Integrated Continuous-time Hidden Markov Models

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Abstract

Motivated by applications in movement ecology, in this paper I propose a new class of integrated continuous-time hidden Markov models in which each observation depends on the underlying state of the process over the whole interval since the previous observation, not only on its current state. This class gives a new representation of a range of existing models, including some widely-applied switching diffusion models. I show that under appropriate conditioning, a model in this class can be regarded as a conventional hidden Markov model, enabling use of the Forward Algorithm for efficient evaluation of its likelihood without sampling of its state sequence. This leads to an algorithm for inference which is more efficient, and scales better with the number of data, than existing methods. Examples of applications to animal movement data are given, along with some related simulation experiments.

1 Introduction

The motivation for this paper comes from the analysis of animal movement data, arising for example from GPS tagging. This type of application has received a great deal of attention recently; see for example the review by Patterson et al. (2017). Typically the animal’s location $X(t)$ is observed at discrete, sometimes regular, instants in time $t_1, t_2, \ldots$. Conceptualisation of the process often involves an underlying behavioural state $S(t)$, with the
movement process switching between different forms depending on that behaviour. Hidden Markov Models (HMMs, defined in §2.1) have thus been widely used to model movement, with the ‘hidden’ state representing the behaviour. However, the desire to extend this approach to continuous-time modelling (e.g. Blackwell et al., 2016) has been limited by computational complexity, as the existing algorithms for HMMs do not immediately apply; see Patterson et al. (2017) for discussion. The aim of this paper is to show how to carry out fast, exact computation, with an algorithm closely related to the Forward Algorithm of a conventional HMM (see §2.1), for a broad class of continuous-time models, including many suitable for representing animal movement. Its use is illustrated in some real examples using telemetry data, and its performance compared with existing methods.

2 Existing classes of model

2.1 Hidden Markov Models

A Hidden Markov Model (HMM) is an unobserved discrete-time Markov chain \( \{ S_k \} \) accompanied by observations \( Y_k \), with the distribution of each observation determined by the corresponding value of the chain, so that

\[ Y_j \sim f_{S_j}(\cdot). \]

In the simplest case, the observations are conditionally independent given the chain. In a movement context, the ‘observation’ in this sense is some function of the sequence of observed locations, for example the displacement

\[ Y_j = X(t_j) - X(t_{j-1}). \]

HMMs are very widely studied and applied, and it is beyond the scope of the current work to review HMM modelling and methods for inference. However, one key factor in their wide adoption is the existence of a highly efficient algorithm, the Forward Algorithm, allowing the calculation of the probability of a sequence of observations by indirectly summing over all possible state sequences—a calculation that would be prohibitively expensive if carried out naïvely. See for example Zucchini and MacDonald (2009) for general background, and Michelot et al. (2016) for specific applications to discrete-time models of animal movement.

2.2 Continuous-time Hidden Markov Models

A continuous-time Hidden Markov Model is an unobserved continuous-time Markov chain \( \{ S(t) \} \) accompanied by conditionally independent observations
\(Y_{t_1}, Y_{t_2}, \ldots\) with distributions determined by the values of the chain at a countable set of times, so that

\[Y_{t_i} \sim f_{S(t_i)}(\cdot).\]

For examples in medical contexts, see Jackson and Sharples (2002); Liu et al. (2017). This case can be handled using broadly the same inferential methods as a standard HMM, with the form of the transition matrices dependent on the time intervals \(t_i - t_{i-1}\), and subject to some constraints even if the observations are equally spaced (since not every discrete-time Markov chain can be expressed as a restriction of any continuous-time Markov chain to equally-spaced times). Note that this model has what is known as the ‘snapshot’ property: the distribution of the observation \(Y_{t_i}\) depends only on the state at the same instant, \(S(t_i)\), and conditional on \(S(t_i)\) is independent of \(S(t), t \neq t_i\).

Thinking about movement in continuous time, an animal’s location \(X(t_i)\) naturally depends on its behaviour between \(t_{i-1}\) and \(t_i\); that is, \(X(t_i)\) depends both on \(X(t_{i-1})\) and on the whole of \(\{S(t), t_{i-1} < t < t_i\}\), as discussed by Patterson et al. (2017, §4.4). The process does not have the ‘snapshot’ property and as a consequence, cannot be represented as a continuous-time Hidden Markov Model in the sense defined above. The computational approach—in particular, the Forward Algorithm—that gives such power to the usual HMM does not immediately apply.

