MAXIMUM LIKELIHOOD ESTIMATION OF
MARK-RECAPTURE-RECOVERY MODELS IN THE
PRESENCE OF CONTINUOUS COVARIATES

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We consider mark-recapture-recovery (MRR) data of animals
where the model parameters are a function of individual time-varying
continuous covariates. For such covariates, the covariate value is un-
observed if the corresponding individual is unobserved, in which case
the survival probability cannot be evaluated. For continuous-valued
covariates, the corresponding likelihood can only be expressed in the
form of an integral that is analytically intractable, and, to date, no
maximum likelihood approach that uses all the information in the
data has been developed. Assuming a first-order Markov process for
the covariate values, we accomplish this task by formulating the MRR
setting in a state-space framework and considering an approximate
likelihood approach which essentially discretizes the range of covari-
ate values, reducing the integral to a summation. The likelihood can
then be efficiently calculated and maximized using standard tech-
niques for hidden Markov models. We initially assess the approach
using simulated data before applying to real data relating to Soay
sheep, specifying the survival probability as a function of body mass.
Models that have previously been suggested for the corresponding
covariate process are typically of the form of diffusive random walks.
We consider an alternative non-diffusive AR(1)-type model which
appears to provide a significantly better fit to the Soay sheep data.

1. Introduction. Mark-recapture-recovery (MRR) data are commonly
collected on animal populations in order to gain some understanding of the
underlying system. Data are collected by repeated surveyings of the pop-
ulation under study. In the initial survey all individuals that are observed
are uniquely identified (via natural features or by applying some form of
mark, such as a ring or tag) and released back into the population. At
each subsequent survey all individuals observed are recorded, and those
that have not previously been observed are again uniquely identified, be-
fore all are released back into the population. We assume that individuals

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can be observed alive or recovered dead in each survey. The resulting MRR data can be summarised as the observed encounter histories for each individual observed within the population, detailing for each survey event whether an individual was observed alive or recovered dead. Conditioning on the initial capture time of each individual leads to Cormack-Jolly-Seber-type models (see Schwarz and Seber, 1999, for a review of these models).

The original Cormack-Jolly-Seber model considered only live captures (i.e., mark-recapture data), and was extended to additional recoveries by Barker (1997). The corresponding MRR likelihood function of these data can be written as a function of survival, recapture and recovery probabilities.

Recent research has focussed on linking environmental and individual covariates to demographic parameters, most notably the survival probabilities, in order to explain temporal and individual variability (Brooks et al., 2000; Catchpole et al., 2000; Coulson et al., 2001; Pollock, 2002; King and Brooks, 2003; King et al., 2006; Gimenez et al., 2006; Catchpole et al., 2008; Schofield and Barker, 2011, to name but a few). We consider individual time-varying continuous covariates. These have traditionally been difficult to deal with due to the missing covariate values (if an individual is unobserved the corresponding covariate value is also unknown). The corresponding likelihood is expressible in the form of an integral, integrating over the set of missing covariate values, but is analytically intractable. One of the initial approaches to dealing with such covariates was to (coarsely) discretize the covariate space, essentially defining discrete covariate “states”. Nichols et al. (1992) considered data relating to meadow voles (Microtus pennsylvanicus) and categorised weight into four different categories. Such a discretization reduces the model to the Arnason-Schwarz model (Brownie et al., 1993; Schwarz et al., 1993). Transition probabilities between the covariate states are estimated within the optimisation of the likelihood (possibly with additional restrictions on the state transitions). With the coarse discretization arbitrarily defined, this approach leads to a (potentially significant) loss of information. Catchpole et al. (2008) have proposed a conditional likelihood approach (often referred to as the “trinomial approach”). By conditioning on only the observed covariate values, this approach results in a simple, closed-form likelihood expression. However, this involves discarding a proportion of the available data, leading to a decreased precision of the parameter estimates. In addition, Bayesian approaches have been proposed (Bonner and Schwarz, 2006; King et al., 2008), and the corresponding model fitted using a data augmentation approach (Tanner and Wong, 1987). This involves treating the unobserved continuous covariate values as parameters (or auxiliary variables) that are essentially integrated out numerically within the associa-
ated Markov chain Monte Carlo (MCMC) algorithm. Within the Bayesian approach priors need to be specified on the model parameters (and possibly models in the presence of model uncertainty). In addition, model selection is generally more difficult due to computational complexity, and posterior model probabilities can be sensitive to the prior distributions specified on the parameters. See Bonner et al. (2010) for further discussion and a comparison of the Bayesian and trinomial approaches, and Catchpole et al. (2008) for an overview of the existing approaches.

For the considered type of MRR data, Bonner et al. (2010) state that “except when few values are missing, the large number of integrals [...] will make it impossible to perform maximum likelihood estimation” (p. 1258). We claim that this statement is not true, and present a novel approach based on a hidden Markov-type formulation of the MRR setting. This formulation leads to a likelihood that is easy to compute and to maximize numerically. The underlying idea is to finely discretize the space of possible covariate values, which corresponds to a numerical integration of the likelihood function. The numerical integration enables us to augment the resulting discrete space of covariate values with the state space of the survival process, leading to a single, partially hidden Markov process for each observed encounter history. This approach essentially extends the previous coarse discretization approach of Nichols et al. (1992) by considering a very fine discretization of the covariate space, coupled with specifying structured transition probability matrices defined using a covariate process model. The corresponding likelihood can be written in a closed, efficient, matrix product form that is characteristic of hidden Markov models (HMMs) (Zucchini and MacDonald, 2009). The likelihood is only approximate due to the discretization, but the approximation can be made arbitrarily accurate. Notably, model selection can be carried out using standard model selection techniques.

We apply the method to data relating to Soay sheep (Ovis aries). The Soay sheep on the uninhabited island of Hirta in the St Kilda archipelago, Scotland, are a well-studied biological system (Clutton-Brock and Pemberton, 2004). Intensive annual surveys involve physical recaptures of individuals, tagging of lambs, visual resightings and searches for dead carcasses. A range of individual covariate data are recorded for each sheep. We focus on the body mass recorded, collected (when possible) when an individual is physically recaptured. Males and females have different life strategies, and we consider data relating to only females, tagged as lambs between 1985-2008 and recaptured/recovered annually from 1986-2009. We investigate the effect of body mass on survival, and consider a variety of models for the change of body mass over time. The latter aspect is usually not the
primary focus of MRR studies, although it is clearly of biological interest. In particular, we demonstrate that the (diffusive) models that have previously been considered for the change of body mass over time are outperformed by alternative (non-diffusive) AR(1)-type processes.

The manuscript is structured as follows. Section 2 introduces the HMM-type estimation method for the specific MRR setting under consideration. An extensive simulation study investigating the performance of the proposed method, including a comparison to the trinomial approach, is given in Section 3. In Section 4, we analyse MRR data collected on Soay sheep, where the time-varying covariate of interest corresponds to body mass. We conclude with a discussion in Section 5.

