ON ESTIMATION FOR BROWNIAN MOTION GOVERNED BY TELEGRAPH PROCESS WITH MULTIPLE OFF STATES

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ABSTRACT. Brownian motion whose infinitesimal variance changes according to a three-state continuous time Markov Chain is studied. This Markov Chain can be viewed as a telegraph process with one on state and two off states. We first derive the distribution of occupation time of the on state. Then the result is used to develop a likelihood estimation procedure when the stochastic process at hand is observed at discrete, possibly irregularly spaced time points. The likelihood function is evaluated with the forward algorithm in the general framework of hidden Markov models. The analytic results are confirmed with simulation studies. The estimation procedure is applied to analyze the position data from a mountain lion.

KEYWORDS: Forward algorithm, Likelihood estimation, Markov process, Occupation time

1. INTRODUCTION

Random walks on a plane, whether simple, biased, or correlated, have a long history of being employed by ecologists to model the movement of animals, micro-organisms, and cells on a small time scale. By the functional Central Limit Theorem, from an appropriate distance any random walk (under some mild regularity conditions) looks like a Brownian Motion (BM). So, it is not

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surprising that recently diffusions are often used to model animal movement on a large time scale (e.g., Preisler et al., 2004; Tilles and Petrovskii, 2016). An excellent review on applications of random walks and diffusions in this area of research can be found in Codling et al. (2008).

Horne et al. (2007) introduced the Brownian bridge movement model (BBMM) that, in essence, assumes that animal movement is perpetual and described by a BM. Pauses in animal movement (on a small time scale) were first introduced in Othmer et al. (1988) where the dispersal of cells or organisms is modeled by a process that comprises a sequence of alternating pauses and jumps. The moving-resting process introduced in Yan et al. (2014) and further investigated in Pozdnyakov et al. (2017) allows an animal to have two states, moving and resting. In the moving state, the motion is characterized by a BM; in the resting state, there is no movement. The duration in either moving or resting states is assumed to be exponentially distributed.

Properties and fitting of the moving-resting model are based on results for telegraph processes (the alternating renewal process or the on-off process) that were obtained in Perry et al. (1999), Di Crescenzo (2001), Stadje and Zacks (2004), and Zacks (2004). The distribution of total time spent in a state plays a critical role in applications driven by a telegraph process (Zacks, 2012). In particular, a BM governed by a telegraph process is an active area of research such as being recently employed in continuous-time option pricing theory (e.g., Di Crescenzo and Pellerey, 2002; Kolesnik and Ratanov, 2013; Di Crescenzo et al., 2014; Di Crescenzo and Zacks, 2015).

In animal movement ecology, it is reasonable to assume that there are very different explanations for why a predator is not moving. For example, an animal might spend time resting (as in Yan et al. (2014)), consuming a prey item, or denning. Resting can be assumed to not last even a single day. However, some predators that can kill a (relatively) large prey item evolved highly elastic guts, and they consume the kill by repeatedly gorging and digesting over a prolonged period called handling. For example, mountain lions (Puma concolor) might remain at a kill for days. Both resting and handling are periodic in the time scales of this model but denning is not, and it is inapplicable to
male mountain lions in any case. Therefore, this model concerns only two non-moving activities, resting and handling, and it is clear that their durations must be different.

This observation motivates our model. In the new model we have one moving state and two motionless states. From a motionless state one always switches to the moving state. Nonetheless, when moving ends, the motionless state type is chosen randomly. For tractability, all the durations (or holding times) are exponentially distributed. We will call this continuous-time process a moving-resting-handling process, or MRH process. An extension of the telegraph process to an alternating process with three states is studied in Bshouty et al. (2012). The difference is that in Bshouty et al. (2012) three states alternate deterministically within a renewal cycle. In our case we have only two states within a renewal cycle but one of the motionless states is chosen at random.

In practice, a MRH process is typically observed at discrete, possibly irregularly spaced time points. Estimation of MRH process parameters is challenging because the states are unobserved, and the observed sequence is not Markov. Our estimation procedure uses techniques developed for the hidden Markov model (HMM). More specifically, the dynamic programming, or the forward algorithm, for HMM is employed to construct the true likelihood (e.g. Cappé et al., 2005). As will be seen, the key to this problem is the distribution of the time that the MRH process spends in the moving state. Our methodology differs from the standard approach to occupation time distribution in continuous-time Markov chain (Sericola, 2000). The method is general so that it remains valid when the holding times are not exponentially distributed, in which case, the state process is semi-Markov; see discussion in Section 9. An implementation of the methods in this paper is publicly available in R package smam (Yan and Pozdnyakov, 2016).
2. Formal Description of MRH Process

Let $S(t)$, $t \geq 0$, be a continuous-time Markov Chain with the state space $\{0,1,2\}$ and the transition rate matrix

$$Q = \begin{pmatrix} -\lambda_0 & \lambda_0 p_1 & \lambda_0 p_2 \\ \lambda_1 & -\lambda_1 & 0 \\ \lambda_2 & 0 & -\lambda_2 \end{pmatrix}$$

where $p_1, p_2, \lambda_0, \lambda_1, \lambda_2 > 0$ and $p_1 + p_2 = 1$. The zero entries in the matrix mean that state 1 or state 2 do not transit between themselves; only a transition to state 0 is allowed from either of them. In animal movement modeling, the mean duration in state 0, 1, and 2 are, respectively, $1/\lambda_0$, $1/\lambda_1$, and $1/\lambda_2$. We assume that the initial distribution $\nu_0$ of $S(0)$ is stationary, that is,

$$\nu_0 = \pi = (\pi_0, \pi_1, \pi_2) = \frac{1}{1/\lambda_0 + p_1/\lambda_1 + p_2/\lambda_2} \left( \frac{1}{\lambda_0}, \frac{p_1}{\lambda_1}, \frac{p_2}{\lambda_2} \right).$$

Recall that $\pi$ has to satisfy $0 = \pi Q$.

