

Supplementary material

Appendix 1. Cormack–Jolly Seber family of models used in Program MARK for the preliminary analysis of apparent annual adult survival of 17 species at our South African study site. Both apparent survival (ϕ) and resighting probability (p) were modelled as constant (.) or varying with time (t). The species were monitored for a variable number of years.

Model	K^1	AIC _c or QAIC _c ²	Δ AIC _c or Δ QAIC _c ³	w_i^4
<i>Emberiza capensis</i> (Cape bunting) $\hat{c} = 0.95$				
$\phi(.) p(.)$	2	86.4	0.00	0.941
$\phi(.) p(t)$	7	92.5	6.19	0.043
$\phi(t) p(.)$	7	94.6	8.21	0.016
$\phi(t) p(t)$	11	101.9	15.53	0.000
<i>Crithagra albogularis</i> (White-throated canary) $\hat{c} = 0.80$				
$\phi(.) p(.)$	2	68.8	0.00	0.938
$\phi(t) p(.)$	5	75.5	6.73	0.032
$\phi(.) p(t)$	5	75.9	7.11	0.027
$\phi(t) p(t)$	7	80.6	11.77	0.003
<i>Crithagra flaviventris</i> (Yellow canary) $\hat{c} = 0.86$				
$\phi(t) p(t)$	11	281.8	0.00	0.697
$\phi(.) p(t)$	7	283.4	1.67	0.302
$\phi(t) p(.)$	7	297.6	15.86	0.000
$\phi(.) p(.)$	2	305.7	23.94	0.000
<i>Cinnyris chalybeus</i> (Southern double-collared sunbird) $\hat{c} = 0.93$				
$\phi(.) p(.)$	2	220.3	0.00	0.558
$\phi(.) p(t)$	7	220.8	0.55	0.423
$\phi(t) p(.)$	7	228.3	7.97	0.010
$\phi(t) p(t)$	11	228.7	8.46	0.008
<i>Cercotrichas coryphaeus</i> (Karoo scrub-robin) $\hat{c} = 1.05$				
$\phi(.) p(.)$	2	833.2	0.00	0.861
$\phi(.) p(t)$	8	837.3	4.17	0.107
$\phi(t) p(.)$	8	840.0	6.82	0.029
$\phi(t) p(t)$	13	844.1	10.96	0.004
<i>Cossypha caffra</i> (Cape robin-chat) $\hat{c} = 1.77$				
$\phi(.) p(.)$	2	165.9	0.00	0.934
$\phi(.) p(t)$	7	172.0	6.04	0.045
$\phi(t) p(.)$	7	173.7	7.75	0.019
$\phi(t) p(t)$	11	179.0	13.07	0.001
<i>Zosterops capensis</i> (Cape white-eye) $\hat{c} = 1.11$				
$\phi(.) p(t)$	7	152.0	0.00	0.689
$\phi(.) p(.)$	2	153.6	1.66	0.300
$\phi(t) p(t)$	11	161.1	9.06	0.007
$\phi(t) p(.)$	7	162.5	10.52	0.004
<i>Apalis thoracica</i> (Bar-throated apalis) $\hat{c} = 1.43$				
$\phi(.) p(.)$	2	336.1	0.00	0.824
$\phi(.) p(t)$	7	340.1	4.05	0.109
$\phi(t) p(.)$	7	341.5	5.41	0.055
$\phi(t) p(t)$	11	344.5	8.48	0.012
<i>Cisticola subruficapilla</i> (Grey-backed cisticola) $\hat{c} = 2.09$				
$\phi(.) p(.)$	2	34.77	0.00	0.889
$\phi(.) p(t)$	6	40.22	5.45	0.058