2. Hidden Markov-type formulation of the MRR setting. We initially develop the form of the (partially) hidden Markov model for standard MRR data (i.e., without any covariate information, in Section 2.1), before extending to include individual time-varying continuous covariate information (in Section 2.2).

2.1. Formulation in absence of covariate information.

2.1.1. General model formulation and notation. MRR data are typically most easily expressed in the form of the capture history of each individual animal observed within the study. We initially consider the probability of an encounter history for a given individual. Suppose that there are $T$ capture occasions within the study. The capture history for the individual is denoted by $(x_1, \ldots, x_T)$, such that

$$x_t = \begin{cases} 1 & \text{if the individual is observed at time } t; \\ 2 & \text{if the individual is recovered dead in the interval } (t-1,t]; \\ 0 & \text{otherwise.} \end{cases}$$

Following the initial capture of the individual, the encounter history can be regarded as the combination of two distinct processes: an underlying survival process and an observation process, conditional on the survival state of an individual. Thus, MRR data can be modelled via a (discrete) state-space model (i.e., HMM), separating the underlying state process (i.e., survival process) from the observation process (i.e., recapture/recovery processes). For further discussion we refer the reader to Gimenez et al. (2007), Schofield and Barker (2008), Royle (2008), King et al. (2009) and King (2012). Let $g$ denote the occasion on which the individual is initially observed and marked.
We define the survival process, \((s_g, \ldots, s_T)\), such that
\[
 s_t = \begin{cases} 
 1 & \text{if the individual is alive at time } t; \\
 2 & \text{if the individual is dead at time } t, \text{ but was alive at time } t-1; \\
 3 & \text{if the individual is dead at time } t, \text{ and was dead at time } t-1. 
\end{cases}
\]
Note that here we explicitly distinguish between “recently dead” individuals \((s_t = 2)\) and “long dead” individuals \((s_t = 3)\), and assume that only recently dead individuals can be recovered dead at a given capture event. This is a standard assumption within MRR models, due to the decay of marks for identifying individuals once they have died (although see, e.g., Catchpole et al., 2001, where this assumption is not valid).

The likelihood of the observed capture histories is a function of survival, recapture and recovery probabilities. In particular, we set
\[
 \phi_t = P(s_{t+1} = 1|s_t = 1) \quad \text{(Survival probability)}, \\
 p_t = P(x_t = 1|s_t = 1) \quad \text{(Capture probability)}, \\
 \lambda_t = P(x_t = 2|s_t = 2) \quad \text{(Recovery probability)}.
\]
We note that the survival process is only partially observed (i.e., it is partially hidden). For a capture history that includes a dead recovery, the corresponding survival process is completely known following initial capture (i.e., if \(x_\tau = 2\) then \(s_t = 1\) for \(t = g, \ldots, \tau - 1\), \(s_t = 2\) for \(t = \tau\) and \(s_t = 3\) for \(t = \tau + 1, \ldots, T\)). Similarly, if an individual is observed at the final capture event, then the associated survival process following initial capture is also fully known (i.e., if \(x_T = 1\) then \(s_t = 1\) for \(t = g, \ldots, T\)). However, for all other histories the survival process following the final capture of the individual is unknown. For notational convenience, we let \(S = \{t \geq g : s_t \text{ is known}\}\) denote the set of all occasions at which the survival state of the individual is known, and \(S^c\) the corresponding complement, i.e., the set of occasions at which the survival state is unknown, following initial capture.

2.1.2. The likelihood. Conditional on the initial capture, the likelihood for a single capture history can be written in the form
\[
 L = \sum_{\tau \in S^c} \sum_{s_\tau \in \{1, 2, 3\}} \prod_{t=g+1}^{T} f(s_t|s_{t-1}) f(x_t|s_t),
\]
taking into account all possible survival histories for the animal, given its observed capture history. For notational simplicity, we use \(f\) as a general
symbol for a probability mass function or a density function, possibly condition-AL

\[
\begin{align*}
  f(s_t | s_{t-1}) &= \begin{cases} 
    \phi_{t-1} & s_t = 1; s_{t-1} = 1; \\
    1 - \phi_{t-1} & s_t = 2; s_{t-1} = 1; \\
    1 & s_t = 3; s_{t-1} \in \{2, 3\}; \\
    0 & \text{otherwise}
  \end{cases} \\
  f(x_t | s_t) &= \begin{cases} 
    p_t & s_t = 1; x_t = 1; \\
    1 - p_t & s_t = 1; x_t = 0; \\
    \lambda_t & s_t = 2; x_t = 2; \\
    1 - \lambda_t & s_t = 2; x_t = 0; \\
    1 & s_t = 3; x_t = 0; \\
    0 & \text{otherwise}
  \end{cases}
\end{align*}
\]

Expression (2.1) represents an inefficient way of computing the likelihood, since some impossible state sequences are taken into account (such as, e.g., \ldots, 1, 2, 1, 1, \ldots) that have a zero contribution to the likelihood. Clearly, only possible state sequences need to be evaluated, but we retain the full summation for notational simplicity.

An alternative expression for the likelihood is available using matrix products. In particular, at time \( t \), we define the transition probability matrix associated with the transitions between different survival states by \( \Gamma_t \), such that

\[
\Gamma_t = \begin{pmatrix} 
  \phi_t & 1 - \phi_t & 0 \\
  0 & 0 & 1 \\
  0 & 0 & 1
\end{pmatrix}.
\]

Furthermore, let \( Q(x_t) \) denote the diagonal matrix giving the state-dependent probabilities of observations at time \( t \) on the diagonal:

\[
Q(x_t) = \begin{cases} 
  \text{diag}(1 - p_t, 1 - \lambda_t, 1) & \text{if } x_t = 0; \\
  \text{diag}(p_t, 0, 0) & \text{if } x_t = 1; \\
  \text{diag}(0, \lambda_t, 0) & \text{if } x_t = 2,
\end{cases}
\]

where diag(\ldots) denotes the diagonal matrix with given diagonal elements. The likelihood (2.1) can then be written in the HMM form

\[
\mathcal{L} = \delta \left( \prod_{t=g+1}^{T} \Gamma_{t-1}Q(x_t) \right) 1_3
\]

(2.2)

\[
= \delta \Gamma_g Q(x_{g+1}) \Gamma_{g+1} Q(x_{g+2}) \ldots \Gamma_{T-1} Q(x_T) 1_3,
\]
where \( \mathbf{1}_3 \) denotes a column vector of length 3 with each element equal to 1, and \( \mathbf{\delta} = (1, 0, 0) \) is the row vector giving the conditional probabilities of occupying the different survival states at the initial capture occasion, given that the individual was captured. The likelihood (2.2) is that of a partially hidden Markov model, and one effectively sums only over the unknown states, rather than over all possible state sequences. We further note that in general for MRR data, the likelihood can be calculated more efficiently using sufficient statistics, but we introduce this form of notation here for facilitating the extension to time-varying individual covariates. In an MRR setting, the HMM-type matrix product likelihood form has previously been given by Pradel (2005), who also discusses the general benefits of being able to apply the powerful HMM machinery.

