaving the carcasses out for 1 rotation, I did not use these variants for the analyses described here.

Table 1. Four variations of models for estimating the detection probability as a function of age (time since fatality). Assumes carcasses are left out for 90 days and all regressions are fitted to the un-transformed age variable.

	Model Number			
	1	**2**	**3**	**4**
Age				
Known	✓		✓	
Estimated		✓		✓
Searches				
primary + secondary	✓	✓		
Primary			✓	✓

Figure 2. Estimated detection functions and 95% confidence interval (dashed lines) based on four models fitted to one example of a dataset simulated using an aggregate detection function based on estimates from Smallwood (2007) (bold solid line). This simulation assumed a sample size of 50 fresh carcass trials.



Notes:

1. The precision of the estimate detection function is higher when the age of the carcass is known (such as when starting the trial with fresh carcasses) and when primary and secondary searches are both conducted.
2. The actual detection function does not have the same form as a logistic regression equation. Thus, as precision increases and the confidence intervals become tighter, the estimated detection function may or may not converge close to the actual detection function. Excessively large sample sizes could have diminishing value if the increase in precision is outweighed by the error resulting from model misspecification. However, a large sample size would offer additional value in a broader modeling framework in which the data can be analyzed with a class of more flexible models which captures the true detection function better.

Figure 3. Same, with 75 carcass trials.

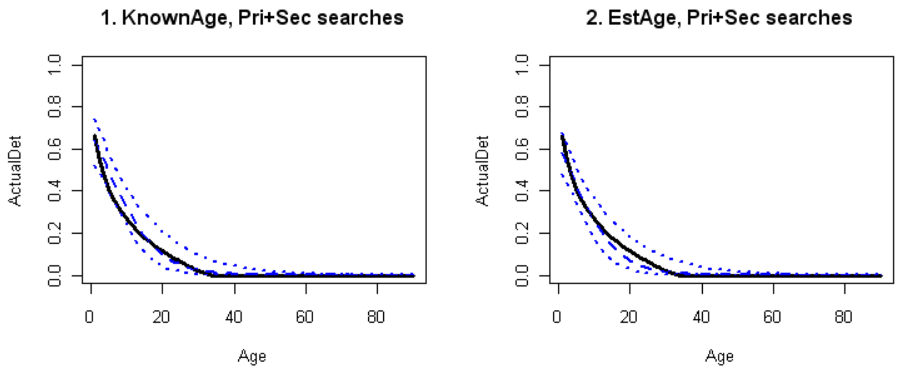


Figure 4. With 100 carcass trials.

