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Incorporating Periodic Variability in Hidden Markov Models for Animal Movement

Michael Li^{1*} and Benjamin M. Bolker^{1,2}

*Correspondence:

lim88@mcmaster.ca

¹ Department of Biology,

McMaster University, 1280 Main

St. West, L8S 4K1, Hamilton,

Ontario, Canada

Full list of author information is available at the end of the article

Abstract

Background: Clustering time-series data into discrete groups can improve prediction and provide insight into the nature of underlying, unobservable states of the system. However, temporal variation in probabilities of group occupancy, or the rates at which individuals move between groups, can obscure such signals. We use finite mixture and hidden Markov models (HMMs), two standard clustering techniques, to model long-term hourly movement data from Florida panthers (*Puma concolor coryi*). Allowing for temporal heterogeneity in transition probabilities, a straightforward but little-used extension of the standard HMM framework, resolves some shortcomings of current models and clarifies the behavioural patterns of panthers.

Results:

Simulations and analyses of panther data showed that model misspecification (omitting important sources of variation) can lead to overfitting/overestimating the underlying number of behavioural states. Models incorporating temporal heterogeneity identify fewer underlying states, and can make out-of-sample predictions that capture observed diurnal and autocorrelated movement patterns exhibited by Florida panthers.

Conclusion:

Incorporating temporal heterogeneity improved goodness of fit and predictive capability as well as reducing the selected number of behavioural states to a more biologically interpretable level. Our results suggest that incorporating additional structure in statistical models of movement behaviour can allow more accurate assessment of appropriate model complexity.

Keywords: Hidden Markov Model; Animal Movement; Temporal Autocorrelation; Temporal Heterogeneity; Florida Panther

Background

Given a sequence of animal movements, movement models aim to find a parsimonious description that can be used to understand past movements and predict future movements. Ecologists have long considered the effects of individual-level covariates (sex, age, nutritional status) and environmental covariates (habitat type, location of predators or prey) on movement [1–3]. More recently, modelers have developed *hidden Markov models* (HMMs) [4–6] — used in animal ecology under the rubric

of the “multiphasic movement framework” [7] — that consider the effects of organisms’ *internal* states; in particular, HMMs model animal movement as though individual animals’ movement behaviour at particular times is determined by which of a discrete set of unobserved movement states (e.g. “foraging”, “traveling”, “resting”) they currently occupy. Conditional on the state occupied by an individual, HMMs typically assume that animals follow a standard correlated random walk model [8, 9].

Ever-increasing capabilities of remote sensors are making movement data available over an ever-wider range of time scales, at both higher resolution (e.g. hourly data from GPS collars vs. daily or weekly fixes for radio or VHF collars) and longer extent (e.g. from a few days to significant fractions of a year, or longer). When analyzing such long-term data, ecologists will more often have to account for temporal variability in movement behaviour at diurnal and seasonal scales that were previously not captured in the data.

HMMs have typically been used to model movements over short time scales, where the probability of transitioning between movement states is approximately constant. Changes in transition probabilities based on the local environment can be accounted for by incorporating environmental covariates in the HMM [10], or inferred from direct comparisons between inferred states and environmental conditions [7]. Schliehe-Diecks et al. [11] considered temporal trends in behavioural transitions over the time scales of a six-hour observation period, but in general ecologists have turned to other tools to describe behavioural changes over longer (diurnal, seasonal, or ontogenetic) time scales [12].

For movement behaviours that change on a fast time scale, such that movement behaviours recorded at successive observations are effectively independent, *finite mixture models* (FMMs) — which can be considered a special case of HMMs where the probability of state occupancy is independent of the previous state — can

adequately describe movement [13]. When movement varies over long time scales (relative to the time between observations) with little short-term persistence or correlation, movement could be well represented by FMMs where the occupancy probabilities change deterministically over time. Thus FMMs and HMMs, with or without temporal variation in the occupancy or transition probabilities, form a useful family of models for capturing changes in movement behaviour over a range of time scales.