### 3 Integrated continuous-time Hidden Markov Models

For more flexible modelling, it is useful to consider a Markov process \(Z(t) = (X(t), S(t))\) on \(\mathcal{X} \times S\), where \(S\) is discrete. If either (a) \(\mathcal{X}\) is continuous and regularity conditions given by Berman (1994) are satisfied, or (b) \(\mathcal{X}\) is discrete, then \(S(t)\) is piecewise constant over time, with transition rates \(\lambda_{ij}(t, x), i, j \in S\) say.

I define an integrated continuous-time Hidden Markov Model (InCH) to be a Markov process \(Z(t)\) as above, satisfying one of the conditions (a) and (b), with rates \(\lambda_{ij}(t, x)\) that are bounded. In general, it lacks the snapshot property defined in §2.2 since the way \(X(t)\) is changing depends on \(S(t)\). This class includes a wide range of existing models; the reason for formulating them in this particular way is the potential improvement in computational efficiency permitted if these conditions are met, as described in §4.3.

In a movement context, often \(\mathcal{X}\) will be continuous. In particular, the separable switching diffusion models of Blackwell et al. (2016) can be thought
of as InCH models on $\mathbb{R}^d \times \{1, \ldots, n\}$. Usually we will be interested in $d = 2$, but cases with $d = 1$ and $d = 3$ arise naturally. Related applications involving multiple animals lead to higher values of $d$; see Niu et al. (2016).

It is useful to distinguish some particular cases. An InCH is **spatially homogeneous** if $\lambda_{ij}(t, x)$ is independent of $x$; otherwise it is **spatially heterogeneous**. Of course, $X(t)$ need not represent geographical space, but the terminology is appropriate to many applications, and makes the necessary distinction from time-homogeneity.

In the next section, I show how to carry out computation using ideas closely related to the conventional HMM or the ‘snapshot’ case, for both spatially heterogeneous and spatially homogeneous InCH models. While the applications are certainly not limited to animal movement, it is convenient to use the terms ‘location’ and ‘behaviour’ to refer to the components of a process $Z$. Similarly, while models with discrete $X$ are certainly possible, the particular interest here is in continuous $X$, and I will refer to the density of $X$, for simplicity.

4 Representation and Algorithms

4.1 Uniformization

Consider an InCH process with transition rates $\lambda_{ij}(t, x)$. Let $\lambda_i(t, x) = \sum_{j \neq i} \lambda_{ij}(t, x)$ represent the rate of switching out of behaviour $i$, at time $t$, when at location $x$, and let $\kappa$ be an upper bound so that $\kappa \geq \lambda_i(t, x) \forall i, t, x$. Then, following Blackwell et al. (2016), the occurrences of changes in behaviour can be represented as a dynamic thinning of a Poisson process of potential switches of uniform rate $\kappa$, with retention probability

$$\lambda_{S(t)}(t, X(t))/\kappa.$$

The unthinned Poisson process of potential switches does not depend on $t$ and $x$, enabling us to partially separate location and behaviour in a way that turns out to be crucial for inference.

If the $\lambda_{ij}(t, x)$ are known, for example if we are interested purely in simulating a known process, then we can simply take $\kappa = \sup_{i, t, x} \{\lambda_i(t, x)\}$. In the more general inference context, the most straightforward case, for both exposition and implementation, is when the prior support of $\lambda_{ij}(t, x)$ is bounded above by $u_{ij}(t, x)$, with the function $u_{ij}(t, x)$ also bounded above. We can then define $u_i(t, x) = \sum_{j \neq i} u_{ij}(t, x)$ and take $\kappa = \sup_{i, t, x} \{u_i(t, x)\}$. This is the approach taken in §6 and §7. If the priors are not all bounded above,
then $\kappa$ is not fixed, and must be sampled in the inference process—see the discussion in §8.

In the spatially homogeneous case, the behaviour process can be thought of as a Markov chain on $\mathcal{S}$ subordinated to a Poisson($\kappa$) process i.e. a continuous-time Markov chain in which some ‘events’ do not change the state of the process.

Rao and Teh (2013) make use of the idea of uniformization, in the context of inference for a continuous-time Markov chain, and give additional background on the concept, including a proof (in the time-homogeneous case) of the representation described above.