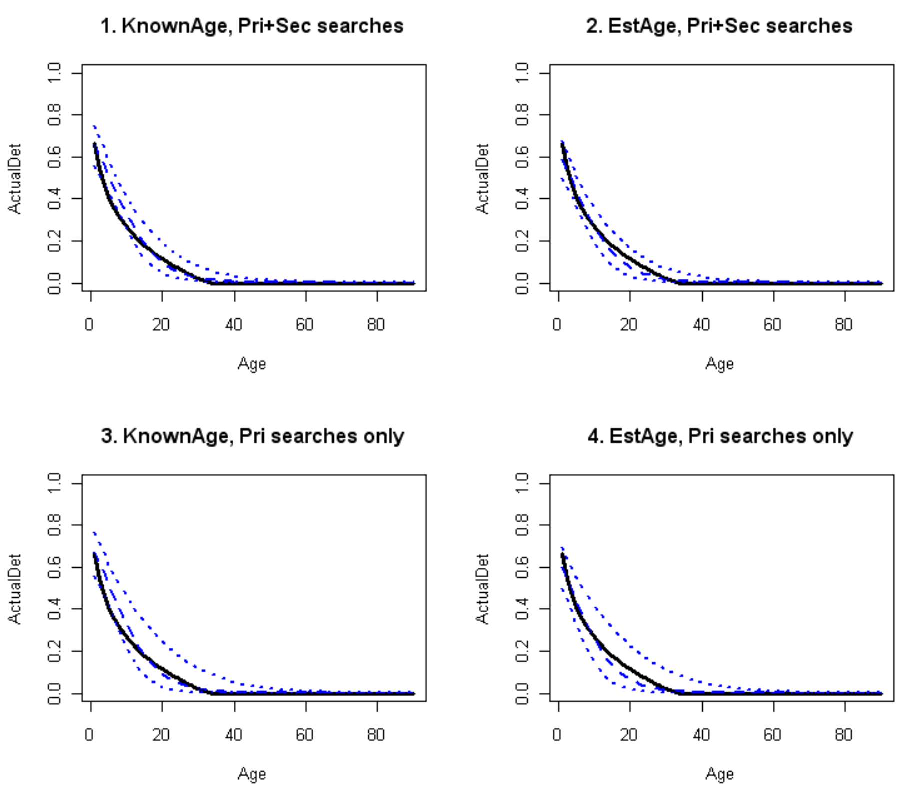


Figure 5. With 200 carcass trials.

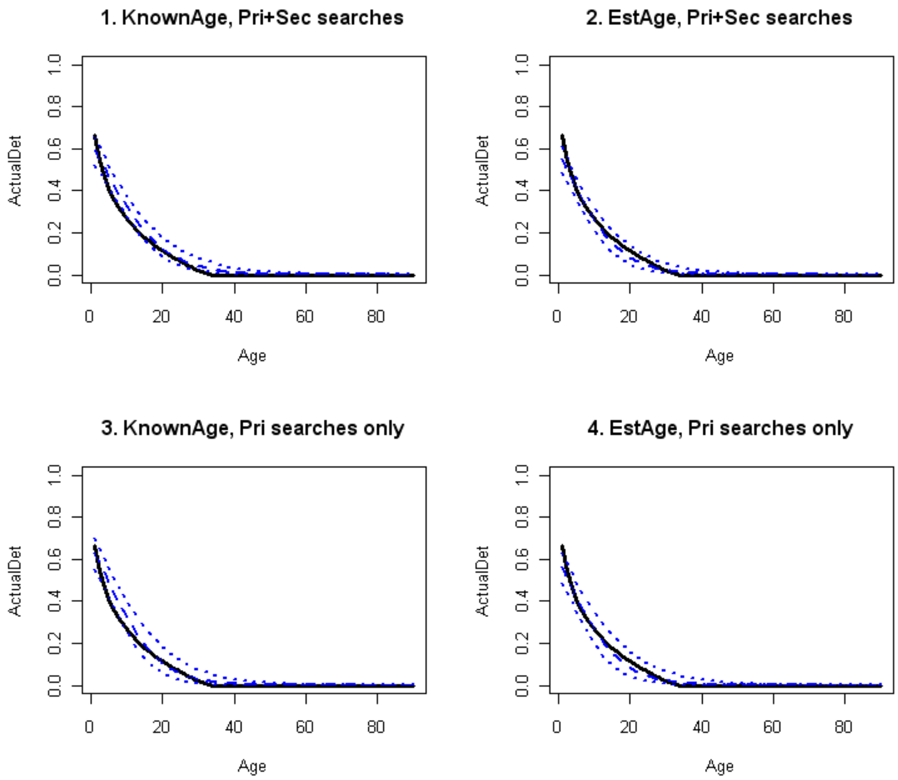


Figure 6. With 1000 carcass trials.