Our primary goal in this paper is to introduce the use of HMMs with temporally varying transition probabilities – in particular, transition probabilities that follow a diurnal cycle – for modeling animal movement recorded over long time scales. In addition to simulation-based examples, we also re-analyze data from van de Kerk et al. [14], who used temporally homogeneous hidden semi-Markov models (HSMMs: an extension of HMMs that allow flexible modelling of the distribution of *dwell times*, the lengths of consecutive occupancy of a behavioural state) to describe the movement and putative underlying behavioural states of Florida panthers (*Puma concolor coryi*).

van de Kerk et al. [14] found that the best-fitting HSMMs incorporated a surprisingly large number of hidden behavioural states (as many as six for individuals with a large amount of available data); for reasons of computational practicality and biological interpretability, they restricted their detailed analysis to models with only three underlying states. In contrast, most studies using HMM have chosen the number of underlying states *a priori*, typically using either two [6, 7, 11, 15], or three states [16–18]. In contrast, Dean et al. [16] evaluated models with up to 10 states, but like van de Kerk et al. they chose to consider only models with three states. As van de Kerk et al. [14] comment, and as we discuss further below, behavioural repertoires with more than three distinct states are difficult to interpret — one rea-

son that other authors have not adopted van de Kerk et al.'s model-based approach to identifying the number of latent states.

Our second goal, therefore, is to explore whether van de Kerk et al.'s results on optimal model complexity might be driven at least in part by structural problems with their statistical model, i.e. the assumption of temporally homogeneous behaviour. For large data sets, information-theoretic model selection methods will typically choose complex, highly parameterized models; when there is only one way in which models can become more complex (e.g. by increasing the number of latent states), complexity that is present in the data but not accounted for in the model (e.g. spatial or temporal heterogeneity) can be misidentified as other forms of complexity. We predict that increasing volumes of data will increasingly lead researchers who are accustomed to fitting small models to sparse data into such traps. We examine whether allowing for diurnal variation in the Florida panther data allows us to select models with fewer latent states; we also fit models to simulated data with varying numbers of latent states, and with and without temporal heterogeneity, to test our conjecture that heterogeneity can be misidentified as behavioural complexity.

Methods

Data and previous analyses

GPS collars were fitted to 18 Florida panthers in 2005-2012 by Florida Fish and Wildlife and Conservation Commission staff using trained hounds and houndsmen. Of these animals, 13 had sufficient data to be used by van de Kerk et al. [14]. Here we focus on the four cats with the most data (all with approximately 10,000-15,000 observations: see Table 1), in part because our goal is to understand the issues that arise when simple models are fitted to large data sets, and in part because the general trend in telemetry studies is toward larger data sets. As is typical in studies of animal movement, we took first differences of the data by decomposing

contiguous sequences of hourly GPS coordinates into successive step lengths (in meters) and turning angles (in radians) [9, 14].

van de Kerk et al. [14] used hidden semi-Markov models (HSMM), an extension of HMM that permits explicit modelling of dwell times [6], considering both Poisson and negative binomial distributions for dwell times. As shown by van de Kerk et al. [14] (Figure S3b, top row, middle panel), the estimated shape parameter of the negative binomial dwell time distribution was typically close to 1 ($\approx 0.4 - 1.6$; confidence intervals were not given), implying that a geometric distribution (i.e., negative binomial with shape=1) might be adequate. In turn, this suggests that we might not lose much accuracy by reverting to a simpler HMM framework, which corresponds to making precisely this assumption.

van de Kerk et al. [14] considered time-homogeneous models with a variety of candidate distributions — log-Normal, Gamma, and Weibull distributions for step lengths and von Mises and wrapped Cauchy distributions for the turning angle — concluding on the basis of the Akaike information criterion (AIC) that Weibull step length and wrapped Cauchy turning angle distributions were best. Since our analysis aims for simplicity and qualitative conclusions rather than for picking the very best predictive model, we focus on models that treat each step as a univariate, log-Normally distributed observation, glossing over both the differences in shape between the three candidate step-length distributions and the effects of considering multivariate (i.e., step length plus turning angle) observations. However, we do briefly compare log-Normal and Weibull step-length distributions, with and without a von Mises-distributed turning angle included in the model (Figure 2). (Note that most movement analyses, including van de Kerk et al. [14], are only partially multivariate, treating step length and turning angle at a particular time as multivariate observations for the purpose of HMM analysis but neglecting possible correlations between the two measures.)