$\phi(t) p(\cdot)$	6	40.48	5.70	0.051
$\phi(t) p(t)$	9	47.58	12.80	0.001
<i>Prinia maculosa</i> (Karoo prinia) $\hat{c} = 1.27$				
$\phi(\cdot) p(\cdot)$	2	743.73	0.00	0.740
$\phi(\cdot) p(t)$	8	745.97	2.24	0.241
$\phi(t) p(\cdot)$	8	752.07	8.34	0.011
$\phi(t) p(t)$	13	752.92	9.19	0.007
<i>Pycnonotus capensis</i> (Cape bulbul) $\hat{c} = 1.17$				
$\phi(\cdot) p(\cdot)$	2	155.74	0.00	0.962
$\phi(t) p(\cdot)$	7	162.97	7.23	0.026
$\phi(\cdot) p(t)$	7	164.68	8.94	0.011
$\phi(t) p(t)$	11	169.69	13.95	0.001
<i>Parisoma subcaeruleum</i> (Chestnut-vented tit-babbler) $\hat{c} = 1.06$				
$\phi(\cdot) p(\cdot)$	2	229.67	0.00	0.922
$\phi(\cdot) p(t)$	8	236.05	6.38	0.038
$\phi(t) p(\cdot)$	8	236.05	6.38	0.038
$\phi(t) p(t)$	13	241.55	11.87	0.002
<i>Sphenoeacus afer</i> (Cape grassbird) $\hat{c} = 1.50$				
$\phi(\cdot) p(\cdot)$	2	53.87	0.00	0.980
$\phi(t) p(\cdot)$	7	62.38	8.51	0.014
$\phi(\cdot) p(t)$	7	63.95	10.08	0.006
$\phi(t) p(t)$	11	72.51	18.65	0.000
<i>Sylvietta rufescens</i> (Long-billed crombec) $\hat{c} = 1.30$				
$\phi(\cdot) p(\cdot)$	2	149.18	0.00	0.990
$\phi(t) p(\cdot)$	8	159.68	10.50	0.005
$\phi(\cdot) p(t)$	8	159.91	10.73	0.005
$\phi(t) p(t)$	13	169.54	20.36	0.000
<i>Anthoscopus minutus</i> (Cape penduline tit) $\hat{c} = 1.40$				
$\phi(\cdot) p(\cdot)$	2	65.87	0.00	0.861
$\phi(t) p(\cdot)$	6	70.64	4.77	0.079
$\phi(\cdot) p(t)$	6	71.84	5.97	0.043
$\phi(t) p(t)$	9	73.78	7.92	0.016
<i>Telophorus zeylonus</i> (Bokmakierie) $\hat{c} = 0.98$				
$\phi(\cdot) p(\cdot)$	2	54.68	0.00	0.968
$\phi(\cdot) p(t)$	7	61.69	7.01	0.029
$\phi(t) p(\cdot)$	7	66.57	11.89	0.003
$\phi(t) p(t)$	11	76.02	21.34	0.000
<i>Colius colius</i> (White-backed mousebird) $\hat{c} = 1.03$				
$\phi(\cdot) p(\cdot)$	2	157.62	0.00	0.843
$\phi(\cdot) p(t)$	5	161.77	4.15	0.106
$\phi(t) p(\cdot)$	5	164.00	6.38	0.035
$\phi(t) p(t)$	7	165.44	7.82	0.017

¹ Number of parameters estimated.

² Akaike's Information Criterion corrected for small sample size (AIC_c) or Quasi-AIC ($QAIC_c$) adjusted for small sample size and a lack-of-fit coefficient \hat{c} when $\hat{c} > 1.1$.

³ Increase over the lowest observed value of AIC_c or $QAIC_c$.

⁴ Akaike weight: likelihood of a model to be the best in the set of candidate models given the data.