4.2 Existing inference methods

For discrete-time HMMs, ‘snapshot’ continuous-time HMMs and continuous-time Markov chains, a range of efficient algorithms for inference are available, as already indicated. Here, I focus on existing methods specific to switching diffusions and similar models, for comparison with the new methods in §4.3 below.

Blackwell et al. (2016) make use of the uniformization representation in §4.1, with a Markov chain Monte Carlo (MCMC) algorithm that relies on forward simulation of the model between potential switches, sampling not only the times of the potential switches but also the locations and states at those times. This enables exact inference, in the sense that there is no time discretisation or approximation, and so the limiting distribution for the chain is exactly the joint posterior distribution of trajectories and parameters. It is widely applicable because of the flexibility in specifying the transition rates. However, because the state space for the MCMC algorithm includes the behaviour not only at the observation times but also at the unknown collection of potential switching times, the algorithm is computationally demanding and mixes relatively slowly.

In the spatially heterogeneous case, more efficient updates that do not rely purely on forward simulation are possible, by proposing locations and states in a more general way. For example, it is possible to propose a reconstruction of part of the behaviour sequence without reference to the locations, from a (spatially homogeneous) continuous-time Markov chain, conditioning only on the behaviour at the start and end of the interval being updated, and then propose corresponding locations, given the behaviour, from the movement process conditioned to give the appropriate time-inhomogeneous bridge; the acceptance probability then accounts for the difference between the true behaviour process and the proposal distribution. Alternatively, locations can be proposed at potential switching times using some time-homogeneous bridge
process, and then behaviours proposed from the true behaviour process given
the locations; again, the acceptance probability can account for the differ-
ence between the true and proposal movement processes. Experimentation
suggests that these algorithms can be worthwhile in particular cases; how-
ever, for most purposes they are likely to be superseded by the algorithms
introduced in §4.3 below.

In the spatially homogeneous case of Blackwell (1997), where tran-
sition rates do not depend on location, behavioural trajectories \( S(\cdot) \) can be sampled
within an MCMC algorithm without sampling the locations \( X(\cdot) \) associated
with the transitions. This kind of algorithm, as detailed in Blackwell (2003),
does not use uniformization, nor would it particularly benefit from it. How-
ever, the algorithms of the next section offer great benefits in efficiency in
this homogeneous case too, and do rely on uniformization, combined with
some additional simplification that exploits the homogeneity.

### 4.3 The InCH approach

A much more efficient inferential approach can be developed by exploiting the
fact that, conditional on the times and locations corresponding to potential
switches, an InCH process is effectively a time-inhomogeneous version of a
conventional discrete-time HMM, defined at the potential switching times,
in which the transition probabilities are given by

\[
p_{ij}(t, x) = \frac{\lambda_{ij}(t, x)}{\kappa}, \quad i \neq j
\]

\[
p_{ii}(t, x) = 1 - \frac{\lambda_i(t, x)}{\kappa},
\]

and the ‘observations’ are given by the changes in location, with

\[
f(X(t_{k+1})|t_k, X(t_k), S(t_k))
\]

given by the density of the movement process corresponding to behaviour
\( S(t_k) \)

\[
f_{S(t_k)}(X(t_{k+1})|t_k, X(t_k)).
\]

This differs from a typical HMM in that the transition probabilities and
observation densities are highly variable between time points. Nevertheless,
the standard Forward Algorithm that enables evaluation of the likelihood for
an HMM without the need for explicit sampling of the states still applies
here, and will enable the calculation of the likelihood for this model very
efficiently.

Of course, the times of potential switches are not known, and the corre-
sponding locations are not observed. Instead, we observe the locations (and
not the behavioural states, generally) at a set of known times, which may or may not be regularly spaced. Thus in practice we need to embed the evaluation of the likelihood using the Forward Algorithm within an MCMC algorithm; but that algorithm now has a much lower-dimensional state space, not involving the behavioural states which are now ‘integrated’ out.

The method of [Rao and Teh (2013)] has some similarities. They are primarily interested in the continuous-time Markov chain (or Markov Jump Process, in their terminology) itself, and do not integrate it out; instead they use the Forward Algorithm to permit fast updating of a part of the realisation of the chain.

The details of the InCH approach are given in the two following sections, which deal separately with the spatially heterogeneous and homogeneous cases. The former is easier to describe, and so is given first; the latter permits the integration out of locations, for further improvement in efficiency where applicable.