2.2. Formulation in the presence of continuous-valued covariates.

2.2.1. General model formulation and notation. We extend the HMM framework to allow for the inclusion of individual-specific, continuous covariate information that varies over time. For example, this may correspond to the condition of the individual (where proxies such as body mass or parasitic load may be used). We consider a single time-varying continuous covariate, such that the survival probabilities are a deterministic function of this covariate. The extension of the method to multiple covariates is, in principle, straightforward, although technically challenging and accompanied by large scale increases in computational time (see Section 5 for further discussion).

Notationally, for a given individual we let \( y_t \) denote the value of the covariate at time \( t, t = g, \ldots, T \), and \( y = \{y_t : t = g, \ldots, T\} \) the set of all covariate values. For all \( t \geq \tau \) such that \( x_{\tau} = 2 \) the value of \( y_t \) (i.e., the covariate value following the observed death) is not defined. We note that usually one observes \( y_t \) when \( x_t = 1 \), but there may still be cases where an individual is observed alive, but no covariate value is recorded. This may occur for example due to a resighting rather than a recapture of the individual, or time constraints making it infeasible to obtain covariate values for all individuals observed. We let \( \mathcal{W} = \{t \geq g : y_t \text{ is observed}\} \) denote the set of times for which the covariate is observed. The corresponding observed covariate values are denoted by \( y_{\mathcal{W}} = \{y_t : t \in \mathcal{W}\} \). Similarly we let \( \mathcal{W}^c \) denote the complement, i.e., the set of times for which the covariate is unobserved, excluding times for which it is known the individual is not in the study (i.e., before initial capture or when known to be dead), so that \( \mathcal{W}^c = \{t \geq g : y_t \text{ is unobserved}\} \backslash \{t \geq g : t \in \mathcal{S}, s_t = 2, 3\} \). Finally, we let the set of missing covariate values be denoted by \( y_{\mathcal{W}^c} = \{y_t : t \in \mathcal{W}^c\} \).

We consider models in which the survival probability depends on the
covariate, and assume that the probability of survival from occasion \( t \) to \( t + 1 \) is determined by the value \( y_t \). Typically a logistic regression of survival probability on covariate value is considered, so that

\[
(2.3) \quad \text{logit}(\phi_t) = \beta_0 + \beta_1 y_t ,
\]

see, e.g., North and Morgan (1979) and Bonner et al. (2010).

Following Bonner et al. (2010), we assume an underlying model for the change in covariate values over time, specified by some first-order Markov process, \( f(y_t|y_{t-1}) \), for \( t = g+1, \ldots, T \). We set the function value of \( f(y_t|y_{t-1}) \) to one for \( s_t = 2, 3 \) (i.e., when an individual is dead). The covariate value may not be recorded at the initial capture, in which case we also require an underlying distribution on the initial covariate values, described by a probability density function \( f_0 \) (but see remarks at the end of Section 2.2.2).

Typically a random walk-type model is assumed for the underlying covariate model. For example, Bonner and Schwarz (2006) and King et al. (2008) consider models along the lines of

\[
(2.4) \quad y_{t+1}|y_t \sim N(y_t + a_t, \sigma^2) ,
\]

with \( a_t \) varying over time, and extensions thereof to allow for additional modelling complexities such as age-dependence. However, fitting such models involves some complexities, due to the unobserved covariate values, which need to be integrated out in order to explicitly calculate the likelihood function of the data. We discuss this in further detail next, and propose a likelihood-based approach that exploits the HMM machinery.

#### 2.2.2. The likelihood

With a first-order Markov process for the covariate values, the likelihood of the capture history and observed covariate values of an individual, conditional on the initial capture event, can be written in the form

\[
(2.5) \quad \mathcal{L} = \int \ldots \int \sum_{\tau \in S^c} \sum_{s_{\tau} \in \{1,2,3\}} f_0(y_g) \\
\times \prod_{t = g+1}^{T} f(s_t|s_{t-1}, y_{t-1}) f(x_t|s_t) f(y_t|y_{t-1}) d\mathbf{y} \mathcal{W}.
\]

In general, the necessary integration within this likelihood expression is analytically intractable. In a Bayesian approach, the missing covariate values are typically treated as auxiliary variables that are essentially integrated out within the MCMC algorithm (King et al., 2009). However, model selection is usually complex in terms of the estimation of the Bayes factors or
posterior model probabilities (although see King et al., 2008, King et al., 2009, and King and Brooks, 2002, with regard to the use of the reversible jump (RJ)MCMC for covariate selection and age/time dependence of the demographic parameters) and the potential sensitivity of these on the prior specified on the model parameters (see King et al., 2009, for further discussion).

We adopt a classical maximum likelihood approach here, where we closely approximate the multiple integral appearing in the likelihood using numerical integration, essentially finely discretizing the space of covariate values. This approach gives an approximation to the likelihood which can be made arbitrarily accurate by increasing the fineness of the discretization. In many MRR settings, the computational effort required to obtain a very close approximation is very reasonable, since one can evaluate the approximate likelihood using an efficient HMM-type recursion (as shown below). The suggested strategy for approximating the likelihood has previously been successfully applied in finance in order to estimate stochastic volatility models (see, e.g., Fridman and Harris, 1998, Bartolucci and De Luca, 2003), but has a much wider scope as pointed out by Langrock (2011).

Mathematically, we define an “essential range” for the covariate values, and split this range into \( m \) intervals of equal length, where \( m \) is some large number (e.g., \( m = 100 \)). Let the \( j \)th interval be denoted by \( B_j = [b_{j-1}, b_j) \), \( j = 1, \ldots, m \). The essential range corresponds to a lower and upper bound for the possible covariate values, given by \( b_0 \) and \( b_m \), respectively. We let \( b^*_j \) denote a representative point in \( B_j \). For large \( m \) the choice of this point only plays a very minor role, and throughout this manuscript we will simply use the interval midpoint. The likelihood (2.5) is then approximated by