van de Kerk et al. [14] used the Bayesian (Schwarz) information criterion (BIC) to test the relative penalized goodness of fit for models ranging from 2 to 6 latent states. In general, BIC values decreased as the number of states increased from three to six states, suggesting that the six-state model was favoured statistically; however, the authors used three-state models in most of their analyses for ease of biological interpretation. We follow van de Kerk et al. [14] in using BIC-optimality (i.e., minimum BIC across a family of models) as the criterion for identifying the best model, because we are interested in explaining the data generation process by identifying the “true” number of underlying movement states.

Using BIC also simplifies evaluation of model selection procedures; it is easier to test whether our model selection procedure has selected the model used to simulate the data, rather than testing whether it has selected the model with the minimal Kullback-Leibler distance [19]. We recognize that ecologists will often be interested in maximizing predictive accuracy rather than selecting a true model, and that as usual in ecological systems the true model will be far more complicated than any candidate model [20]; we believe that the qualitative conclusions stated here for BIC-optimality will carry over to analyses using AIC instead.

Model description

In a HMM, the joint likelihood of *emissions* (i.e., direct observations) $\mathbf{Y} = \mathbf{y}_1, \dots, \mathbf{y}_T$ and a hidden state sequence $\mathbf{Z}, z_t \in \{1, \dots, n\}, t = 1, \dots, T$, given model parameters $\boldsymbol{\theta}$ and covariates $\mathbf{X}_{1:T} = \mathbf{x}_1, \dots, \mathbf{x}_T$, can be written as:

$$P(\mathbf{Y}_{1:T}, \mathbf{Z}_{1:T} | \boldsymbol{\theta}, \mathbf{X}_{1:T}) = P(z_1 | \mathbf{x}_1) P(\mathbf{y}_1 | z_1, \mathbf{x}_1) \times \prod_{k=2}^T P(z_k | z_{k-1}, \mathbf{x}_k) P(\mathbf{y}_k | z_k, \mathbf{x}_k) \quad (1)$$

137 The emissions \mathbf{y}_i are boldfaced to denote that we may have a vector of observations
 138 at each time point (e.g., step length and turning angle). The model contains three
 139 distinct components:

140 **Initial probability** $P(z_1 = i | \mathbf{x}_1)P(\mathbf{y}_1 | z_1, \mathbf{x}_1)$: the probability of state i at time
 141 $t = 1$ given that the covariates are \mathbf{x}_1 , times the vector of observations \mathbf{y}_1
 142 conditioned on state z_1 and covariates \mathbf{x}_1 .

143 **Transition probability** $P(z_k = j | z_{k-1} = i, \mathbf{x}_k)$: the probability of a transition
 144 from state i at time $t = k - 1$ to state j at time $t = k$, given covariates \mathbf{x}_k .

145 **Emission probability** $P(\mathbf{y}_k | z_k, \mathbf{x}_k)$: a vector of observations \mathbf{y}_k given state z_k at
 146 time $t = k$ and covariates \mathbf{x}_k .

147 Eq. 1 gives the likelihood of the observed sequence given (conditional on) a partic-
 148 ular hidden sequence. In order to calculate the overall, unconditional (or marginal)
 149 likelihood of the observed sequence, we need to average over all possible hidden
 150 sequences. There are several efficient algorithms for computing the marginal like-
 151 lihood and numerically estimating parameters [21]; we used those implemented in
 152 the `depmixS4` package for R [22, 23].