### 4.4 Spatially heterogeneous case

Here we need to consider an HMM defined at a set of times which is the union of the potential switching times, at which the transition matrix is defined as above in §4.3, and the observation times, at which (with probability 1) no change in state occurs and so the transition matrix is just the identity matrix $I_n$. Spatial locations at the potential switching times need to be sampled within an MCMC algorithm, but the states do not.

Write $t_c$ for the $c$th observation time, and $t_{c,k}$ for the $k$th potential switching time between $t_c$ and $t_{c+1}$, for $k = 1, \ldots, M_c$. Of course, for any given $c$, $M_c$ may be zero.

An outline of the key step in the new MCMC algorithm is as follows. Choose $a, b$ such that $1 \leq a < b \leq n_{obs}$. Propose new times and locations $t_{c,k}'$ and $x(t_{c,k}')$, for $k = 1, \ldots, M_c', c = a, \ldots, b - 1$. Evaluate the Hastings ratio based on likelihoods that integrate over all state sequences, replacing $t_{c,k}, x(t_{c,k})$ with $t_{c,k}', x(t_{c,k}')$, and accept or reject accordingly.

We could choose new values $X(t_{c,k}')$ independently of $X(t_{c,k})$, for simplicity, or close to $X(t_{c,k})$, to allow ‘small’ steps that retain the information in $X(t_{c,k})$. That is, we could take either an independence sampling or a random walk approach. For maximum flexibility, we formulate the proposals as a mixture of these two extremes.

In more detail, we propose $t_{c,k}'$ and $X(t_{c,k}')$ for a given $c$ as follows. $M_c'$ is proposed independently of $M_c$, with $M_c' \sim \text{Poisson}((t_{c+1} - t_c)\kappa)$, and $t_{c,k}'$ are defined as the order statistics of $M_c'$ independent uniform r.v.s on $(t_c, t_{c+1})$. We define $\mu_1, \Sigma_1$ as the mean and covariance respectively of a Brownian bridge
with diffusion parameter $\omega$ from $X(t_c)$ to $X(t_{c+1})$, evaluated at times $t'_{c,k}$, $k = 1, \ldots, M'_c$, corresponding to the idea of an independent proposal. Similarly we write $\mu_D, \Sigma_D$ for the mean and covariance of a series of Brownian bridges with diffusion parameter $\omega$ passing through $X(t_c), X(t_{c,1}), \ldots, X(t_{c,M_c}), X(t_{c+1})$, again evaluated at $t'_{c,k}$, $k = 1, \ldots, M'_c$. We propose new locations from a weighted mixture of these bridges,

$$X(t'_{c,1}), \ldots, X(t'_{c,M'_c}) \sim \text{Normal}(p\mu_1 + (1 - p)\mu_D, p^2\Sigma_1 + (1 - p)^2\Sigma_D).$$

Both $\omega$ and $p$ are effectively tuning parameters. The Hastings ratio has the usual form, with the likelihood terms being evaluated using the Forward Algorithm, and the proposal densities in each direction coming from joint densities of the sampled locations from the weighted mixtures of Brownian bridges.

### 4.5 Spatially homogeneous case

In the special case where the InCH process is spatially homogeneous and the movement processes are solutions to a linear stochastic differential equation (SDE), we can completely avoid the need to sample the locations $x(t_{c,k})$, integrating them out using a matrix calculation which can be thought of as a special case of Kalman Filtering. As discussed at length elsewhere [Blackwell (1997, 2003); Blackwell et al. (2016)], models where the movement process for each state is defined by a linear SDE can lead to surprisingly rich behaviour, so this case is of practical importance. In particular, even the case where movement simply switches between different speeds of Brownian motion is important in data analysis; see Kranstauber et al. (2012) and the example in §7.2.

Spatially homogeneous but non-linear models are not explicitly considered in this paper; one straightforward option would be to apply the ‘heterogeneous’ methods above, but the example from Parton and Blackwell (2017) of continuous-time step-and-turn models suggests that a more efficient compromise ought to be possible.

Spatial homogeneity means that the transition probabilities of the uniform chain do not depend on the locations at the potential switching times, and linearity implies that for any given sequence of behaviours, movement densities can be calculated explicitly even over time intervals that incorporate changes in behaviour.