\[
\mathcal{L} \approx \sum_{\kappa \in W^c} \sum_{j=1}^m \sum_{s_{t-1} \in \{1, 2, 3\}} \sum_{t=g+1}^T f_0(y_{t-1}) I_{\{s \in W\}} \left( \int_{b_{j-1}}^{b_j} f_0(z)dz \right) I_{\{s \in W^c\}} \\
\times \prod_{t=g+1}^T \left[ f(s_t \mid s_{t-1}, y_{t-1}) I_{\{(t-1) \in W\}} f(s_t \mid s_{t-1}, b^*_j) I_{\{(t-1) \in W^c\}} f(x_t \mid s_t) \right. \\
\times f(y_t \mid y_{t-1}) I_{\{(t-1) \in W, t \in W\}} f(y_t \mid b^*_j) I_{\{(t-1) \in W^c, t \in W\}} \\
\times f(y_t \in B_j \mid y_{t-1}) I_{\{(t-1) \in W, t \in W^c\}} f(y_t \in B_j \mid b^*_j) I_{\{(t-1) \in W^c, t \in W^c\}} \right],
\]

where \( I \) denotes the indicator function. In the last three lines in (2.6), the indicator function is used to distinguish between the cases where the covariate value is known (so that the observed value can be used) or unknown (so that
the defined intervals and associated representative values are used), at times \( t - 1 \) and \( t \). The final two lines correspond to the likelihood contribution of the underlying model for the covariate process, and

\[
(2.7) \quad f(y_t \in B_j | z) = \int_{b_{j-1}}^{b_j} f(y_t | z) dy_t .
\]

Note this is essentially the same numerical integration strategy that has previously been implemented by Langrock (2011) and Langrock et al. (2012); see the latter reference for more details. The major difference to those approaches is that here we allow for some covariate values to be observed, and hence do not integrate over these observed covariate values. Also here there is the additional difficulty of a second level of missing values, given by those \( s_t \) with \( t \in S^c \), which need to be summed over. Alternative numerical procedures for evaluating the likelihood are discussed in Section 5. In cases where the integral appearing in (2.7) cannot be solved analytically, it can be approximated by \((b_j - b_{j-1}) f(b_j^* | z)\).

The likelihood (2.6) can be written in HMM-type matrix notation, corresponding to an efficient recursive scheme for evaluating the likelihood (see Zucchini et al., 2008, for a more detailed description of the recursion). This makes maximum likelihood estimation feasible and has the general benefit that the well-developed HMM machinery becomes applicable. To do this, we essentially augment the “alive” survival state by dividing it into \( m \) distinct states, corresponding to “alive and with covariate value in \( B_j \), \( j = 1, \ldots, m \). The complete state space of the (partially) hidden process – now giving survival state and covariate value – comprises these \( m \) states plus the “recent dead” (state \( m + 1 \)) and the “long dead” (state \( m + 2 \)) survival states. To obtain the matrix product form of the likelihood, we extend the HMM form described in Section 2.1.2, allowing for the augmentation of the single alive state \( s_t = 1 \) to the set of \( m \) states. In particular we need to extend the definitions of the (system process) matrix, \( \Gamma_t \), observation matrix, \( Q_t \), and an initial distribution for the covariate values, \( \delta \) (assuming that these are not always observed). First, we define the \((m + 2) \times (m + 2)\) system process matrix

\[
\Gamma_t^{(m)} = \begin{pmatrix}
\phi_t(1)\Psi_t(1, 1) & \ldots & \phi_t(1)\Psi_t(1, m) & 1 - \phi_t(1) & 0 \\
\vdots & \ddots & \vdots & \vdots & \vdots \\
\phi_t(m)\Psi_t(m, 1) & \ldots & \phi_t(m)\Psi_t(m, m) & 1 - \phi_t(m) & 0 \\
0 & \ldots & 0 & 1 & 0 \\
0 & \ldots & 0 & 1 & 1
\end{pmatrix},
\]
where

\[
\Psi_t(i, j) = \begin{cases} 
  f(y_{t+1} | y_t) & \text{if } t, t+1 \in W, y_t \in B_i, y_{t+1} \in B_j; \\
  f(y_{t+1} | y^*_t) & \text{if } t \in W^c, t+1 \in W, y_{t+1} \in B_j; \\
  f(y_{t+1} \in B_j | y_t) & \text{if } t \in W, t+1 \in W^c, y_t \in B_i; \\
  f(y_{t+1} \in B_j | y^*_t) & \text{if } t, t+1 \in W^c; \\
  0 & \text{otherwise,}
\end{cases}
\]

and

\[
\phi_t(i) = \begin{cases} 
  f(s_{t+1} = 1 | s_t = 1, y_t) & \text{if } t \in W, y_t \in B_i; \\
  f(s_{t+1} = 1 | s_t = 1, y^*_t) & \text{if } t \in W^c; \\
  0 & \text{otherwise.}
\end{cases}
\]

Here the product \( \phi_t(i) \Psi_t(i, j) \) corresponds to the probability of the individual surviving from time \( t \) to time \( t+1 \), with the covariate value changing from a given value in the interval \( B_i \) at time \( t \) (either the observed covariate value or the representative value) to some value in the interval \( B_j \) at time \( t+1 \) (either the observed covariate value or any point within the interval). We note that this formulation is similar to the Arnason-Schwarz model, where the transition probabilities are defined between discrete states. However, within our model specification the transition probabilities are of a more complex form, as they are determined via the underlying model specified on the covariate process (rather than estimated freely), and also as they depend on whether the (continuous) covariate value is observed or not. For example, the probability \( f(y_{t+1} \in B_j | b^*_t) \) is determined by the model used for the covariate process. If the model given by (2.4) is considered, then

\[
f(y_{t+1} \in B_j | b^*_t) = \Phi \left( \frac{b_j - (b^*_t + a_t)}{\sigma} \right) - \Phi \left( \frac{b_{j-1} - (b^*_t + a_t)}{\sigma} \right),
\]

where \( \Phi \) denotes the cumulative distribution function of the standard normal distribution.

We now consider the matrix comprising the state-dependent observation probabilities, which is a diagonal matrix of dimension \((m + 2) \times (m + 2)\), such that

\[
Q^{(m)}(x_t) = \begin{cases} 
  \text{diag}(1 - p_t, \ldots, 1 - p_t, 1 - \lambda_t, 1) & \text{if } x_t = 0; \\
  \text{diag}(p_t, \ldots, p_t, 0, 0) & \text{if } x_t = 1; \\
  \text{diag}(0, \ldots, 0, \lambda_t, 0) & \text{if } x_t = 2.
\end{cases}
\]

Finally, one may need to model the initial distribution for the covariate value (since the initial value may not be observed). In general the distribution will
depend on the model assumed for the covariate process. For a (conditional) probability density function of initial covariate values given by \( f_0 \) (given the individual was captured during the study), we define the row vector \( \delta^{(m)} \) of length \( m + 2 \) with the \( i \)th element,

\[
\delta^{(m)}_i = \begin{cases} 
\int_{b_i}^{b_{i-1}} f_0(z) \, dz & \text{if } g \in W^c, \, i \in \{1, \ldots, m\}, \\
 f_0(y_g) & \text{if } g \in W, \, y_g \in B_i, \\
0 & \text{otherwise.}
\end{cases}
\]

If all initial covariate values are observed and the initial covariate distribution itself is not of interest, then one can set \( \delta^{(m)}_i = 1 \) for \( g \in W, \, y_g \in B_i \), which corresponds to conditioning the likelihood on the initial covariate value (with the advantage that less parameters have to be estimated).

