The two oxpecker species reveal the role of movement rates and foraging intensity in species coexistence, by Guillaume Péron, Christophe Bonenfant, Roxanne Gagnon, and Cheryl Mabika

Appendix S1

R-code for estimating the rate of mis-identification in a two-species, three-observer setting.

The data is summarized into 8 numbers $n_{i,j,k}$ = the number of oxpeckers identified as species *i* by observer 1, species *j* by observer 2, and species *k* by observer 3, with *i*, *j*, and *k* taking value 1 or 2. These values are manually entered into the R environment by typing n111 = ..., and so forth.

In practice, the same observer performed the identification challenge twice (with a two week interval). We applied the same observer mis-identification probability, allowing us to spare some parameters relative to if we had three different observers.

The negative log-likelihood function was then:

```
nll <- function(theta) {</pre>
       pi1 = plogis(theta[1]) ## proportion of species 1
      p1 = plogis(theta[2]) ## probability of correct identification species 1 by observer 1
p2 = plogis(theta[3]) ## probability of correct identification species 2 by observer 1
       q1 = plogis(theta[4]) ## probability of correct identification species 1 by observer 2
       q2 = plogis(theta[5]) ## probability of correct identification species 2 by observer 2
       P111 = pi1*p1*p1*q1 + (1-pi1)*(1-p2)*(1-p2)*(1-q2)
                                                                                       ## proba obs 1 says species 1 twice, obs 2 also says species 1
       P112 = pi1*p1*p1*(1-q1) + (1-pi1)*(1-p2)*(1-p2)*q2
       P121 = pi1*p1*(1-p1)*q1 + (1-pi1)*(1-p2)*p2*(1-q2)
       P122 = pi1*p1*(1-p1)*(1-q1) + (1-pi1)*(1-p2)*p2*q2
       P221 = pi1*(1-p1)*(1-p1)*q1 + (1-pi1)*p2*p2*(1-q2)
       P222 = pi1*(1-p1)*(1-p1)*(1-q1) + (1-pi1)*p2*p2*q2
       P211 = pi1*(1-p1)*p1*q1 + (1-pi1)*p2*(1-p2)*(1-q2)
       P212 = pi1*(1-p1)*p1*(1-q1) + (1-pi1)*p2*(1-p2)*q2
       lik = n111 \times log(P111) + n121 \times log(P121) + n211 \times log(P211) + n221 \times log(P221) + n221 
                          n112*log(P112) + n122*log(P122) + n212*log(P212) + n222*log(P222)
       return(-(lik))
 }
s=nlm(nll,rnorm(5,2,1),hessian=TRUE) ## minimize starting from a random initial value
```

We minimized the negative log-likelihood using the nlm function in R with default options, and backtransformed the estimates from the logit to the natural scale.

In practice, after a first round of identification, the estimated rates of mis-identification were not satisfactory (>5%). Thus GP conducted a second round of identification, taking into account the outcome of the previous round and focusing in particular on cases with disagreements between the three previous passages.