For particular states $i$ and $j$ at times $t_c$ and $t_{c+1}$, with potential switching times

$$T_c = t_{c,1}, \ldots, t_{c,M_c},$$

we have

$$X(t'_{c,1}), \ldots, X(t'_{c,M'_c}) \sim \text{Normal}(p\mu_1 + (1 - p)\mu_D, p^2\Sigma_1 + (1 - p)^2\Sigma_D).$$
we have
\[ f_{ij}(x(t_{c+1})|x(t_c), T_c) = \sum_s \pi_{ij}(s) \phi_{ij}(x(t_{c+1})|x(t_c), T_c, s) \]

where
\[ s = (s_1, \ldots, s_{M_c-1}) \]
is a possible sequence of states entered at times \( t_{c,1}, \ldots, t_{c,M_c-1} \),
\[ \pi_{ij}(s) = p_{i,s_1} \cdots p_{s_{M_c-1},j}, \]
each \( p_{i,j} \) is a transition probability as derived in §4.3, and \( \phi_{ij}(\cdot|\cdot) \) is the transition density conditional on the sequence and timing of states. In general, \( \phi_{ij}(\cdot|\cdot) \) can be calculated as a density from a \( d \)-dimensional normal distribution with parameters calculated recursively as in §3.3 of Blackwell (2003). See §7.2 below for a special case.

This summation over sequences of states is, of course, exactly the kind of calculation that the HMM Forward Algorithm is designed to avoid, because its computational cost increases rapidly with the number of time points. As a brute-force way of calculating the likelihood globally, it would be impractical because it scales so badly with the size of the data-set. As used here however, for calculation of the likelihood locally between successive observations, it is feasible provided \( \kappa \) is not too large, which will be true in cases where the data are reasonably informative about the model.

5 Implementation

In each of the examples below, I chose to fix \( \kappa \) so that \( \kappa \delta t = 1 \) for the typical interval between observations. This ensures that for such an interval, the probabilities of 0, 1 or 2 potential switches are not too small (approximately 0.368, 0.368, 0.184 respectively), permitting visits to a behaviour to have a chance of being represented even if they do not span an observation.

All runs were carried out on the same low-specification desk-top PC (2.90 GHz, 8.0GB), run for 100,000 iterations with burn-in of 10,000 iterations and thinning by a factor of 100. The various tuning parameters, such as proposal variances for the Metropolis-Hastings steps, were optimised after Latin hypercube sampling, with 5 replicates at each sampled point.

Coding is in R (R Core Team, 2017), for ease of development, and there is in all cases scope for improvement by re-writing in a fully-compiled language. Relative speeds are therefore much more informative than absolute speeds.

Effective sample size was calculated using the package Coda (Plummer et al., 2006), minimizing over the unknown parameters and, where applicable, over
the index of the observation times for which behavioural states were sampled. This minimum effective sample size was compared with the running time required, to give an effective sample size per second.

6 Example—heterogeneous case

6.1 Data

As a small-scale example, I use irregular data consisting of 71 GPS relocations at approximately 4-hour intervals of an ibex in the Belledonne mountain in the French Alps, originating with the French Office national de la chasse et de la faune sauvage and made available in the ADEhabitatLT package (Calenge, 2006) for R. The majority of the intervals between observations were around 4 hours, plus or minus 90 seconds, but there were some ‘missing values’ leading to eight intervals of around 8 hours, one of 12 hours, and one of 16 hours.

6.2 Model

The model fitted was a two-state switching diffusion based on a division of the space into two regions, inside and outside a circular boundary. The boundary is intended as a simple representation of the animal’s home range; its behaviour switches at some finite rate to ‘match’ its location, inside or outside the boundary. The movement processes for the two states are Ornstein-Uhlenbeck processes (Dunn and Gipson, 1977; Blackwell, 1997; Blackwell et al., 2016) with a common centre of attraction. The boundary is taken to be known and fixed; this gives an adaptive model, in the sense of Blackwell et al. (2016). Estimation of the boundary is possible within the MCMC part of the algorithm, and is tackled by Tishkovskaya and Blackwell (in prep.) and also Alkhezi (2019), but omitted here for simplicity.

6.3 Comparison of methods

This adaptive model can be fitted exactly using the algorithm of Blackwell et al. (2016), sampling potential switching times, corresponding locations, and the full behavioural trajectory. It can also be fitted using the InCH approach introduced in §4.4, obviating the need to sample the behaviours. In each case I took $\kappa = 0.25$.

