

Wildlife Biology

WLB-00529

Lyons, T. P., Stodola, K. W. and Benson, T. J. 2019.
Estimating the survival of unmarked young from
repeated counts. – Wildlife Biology 2019: wlb.00529

Supplementary material

```

1  APPENDIX 1. R CODE TO SIMULATE DATA ASSUMING DAILY SURVIVAL
2  BETWEEN COUNTS IS 1
3  #data simulation when daily survival assumed to be 1
4  brood.sim<-function(broods,visits,meanD, meanS){
5  broods<-broods
6  visits<-2
7  meanS=meanS
8  p=meanD
9  hatch<-rbinom(n=broods,15,0.85)+1          # number of eggs that hatch, preventing any
10  0's from occurring
11  scov<-runif(n=broods,-2,2)                #
12  survival covariate value
13  est.surv<-plogis(qlogis(meanS)+0.8*scov)   #brood-specific survival
14  probability
15  chicks.d1<-rbinom(n=broods,size=hatch,prob=est.surv) # N chicks surviving to 1st
16  detection
17  #detection probability
18  alpha0<-qlogis(p)
19  dcov<-array(runif(n=broods*visits,-1,1),dim=c(broods,visits))
20  alpha1<--1
21  obs.p<-plogis(alpha0+alpha1*dcov)
22  obsv.data<-matrix(NA,nrow=broods,ncol=visits)
23  #observation data
24  for (v in 1:visits){
25  obsv.data[,v]<-rbinom(n=broods,size=chicks.d1,prob=obs.p[,v])}

```

26 **APPENDIX 2. R CODE TO SIMULATE DATA WHEN DAILY SURVIVAL IS NOT 1**
27 **BETWEEN COUNTS.**

```
28 brood.simDSR<-function(broods,visits,meanS,meanD,dsr,lagD){
29   broods<-broods
30   visits<-visits
31   meanS=meanS
32   p=meanD
33   hatch<-rbinom(n=broods,15,0.85)+1
34           # number of eggs that hatch, preventing any 0's from occurring
35   scov<-runif(n=broods,-2,2)
36           #covariate value
37   est.surv<-plogis(qlogis(meanS)+0.8*scov)
38           #brood-specific survival probability
39   chicks.d1<-rbinom(n=broods,size=hatch,prob=est.surv)           # N chicks surviving to 1st
40   detection
41   chicks.d2<-rbinom(n=broods,size=chicks.d1,prob=dsr^lagD) #N chicks surviving to 2nd detection
42   #detection probability
43
44   alpha0<-qlogis(p)
45   dcov<-array(runif(n=broods*visits,-1,1),dim=c(broods,visits))
46   alpha1<--1
47
48   obs.p<-plogis(alpha0+alpha1*dcov)
49
50   obs1<-rbinom(n=broods,size=chicks.d1,prob=obs.p[,1])
51   obs2<-rbinom(n=broods,size=chicks.d2,prob=obs.p[,2])
```

```
52
53 #format simulated data to a matrix
54 test.data<-cbind(hatch,scov,obs1,obs2, dcov,chicks.d1)
55
56 return(test.data)
57
58 }
```

59 **APPENDIX 3. JAGS MODEL FOR ESTIMATING CHICK SURVIVAL FROM 2**

60 **REPEATED COUNTS**

61 #the brood survival model assuming two visits

62 sink("broodsim_logit.txt")

63 cat(" "

64 model {

65

66 for (i in 1:broods)

67 {

68 #the model

69 C[i]~dbin(surv[i], hatched[i]) #C-

70 chicks surviving to be detected

71 logit(surv[i])<-s.int+h1*scov[i]

72 #model for survival

73

74

75 for (j in 1:visits){

76

77 X[i,j]~dbin(det[i,j],C[i])

78 #count on visit j

79 logit(det[i,j])<-d.int+p1*pcov[i,j]

80 #model for detection

81

82

83 }

84 }

```
85
86     #priors
87         s.int~dlogis(0,1)
88         h1~dlogis(0,1)
89         p1~dlogis(0,1)
90         d.int~dlogis(0,1)
91
92     }
93
94     ",fill=TRUE)
95     sink()
```

96 **APPENDIX 4. SUMMARY STATISTICS FROM SIMULATED DATA**

97 Table A4.1.

98 Calibration error, convergence, coverage, and 95% CRI range of all parameter estimates from 100
 99 simulations under differing scenarios of sample size and detection probability.