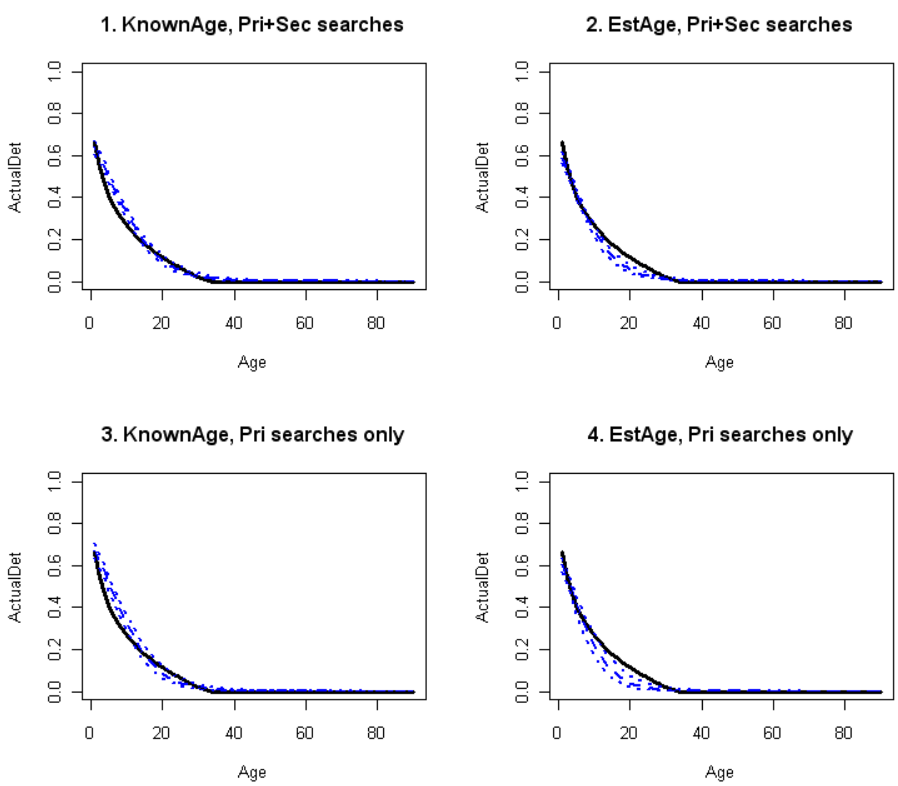
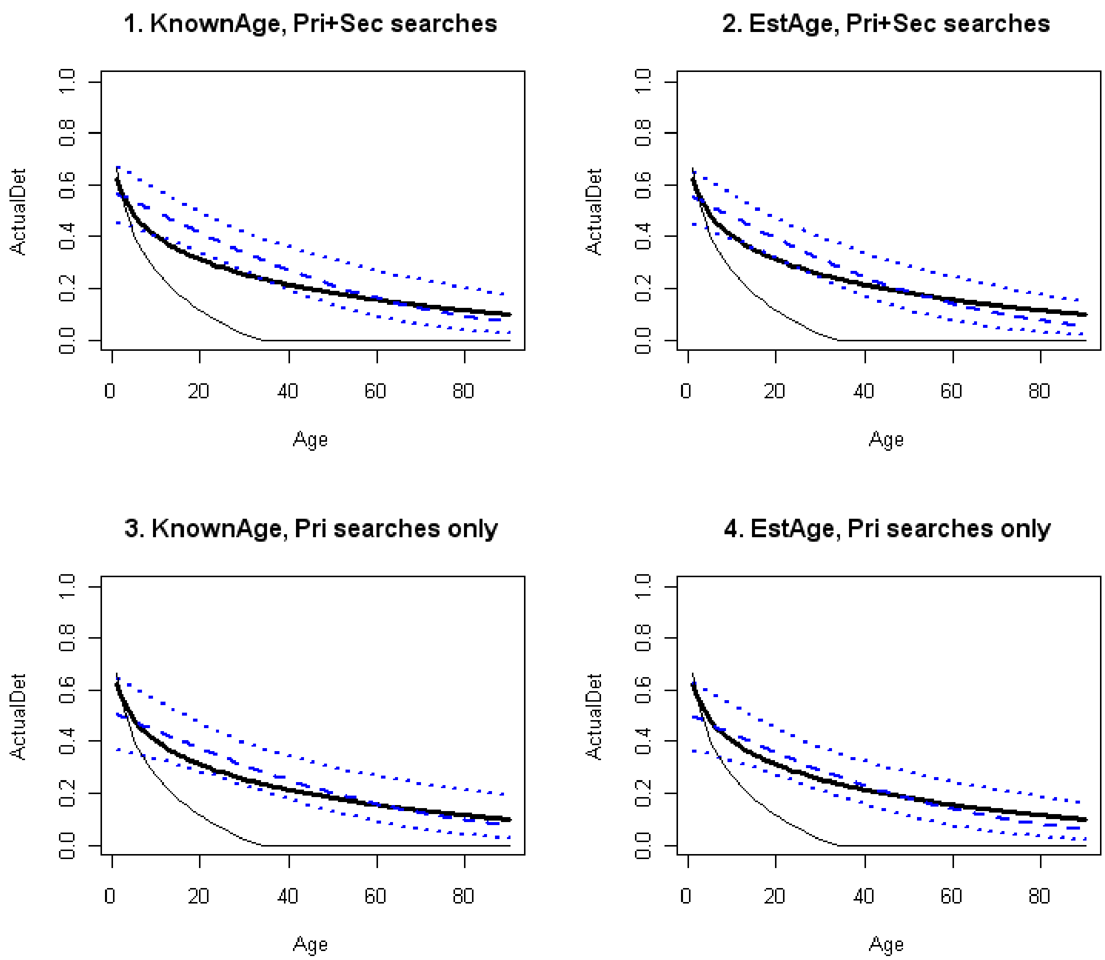