Putting all these components together, the matrix formulation of (2.6) is

\[
L = \delta^{(m)} \left( \prod_{t=g+1}^{T} \Gamma^{(m)}_{t-1} Q^{(m)}(x_t) \right) \mathbf{1}_{m+2}
\]

(2.8) = \( \delta^{(m)} \Gamma^{(m)}_g Q^{(m)}(x_{g+1})\Gamma^{(m)}_{g+1} Q^{(m)}(x_{g+2}) \cdots \Gamma^{(m)}_{T-1} Q^{(m)}(x_T) \mathbf{1}_{m+2} \),

i.e., the likelihood has exactly the same structure as in the case of absence of covariates (cf. Expression (2.2)). It should perhaps be emphasized here that although (2.8) has precisely the same structure as an HMM likelihood (and hence can easily be maximized numerically), it is not the likelihood of an HMM, since (for any given \( t \)) the rows of the matrix \( \Gamma^{(m)}_t \) in general do not sum to one. This is because some of the covariate values are known, and also because we restrict the range of covariate values to some essential range.

2.2.3. Inference. For multiple individuals, the likelihood is simply the product of likelihoods of type (2.8), corresponding to each encounter history. It is then a routine matter to numerically maximize this joint likelihood with respect to the model parameters, subject to well-known technical issues arising in all optimization problems; see Chapter 3 in Zucchini and MacDonald (2009) for a detailed account of the particular issues that arise in the case of HMMs. Approximate confidence intervals for the parameters can be obtained based on the estimated Hessian, or, alternatively, using a parametric bootstrap. Model selection, including for the underlying covariate process model, can easily be carried out using model selection criteria such as the Akaike information criterion (AIC).

The accuracy of the likelihood approximation increases with increasing \( m \). The influence on the estimates can be checked by considering different values
of \( m \): if for some relatively large \( m \) a further increase does not change the likelihood value and/or the estimates, then this is a very strong indication that \( m \) is sufficiently large to ensure a very close approximation. From our experience we suggest using 20 – 80 intervals in the discretization (cf. the simulation study in Langrock et al., 2012, and further remarks on this issue in Section 4 below).

We note that the computational expense is not only a function of \( m \) and \( T \) and of the proportion of missing covariates, but also of the pattern that the missing values occur in. Consecutive missing covariate values lead to the highest computational burden (since they imply that all entries of the corresponding system process matrix associated with the underlying covariate process need to be calculated, a total of \( m^2 \) entries). If an unobserved covariate value is followed by an observed covariate value, then the corresponding system process matrix consists of only one column with non-zero entries (and likewise, if an observed covariate value is followed by an unobserved covariate value, then there is only one row with non-zero entries). Consecutive observed covariate values are clearly least computationally intensive (the system process matrix then consists of only one non-zero element).

3. Simulation study. In this section, we present the results of a simulation study for evaluating the performance of the HMM-based method. As a benchmark method we consider the trinomial method suggested by Catchpole et al. (2008), which currently appears to be the most popular classical inference method for MRR models with continuous-valued covariates (Bonner et al., 2010). We considered four different simulation scenarios, using different values for the recapture and the recovery probabilities, respectively. Table 1 gives the combinations of these parameters that were considered. The different scenarios represent, inter alia, different amounts of information on the survival states (the lower \( \lambda \) and the lower \( p \), the less information) and on the covariate values (the lower \( p \), the less information), respectively. For each of the scenarios we conducted 500 simulation experiments, in each experiment considering simulated capture histories for \( N = 500 \) individuals, each of them observed on at most \( T = 10 \) occasions. For each individual the time of the initial capture occasion was chosen uniformly from \{1, \ldots, 9\}.

In each scenario we used the same underlying process to generate the covariate values. More precisely, for each individual we generated the values of the covariate process using an autoregressive-type process of order 1 with a deterministic (sine-shaped) trend:

\[
y_t - 25 = \eta(y_{t-1} - 25) + \alpha_t + \sigma \epsilon_t,
\]

where \( \alpha_t = \gamma \sin(2\pi t/T) \) and \( \epsilon_t \overset{iid}{\sim} N(0,1) \). In all scenarios we used the
Table 1
Configurations of true recovery and recapture probabilities used in four different simulation scenarios.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>$p$</th>
<th>$\lambda$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.95</td>
<td>0.95</td>
</tr>
<tr>
<td>2</td>
<td>0.90</td>
<td>0.30</td>
</tr>
<tr>
<td>3</td>
<td>0.30</td>
<td>0.90</td>
</tr>
<tr>
<td>4</td>
<td>0.30</td>
<td>0.30</td>
</tr>
</tbody>
</table>

following values for the parameters determining the covariate process: $\eta = 0.6$, $\sigma = 1.2$ and $\gamma = 2$. For the initial (conditional) covariate distribution, associated with the first capture event, we used a normal with mean 15 and standard deviation 2. We assume a logistic link function for the survival probabilities regressed on the covariate values, with intercept $\beta_0 = -3$ and slope $\beta_1 = 0.2$. For this model the survival probability is 0.5 for $w_{t-1} = 15$ and greater than 0.9 for $w_{t-1} > 26$. The parameter values were chosen roughly similar to those estimated in the application to Soay sheep MRR data given in Bonner et al. (2010). In particular, a typical covariate time series starts at around 15 at the initial capture occasion, over the years approaches 25 and then fluctuates around that value. The deterministic trend $\alpha_t$ was included to enable us to conduct a simple check for robustness of our method to model misspecification (see below).