153 For an n -state HMM, we need to define an $n \times n$ matrix that specifies the proba-
 154 bilities π_{ij} of being in movement states j at time $t + 1$ given that the individual is
 155 in state i . The FMM is a special case of HMM where the probabilities of *entering*
 156 a given state are identical across all states — i.e., the probability of occupying a
 157 state at the next time step is independent of the current state occupancy. It can be
 158 modelled in the HMM framework by setting the transition probabilities $\pi_{ij} = \pi_{i*}$.

159 In any case, the transition matrix π_{ij} must respect the constraints that (1) all
 160 probabilities are between 0 and 1 and (2) transition probabilities out of a given state
 161 sum to 1. As is standard for HMMs with covariates [22], we define this multinomial
 162 logistic model in terms of a linear predictor η_{ij} , where η_{i1} is set to 1 without loss

of generality (i.e. we have only $n \times (n - 1)$ distinct parameters; we index j from 2 to n for notational clarity):

$$\begin{aligned}\pi_{ij} &= \exp(\eta_{ij}(t)) / \left(1 + \sum_{j=2}^n \exp(\eta_{ij}(t)) \right), \text{ for } j = 2, \dots, n \\ \pi_{i1} &= 1 - \sum_{j=2}^n \pi_{ij}\end{aligned}\tag{2}$$

We considered four different transition models for diurnal variation in behaviour, incorporating hour-of-day as a covariate following the general approach of Morales et al. [17] of incorporating covariate dependence in the transition matrix.

Multiple block transition Here we assume piecewise-constant transition probabilities. The transition probability π_{ij} is a function of time (hour of day), where it is assigned to one of M different time blocks:

$$\eta_{ij}(t) = \sum_{m=1}^M a_{ijm} \delta_{m=t}$$

where a_{ijm} are parameters, and $\delta_{m=t}$ is a Kronecker delta ($\delta_{m=t} = 1$ for the time block corresponding to time t , and 0 otherwise).

Quadratic transition model We assume the elements of the linear predictor are quadratic functions of hour:

$$\eta_{ij}(t) = b_{ij1} + b_{ij2} \left(\frac{t}{24} \right) + b_{ij3} \left(\frac{t}{24} \right)^2.$$

The quadratic model is not diurnally continuous, i.e. there is no constraint that forces $\eta_{ij}(0) = \eta_{ij}(24)$; imposing a diurnal continuity constraint would collapse the model to a constant.

178 **Sinusoidal transition model** A sinusoidal model with a period of 24 hours is
 179 identical in complexity to the quadratic model, but automatically satisfies
 180 the diurnal continuity constraint:

$$\eta_{ij}(t) = b_{ij1} + b_{ij2} \cos\left(\frac{2\pi t}{24}\right) + b_{ij3} \sin\left(\frac{2\pi t}{24}\right).$$

181 **Hourly model** Lastly, we extended the multi-block approach and assign a differ-
 182 ent transition matrix for every hour of the day. This model is included for
 183 comparative purposes; due to the large number of parameters in the model
 184 (more than $24n(n-1)$ for a HMM with n states), it is not really practical.
 185 We only fitted up to four states using the hourly model.

186 Other periodic functions, such as Fourier series (i.e., the sinusoidal transition
 187 model augmented by additional sinusoidal components at higher frequencies) or
 188 periodic splines, could also be considered.

189 Model evaluation

190 We used the `depmixS4` package to fit covariate-dependent transition HMMs, simu-
 191 late states and step lengths using the estimated parameters, and estimate the most
 192 likely states with the Viterbi algorithm.

193 A simple simulation was conducted to see whether fitting homogeneous tran-
 194 sition probability HMMs to heterogeneous transitions simulated data will over es-
 195 timate the number of states and estimate the correct number of states using the
 196 heterogeneous transitioning model. We used 100 realizations of a two-state HMM
 197 with sinusoidal temporal transitions and fitted it with 2- to 5-state HMMs with and
 198 without temporal heterogeneity in the transition probabilities.