Let $B(t)$ be the standard BM independent of $S(t)$. Then the MRH process is given by

$$X(t) = \sigma \int_0^t 1_{\{S(s)=0\}} dB(s),$$

where $\sigma > 0$ is an infinitesimal standard deviation.

Estimation of the MRH process parameters $\theta = (\lambda_0, \lambda_1, \lambda_2, p_1, \sigma)$ is based on observations at discrete, possibly irregularly spaced time points. The observed data are represented by the vector of observed changes in location

$$X = (X(t_1) - X(0), X(t_2) - X(t_1), \ldots, X(t_n) - X(t_{n-1})), $$

where $0 < t_1 < \cdots < t_n$ are the time points of the observations. As mentioned earlier, the difficulty is that the MRH process itself is not Markov. However, the location-state process $\{X(t), S(t)\}$ is
Markov. So, our first objective is to derive formulas for transitional probabilities of the location-state process. The key random variable here is the total time spent in state 0 in the time interval 

\[ M(t) = \int_0^t 1_{S(s)=0} ds. \]

We also can call this random variable 0-state occupation time by time \( t \).

A continuous-time Markov Chain can be alternatively described by representing the process \( S(t) \) as a combination of a discrete time Markov Chain, holding times, and initial distribution \( \nu \). More specifically, let \( p_{ij} \) be the probability of switching to state \( j \) at the next jump given that we are currently in state \( i \). The matrix

\[
P = (p_{ij}) = \begin{pmatrix}
0 & p_1 & p_2 \\
1 & 0 & 0 \\
1 & 0 & 0 \\
\end{pmatrix}
\]

is a stochastic matrix, and it is the transition matrix of the embedded (discrete time) Markov Chain of process \( S(t) \). The time spent in a particular state \( i \) between two consecutive jumps is called the holding time. The holding time has exponential distribution with rate \( \lambda_i \). For our task this representation (via an embedded Markov Chain and holding times) is a bit more convenient. Note also that in the case of the standard telegraph process the associated stochastic matrix of the embedded Markov chain is

\[
\begin{pmatrix}
0 & 1 \\
1 & 0 \\
\end{pmatrix}.
\]

Our technique is different from the general approach to the distribution of occupation times in homogeneous finite-state Markov processes (e.g., Sericola (2000)). To develop computationally efficient estimation procedure we exploit the specific structure of our Markov chain. More specifically, a telegraph process can be associated with \( S(t) \) if we collapse states 1 and 2 into one state. For
this new state the holding time is distributed as a mixture of two exponential distributions. As a consequence, the telegraph process is not Markov. This makes computing the likelihood function for $X$ challenging, because algorithms like the forward algorithm are not applicable. That is, results for telegraph processes can not be directly employed, because we do need to distinguish states 1 and 2. We use a certain periodicity of the Markov Chain and extend the technique developed in Di Crescenzo (2001) for telegraph processes to obtain the joint distribution of $M(t)$ and $S(t)$. An alternative approach can be developed by extending the method presented in Zacks (2012).

3. Distribution of Occupation Time $M(t)$ Given $S(0) = 0$

To simulate process $S(t)$ that starts with $S(0) = 0$, we need the following independent sequences of random variables:

1. $\{M_k\}_{k \geq 1}$ are independent identically distributed (iid) random variables with $\text{Exp}(\lambda_0)$ distribution,

2. $\{R_k\}_{k \geq 1}$ are iid random variables with $\text{Exp}(\lambda_1)$,

3. $\{H_k\}_{k \geq 1}$ are iid random variables with $\text{Exp}(\lambda_2)$,

4. $\{\xi_k\}_{k \geq 1}$ are iid random variables with $P(\xi_k = 1) = p_1$ and $P(\xi_k = 0) = p_2$.

Having these sequences defined we can proceed as follows. To generate a particular realization of $S(t)$, first, generate $M_1$, the time duration the process spends in state 0. Then generate $\xi_1$ to decide whether it jumps to state 1 or 2. Depending on $\xi_1$ generate the duration $R_1$ or $H_1$. After that, switch back to state 0, and so on.

Let us introduce some auxiliary random variables. Let $U_k = \xi_k R_k + (1 - \xi_k) H_k$, $C_k = M_k + U_k$, and

$$N(t) = \sup \{ n \geq 0 : \sum_{k=1}^{n} C_k \leq t \}.$$ 

Here and everywhere in the text, by convention, a summation over an empty set is 0, for instance, $\sum_{k=1}^{0} C_k = 0$. Random variable $N(t)$ is the number of full cycles $C_k$ by time $t$. 

Figure 1. \( S(t) = 0 \) and \( N(t) = n \) given that \( S(0) = 0 \).