We here focus on the estimation of the parameters $\beta_0$ and $\beta_1$, and in each case give the following summary statistics: sample mean relative bias $((\hat{\beta}_i - \beta_i)/\beta_i)$, 2.5 and 97.5% quantiles of the relative bias, sample mean width of the estimated 95% confidence intervals and coverage probability of the confidence intervals. Confidence intervals were obtained based on the estimated Hessian matrix. For the HMM-based method we considered three different covariate process models in the simulation experiments: 1) the correctly specified model (i.e., the one that was used for simulating the data; denoted model HMM-C), 2) a slightly misspecified model which assumes a homogeneous AR(1) for the covariate process (i.e., one that neglects the deterministic sine-shaped component of the trend; model HMM-M1), and 3) a substantially misspecified model which assumes that at all ages (and across all individuals) the covariate is independently and identically normally distributed, with mean and standard error being estimated in the simulation experiments (model HMM-M2; this model neglects both trend components as well as the correlation over time). The latter two explore the robustness of our method to misspecification of the covariate process model. In the implementation of the HMM approach we used $m = 40$ intervals in the dis-
cretization of the covariate space, and the function `nlm` in R to maximize the approximate likelihood numerically. In the implementation of the trinomial approach we used the function `optim` in R instead, since `nlm` had problems in estimating the Hessian when \( p \) or \( \lambda \) are estimated at the boundaries of their support (which happens occasionally when using the trinomial method). Results are provided in Table 2.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Meth.</th>
<th>RB((\beta_0 = -3))</th>
<th>CW</th>
<th>CC</th>
<th>RB((\beta_1 = 0.2))</th>
<th>CW</th>
<th>CC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Tri</td>
<td>0.00(-0.23,0.22) 1.39 0.96</td>
<td>0.00(-0.20,0.20)</td>
<td>0.08 0.94</td>
<td>0.00(-0.24,0.23) 1.33 0.94</td>
<td>0.00(-0.19,0.21)</td>
<td>0.07 0.93</td>
</tr>
<tr>
<td></td>
<td>HMM-C</td>
<td>0.00(-0.24,0.23) 1.34 0.94</td>
<td>0.00(-0.18,0.21)</td>
<td>0.08 0.94</td>
<td>0.00(-0.24,0.22) 1.34 0.95</td>
<td>0.01(-0.19,0.21)</td>
<td>0.08 0.94</td>
</tr>
<tr>
<td></td>
<td>HMM-M1</td>
<td>-0.01(-0.24,0.22) 1.34 0.95</td>
<td>0.01(-0.19,0.21)</td>
<td>0.08 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>HMM-M2</td>
<td>-0.01(-0.24,0.22) 1.34 0.95</td>
<td>0.01(-0.19,0.21)</td>
<td>0.08 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Tri</td>
<td>0.00(-0.28,0.26) 1.60 0.95</td>
<td>0.00(-0.27,0.30)</td>
<td>0.12 0.95</td>
<td>0.00(-0.24,0.22) 1.37 0.95</td>
<td>0.00(-0.18,0.20)</td>
<td>0.08 0.95</td>
</tr>
<tr>
<td></td>
<td>HMM-C</td>
<td>0.00(-0.24,0.22) 1.37 0.95</td>
<td>0.00(-0.18,0.20)</td>
<td>0.08 0.95</td>
<td>0.00(-0.24,0.21) 1.38 0.96</td>
<td>0.00(-0.18,0.20)</td>
<td>0.08 0.95</td>
</tr>
<tr>
<td></td>
<td>HMM-M1</td>
<td>-0.03(-0.28,0.20) 1.41 0.95</td>
<td>0.02(-0.17,0.23)</td>
<td>0.08 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>HMM-M2</td>
<td>-0.03(-0.28,0.20) 1.41 0.95</td>
<td>0.02(-0.17,0.23)</td>
<td>0.08 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Tri</td>
<td>0.03(-0.52,0.34) 3.08 0.97</td>
<td>0.02(-0.26,0.35)</td>
<td>0.14 0.97</td>
<td>0.00(-0.26,0.24) 1.46 0.94</td>
<td>0.00(-0.21,0.22)</td>
<td>0.08 0.95</td>
</tr>
<tr>
<td></td>
<td>HMM-C</td>
<td>0.00(-0.26,0.24) 1.46 0.94</td>
<td>0.00(-0.21,0.22)</td>
<td>0.08 0.95</td>
<td>0.00(-0.27,0.26) 1.50 0.93</td>
<td>0.01(-0.21,0.24)</td>
<td>0.09 0.94</td>
</tr>
<tr>
<td></td>
<td>HMM-M1</td>
<td>-0.01(-0.28,0.28) 1.57 0.93</td>
<td>-0.01(-0.23,0.23)</td>
<td>0.09 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>HMM-M2</td>
<td>-0.03(-0.28,0.20) 1.41 0.95</td>
<td>0.02(-0.17,0.23)</td>
<td>0.08 0.94</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Tri</td>
<td>0.00(-0.58,0.60) 3.73 0.98</td>
<td>0.01(-0.45,0.57)</td>
<td>0.20 0.95</td>
<td>0.00(-0.30,0.32) 1.92 0.95</td>
<td>0.00(-0.26,0.25)</td>
<td>0.11 0.95</td>
</tr>
<tr>
<td></td>
<td>HMM-C</td>
<td>0.00(-0.30,0.32) 1.92 0.95</td>
<td>0.00(-0.26,0.25)</td>
<td>0.11 0.95</td>
<td>-0.01(-0.34,0.33) 2.01 0.95</td>
<td>0.02(-0.26,0.31)</td>
<td>0.11 0.95</td>
</tr>
<tr>
<td></td>
<td>HMM-M1</td>
<td>-0.09(-0.45,0.30) 2.20 0.92</td>
<td>0.09(-0.23,0.40)</td>
<td>0.13 0.92</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>HMM-M2</td>
<td>-0.09(-0.45,0.30) 2.20 0.92</td>
<td>0.09(-0.23,0.40)</td>
<td>0.13 0.92</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

In all four simulation scenarios, the interval estimates obtained using the HMM-based method were narrower than those obtained using the trinomial method, with the differences being substantial in Scenarios 3 and 4 (those with low capture probabilities). Using the HMM-based method, with both the correct specification (HMM-C) and with a slight misspecification (HMM-M1) of the model for the covariate process, no significant bias was found in the estimates of the logistic regression parameters (for each scenario). The experiment involving a substantial misspecification of the covariate process model (HMM-M2) led to a 9% negative bias in Scenario 4 (with both low capture and recovery probabilities), whereas in all other scenarios there still was only a small bias. In all considered settings, coverage probabilities of the interval estimates were close to 95%. We note that it is immediate to consider a model selection approach for the underlying covariate process, for
example using the AIC statistic. For the present simulation experiment, the correct underlying covariate model (model HMM-C) was deemed optimal by the AIC statistic in all 500 simulation runs (when compared to the models HMM-M1 and HMM-M2, respectively).

We conclude this section with some remarks on the computing times involved. On an octa-core i7 CPU, at 2.7 GHz and with 4 GB RAM, the simulation runs took, on average per run, 15, 18, 14 and 15 seconds for Scenarios 1, 2, 3 and 4, respectively, when applying the trinomial method, and 3, 15, 8 and 20 minutes for the same scenarios when applying the HMM method (with the correct model specification and $m = 40$). The computational effort is thus extremely low for the trinomial method, and modest for the HMM approach (for reasonable $m$). In case of the HMM approach, the computational effort is highly dependent on the desired accuracy of the likelihood approximation: e.g., in Scenario 3, the average computing time per simulation run is 2 minutes when using $m = 10$ intervals in the discretization, and 54 minutes when using $m = 150$.