The algorithm of Blackwell et al. (2016) mixes rather poorly, because the space to be explored by the MCMC includes the complete state trajectory
at the potential switching times, behaviours as well as locations. The runs reported here, five replicates of 100,000 iteration as described in \S \ref{5}, give effective samples sizes in some cases too small for definitive analysis, but sufficient for comparison with the new approach.

6.4 Results—real data

Fitting the two-state adaptive model with fixed boundary, using the state-sampling algorithm of \cite{blackwell2016}, five replicates of $10^5$ iterations with the optimal tuning parameters took 933.3s and gave an effective sample size of 23.5, equivalent to 0.0252 samples per second. Using the InCH approach, the corresponding running time was 2368.1s, for an effective sample size of 383.4, giving 0.136/s. In this small heterogeneous example, the InCH approach is around 5.4 times as efficient as the original ‘exact’ algorithm—and of course remains exact in the same sense.

6.5 Results—simulated data

Using the point estimates from the analysis in \S \ref{6.4}, I simulated a larger data-set of 201 observations at 4 hour intervals (so approximately three times the size of the real data). I analysed these simulated data in the same way as before, re-running the Latin hypercube tuning since a larger data-set changes the trade-off between running time, acceptance rate and mixing.

The method of \cite{blackwell2016} took 958.0s for an effective sample size of only 10.31, giving a sampling rate of 0.0108 per second. The InCH approach took 3386.2s for an effective sample size of 458.6, giving a sampling rate of 0.135 per second.

Both these results are better than might be expected, since the time taken per effective sample increases more slowly than the amount of data—and hardly at all in the InCH case. Initial investigations suggest that this is due to the increased regularity in the simulated data, which for simplicity were simulated at regular intervals within no missing data. The few larger intervals in the real data impose a disproportionate computational cost, in both algorithms.

For this case, the InCH approach is around 12 times as efficient as the original algorithm.
7 Example—homogeneous case

7.1 Data
As an example, I consider a small data-set of two-dimensional GPS locations for a kinkajou (Potos flavus), taken from the Movebank Repository (Kays and Hirsch, 2015). The data-set consists of 61 fixes, mostly of intervals of 9 and 11 minutes but with a few missing values leading to intervals of 20 to 30 minutes.

7.2 Model
The model fitted is a simple InCH process, with \( n \) different states each involving isotropic Brownian motion on \( \mathbb{R}^2 \) with a different speed (i.e. diffusion parameter) \( v_l, l = 1, \ldots, n \), in increasing order to avoid label switching.

In this case, the calculation of transition densities between observations, given in §4.5, has a particularly simple form. For particular states \( i \) and \( j \) at times \( t_c \) and \( t_{c+1} \), \( \phi_{ij}(X(t_{c+1})|X(t_c), T_c, s) \) in the notation of §4.5 is specified by

\[
X(t_{c+1})|X(t_c), T_c, s \sim N(0, v_{ij}(X(t_c), T_c, s)I_2)
\]

where

\[
v_{ij}(X(t_c), T_c, s) = (t_{c,1} - t_c)v_i + \sum_{k=1}^{M_c-1} (t_{c,k+1} - t_{c,k})v_{sk} + (t_{c+1} - t_{c,m_c})v_j,
\]

that is, the appropriately time-weighted average of the diffusion parameters in different states, and \( I_2 \) is the \( 2 \times 2 \) identity matrix.

All runs reported here have \( n = 3 \).

7.3 Comparison of methods
The model being fitted is spatially homogeneous, so the method of §4.5 is appropriate here. For comparison, the same model could be fitted using the forward simulation method of Blackwell et al. (2016), which is the origin of the thinned Poisson representation. The method there does not exploit HMM computational methods, but instead tracks the whole state trajectory as part of its MCMC algorithm, re-sampling a part of it at each iteration. Since the ‘full data’ likelihood conditional on a complete trajectory for the states can be calculated more easily than the ‘integrated’ likelihood of §4.5, the algorithm of Blackwell et al. (2016) runs more quickly. However, it mixes much less well, because the space to be explored by the MCMC includes the
complete state trajectory at the potential switching times, both behaviours and locations. This comparison is arguably unfair, however, as the existing algorithm does not exploit the spatial homogeneity of the model or the simplification described in §7.2. Instead, therefore, performance is shown for a version in which the behavioural sequence is sampled, and the simplification of §7.2 is applied. This is essentially the algorithm applied by Blackwell (2003), in the particular case where all movement processes are versions of Brownian motion, representing the state of the art for an exact analysis in the spatially homogeneous case, and therefore a fairer comparison.