First, we consider the distribution of occupation time \( M(t) \) when \( S(t) = 0 \). Denote \( P_i(\cdot) = P(\cdot | S(0) = i) \), where \( i = 0, 1, 2 \). With probability 1 the random variable \( M(t) \in [0, t] \), and it has an atom at \( t \) in the following sense:

\[
P_0(M(t) = t, S(t) = 0) = P_0(M(t) = t) = P(M_1 > t) = e^{-\lambda_0 t}.
\]

Now, fix \( 0 < s < t \). Then we have

\[
P_0(M(t) \in ds, S(t) = 0) = \sum_{n=0}^{\infty} P_0(M(t) \in ds, S(t) = 0, N(t) = n)
= \sum_{n=1}^{\infty} P_0(M(t) \in ds, S(t) = 0, N(t) = n),
\]

because \( S(0) = 0, S(t) = 0 \) and \( N(t) = 0 \) implies \( M(t) = t \).

Next, for \( n \geq 1 \) we get, from Figure 1, that

\[
P_0(M(t) \in ds, S(t) = 0, N(t) = n)
= P \left( \sum_{k=1}^{n} M_k + \sum_{k=1}^{n} U_k \leq t, \sum_{k=1}^{n+1} M_k + \sum_{k=1}^{n} U_k > t, t - \sum_{k=1}^{n} U_k \in ds \right)
= P \left( \sum_{k=1}^{n} M_k \leq s, \sum_{k=1}^{n+1} M_k > s, \sum_{k=1}^{n} U_k \in t - ds \right)
= P \left( \sum_{k=1}^{n} M_k \leq s, \sum_{k=1}^{n+1} M_k > s \right) P \left( \sum_{k=1}^{n} U_k \in t - ds \right)
= \left[ P \left( \sum_{k=1}^{n} M_k \leq s \right) - P \left( \sum_{k=1}^{n+1} M_k \leq s \right) \right] P \left( \sum_{k=1}^{n} U_k \in t - ds \right).
\]
Figure 2. \( S(t) = 1 \) and \( N(t) = n \) given that \( S(0) = 0 \).

Here we use independence of \( \{M_k\}_{k \geq 1} \) and \( \{U_k\}_{k \geq 1} \).

The sums \( \sum_{k=1}^{n} M_k \) and \( \sum_{k=1}^{n+1} M_k \) have gamma distributions, Gamma\((n, \lambda_0)\) and Gamma\((n + 1, \lambda_0)\), respectively. The distribution of \( \sum_{k=1}^{n} U_k \) can be expressed in terms of the convolution of gamma distributions. More specifically, by conditioning on \( \{\xi_k\}_{1 \leq k \leq n} \) one can show that

\[
P\left( \sum_{k=1}^{n} U_k \leq s \right) = \sum_{k=0}^{n} P\left( \sum_{j=1}^{k} R_j + \sum_{j=1}^{n-k} H_j \leq s \right) \binom{n}{k} p_1^k p_2^{n-k}.
\]

Random variables \( \sum_{j=1}^{k} R_j \) and \( \sum_{j=1}^{n-k} H_j \) are independent, and they have Gamma\((k, \lambda_1)\) and Gamma\((n - k, \lambda_2)\) distributions, respectively. For the convolution of gamma distributions, we refer the reader to Mathai (1982) and Moschopoulos (1985).

Next, let us work out the case when \( S(t) = 1 \). Again, the random variable \( M(t) \in [0, t] \), but now it has no atoms. For any \( 0 < s < t \), we have

\[
P_0(M(t) \in ds, S(t) = 1) = \sum_{n=0}^{\infty} P_0(M(t) \in ds, S(t) = 1, N(t) = n)
\]

Then for \( n \geq 0 \) we get, from Figure 2, that

\[
P_0(M(t) \in ds, S(t) = 1, N(t) = n)
\]

\[
= P\left( \sum_{k=1}^{n+1} M_k + \sum_{k=1}^{n} U_k \leq t, \sum_{k=1}^{n+1} M_k + \sum_{k=1}^{n} U_k + R_{n+1} > t, \sum_{k=1}^{n+1} M_k \in ds, \xi_{n+1} = 1 \right)
\]

\[
= P\left( \sum_{k=1}^{n} U_k \leq t - s, \sum_{k=1}^{n} U_k + R_{n+1} > t - s, \sum_{k=1}^{n+1} M_k \in ds, \xi_{n+1} = 1 \right)
\]
\[
\begin{align*}
&= p_1 P \left( \sum_{k=1}^{n} U_k \leq t - s, \sum_{k=1}^{n} U_k + R_{n+1} > t - s \right) P \left( \sum_{k=1}^{n+1} M_k \in ds \right) \\
&= p_1 \left[ P \left( \sum_{k=1}^{n} U_k \leq t - s \right) - P \left( \sum_{k=1}^{n} U_k + R_{n+1} \leq t - s \right) \right] P \left( \sum_{k=1}^{n+1} M_k \in ds \right).
\end{align*}
\]

Random variable \( \sum_{k=1}^{n+1} M_k \) has Gamma\((n + 1, \lambda_0)\) distribution. As before,

\[
P \left( \sum_{k=1}^{n} U_k \leq s \right) = \sum_{k=0}^{n} P \left( \sum_{j=1}^{k} R_j + \sum_{j=1}^{n-k} H_j \leq s \right) \binom{n}{k} p_1^k p_2^{n-k},
\]

and

\[
P \left( \sum_{k=1}^{n} U_k + R_{n+1} \leq s \right) = \sum_{k=0}^{n} P \left( \sum_{j=1}^{k+1} R_j + \sum_{j=1}^{n-k} H_j \leq s \right) \binom{n}{k} p_1^k p_2^{n-k}.
\]