Figure 7. Estimated detection functions and 95% confidence interval (dashed lines) based on four models fitted to one example of a dataset simulated using an aggregate detection function based on a hypothetical and shallower removal function (P-207) (bold solid line). For reference, the Smallwood detection curve is also shown (solid line). This simulation assumed a sample size of 50 fresh carcass trials.



Notes:
3. There is very little difference in the estimates and confidence intervals among all four models.
4. A sample size of 50 fresh carcasses should be sufficient to distinguish some substantive differences in detection probability.
5. The effects of model misspecification are more pronounced with simulations generated by the P207 model than with the simulations generated by the Smallwood model. By 100 trials (Figure 8), the model misspecification error would result in an overestimation of the detection probability function over the 1-30 day range.

Figure 8. Same, with 75 carcass trials.

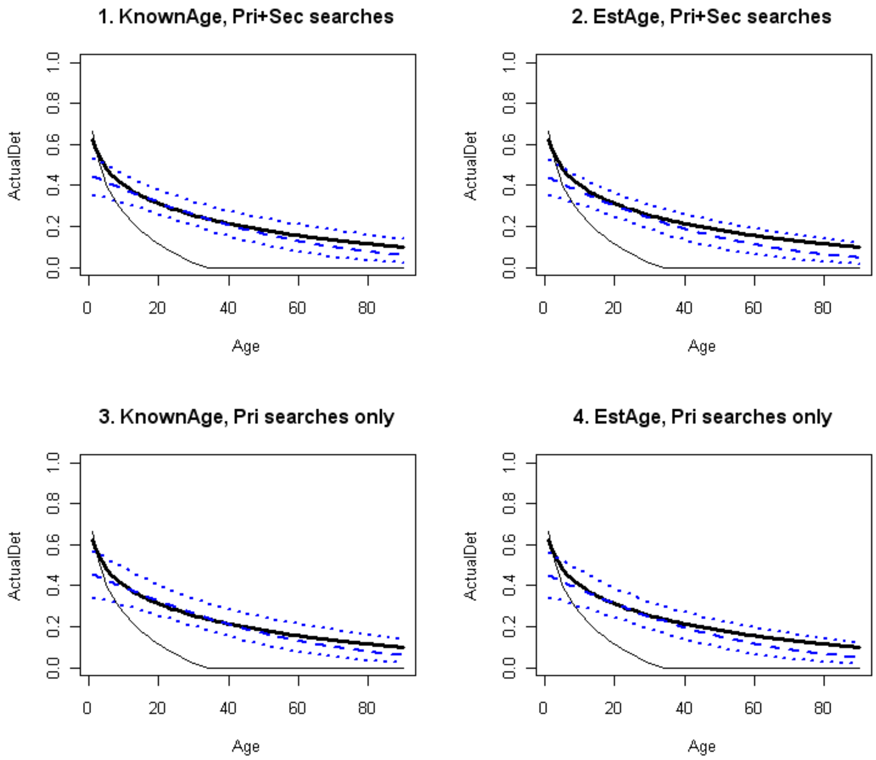


Figure 9. 100 trials.