4. Application to Soay sheep data. We consider capture histories for Soay sheep that were born and tagged on the Island of Hirta, off the west coast of Scotland, between 1985 and 2009, with the annual surveys being carried out in the summer. These sheep have been the subject in numerous studies on population dynamics, due to their isolated nature with no natural predators – Hirta was left by the last residents in 1932, after which the sheep established a wild population – and the ease with which individuals can be marked and recaptured. Annual studies involving, inter alia, captures, searches for dead animals, and weighings, are conducted. We consider only female sheep, with at least one recorded body mass, leading to a total of 1344 individual capture histories. The mean number of observations per sheep is 4.64, with a total of 900 sheep recovered dead during the observation period.

We assume that the survival probabilities are a function of body mass, noting that the primary cause of mortality is starvation, with the risk of dying from starvation being highest for young individuals. It is not the objective of the given analysis to perform a full investigation of the factors that affect the survival of the individuals. For details on the population dynamics of the Soay sheep we refer to Clutton-Brock and Pemberton (2004).

Not all observations are associated with the animal being physically captured, and thus for 38% of the observations the corresponding body mass was not recorded. Following Bonner et al. (2010), we consider four different age groups: lambs (age $< 1$), yearlings (age $\in [1, 2)$), adults (age $\in [2, 7)$) and seniors (age $\geq 7$). We assume a logistic relationship between the covariate
body mass and the survival probability, so that

\[ \logit (\phi_t) = \beta_{a_t,0} + \beta_{a_t,1} y_t. \]

For a given sheep, \( a_t \) indicates the age group the sheep is in at time \( t \) (lamb, yearling, adult or senior). We consider five different possible models in total, summarised as follows:

Model 1: \( y_t = y_{t-1} + \eta_{a_t} (\mu_{a_t} - y_{t-1}) + \sigma_{a_t} \epsilon_t \) (i.e., distinct covariate process parameters across age groups), time-dependent recapture probabilities, time-dependent recovery probabilities (68 parameters);
Model 2: \( y_t = y_{t-1} + \eta (\mu - y_{t-1}) + \sigma \epsilon_t \) (i.e., covariate process parameters fixed across age groups), time-dependent recapture probabilities, time-dependent recovery probabilities (59 parameters);
Model 3: Same covariate model as for Model 1, constant recapture probability, constant recovery probability (22 parameters);
Model 4: Same covariate model as for Model 1, constant recapture probability, time-dependent recovery probability (45 parameters);
Model 5: \( y_t = y_{t-1} + \mu_{a_t} + \sigma_{a_t} \epsilon_t \), time-dependent recapture probabilities, time-dependent recovery probabilities (64 parameters).

For each model, \( \epsilon_t \) denote independently and identically distributed standard normal random variables. Model 5 has a covariate process model similar to those used by Bonner and Schwarz (2006), King et al. (2008) and Bonner et al. (2010) (although, for example, Bonner et al., 2010, assume \( \mu \) not only depends on the age group of the sheep but also on the year and King et al., 2008, consider a further additive year effect). Notably, this covariate process model is diffusive and thus, in general, not biologically realistic (see later discussion).

Each of the models was fitted using the HMM-based approach using \( m = 50 \) intervals in the discretization. The assumed essential range of covariates values is given by \( b_0 = 0.8 b_{\text{min}} \) and \( b_m = 1.2 b_{\text{max}} \), where \( b_{\text{min}} \) and \( b_{\text{max}} \) denote the minimum and the maximum of the observed covariate values, respectively. For the given data, \( b_{\text{min}} = 2.9 \) and \( b_{\text{max}} = 33.9 \). For the initial covariate value we assumed a normal distribution, and estimated the corresponding mean and variance parameter alongside the other parameters. For the different models considered, the computing time ranged from 14 hours (for Model 3) to 45 hours (for Model 1); the computing times are much higher than those observed in the simulation experiments described in Section 3, which is primarily due to the high-dimensional parameter spaces associated with the models fitted to the real data. The AIC values obtained for the five different models described above are provided in Table 3. Clearly,
Table 3
Log-likelihood, number of parameters ($q$) and AIC values for different models, fitted to the Soay sheep data.

<table>
<thead>
<tr>
<th>Model</th>
<th>log $\mathcal{L}$</th>
<th>$q$</th>
<th>AIC</th>
<th>$\Delta$AIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model 1</td>
<td>-10221.85</td>
<td>70</td>
<td>20583.70</td>
<td>0</td>
</tr>
<tr>
<td>Model 2</td>
<td>-10350.66</td>
<td>61</td>
<td>20823.32</td>
<td>239.62</td>
</tr>
<tr>
<td>Model 3</td>
<td>-10309.28</td>
<td>24</td>
<td>20666.56</td>
<td>82.86</td>
</tr>
<tr>
<td>Model 4</td>
<td>-10260.68</td>
<td>47</td>
<td>20615.36</td>
<td>31.66</td>
</tr>
<tr>
<td>Model 5</td>
<td>-10404.45</td>
<td>66</td>
<td>20940.90</td>
<td>357.20</td>
</tr>
</tbody>
</table>

Model 1 is identified as optimal via the AIC statistic by quite a substantial margin.

Figure 1 displays the estimated year-dependent recapture and recovery probabilities for Model 1. The results generally match those of Bonner et al. (2010) well for the years common between the analyses (i.e., 1986-2000), except of in the initial two years. This mismatch appears to be related to the use of slightly different data: e.g., in our data set there are no recoveries in 1987, but Bonner et al. (2010) estimate a positive recovery probability in
that year. The variability over time in the recovery probabilities is considerably greater than for the recapture probabilities, which is also identified via the model selection procedure above (see ΔAIC values in Table 3).

Figure 2 displays the estimated survival probabilities for Model 1 for the different age groups, in each case as a function of body mass. Pointwise confidence intervals were obtained based on the Hessian (via the delta method). Again, the results are similar to those of Bonner et al. (2010). The survival probability increases with increasing body mass, with this effect found strongest for lambs and seniors, and weakest for adults. The interval estimates are slightly narrower than those obtained by Bonner et al. (2010), which is not surprising given that we consider a larger data set.

In Figure 3, the observed body masses of sheep at ages 0–12 are compared to the model-derived distributions of body masses (of alive sheep) for these ages. We omitted Models 3 and 4 since the covariate process model in these
models is identical to that of Model 1. Models 1 and 2 appear to capture the development of the body mass over the years. However, the diffusive nature of the covariate process in Model 5 leads to increasingly wider interval estimates for body mass as age increases, with the intervals not capturing well.
the observed quantiles. Thus, as already identified via the AIC statistic, it appears that the non-diffusive, auto-regressive type covariate process models are more appropriate in this application.