Appendix 2. WinBUGS code for the multi-species, hierarchical capture-mark-recapture

model.

```

*****
# WinBUGS codes used to fit multispecies hierarchical model
*****
model
{
  *****
  # Priors and constraints
  *****

  for(i in 1:nind)
  {
    for(t in f[i]:(nocc-1))
    {
      *****
      # Survival (phi): species-specific and constant over time
      *****
      logit(phi[i,t]) <- beta[gr[i]]

      *****
      # Recapture (p) - species-specific and time dependent
      # Time treated as random
      *****
      logit(p[i,t]) <- gamma[gr[i]] + eta[t]
    } #t
  } #i

  for(t in 1:(nocc-1))
  {
    eta[t] ~ dnorm(0,taueta)I(-5,5)
  }#t

  sigeta ~ dunif(0,5) ; taueta <- pow(sigeta,-2)

  for(j in 1:g)
  {
    beta[j] ~ dunif(-5,5)
    gamma[j] ~ dunif(-5,5)

    phi.g[j] <- exp(beta[j])/(1 + exp(beta[j]))
    p.g[j] <- exp(gamma[j])/(1 + exp(gamma[j]))
  }#j

  *****
  # Define the likelihood using state-space formulation
  # z is the state process
  # y is the observation process (capture history)

```

```

# eff is an effort matrix
#*****

for (i in 1:nind)
{
  z[i,f[i]] <- 1
  for (t in (f[i]+1):nocc)
  {
    #*****
    # State process
    #*****
    z[i,t] ~ dbern(mu1[i,t])
    mu1[i,t] <- phi[i,t-1]*z[i,t-1]

    #*****
    #Observation process
    #*****
    y[i,t] ~ dbern(mu2[i,t])
    mu2[i,t] <- p[i,t-1]*z[i,t]*eff[i,t]
  }#t
}#i
}#model

```

Appendix 3. WinBUGS code for comparison of survival and clutch size between South Africa and Malawi.

```
#####  
# Analysis for comparing survival estimates between South Africa and Malawi  
# #####  
  
# The data are mean survival per species ('surv')  
  
# and their standard errors ('se.surv')  
  
# 'group' indicates whether the estimate is from South Africa (group=0) or Malawi (group=1)  
  
model {  
  
# Priors  
  
mu.sa ~ dnorm(0, 0.0000001) # mean survival for South African estimates  
beta ~ dnorm(0, 0.0000001) # difference between South Africa and Malawi  
  
tau.species <- pow(sd.species, -2)  
sd.species ~ dunif(0, 100) # Heterogeneity among species  
  
tau.genus <- pow(sd.genus, -2)  
sd.genus ~ dunif(0,100) # genus effect  
  
# Likelihood  
  
for (i in 1:8) # for each of the 8 species comparisons  
{  
  spp[i] ~ dnorm(0, tau.genus) # random species-'pair' effect  
}  
  
for (i in 1:n){  
  surv[i] ~ dnorm(mu[i], tau.error[i])  
  mu[i] ~ dnorm(mu.a[i], tau.species)  
  mu.a[i] <- mu.sa + beta * group[i] + spp[genus[i]]  
  tau.error[i] <- pow(se.surv[i], -2)
```

```

}

# Derived quantities

mu.malawi <- mu.sa + beta      # mean estimate for Malawi

} # end model

#*****
# Analysis for comparing clutch size estimates between South Africa and Malawi
# *****

# The data are mean clutch size per species ('clutch')

# 'group' indicates whether the estimate is from South Africa (group=0) or Malawi (group=1)

model {

# Priors

mu.sa ~ dnorm(0, 0.0000001)    # mean clutch for South African estimates

beta ~ dnorm(0, 0.0000001)    # difference between South Africa and Malawi

tau.species <- pow(sd.species, -2)

sd.species ~ dunif(0, 100)    # Heterogeneity among species

tau.genus <- pow(sd.genus, -2)

sd.genus ~ dunif(0,100)    # genus effect

# Likelihood

for (i in 1:8) # for each of the 8 species comparisons

{

  spp[i] ~ dnorm(0, tau.genus) # random species-'pair' effect

}

for (i in 1:n){

  clutch[i] ~ dnorm(mu.a[i], tau.species)

  mu.a[i] <- mu.sa + beta * group[i] + spp[genus[i]]
}

```

```
}  
# Derived quantities  
mu.malawi <- mu.sa + beta      # mean estimate for Malawi  
} # end model
```