# Appendix S1. Updating of latent encounter history frequencies in multimark

# Brett T. McClintock<sup>1</sup>

### National Marine Mammal Laboratory

Alaska Fisheries Science Center NOAA National Marine Fisheries Service Seattle, Washington, U.S.A. <sup>1</sup>Email: brett.mcclintock@noaa.gov

#### May 11, 2015

The feasible set of latent encounter histories ( $\mathbf{Y}$ ) is explored in multimark using an extension of the MCMC algorithms proposed by Bonner & Holmberg (2013) and McClintock et al. (2013, 2014) that were originally conceived for a different application by Link et al. (2010). The new algorithm conditions on the observed data (thus reducing the dimension of the problem) and only proposes updates with non-negative latent encounter history frequencies,  $\mathbf{f} = (f_1, f_2, \dots, f_{5^T})$ . Let  $\mathbf{r}$  denote the set of  $\mathbf{4}^T - \mathbf{2}^{T+1} + 1$  indices for latent encounter histories that spawn >1 observed history, and let  $f_{j(1)}$  and  $f_{j(2)}$  denote the corresponding frequencies for type 1 and type 2 histories that arise from latent encounter history  $j \in \mathbf{r}$ . Referring back to Table 2 with T = 2,  $\mathbf{r} = \{4, 8, 9, 12, 14, 16, 17, 18, 19\}$  and one potential update would involve frequencies for latent history '31'  $(f_{17})$  and its progeny '11'  $(f_{17(1)} = f_7)$  and '20'  $(f_{17(2)} = f_{11})$ .

- When conditioning on the observed encounter histories, the size of the problem is typically greatly reduced because many of the potential latent histories and corresponding moves are not permissable. For example, with T=2, if encounter history '11' was never observed, then  $f_7=f_9=f_{17}=f_{19}=0$  can be ignored and  $j \in \{9,17,19\}$  can be removed from  $\mathbf{r}$  for subsequent computations.
- Starting from a permissible **f** conditional on the observed encounter histories, the algorithm proceeds as follows:
- 1. Randomly draw a latent encounter history index  $r \in \mathbf{r}^*$ , where  $\mathbf{r}^*$  is the subset of  $\mathbf{r}$  with corresponding frequencies that satisfy  $\min(f_1, f_j) + \min(f_{j(1)}, f_{j(2)}) > 0$  for  $j \in \mathbf{r}$ .
- 2. Randomly draw  $c_r$  from the integer set  $\{-\min(f_1, f_r), \ldots, -1, 1, \ldots, \min(f_{r(1)}, f_{r(2)})\}$ .
- 3. Propose  $f_r^* = f_r + c_r$ ,  $f_{r(1)}^* = f_{r(1)} c_r$ , and  $f_{r(2)}^* = f_{r(2)} c_r$ .
- <sup>25</sup> 4. Apportion **f**\* to individuals following McClintock *et al.* (2014), and accept proposed move based on the Metropolis-Hastings ratio described therein [pp. 2470-2472, steps 9(b)-9(c)].
- Any additional constraints, such as those resulting from encounter histories being designated as known with certainty using the *known* argument in *processdata()*,
  are accounted for by simple modifications to steps 1-2. In terms of mixing, it can
  sometimes be advantageous to explore more than one move at a time. At each iteration of the chain, the argument *maxnumbasis* specifies how many times to perform
  steps 1-3 in sequence before evaluating step 4. The default for *multimarkCJS()* and *multimarkClosed()* is *maxnumbasis=1*.

Note that because multimark uses "semi-complete" data likelihoods that condition on the number of unique individuals encountered at least once (n), the dimension of the data-augmented encounter histories (M) described in McClintock  $et\ al.\ (2014)$  is determined by the number of observed encounter histories (i.e.  $M=n_1+n_2+n_{known}$ ) such that  $f_1=M-n$ . Letting  $q_i\sim \text{Bernoulli}\ (\psi)$  be an indicator for whether or not individual i belongs to the n unique individuals encountered at least once (i.e.  $\sum_{i=1}^M q_i=n$ ), then  $q_i=1$  if  $H_i>1$  (otherwise  $q_i=0$ ), where  $H_i$  is the latent encounter history index for individual i  $\left(\sum_{i=1}^M I(H_i=j)=f_j\right)$ , and  $\psi\sim \text{Beta}\ (a_\psi^0,b_\psi^0)$  is the probability that a randomly selected individual from the M observed individuals belongs to the n unique individuals encountered at least once. The defaults in multimarkCJS() and multimarkClosed() are  $a_\psi^0=b_\psi^0=1$ .

# 46 References

- Bonner, S.J. & Holmberg, J. (2013) Mark-recapture with multiple, non-invasive marks. *Biometrics*, **69**, 766–775.
- Link, W.A., Yoshizaki, J., Bailey, L.L. & Pollock, K.H. (2010) Uncovering a latent multinomial: analysis of mark-recapture data with misidentification. *Biometrics*, **66**, 178–185.
- McClintock, B.T., Bailey, L.L., Dreher, B.P. & Link, W.A. (2014) Probit models for
   capture-recapture data subject to imperfect detection, individual heterogeneity
   and misidentification. The Annals of Applied Statistics, 8, 2461–2484.
- McClintock, B.T., Conn, P.B., Alonso, R.S. & Crooks, K.R. (2013) Integrated mod-

- eling of bilateral photo-identification data in mark-recapture analyses. *Ecology*,
- , 1464–1471.