199 We used three approaches to assess the fit of both time-homogeneous and time-
 200 inhomogeneous HMMs with 3 to 6 states to step-length data from the four of the
 201 thirteen Florida panthers with the most data (> 9000 observations). (1) BIC was

used to compare the goodness of fit of each model type. The model with the lowest BIC was selected to be the optimal-BIC model and all BICs were adjusted to ΔBIC based on the optimal-BIC model ($\Delta\text{BIC} = \text{BIC} - \min(\text{BIC})$). (2) Comparing average step-length by hour of day for the observed data and for data simulated from the models shows how well a particular class of models can capture diurnal variation in behaviour. (3) Comparing temporal autocorrelations for the observed data and for data simulated from the models shows how well a particular class of models can capture serial correlation at both short and long time scales. As a complement, we also fitted FMM and FMM with priors on state occupancy that varied sinusoidally over time to compare the temporal effects in goodness of fit. As a reminder, FMMs assume that the latent state in each time step is *independent* of the latent state at the previous time step; time-varying FMMs can accurately describe movement when behaviour can change on a short time scale, but the average propensity for different behaviours changes over time.

Model complexity and the number of parameters increase as the number of latent states increase. For a fixed number of states homogeneous FMMs are simplest, followed by homogeneous HMMs and finally by FMMs and HMMs incorporating temporal heterogeneity. In general, the number of free parameters in an HMM is the sum of the number of free parameters for each of the three model components. Let n be the number of hidden states and k_i, k_t, k_e be the number of parameters describing the covariate-dependence of the prior distribution, transition function and emission distributions; that is, for a homogeneous model, $k = 1$, while a single numeric covariate or a categorical predictor with two levels would give $k = 2$. Then the number of free parameters of an HMM is:

$$\text{Number of Free Parameters} = \underbrace{k_i \cdot (n - 1)}_{\text{Initial}} + \underbrace{k_t \cdot n \cdot (n - 1)}_{\text{Transition}} + \underbrace{k_e \cdot n}_{\text{Emission}} . \quad (3)$$

As the number of states increases, the number of free parameters in (homogeneous or heterogeneous) FMMs and time-homogeneous HMMs will increase linearly, whereas for HMMs with temporal heterogeneity (or covariate-dependent transitions more generally) the number increases quadratically (Eq. 3). When comparing BICs, it is important to account for the tradeoff between log-likelihood and number of states, but also log-likelihood and number of free parameters.

We used simulations to predict expected hourly step lengths and autocorrelation functions (ACF). While the computation of expected step length and ACF is straightforward for FMMs, and feasible for homogeneous HMMs, the interaction between the geometric dwell time within each state and the temporally varying interaction probabilities makes it infeasible for more complex models. We used this approach to validate our models, comparing our simulated predictions with the observed movements. The more usual approach, generating predictions from the expected step lengths conditional on the most likely state sequence predicted by the Viterbi algorithm or pseudo-residuals [6, 21], is somewhat problematic because the predictions by these methods rely on the observed data. These approach is useful to predict missing data in the observation sequence, but because it is conditional on the observed values, it can not reliably evaluate goodness of fit for the different structural complexities of HMM models.

Results

The simulation agrees with our hypothesis that homogeneous transition HMMs can over estimate the number of hidden states. Heterogeneous transition models can always predict the correct number of states, whereas the temporally homogeneous models overestimate the number of states (based on BIC-optimality: Figure 1).

The BIC-optimal number of states for time homogeneous models is consistent with van de Kerk et al.'s [14] results. For time homogeneous models, the Weibull-wrapped-Cauchy [14], Weibull von Mises, and log Normal without turn-

ing angles all identify the same BIC-optimal number of states. Furthermore, the homogeneous-HMM models do vary among models (different step-length distributions, with/without turning angles) in how many states they identify, whereas, the heterogeneous-HMM models are consistent among models (Figure 2).