To summarize our findings let us first introduce the following notation:

\( (1) \) \( G(x, \alpha, \beta) \), where \( \alpha \geq 0, \beta > 0 \), is the cdf of Gamma\((\alpha, \beta)\) distribution; by convention, Gamma\((0, \beta)\) distribution is the degenerate distribution with atom 1 at 0;

\( (2) \) \( g(x, \alpha, \beta) \), where \( \alpha, \beta > 0 \), is the pdf of Gamma\((\alpha, \beta)\) distribution;

\( (3) \) \( F(x, \alpha_1, \beta_1, \alpha_2, \beta_2) \), where \( \alpha_1, \alpha_2 \geq 0, \beta_1, \beta_2 > 0 \), is the cdf of the convolution of Gamma\((\alpha_1, \beta_1)\) and Gamma\((\alpha_2, \beta_2)\); note that, for example, \( F(x, 0, \beta_1, \alpha_2, \beta_2) \equiv G(x, \alpha_2, \beta_2) \);

\( (4) \) \( f(x, \alpha_1, \beta_1, \alpha_2, \beta_2) \), where \( \beta_1, \beta_2 > 0, \alpha_1, \alpha_2 \geq 0, \) and \( \alpha_1 + \alpha_2 > 0 \), is the pdf of \( F(x, \alpha_1, \beta_1, \alpha_2, \beta_2) \);

\( (5) \) \( H(x, \alpha_1, \beta_1, \alpha_2, \beta_2) = F(x, \alpha_1, \beta_1, \alpha_2, \beta_2) - F(x, \alpha_1 + 1, \beta_1, \alpha_2, \beta_2) \), where \( \beta_1, \beta_2 > 0, \alpha_1, \alpha_2 \geq 0, \) and \( \alpha_1 + \alpha_2 > 0 \), is the difference in cdf with parameters only differing by \( \alpha_1 \) versus \( \alpha_1 + 1 \).

Finally, let us denote the (defective) densities of \( M(t) \) as

\( (5) \)

\[
p_{ij}(s, t) = P_i(M(t) \in ds, S(t) = j)/ds,
\]

where \( t \geq 0, \ 0 < s < t, \ i, j = 0, 1, 2. \)

Here is the main result of the section.

**Theorem 1.** Let \( t \geq 0 \) and \( 0 < s < t. \) Then

\( (6) \)

\[
P_0(M(t) = t, S(t) = 0) = e^{-\lambda_0 t},
\]
and the densities are given by

\begin{align*}
(7) \quad p_{00}(s, t) &= \sum_{n=1}^{\infty} \left[ G(s, n, \lambda_0) - G(s, n + 1, \lambda_0) \right] \sum_{k=0}^{n} f(t - s, k, \lambda_1, n - k, \lambda_2) \binom{n}{k} p_1^k p_2^{n-k}, \\
(8) \quad p_{01}(s, t) &= \sum_{n=0}^{\infty} p_1 g(s, n + 1, \lambda_0) \sum_{k=0}^{n} H(t - s, k, \lambda_1, n - k, \lambda_2) \binom{n}{k} p_1^k p_2^{n-k}, \\
\text{and} \\
(9) \quad p_{02}(s, t) &= \sum_{n=0}^{\infty} p_2 g(s, n + 1, \lambda_0) \sum_{k=0}^{n} H(t - s, k, \lambda_2, n - k, \lambda_1) \binom{n}{k} p_1^k p_2^{n-k}.
\end{align*}

Note that the last formula of Theorem 1 can be obtained from the previous one by interchanging state 1 and state 2.

4. Distribution of Occupation Time \( M(t) \) Given \( S(0) = 1 \)

Let \( \{M_k\}_{k \geq 1}, \{R_k\}_{k \geq 1}, \{H_k\}_{k \geq 1}, \{\xi_k\}_{k \geq 1}, \) and \( \{U_k\}_{k \geq 1} \) be the same sequences of random variables as in Section 3. Let \( R_0 \) be an independent-of-everything random variable with \( \text{Exp}(\lambda_1) \) distribution. When \( S(0) = 1 \), the sequence of holding times starts from \( R_0 \); that is, we have: \( R_0, M_1, U_1, M_2, U_2, \ldots \). This requires us to modify the definition of cycles. Now \( C_1 = R_0 + M_1 \), and \( C_k = U_{k-1} + M_k \) for \( k \geq 1 \). As before, the random variable \( N(t) \) is the number of cycles in time interval \([0, t]\):

\[ N(t) = \sup \{n \geq 0 : \sum_{k=1}^{n} C_k \leq t \}. \]

Let us first consider the distribution of \( M(t) \) when \( S(t) = 1 \). Again, in this case there is an atom, but now the atom is at \( s = 0 \):

\[ P_1(M(t) = 0, S(t) = 1) = P_1(M(t) = 0) = P(R_0 > t) = e^{-\lambda_1 t}. \]