7.4 Results—real data

Firstly, results are shown for the analysis of the small data-set of 61 observations. The results support a 3-state model as being plausible, but the key point of interest here is computational performance, compared for the existing and proposed algorithms.

Using the homogeneous version of the existing algorithm, as described above, five replicates of $10^5$ iterations took 753.9s. The effective sample size was 481.5, giving 0.639 samples per second.

Regarding the model as an InCH and using the Forward Algorithm to calculate the likelihood, five replicates of $10^5$ iterations took 1185.6s and produced an effective sample size of 1381.5, giving 1.17/s. For this small sample, the InCH approach is around 1.8 times as efficient as the existing approach.

7.5 Results—simulated data

The real strength of the InCH approach is that its efficiency scales better with the size of the data-set than existing methods. To illustrate this, I simulated data from the estimated parameters in §7.4 to obtain 301 observations (i.e. simulating an observation period 5 times longer than the data used in §7.4) and then analysed them in the same way as before. Note that values of the tuning parameters differ between the two data-sets, based on separate Latin hypercube optimization.

With the existing algorithm, five replicates of $10^5$ iterations took 1327.1s, so the running time is only around 1.8 times as long as for the smaller data-set. This is because much of the computational effort goes on localised updates to the behavioural sequence, for which only part of the likelihood needs to be evaluated. However, the effective sample size is only 27.4, giving a sampling rate of 0.0207/s.
The InCH approach ran five replicates of $10^5$ iterations in 4228.3s, about 3.6 times as long as for the small data-set. It gave an effective sample size of 592.6, decreasing much more slowly than was the case for the existing method. This is because the dimension of the space over which the MCMC algorithm is sampling is not increasing with size of the data-set, so mixing does not degrade so quickly. It does still decrease to some extent, because the optimal proportion of the Poisson $\kappa$ process to resample at each iteration (estimated through the Latin hypercube experiments) is decreasing. The net rate of generating independent samples is 0.140/s, so for this data-set the InCH approach is around 6.8 times as efficient as the existing method.

8 Discussion

8.1 Summary of results

I have shown that, while standard HMM techniques do not apply directly to continuous-time movement models, a very broad class of such models can be be seen as HMMs after conditioning on the Poisson process of potential times of behavioral change. This can be exploited within an MCMC algorithm as a highly efficient way of evaluating likelihood for these models without sampling the behavioural states, resulting in much improved mixing. In an example, the scaling of computational performance with the size of data-set is shown to be much better in the new approach than in existing methods. Thus, it is possible to extend the key benefit of the HMM approach to realistic continuous-time models.

8.2 Extensions

For definiteness of exposition, the models and algorithms above make a number of assumptions that are not in fact essential.

I have assumed that behaviour is not observed at all, which is the most common case—though Blackwell (2003) addresses the opposite case. Increasingly, partial information about behaviour is available, either through direct observation or through other kinds of telemetry such as accelerometry. The methods above can incorporate this extra information readily, by adding an extra term in the calculation of the likelihood at the time of the observation.

As is widespread in movement analysis, including discrete-time HMMs, I have neglected GPS measurement error above. However, it can be readily incorporated by including extra variables in the state of the MCMC chain, representing the true, rather than observed, location at the time of each GPS
As mentioned above, it is conceptually simplest to keep the rate $\kappa$ of potential switches as a constant. However, that requires the prior distributions for the rates $\lambda_i(\cdot)$ to be bounded above. An alternative is to allow $\kappa$ to be data-driven, via the $\lambda_{ij}(\cdot)$s. Some care is needed, since $\kappa$ is not really a parameter but rather a computational device (for example, increasing $\kappa$ does not change the model at all, though it slows the calculation), but Alkhezi and Blackwell (in prep.) show one successful approach.

Finally, it may be desirable to allow behavioural switching to depend on the length of time already spent in the current state, as well as the absolute time and other covariates, as a kind of semi-Markov extension. Again, this can be done readily either by simply incorporating this elapsed time as an argument to $\lambda_{ij}(\cdot)$, which complicates the computation somewhat, or by extending the state space; see Alkhezi and Blackwell (in prep.) for details.

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