Models with temporal heterogeneity are better (lower BIC) than homogeneous models in both FMM and HMM frameworks, but time-homogeneous HMMs are better than FMMs with sinusoidal temporal heterogeneity (Figure 3). Turning to the temporally heterogeneous HMMs (Figure 3, right panel), we see that the model with different transition probabilities for each hour of the day (HMM + THhourly) is overparameterized; it underperforms homogeneous HMM with even 3 states, and gets much worse with 4 states. The multiple-block model gives approximately the same BIC as the homogeneous HMM, although it gives the BIC-optimal number of states as 4, in contrast to 6 for the homogeneous HMM. Finally, the quadratic and sinusoidal models are the best models tested by far; they both give the BIC-optimal number of states as 5, and they have similar goodness of fit. However, this similarity is overstated due to the very large variation in BIC (over thousands of units) across the full range of models; there is a difference of approximately 80 BIC units, which would normally be interpreted as an enormous difference in goodness of fit, between the sinusoidal and quadratic models (both of which have 90 parameters).

The average hourly step lengths from the observed panther data exhibit a clear diurnal pattern (Figure 4). As expected, temporally homogeneous models (whether FMM or HMM) predict the same mean step length regardless of time of day, failing to capture the diurnal activity cycle. All of the models incorporating temporal heterogeneity, including the temporally heterogeneous FMM, can capture the observed patterns. However, the block model does markedly worse than the other temporal models (changing the block definitions might help by re-clustering/grouping different hours or increasing the number of blocks), and the (overparameterized)

hourly model does better than any other model at capturing the early-evening peak (but worse at capturing the mid-day trough). We also included average hourly step lengths from three-state temporally homogeneous HMM Viterbi prediction to illustrate within sample predictions can capture the diurnal patterns, but fail to capture out of sample predictions.

Like the diurnal pattern (Figure 4), the strong autocorrelation of the observed step lengths at a 24-hour lag (Figure 5) shows the need to incorporate temporal heterogeneity in the model — we could have reached this conclusion even without developing any of the temporal-heterogeneity machinery. In contrast to the hourly averages, the autocorrelation (ACF) captures both short- and long-term temporal effects. HMM without temporal heterogeneity captures the short-term autocorrelation, but misses the long-term autocorrelation beyond a 7-hour lag. Temporally homogeneous FMMs, by definition, produce no autocorrelation (neither short- nor long-term autocorrelation). FMMs without temporal heterogeneity, although they capture the diurnal pattern well, underpredict the degree of short-term autocorrelation.

The estimated emission parameter values (mean and standard deviation of the step length in each state) are similar, for both homogeneous and heterogeneous models, across all cats (Figure 7 shows a subset of cats). In general, the states with longer mean step lengths are similar between homogeneous and heterogeneous models. For cats 14 and 15, the states with the longest or next-longest mean step lengths have similar means and standard deviations; for cats 1 and 2, three long-step states in the homogeneous HMM appear to divide two long-step states in the heterogeneous HMM. For short-step states, the heterogeneous HMM tends to identify a high-variance state, while the homogeneous HMM picks up states with very short step lengths (questionable in any case because we have not taken any special efforts to account for GPS error).

307 Discussion

308 HMMs are a widely used and flexible tool for modeling animal movement be-
309 haviour; we need to work harder to make sure they are both appropriately com-
310 plex and biologically interpretable. With the increasing volumes of movement data
311 available, ecologists who naively use traditional homogeneous HMMs and standard
312 information-theoretic criteria to estimate the number of behavioural states will gen-
313 erally overfit their data, in the sense of “discovering” large number of states that
314 are difficult to interpret biologically.

315 On a broad spectrum, it really depends on what kind of question that is being
316 answered. On one side of the spectrum, if the goal is to identify states, it might
317 be sufficient to use a simple/traditional HMM model and pre-specify the number
318 of states and, post hoc, match Viterbi-based states estimates with environmental
319 variation [7]. In our panther study, it is really hard to interpret multiple latent
320 states biologically. We have no way of knowing what panthers are actually thinking
321 (it is certainly more complex than being in one of a small number of discrete latent
322 states); we don’t know the “true” number of latent states, nor are we able to observe
323 them directly, although incorporating additional direct observations of behaviour (if
324 available) can at least partially address this problem [7]. Three distinct movement
325 states seem biologically interpretable for Florida panthers according to van de Kerk
326 et al. [14]: Short step length suggests resting states, intermediate step length a
327 foraging state, and long step length a traveling state.