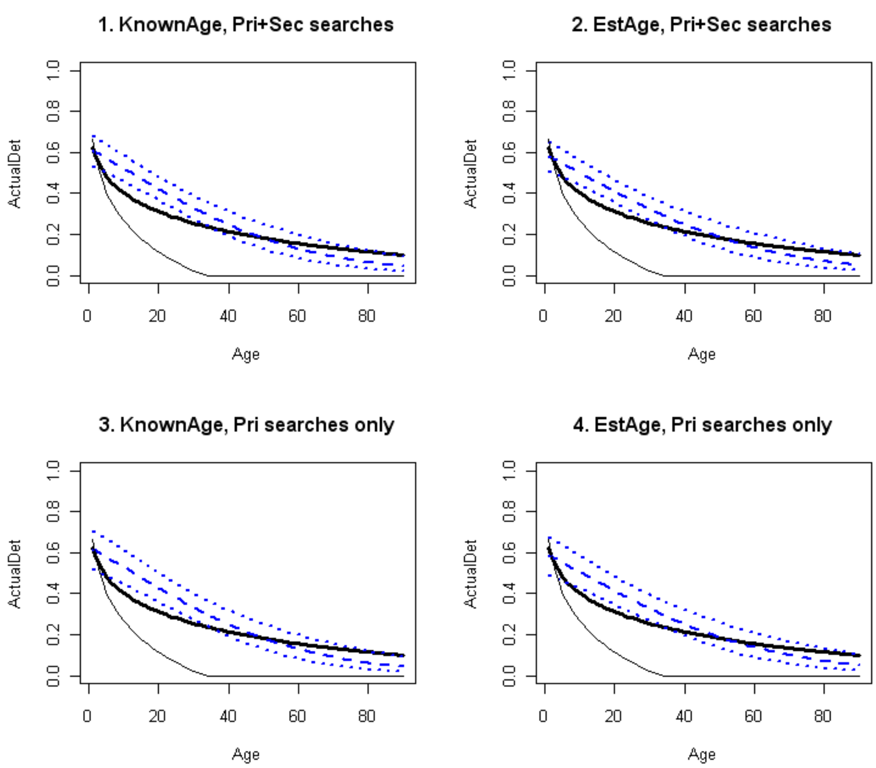


Figure 10. 200 trials.

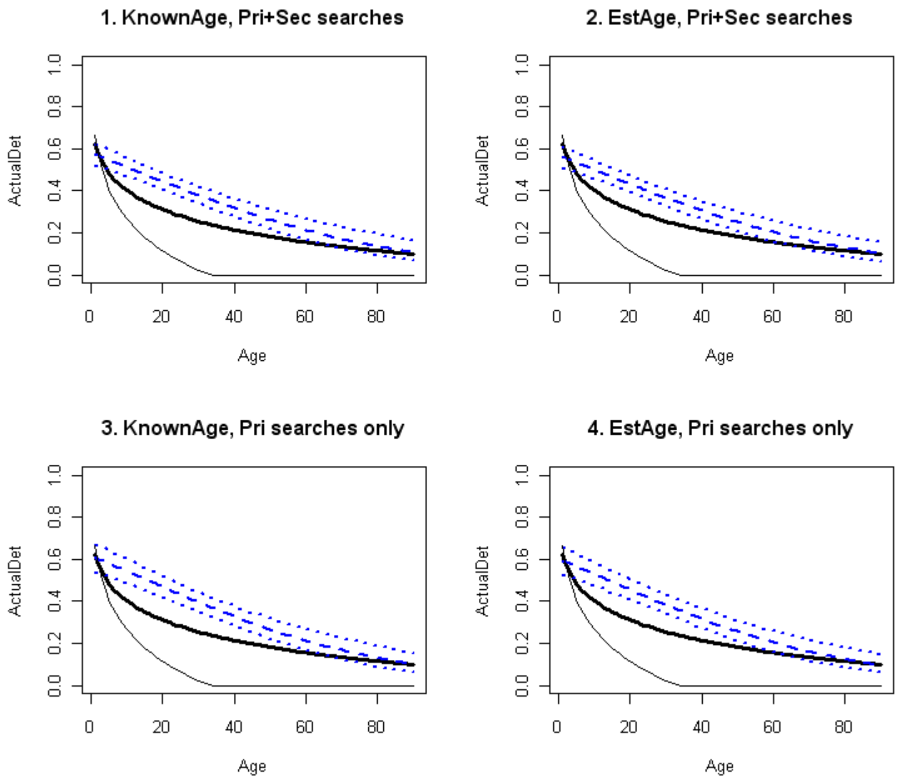


Figure 11. 1000 trials.