Parameter	Sample size	Detection	Calibration error (Median-truth)	Convergence	95% CRI range	Coverage
Survival coefficient	20	0.2	-0.014	100%	1.909	100%
	20	0.4	0.047	100%	1.442	100%
	20	0.6	0.113	100%	1.215	100%
	20	0.8	0.079	100%	0.870	100%
	25	0.2	-0.018	100%	1.713	100%
	25	0.4	0.060	100%	1.332	100%
	25	0.6	0.082	100%	1.084	100%
	25	0.8	0.062	100%	0.792	100%
	30	0.2	-0.013	100%	1.629	100%
	30	0.4	0.068	100%	1.258	100%
	30	0.6	0.066	100%	0.943	100%
	30	0.8	0.044	100%	0.682	100%
	35	0.2	0.023	100%	1.539	100%
	35	0.4	0.054	100%	1.146	100%
	35	0.6	0.060	100%	0.897	100%
	35	0.8	0.037	100%	0.628	100%
	40	0.2	0.039	100%	1.465	100%
	40	0.4	0.039	100%	1.085	100%
	40	0.6	0.053	100%	0.806	100%
	40	0.8	0.041	100%	0.582	100%
Detection coefficient	50	0.2	-0.004	100%	1.334	100%
	50	0.4	0.038	100%	0.965	100%
	50	0.6	0.057	100%	0.725	100%
	50	0.8	0.026	100%	0.495	100%
	20	0.2	-0.057	100%	1.334	100%
	20	0.4	-0.055	100%	1.182	100%
	20	0.6	-0.018	100%	1.201	100%
	20	0.8	0.077	100%	1.392	100%
	25	0.2	-0.039	100%	1.191	100%
	25	0.4	-0.041	100%	1.064	100%
	25	0.6	0.009	100%	1.068	100%
	25	0.8	0.070	100%	1.268	100%
	30	0.2	-0.066	100%	1.081	100%
	30	0.4	-0.022	100%	0.953	100%

	30	0.6	0.000	100%	0.999	100%
	30	0.8	0.050	100%	1.158	100%
	35	0.2	-0.061	100%	1.000	100%
	35	0.4	-0.036	100%	0.901	100%
	35	0.6	0.009	100%	0.920	100%
	35	0.8	0.052	100%	1.064	100%
	40	0.2	-0.035	100%	0.903	100%
	40	0.4	-0.027	100%	0.827	100%
	40	0.6	-0.003	100%	0.868	100%
	40	0.8	0.060	100%	0.996	100%
	50	0.2	-0.054	100%	0.827	100%
	50	0.4	-0.032	100%	0.747	100%
	50	0.6	0.011	100%	0.768	100%
	50	0.8	0.024	100%	0.907	100%
	20	0.2	0.031	100%	0.332	100%
	20	0.4	0.014	100%	0.320	100%
	20	0.6	-0.006	100%	0.288	100%
	20	0.8	-0.017	100%	0.227	100%
	25	0.2	0.030	100%	0.306	100%
	25	0.4	0.014	100%	0.301	100%
	25	0.6	-0.009	100%	0.271	100%
	25	0.8	-0.018	100%	0.210	100%
	30	0.2	0.026	100%	0.284	100%
	30	0.4	0.006	100%	0.276	100%
	30	0.6	-0.007	100%	0.255	100%
	30	0.8	-0.014	100%	0.195	100%
Mean detection	35	0.2	0.026	100%	0.267	100%
	35	0.4	0.015	100%	0.268	100%
	35	0.6	-0.011	100%	0.243	100%
	35	0.8	-0.012	100%	0.182	100%
	40	0.2	0.023	100%	0.246	100%
	40	0.4	0.007	100%	0.253	100%
	40	0.6	-0.003	100%	0.231	100%
	40	0.8	-0.013	100%	0.170	100%
	50	0.2	0.024	100%	0.237	100%
	50	0.4	0.009	100%	0.232	100%
	50	0.6	-0.008	100%	0.209	100%
	50	0.8	-0.009	100%	0.154	100%
	20	0.2	-0.038	100%	0.644	100%
	20	0.4	0.010	100%	0.476	100%
	20	0.6	0.029	100%	0.366	100%
	20	0.8	0.019	100%	0.259	100%
	25	0.2	-0.040	100%	0.614	100%
	25	0.4	0.002	100%	0.455	100%
	25	0.6	0.026	100%	0.345	100%
Mean survival						