328 On the other side of the spectrum, if the goal of interest is to make predictions
329 (out of sample), it might be better to fit a covariate-dependent model so that we can
330 explicitly model the switching process. In that case, fitting a covariate-dependent
331 model is better for out of sample prediction because Viterbi can only estimate state
332 occupancy if observed movements are available (within sample predictions).

333 Finally, if we want to estimate the number of states, BIC is not necessarily good
334 for estimation of number of states [24], but it can be useful as an approximate
335 upper limit estimate. This is a common problem when using BICs, thus, the "knee
336 point" (jump point) was proposed for BIC in partitioning based clustering via angle-
337 based method [25]. A similar method was used with likelihood [16] where both are
338 applicable in our case, and suggest fewer number of states, but we do not know the
339 reliability when fitting more complex models (ie. the shape of the BIC curve can be
340 affected by the non-linear increase of parameters with every additional state).

341 Incorporating temporal heterogeneity in animal movement is one step in the right
342 direction, but much remains to be done. Our model neglects other predictors, such
343 as habitat type or location with respect to environmental features such as roads,
344 that can potentially improve goodness of fit and predictions and further reduce the
345 estimated number of states. While adding more covariates is in principle straight-
346 forward using existing frameworks, including all possible biological complexities in
347 a HMM with state-dependent transitions may rapidly become intractable in terms
348 of both computational time and complexity of choosing among possible reduced
349 models and numbers of states. Better diagnostic procedures and tests are needed:
350 these can both test overall goodness-of-fit [26] and, more importantly, localize fit-
351 ting problems to particular aspects of the data so that models can be constructed
352 without needing to include all possible features of interest. Because there are a
353 huge number of potential complexities that can be added to movement models (e.g.
354 spatial/temporal/among-individual heterogeneity; effects of conspecific attraction
355 or avoidance; memory or cognitive effects), each with associated costs in researcher
356 and computational effort, such diagnostic plots are invaluable.

357 Conclusion

358 We have presented a relatively simple but little-used extension (time-dependent
359 transitions) that partly resolves the problem. Time-dependent transitions appear to

offer a simple way to (1) reduce the selected number of states closer to a biologically interpretable level; (2) capture observed diurnal and autocorrelation patterns in a predictive model; (3) improve overall model fit (i.e., lower BIC) and reduce the level of complexity (number of parameters) of the most parsimonious models. Simple simulations where the true number of states is known, and transitions among states vary over time, confirm that using BIC with homogeneous HMMs overestimates the number of behavioural states, while time-dependent HMMs correctly estimate the number.

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Ethics approval

All data used are secondary, drawn from an existing institutional data repository.

Consent for publication

Not applicable.

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1 Data accessibility

Hourly step lengths and turning angles of male and female Florida panthers available at <http://ufdc.ufl.edu/IR00004241/00001>.

Authors' contributions

ML designed analyses and simulations; ran analyses and simulations; and co-wrote the text of the paper. BMB designed analyses and simulations and co-wrote the text of the paper.

Competing interests

The authors declare that they have no competing interests.

Author details

¹ Department of Biology, McMaster University, 1280 Main St. West, L8S 4K1, Hamilton, Ontario, Canada. ² Department of Mathematics and Statistics, McMaster University, 1280 Main St. West, L8S 4K1, Hamilton, Ontario, Canada.