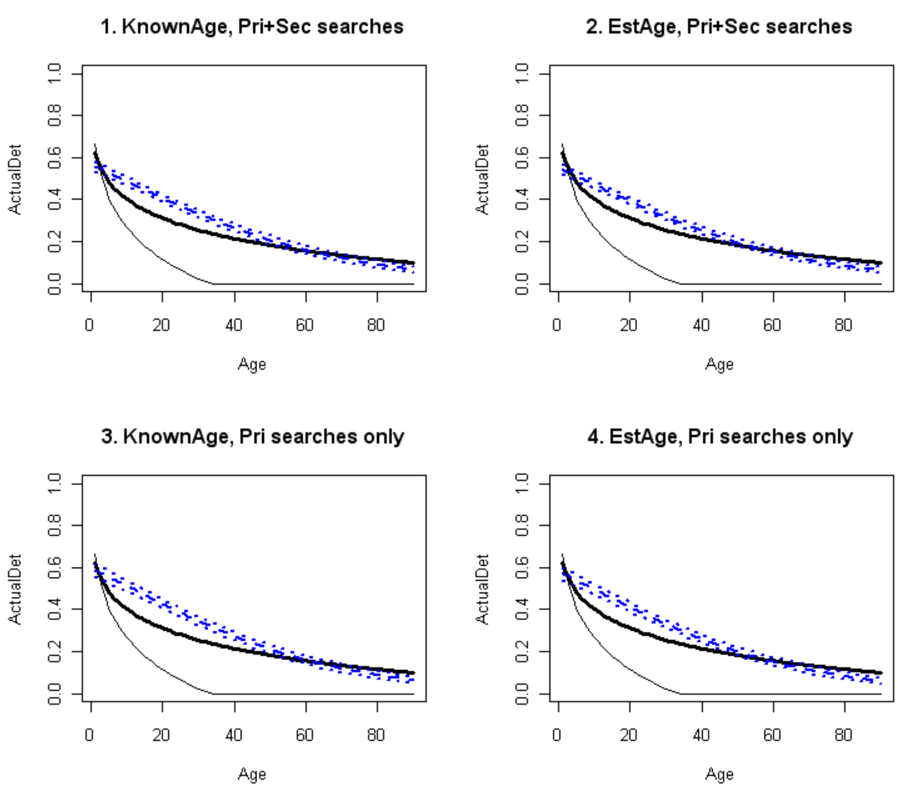


Figure 12. Coefficient of variations (CV) and standard errors (SE) of detection probability estimate, as a function of age, based on one simulation of 50 (solid line), 75 (dashed line), 100 (dotted line), 200 (dotted and dashed line), and 1000 carcass trials (long dash line), generated using the Smallwood estimate of the aggregate detection probability. CV is the ratio of SE divided by detection probability estimate.