Fix \( 0 < s < t \). First note that \( S(0) = 1, S(t) = 1, \) and \( N(t) = 0 \) implies that \( M(t) = 0 \), therefore,

\[ P_1(M(t) \in ds, S(t) = 1) = \sum_{n=0}^{\infty} P_1(M(t) \in ds, S(t) = 1, N(t) = n). \]
Finally, for \( n \geq 1 \) one can show (see Figure 3) that

\[
P_1(M(t) \in ds, S(t) = 1, N(t) = n) = \sum_{n=1}^{\infty} P_1(M(t) \in ds, S(t) = 1, N(t) = n).
\]

The next case is when \( S(t) = 2 \). In this situation \( M(t) \) does not have atoms, because we cannot switch from state 1 to state 2 without visiting state 0. Since event \( \{S(0) = 1, S(t) = 2, \) and
\( N(t) = 0 \) is impossible, for \( 0 < s < t \) we have

\[
P_1(M(t) \in ds, S(t) = 2) = \sum_{n=0}^{\infty} P_1(M(t) \in ds, S(t) = 2, N(t) = n)
\]

\[
= \sum_{n=1}^{\infty} P_1(M(t) \in ds, S(t) = 2, N(t) = n),
\]

and for \( n \geq 1 \)

\[
P_1(M(t) \in ds, S(t) = 2, N(t) = n)
\]

\[
= P \left( R_0 + \sum_{k=1}^{n} M_k + \sum_{k=1}^{n-1} U_k \leq t, R_0 + \sum_{k=1}^{n} M_k + \sum_{k=1}^{n-1} U_k + H_n > t, \sum_{k=1}^{n} M_k \in ds, \xi_n = 0 \right)
\]

\[
= P \left( R_0 + \sum_{k=1}^{n-1} U_k \leq t - s, R_0 + \sum_{k=1}^{n-1} U_k + H_n > t - s, \sum_{k=1}^{n} M_k \in ds, \xi_n = 0 \right)
\]

\[
= p_2 P \left( R_0 + \sum_{k=1}^{n-1} U_k \leq t - s, R_0 + \sum_{k=1}^{n-1} U_k + H_n > t - s \right) P \left( \sum_{k=1}^{n} M_k \in ds \right)
\]

\[
= p_2 \left[ P \left( R_0 + \sum_{k=1}^{n-1} U_k \leq t - s \right) - P \left( R_0 + \sum_{k=1}^{n-1} U_k + H_n > t - s \right) \right] P \left( \sum_{k=1}^{n} M_k \in ds \right)
\]

\[
= p_2 g(s, n, \lambda_0)
\]

\[
\times \sum_{k=0}^{n-1} \left[ F(t - s, k + 1, \lambda_1, n - 1 - k, \lambda_2) - F(t - s, k + 1, \lambda_1, n - k, \lambda_2) \right] \binom{n - 1}{k} p_1^k p_2^{n-1-k} ds
\]

\[
= p_2 g(s, n, \lambda_0) \times \sum_{k=0}^{n-1} \left[ H(t - s, n - 1 - k, \lambda_2, k + 1, \lambda_1) \binom{n - 1}{k} p_1^k p_2^{n-1-k} ds. \right.
\]

Finally, let us consider the case \( S(t) = 0 \). Again, there are no atoms. For \( 0 < s < t \)

\[
P_1(M(t) \in ds, S(t) = 0) = \sum_{n=0}^{\infty} P_1(M(t) \in ds, S(t) = 0, N(t) = n),
\]

and for \( n \geq 0 \)

\[
P_1(M(t) \in ds, S(t) = 0, N(t) = n)
\]

\[
= P \left( R_0 + \sum_{k=1}^{n} M_k + \sum_{k=1}^{n} U_k \leq t, R_0 + \sum_{k=1}^{n} M_k + \sum_{k=1}^{n+1} U_k > t, t - \sum_{k=1}^{n} U_k - R_0 \in ds \right)
\]
Thus, we have the following result.

**Theorem 2.** Let $t \geq 0$ and $0 < s < t$. Then

\[(10) \quad P_1(M(t) = 0, S(t) = 1) = e^{-\lambda_1 t},\]

and the densities are given by

\[(11) \quad p_{10}(s,t) = \sum_{n=0}^{\infty} [G(s, n, \lambda_0) - G(s, n + 1, \lambda_0)] \sum_{k=0}^{\infty} [f(t-s, k+1, \lambda_1, n-k, \lambda_2)] \binom{n}{k} p_1^k p_2^{n-k} ds,\]

\[(12) \quad p_{11}(s,t) = \sum_{n=1}^{\infty} p_1 g(s, n, \lambda_0) \times \sum_{k=0}^{n-1} H(t-s, k+1, \lambda_1, n-1-k, \lambda_2) \binom{n-1}{k} p_1^k p_2^{n-1-k},\]

and

\[(13) \quad p_{12}(s,t) = \sum_{n=1}^{\infty} p_2 g(s, n, \lambda_0) \times \sum_{k=0}^{n-1} H(t-s, n-1-k, \lambda_2, k+1, \lambda_1) \binom{n-1}{k} p_1^k p_2^{n-1-k}.\]

In order to get densities $p_{2j}(s,t)$, $j = 0, 1, 2$ we simply need to interchange state 1 and state 2 in all the formulas of Theorem 2. Also let us note that Theorems 1 and 2 can be easily extended to the case when there are more than two motionless states.
5. Numerical Verification

Figure 4 presents defective densities $p_{ij}(s,t)$ for two cases when the Markov Chain starts in state 0 and state 1. The following model parameters are used: $\lambda_0 = 4$, $\lambda_1 = .5$, $\lambda_2 = .1$, $p_1 = .8$, and $t = 10$. Note that the total probability in both cases is slightly less than 1. When the Markov Chain starts in state 0, the total probability adds up to $1 - e^{-40}$, because $M(10)$ has an atom at $s = 10$. When the Markov Chain starts in state 1, the probability of the atom at $s = 0$ is relatively larger: $e^{-5}$. Because densities $p_{0j}(s,t)$ correspond to the case when at $s = 0$ the state process is in state 0, these occupation times are longer on average than $p_{1j}(s,t)$.