25	0.8	0.024	100%	0.239	100%
30	0.2	-0.036	100%	0.597	100%
30	0.4	0.011	100%	0.432	100%
30	0.6	0.018	100%	0.319	100%
30	0.8	0.013	100%	0.216	100%
35	0.2	-0.035	100%	0.575	100%
35	0.4	0.001	100%	0.411	100%
35	0.6	0.021	100%	0.307	100%
35	0.8	0.016	100%	0.199	100%
40	0.2	-0.024	100%	0.556	100%
40	0.4	0.006	100%	0.401	100%
40	0.6	0.014	100%	0.286	100%
40	0.8	0.015	100%	0.186	100%
50	0.2	-0.030	100%	0.535	100%
50	0.4	0.002	100%	0.370	100%
50	0.6	0.019	100%	0.261	100%
50	0.8	0.010	100%	0.162	100%

100

101

102 Table A4.2

103 Average calibration error, convergence, coverage, and 95% CRI range of all parameter estimates

104 from 100 simulations when daily survival rate is not 1 and the number of days between counts (lag)

105 varies. The mean detection probability and sample size were fixed at 0.6 and 30 broods,

106 respectively.

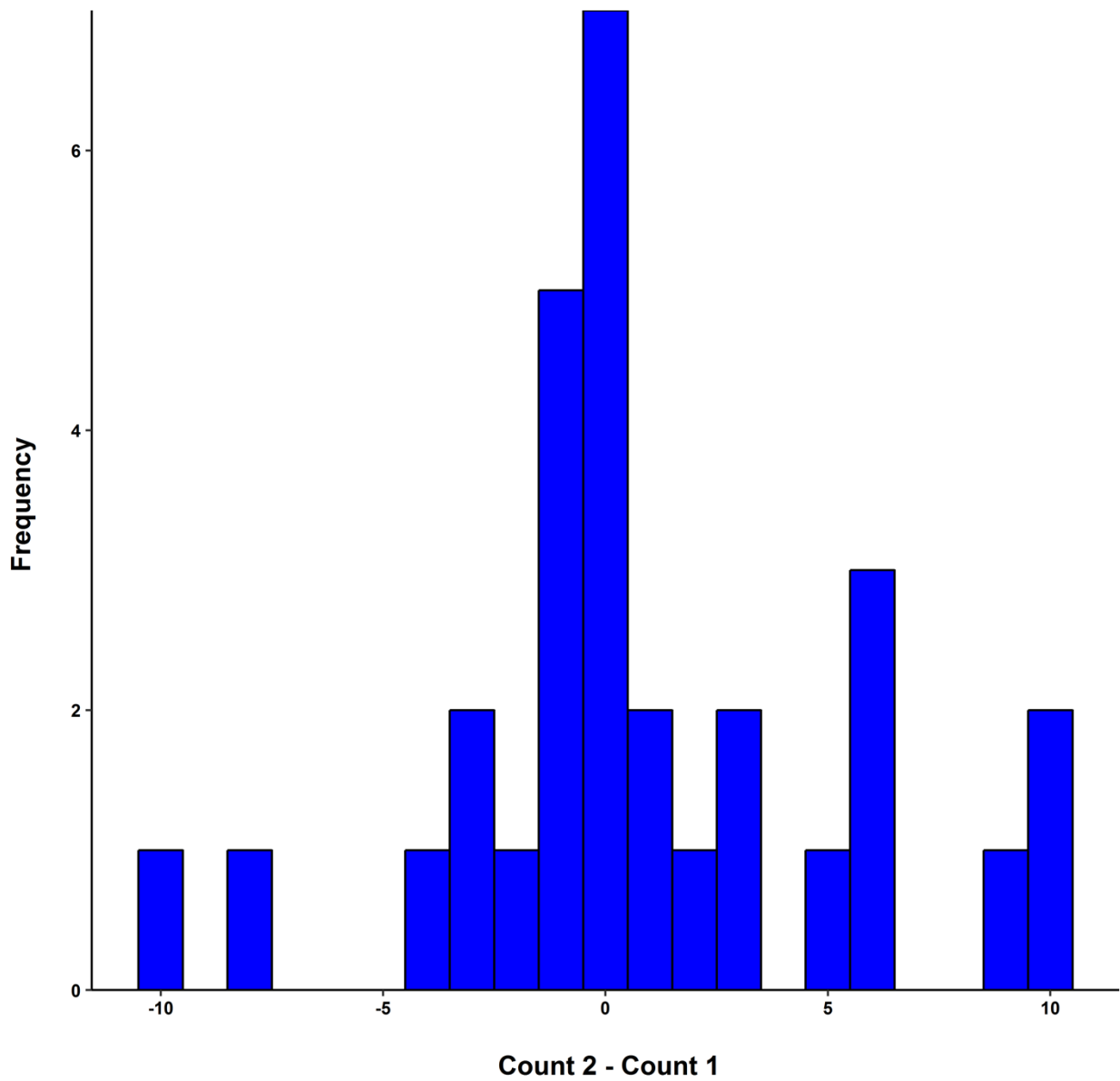
Parameter	Daily survival rate	Lag	Avg. calibration error (Median-truth)	Convergence	CRI range	Coverage
Survival coefficient	0.96	1	0.040	100%	0.934	100%
	0.96	3	0.113	100%	1.028	100%
	0.96	4	0.111	100%	1.004	100%
	0.97	1	0.076	100%	0.958	100%
	0.97	3	0.087	100%	0.963	100%
	0.97	4	0.103	100%	0.986	100%
	0.98	1	0.049	100%	0.950	100%
	0.98	3	0.064	100%	0.966	100%
	0.98	4	0.122	100%	1.008	100%
	0.99	1	0.107	100%	0.982	100%
	0.99	3	0.037	100%	0.922	100%
	0.99	4	0.065	100%	0.960	100%
Detection coefficient	0.96	1	0.038	100%	0.948	100%