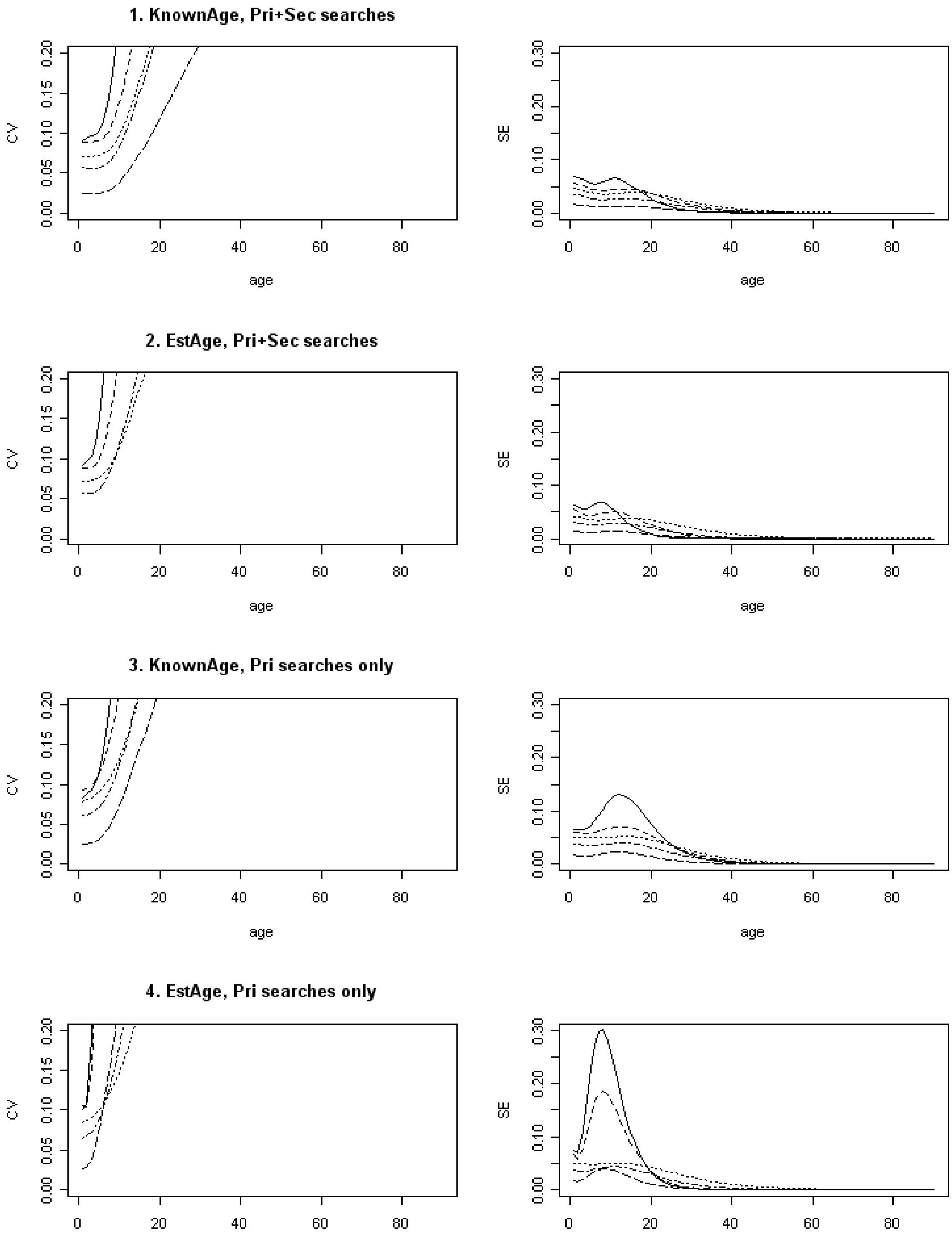
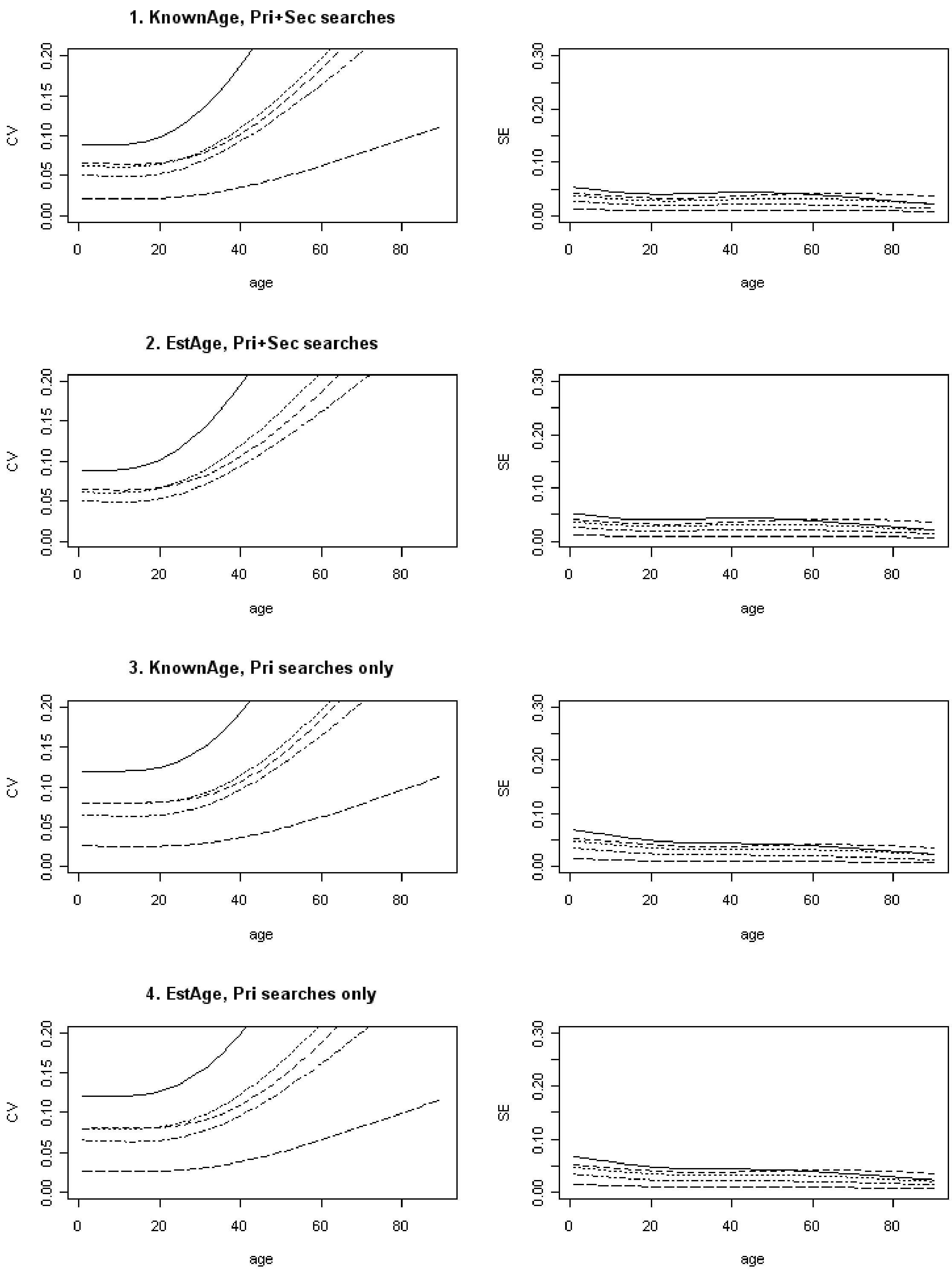