Applications of the formulas in practice depends on how accurately the infinite sums can be implemented. To check the accuracy of the implementation and to verify that our formulas in
Theorem 1 and Theorem 2 are free of errors or typos, we simulated 1,000,000 realizations of the Markov chain $S(\cdot)$ for each theorem. The empirical densities follow theoretical ones extremely closely (not shown).

We also performed another check. There are two cases when the MHR process collapses to the moving-resting process investigated in Yan et al. (2014). If $p_1$ is equal to 0 or 1, then the MHR process (after the first visit of moving state) will alternate only between two states. The other case is when $\lambda_1 = \lambda_2$. The MHR process will hit all three states, but state 1 and state 2 are indistinguishable. This can be verified analytically. For example, one can show that our formula (7) will simplify to the first term of (2.3) in Zacks (2004). For different sets of parameters, we checked numerically that in these two cases our formulas are consistent with the formulas based on modified Bessel functions derived in Zacks (2004).

6. Joint Distribution of $X(t)$ and $S(t)$

Let us first work out the details the formula for $P_0(X(t) \in dx, S(t) = 0)$. Fix $0 < s < t$. Given $M(t) = s$, random variable $X(t)$ has a normal distribution with mean 0 and variance $\sigma^2 s$, because Markov Chain $S(\cdot)$ and Brownian Motion $B(\cdot)$ are independent processes. Let $\phi(\cdot, \sigma^2)$ denote the pdf of a normal random variable with mean zero and variance $\sigma^2$. Then we get that

$$P_0(X(t) \in dx, S(t) = 0, M(t) \in ds) = \frac{\phi(x, \sigma^2 s)p_{00}(s, t)dxds}{ds}.$$ 

Now, recall also that given $S(0) = 0$, random variable $M(t)$ has an atom (with weight $e^{-\lambda_0 t}$ at $s = t$). Therefore, when we integrate $s$ out of the joint distribution of $X(t)$, $S(t)$ and $M(t)$, we get that

$$h_{00}(x, t) = \frac{P_0(X(t) \in dx, S(t) = 0)}{dx} = e^{-\lambda_0 t}\phi(x, \sigma^2 t) + \int_0^t \phi(x, \sigma^2 s)p_{00}(s, t)ds.$$
In a similar fashion, one can show that for $i = 1, 2$

$$h_{0i}(x, t) = P_0(X(t) \in dx, S(t) = i)/dx = \int_0^t \phi(x, \sigma^2 s)p_{0i}(s, t)ds.$$  

When $S(0) = 1$, the distribution of random variable $X(t)$ has an atom at $x = 0$ (if $R_0 > t$, that is, the Markov chain stays in state 1 till time $t$). Taking this into an account we have the following formulas:

$$h_{1i}(x, t) = P_1(X(t) \in dx, S(t) = i)/dx = \int_0^t \phi(x, \sigma^2 s)p_{1i}(s, t)ds, \quad \text{if } x \neq 0 \text{ and } i = 0, 1, 2,$$

and

$$P_1(X(t) = 0, S(t) = 1) = e^{-\lambda_1 t}.$$

Similarly,

$$h_{2i}(x, t) = P_2(X(t) \in dx, S(t) = i)/dx = \int_0^t \phi(x, \sigma^2 s)p_{2i}(s, t)ds, \quad \text{if } x \neq 0 \text{ and } i = 0, 1, 2,$$

and

$$P_2(X(t) = 0, S(t) = 2) = e^{-\lambda_2 t}.$$

It is not essential to use one-dimensional Brownian Motion for these derivations but it simplifies our presentation’s notation. If one does want to consider a Brownian Motion of $d$-dimension, then all we need to do is to substitute the one-dimensional normal pdf in formulas (14)–(17) by the $d$-dimensional normal density with mean zero and covariance matrix $\sigma^2 I_d$, where $I_d$ is the $d$-dimensional identity matrix. Of course, in this case $x$ is a vector in the $d$-dimensional space, not a scalar. In fact, later when we run simulations and analyze real-world data we will use the two-dimensional setup.
7. Likelihood Estimation with Forward Algorithm

Assume that we observe the MRH process $X(t)$ at times $0 = t_0 < t_1 < \cdots < t_n$. Let $X = (X_1, X_2, \ldots, X_n)$, where $X_k = X(t_i) - X(t_{i-1})$, $i = 1, \ldots, n$ are the observed increments of the MHR process. Let $S = (S(0), S(t_1), \ldots, S(t_n))$ be the corresponding states of the the continuous-time Markov Chain, and $\Delta_i = t_i - t_{i-1}$, $i = 1, \ldots, n$.