	0.96	3	0.112	100%	0.907	100%
	0.96	4	0.104	100%	0.889	100%
	0.97	1	0.031	100%	0.954	100%
	0.97	3	0.138	100%	0.893	100%
	0.97	4	0.095	100%	0.901	100%
	0.98	1	0.005	100%	0.998	100%
	0.98	3	0.043	100%	0.972	100%
	0.98	4	0.085	100%	0.922	100%
	0.99	1	0.046	100%	0.960	100%
	0.99	3	0.042	100%	0.974	100%
	0.99	4	0.069	100%	0.966	100%
Mean detection	0.96	1	0.383	100%	0.253	100%
	0.96	3	0.351	100%	0.251	100%
	0.96	4	0.333	100%	0.243	100%
	0.97	1	-0.021	100%	0.253	100%
	0.97	3	-0.047	100%	0.248	100%
	0.97	4	-0.047	100%	0.242	100%
	0.98	1	-0.010	100%	0.262	100%
	0.98	3	-0.026	100%	0.260	100%
	0.98	4	-0.042	100%	0.249	100%
	0.99	1	-0.014	100%	0.255	100%
	0.99	3	-0.009	100%	0.257	100%
	0.99	4	-0.022	100%	0.258	100%

	0.96	1	0.019	100%	0.317	100%
	0.96	3	0.036	100%	0.338	100%
	0.96	4	0.040	100%	0.333	100%
	0.97	1	0.026	100%	0.322	100%
	0.97	3	0.034	100%	0.331	100%
Mean survival	0.97	4	0.034	100%	0.324	100%
	0.98	1	0.013	100%	0.328	100%
	0.98	3	0.021	100%	0.330	100%
	0.98	4	0.039	100%	0.332	100%
	0.99	1	0.022	100%	0.328	100%
	0.99	3	0.021	100%	0.319	100%
	0.99	4	0.020	100%	0.330	100%

107

108

109 APPENDX 5 DIFFERENCE IN FLUSH COUNTS BETWEEN VISITS OF PHEASANT
110 BROODS



111 .
112 Figure A5: A histogram showing the difference in counts between the first and second visits among
113 pheasant broods surveyed. Positive values indicate more chicks were detected on the second visit
114