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455 **Tables**

Table 1 Cat ID and number of observations; ID numbers are given matching those shown by van de Kerk et al. 2015 and those in the data located at the UF Institutional repository (IR@UF).

van de Kerk 2015	IR@UF	Number of Observations
130	1	10286
131	2	9458
48	14	14645
94	15	10250

456 **Figures**

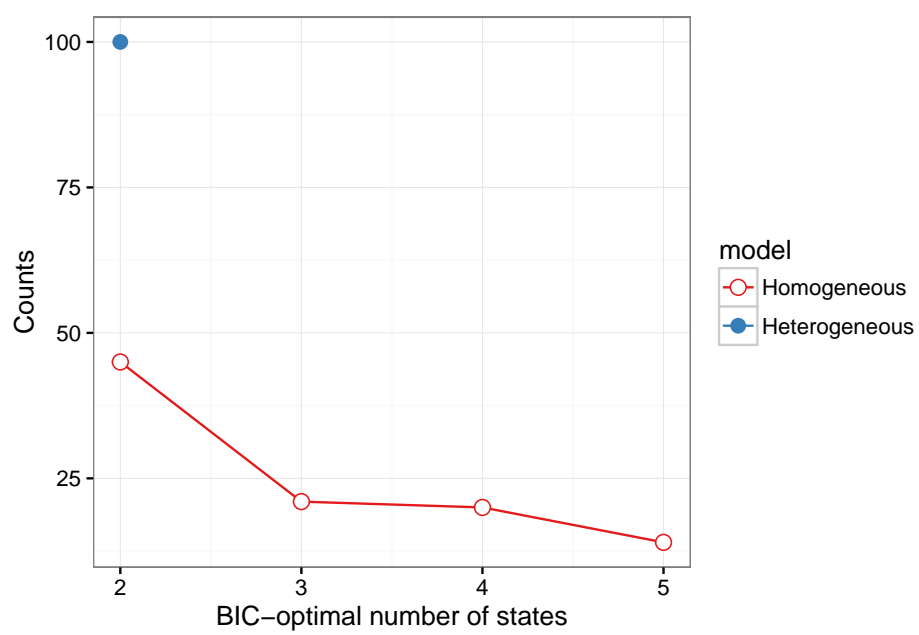


Figure 1 Simulation Results BIC-optimal state frequency for 2-6 state HMMs with and without covariate transition on 100 two-state hidden Markov models with covariate transitioning simulations.

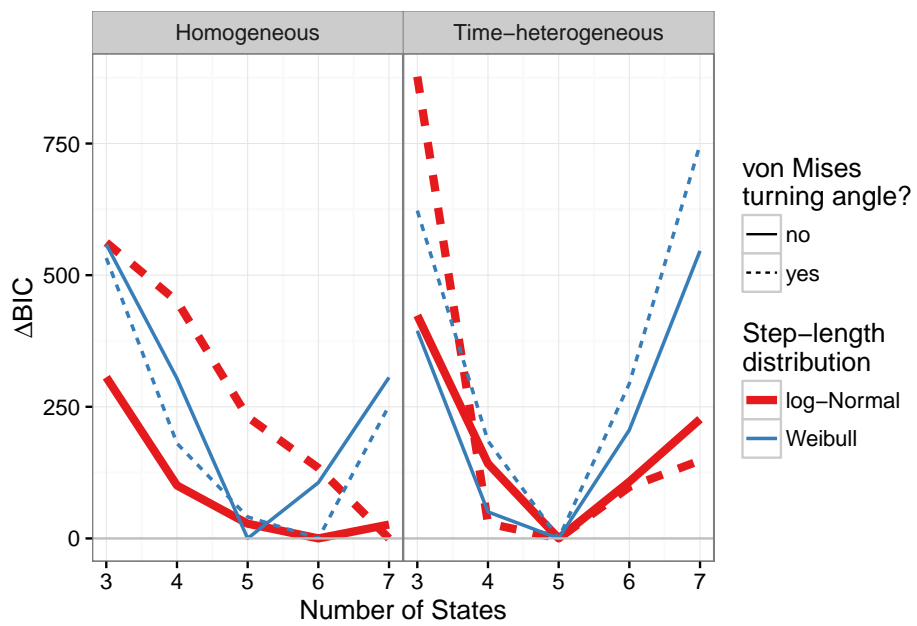


Figure 2 Adjusted BIC Emission Distribution Comparison Adjusted Bayesian information criterion values for 3-7 state HMMs with different step-length distributions, with and without temporal transitions and turning angles.