The location-state process $\{X(t), S(t)\}$ is Markov, so the likelihood function of $(X, S)$ is available in closed-form. More specifically, it is given by

$$L(X, S, \theta) = \nu(S(0)) \prod_{i=1}^{n} f(X_i, S(t_i)|S(t_{i-1}), \Delta_i, \theta),$$

where

$$f(x, u|v, t, \theta) = \begin{cases} 
0 & v \neq u, x = 0, \\
0 & v = u = 0, x = 0, \\
e^{-\lambda_1 t} & v = u = 1, x = 0, \\
e^{-\lambda_2 t} & v = u = 2, x = 0, \\
h_{ij}(x, t) & v = i, u = j, x \neq 0,
\end{cases}$$

$x \in \mathbb{R}$, $u, v = 0, 1, 2$, $t > 0$, and $\theta = (\lambda_0, \lambda_1, \lambda_2, p_1, \sigma)$.

The distribution of the increments of the MRH process is a mixture of absolutely continuous and discrete distributions. Therefore, in order to construct the likelihood function we have to use the Radon–Nikodym derivative of the probability distribution relative to a dominating measure that includes an atom at $x = 0$. That explains the special sets of formulas in the case when $x = 0$.

Now, if the state vector $S_t$ is not observed, then obviously the likelihood of the increment vector $X$ can be computed using

$$L(X, \theta) = \sum_{s_0, \ldots, s_n} L(X, (s_0, \ldots, s_n), \theta),$$
where the summation is taken over all possible trajectories of $S$. However, this formula is not practical since the number of trajectories grows exponentially as sample size $n \to \infty$. This difficulty is addressed with help of the forward algorithm.

First, we need to introduce forward variables:

$$\alpha(X_k, s_k, \theta) = \sum_{s_0, \ldots, s_{k-1}} \nu(s_0) \prod_{i=1}^{k} f(X_i, s_i|s_{i-1}, \Delta_i, \theta),$$

where $X_k = (X_1, X_2, \ldots, X_k)$, and $1 \leq k \leq n$. Then one can show that

$$\alpha(X_{k+1}, s_{k+1}, \theta) = \sum_{s_k} f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta) \alpha(X_k, s_k, \theta).$$

That is, for every $k$ we have three forward variables. To get one $k + 1$st forward variable we need to calculate three transitional values in (19), multiply each $k$th forward variable by an appropriate transitional value, and finally sum up these three quantities. The bottom line is that the transition from $\alpha(X_k, s_k, \theta)$ to $\alpha(X_{k+1}, s_{k+1}, \theta)$ for each $k$ requires a constant (independent of $k$) number of operations. Since

$$L(X, \theta) = \sum_{s_n} \alpha(X_n, s_n, \theta),$$

we get an algorithm that finds $L(X, \theta)$ with computational complexity that is linear with respect to sample size $n$.

The next step is to modify the forward variables to address the underflow problem. The problem is that for large $k$ forward variables $\alpha(X_k, s_k, \theta)$ might be numerically indistinguishable from zero. To resolve this issue the following normalized forward variables are employed:

$$\bar{\alpha}(X_k, s_k, \theta) = \frac{\alpha(X_k, s_k, \theta)}{L(X_k, \theta)},$$

where $L(X_k, \theta) = \sum_{s_k} \alpha(X_k, s_k, \theta)$, the likelihood of vector $X_k$. Then (21) immediately implies that the normalized forward variables satisfy the following equation:

$$\bar{\alpha}(X_{k+1}, s_{k+1}, \theta) = \frac{L(X_{k+1}, \theta)}{L(X_k, \theta)} \sum_{s_k} f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta) \bar{\alpha}(X_k, s_k, \theta).$$
If for $0 \leq k \leq n - 1$ we define

$$d(X_{k+1}, \theta) = \frac{L(X_{k+1}, \theta)}{L(X_k, \theta)},$$

then one can easily verify that

$$d(X_{k+1}, \theta) = \sum_{s_{k+1}} \sum_{s_k} f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta) \bar{\alpha}(X_k, s_k, \theta).$$

Here is the normalized version of the forward algorithm.

1. For observed $X$ and given parameter vector $\theta$, compute $f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta)$ for all possible pairs $(s_k, s_{k+1})$, $k = 0, \ldots, n - 1$.

2. Base case: $\bar{\alpha}(X_0, s_0, \theta) = \nu(s_0)$, where $s_0 = 0, 1, 2$.

3. Induction: for $s_{k+1} = 0, 1, 2$ compute $\bar{\alpha}(X_{k+1}, s_{k+1}, \theta)$ using

$$\bar{\alpha}(X_{k+1}, s_{k+1}, \theta) = \frac{1}{d(X_{k+1}, \theta)} \sum_{s_k} f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta) \bar{\alpha}(X_k, s_k, \theta).$$

and

$$d(X_{k+1}, \theta) = \sum_{s_{k+1}} \sum_{s_k} f(X_{k+1}, s_{k+1}|s_k, \Delta_{k+1}, \theta) \bar{\alpha}(X_k, s_k, \theta).$$

4. Termination: $\log L(X, \theta) = \sum_{k=1}^{n} \log d(X_k, \theta)$.

This algorithm can be easily adapted to a situation when some states are completely observed or partially observed. For example, accelerometer data might be used to infer when an animal is moving or not, and direct inspection of a kill-site can confirm handling. If state $s_k$ is known, then first calculate three $k$th forward variables as usual. Next, set the two forward variables with unobservable states to zero. After that just continue the forward algorithm in the normal fashion until the next location where additional information on the state is available. If at $k$th location only one state is excluded, then we have to set only one forward variable to zero.
Figure 5. Violin plots of the maximum likelihood estimates from 49 replicates using the forward algorithm. The horizontal bar in each panel is the true parameter value.