Figure 13. Coefficient of variations (CV) and standard errors (SE) of detection probability estimate, as a function of age, based on one simulation of 50 (solid line), 75 (dashed line), 100 (dotted line), 200 (dotted and dashed line), and 1000 carcass trials (long dash line), generated using the hypothetical aggregate detection probability (P-207). CV is the ratio of SE divided by detection probability estimate.



(Figure 1 from page 1. Detection probability curves based on Smallwood and P207 demographies. Repeated here for convenience, in reference to Figure 14 below).

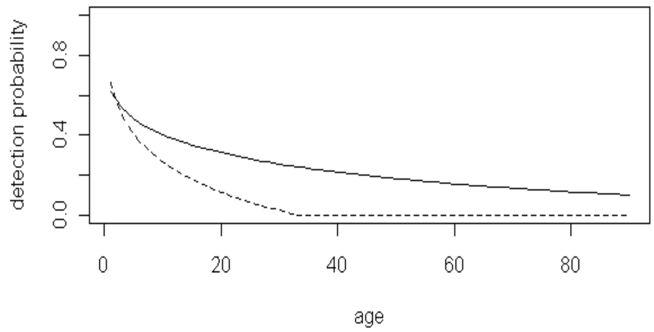


Figure 14. Power of discerning differences in detection probability compared to the Smallwood detection probability curve (above, dashed line), assuming a P207 carcass population demography (above, solid line), and a sample size of 50 trial carcasses.