**Fig 4.** Approximation error arising from the discretization: differences between the estimates $\hat{\beta}_{3,1}^{(m)}$, $\hat{p}_{1994}^{(m)}$, and $\hat{\eta}_{3}^{(m)}$ (for given $m$, with $m = 10, 20, 30, 40, 50, 60, 80, 100$), respectively, and the corresponding estimates obtained for $m = 150$ ($\hat{\beta}_{3,1}^{(150)} = 0.122$; $\hat{p}_{1994}^{(150)} = 0.908$; $\hat{\eta}_{3}^{(150)} = 0.222$), and differences between the log-likelihood value for given $m$ and the log-likelihood value obtained using $m = 150$ ($\text{llk}^{(150)} = -10221.74$).

Finally, to investigate the effect of the choice of $m$, the number of intervals used in the numerical integration of the likelihood, we repeatedly ran the estimation of Model 1, for $m = 10, 20, 30, 40, 50, 60, 80, 100, 150$. Figure 4 illustrates, exemplarily, the convergence of the estimates $\hat{\beta}_{3,1}^{(m)}$, $\hat{p}_{1994}^{(m)}$, and $\hat{\eta}_{3}^{(m)}$ (with the superscript indicating their dependence on $m$) as $m$ increases, and also the convergence of the corresponding log-likelihood. In this application, $m = 50$ seems to provide a reasonable compromise between minimizing the computational effort and maximizing the accuracy of the numerical integration (although we note that even for $m = 20$ the estimates are close to those obtained for $m = 150$). Not surprisingly, the effect of the choice of $m$
is found to be strongest on the estimates of parameters that are related to
the covariate process (in our example: $\hat{\eta}_3^{(m)}$), and weakest on the estimates
of parameters related to the observation process (here: $\hat{p}_{1994}^{(m)}$).

5. Discussion. In recent years, several different methods have been
proposed that address MRR studies that involve individual-specific and
time-varying continuous covariates (see Catchpole et al., 2008, for a sum-
mary of these approaches). The most popular approaches for fitting models
to this type of data are the conditional trinomial method (Catchpole et al.,
2008) and the Bayesian imputation method (Bonner and Schwarz, 2006;
King et al., 2008, 2009; Schofield and Barker, 2011). The former method is
easy to implement, computationally fast and avoids assumptions concern-
ing the underlying model for the covariate process. However, it disregards
a potentially significant amount of information in the data, which can lead
to poor precision of the parameter estimates. Use of the trinomial approach
is not recommended if capture probabilities are low (Bonner et al., 2010)
or clearly if the underlying covariate process is of interest in itself. While
the Bayesian approach is much more computer intensive than the trinomial
method, it makes use of all available information in the data and thus usually
leads to an improved precision of the estimators (provided a correct specifi-
cation of the covariate process model). However, prior distributions need to
be specified on all model parameters, and model selection is generally more
difficult and potentially sensitive to the prior specification.

The proposed HMM-based method for estimating such MRR models is
based on a discretization of the space of covariate values, which reduces the
multiple integral appearing in the likelihood to a multiple sum. The resulting
multiple sum can efficiently be calculated by rewriting it as a matrix prod-
uct that corresponds to a recursive scheme for evaluating the (approximate)
likelihood. While the fitting is based on maximizing only an approximation
to the likelihood, it is very easy to make this approximation extremely accu-
rate (by considering increasingly finer discretizations of the covariate space),
while maintaining computational tractability in typical MRR settings. The
HMM method is fairly easy to implement and to apply (R code is provided in
Supplement A), and, once it is implemented, changes of the model structure
usually only require very minor and straightforward changes to the code,
making this method very user-friendly.

The simulation study demonstrated that if the covariate process is mod-
elled adequately, and even if the model is misspecified to some degree, then
the HMM-based approach leads to more precise estimates than does the
trinomial method. The difference in the precision is small if (and only if)
there are only few missing covariate values, and in such a case the trinomial method can be more attractive due to the extremely low computational effort it involves, and as it is implemented in the widely used software package MARK (Bonner, 2012). If, however, the covariate process is also of interest, then the HMM method has the additional advantage of allowing for formal (and simple) comparison between competing covariate process models (using standard information criteria). Model checking of the covariate process model can be performed by comparing the observed covariate values with those obtained from the fitted process model, for example using graphical means to assess a lack of model fit.

We applied the novel HMM-based approach to MRR data collected on female Soay sheep born between 1985 and 2009, investigating the effect of body mass on survival and comparing a variety of models for the change of the covariate body mass over time. Previous covariate process models that have been suggested for these type of data (including the Soay sheep) are typically of the form of diffusive random walks. For this application, an alternative non-diffusive AR(1)-type model appears to provide a significantly better fit, particularly at increasing age of the sheep (which is due to the model-derived variance of body mass diverging as age increases in case of the diffusive random walk). The AR(1)-type model is similar to, but more flexible than, the von Bertalanffy growth curve model (James, 1991), distinguishing between different age classes within which growth, or change of body mass (in the Soay sheep application), is homogeneous. We believe that this type of model has the potential to be very useful for analyzing growth-related dynamics. The results obtained showed an increasing survival probability with increasing body mass for each age group. The strongest effect was observed for lambs and seniors, and the weakest for adults, corresponding well to findings of previous studies (Bonner et al., 2010). This is biologically sensible with the youngest and the oldest sheep the “weakest” individuals and less able to compete for available resources. Recapture probabilities were estimated to vary only slightly over time, while the estimated recovery probabilities showed great variability over time. Further research involves the consideration of multiple covariates (see below) and different age-dependence structures to identify further biological structure.

The HMM-based approach can be extended in different ways. The extension to allow the observation model parameters to be dependent on the individual covariate is straightforward, with minimal additional computational effort – the only change that is required relates to the matrix comprising the state-dependent probabilities. A drawback of the HMM-based approach is that the computational effort increases dramatically if multiple...
continuous, individual-specific and time-varying covariates are considered, and in such cases a Bayesian approach will often be preferable. However, we anticipate that using more sophisticated numerical procedures in the likelihood approximation, such as, e.g., Gauss-Legendre, will at least render the case of two such covariates feasible even for relatively large MRR data sets. In general, it may also be worthwhile to consider alternative numerical approaches for evaluating the likelihood, such as, e.g., simulated maximum likelihood (which is often used in stochastic volatility modelling; see, e.g., Durbin and Koopman, 1997). Another extension that is straightforward in principle, but accompanied by large scale increases in computational time is that to models involving random effects (see, e.g., King et al., 2008, for an account in an MRR setting in a Bayesian framework, and Schliehe-Diecks et al., 2012, Langrock et al., 2012, for implementations of similar models in a non-Bayesian HMM framework in other ecological applications).

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SUPPLEMENTARY MATERIAL

Supplement A: R code for model fitting
(http://www.e-publications.org/ims/support/...). Sample R code for simulating MRR data and fitting the corresponding model using the HMM-based approach (with MRR model as described in Section 3).

References.
ML ESTIMATION FOR MRR DATA WITH CONTINUOUS COVARIATES


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