8. Simulation and Data Analysis

We ran a small simulation to demonstrate that the forward algorithm successfully recovers the model parameters. The true parameter values were set to be $\lambda_0 = 4$, $\lambda_1 = 0.5$, $\lambda_2 = 0.1$, $p_1 = 0.8$, and $\sigma = 25$. The simulation was small because the computation of the maximum likelihood estimator is very demanding. Evaluation of the terms in Theorems 1–2 involves infinite series that are computationally intensive; evaluation of the terms in the likelihood in Section 6 is very expensive because functions in (19) are numerical integrals of $p_{ij}(s,t)$. We generated 49 two-dimensional datasets on a time grid from 0 to 4000, with increment 20, so the resulting series $X$ is of length 200.
Figure 5 presents the violin plots of the likelihood estimates of the 49 replicates in comparison to the true values of the five parameters. Violin plots are similar to box plots with a rotated kernel density plot on each side, which show more information about the data than box plots. The horizontal bars in the panels are the true parameter values. For each parameter, the true value lies in the bulk part of the violin plot, indicating that the true parameters are recovered well by the likelihood estimates in this small scale simulation study.

We next applied the proposed model to the data from the same mountain lion analyzed by Yan et al. (2014) and Pozdnyakov et al. (2017). This mountain lion was a mature female in the Gros Ventre Mountain Range near Jackson Wyoming tracked with a GPS collar from 2009 to 2012. The collar was designed to collect a fix every 8 hours but the actual sampling times were irregular with sampling intervals having standard deviation 6.45 hours, ranging from 0.5 hours to 120 hours. Mountain lions behave differently in the summer and in the winter, so we focused on the summer of 2012, a total of 389 observations spanning from June 1 to August 31, which makes our results not directly comparable to existing analyses Yan et al. (2014); Pozdnyakov et al. (2017). Field personnel determined that some of the sites were places where the mountain lion consumed a prey item. She typically remained within 250 m of a kill site while it was considered to be “handling”, which is different from shorter, resting periods. To allow for GPS measurement error, we rounded the locations to the nearest 100 meters.

The maximum likelihood estimates of the MRH model parameters are: \( \hat{\lambda}_0 = 9.25 \) hour, \( \hat{\lambda}_1 = 2.49 \) hour, \( \hat{\lambda}_2 = 0.19 \) hour, \( \hat{\sigma} = 1.28 \text{km/hour}^{1/2} \), and \( \hat{p} = 0.70 \). That is, on average, the mountain lions stays for 0.11, 0.40, and 5.1 hours in the moving, resting, and handling states. When moving, the mobility parameter is 1.28 km/hour\(^{1/2}\). This means that if the mountain lion moves without stopping for one hour, the average deviation from the initial position in terms of northing and easting values is 1.28 km. When she stopped moving, she went into resting with probability
0.70 and handling with probability 0.30, respectively. For comparison, we also fitted the moving-resting process to the same data, and the maximum likelihood estimates of the parameters are \( \hat{\lambda}_0 = 0.66/\text{hour} \), \( \hat{\lambda}_1 = 0.27/\text{hour} \), and \( \hat{\sigma} = 0.59 \text{km/hour}^{1/2} \). Because there is no handling state, the average durations in both moving and resting are estimated longer. Consequently, the mobility parameter estimate is much lower, almost halved, because the animal was assumed to be moving longer. We also fitted the BBMM of (Horne et al., 2007) with the original, non-rounded data and the GPS measurement error standard deviation fixed at 0.02km. The BM mobility parameter estimate is even lower, 0.42km/hour\(^{1/2} \), as the animal was assumed to be always moving.

9. Concluding Remarks

The results on occupation times obtained in the paper have their own value and can be used for other applications, such as quality control. Indeed, the continuous-time Markov Chain \( S(t) \) can be viewed as a telegraph process with two off states. These two states will correspond to two different types of breakdown that require different time for repair. The results in Theorems 1 and 2 can be easily generalized to cover \( k \) motionless states instead of just two. The only difference is that, instead of binomial distribution and convolutions of two gamma distributions, we will have multinomial distribution and convolutions of \( k \) gammas.

The methodology developed in Sections 3 and 4 works even if the holding times are not exponentially distributed, which is an advantage of our approach. If we want to keep the Markov property, then all holding times must have exponential distributions. The memoryless distribution might be not appropriate for some species that follow a cyclic daily routine. Nonetheless, if animals under observation do not exhibit a daily periodic behavior (like mountain lions), then using an exponential distribution is acceptable. The behavior of these animals is subject to interruptions that can cut their time spent in a particular activity. For example, handling might be interrupted by a more dominate predator who drives the lion off her kill before she is finished with it.
A different (from exponential) distribution should be used for species with a periodic routine. One interesting possibility is to employ stable distributions (for example, Lévy distribution). Because a linear combination of two independent random variables with a stable distribution has the same distribution, up to location and scale parameters, the formulas in Theorems 1 and 2 will be even nicer. The drawback is that the state process is then semi-Markov, and, as a result, the likelihood inferences from standard HMM tools are not available. Nevertheless, this still might be of interest for practitioners in ecological science, because estimation can be done via alternative methods such as the composite likelihood estimation (Lindsay, 1988).

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