COMMENTS FROM NANCY

Inferring Fine-Scale Animal Behaviors using Hidden Markov Models

You might as well start using the Canadian Journal of Statistics style guide - you can get it here. https://onlinelibrary.wiley.com/page/journal/1708945x/homepage/forauthors.html sample.pdf gives instructions for format.

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June 5, 2020

For instance - abstract is typically about 10 lines long. So some of your abstract can go into intro.

Proof goes in the appendix,

Abstract

The field of animal movement is in the midst of a "data renaissance" where advancements in tagging technology have given rise to an explosion of data available for statistical modeling. In particular, tagging technologies are capable of recording observations at rates of tens of hertz, resulting in time series containing millions of observations over the course of several hours. This results in a vast amount of data which often exhibits many different simultaneous behavioral processes occurring at different time scales.

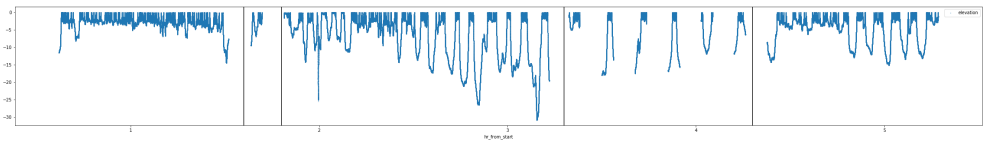
One solution to this issue is to use a hierarchical hidden Markov model (HHMM). HHMMs model the entire system as a nested structure of hidden Markov models (HMM) where each HMM corresponds to one behavioral process. One nice property of HHMMs is that its likelihood is relatively easy to compute, facilitating fast maximum likelihood estimates for its associated parameters.

At the shortest time scales, however, observations often exhibit complicated dependence structures which cannot be easily captured by a traditional HMMs. To address this issue, it is possible to model small-scale animal behavior as the solution to some stochastic differential equation, but these methods tend to be computationally intractable and require approximate inference techniques such as Markov-chain Monte Carlo (MCMC).

This work investigates how to incorporate fine-scale processes into the larger structure of hierarchical hidden Markov models while maintaining computational efficiency. We bridge the gap between discrete hidden Markov models and continuous-time stochastic process models by showing that the two are equivalent under certain conditions. In addition, we extract features from highly structured sub-dive behaviors using signal processing techniques. These features otherwise could not be modeled with a simple HMM. Finally, we apply our method to dive data collected from two Northern resident killer whales off the coast of British Columbia, Canada.

1 Background

Hidden Markov models are useful when inferring a single unobserved process, but biological processes often involve multiple simultaneous hidden processes which can occur and at different time scales. For example, a preliminary observation of the killer whale dive data shown in figure (1) shows that the behavior of this killer whale changes between approximately hour-long periods of predominately short, shallow dives and long, deep dives. Leos-Barajas et al. encounter a similar issue when modeling the movement of a harbor porpoise in the North Sea, and use it as a motivating example when they introduce hierarchical hidden Markov models.



Nice motivating graphic. It will need more explanation (but you probably know that).

Figure 1: Raw depth data of a Killer Whale off the coast of British Columbia, Canada.

Is there any reason to use X_t for states rather than the more usual S_t?
And I think usually papers talk about distributions f_1,..., f_N - one for each state, rather than listing parameters.

1.1 Hidden Markov models

it's good to say that the index is usually time

Hidden Markov models (or HMMs) are comprised of an unobserved Markov chain $X = (X_1, \ldots, X_T)$ and a sequence of (possibly high-dimensional) observations $Y = (Y_1, \ldots, Y_T)$, each of length T. In the field of animal movement, the

you can introduce X_t and Y_t notation here: a sequence of unobserved states, X_t, t=1,...,T and a sequence of .... Y_t, t=1,...,T. The X_t's form a Markov chain. You don't use the X, Y vector notation until further along. So I don't think you need it here - go with the X_t's and Y_t's for awhile. I think that is the more common structure in HMM papers. Up in here, you can say that the Y_t's are often called "emissions".

unobserved chain X usually represents the latent behaviour of an animal (e.g. foraging, resting, migrating, etc.), while the observations Y are often a series of step lengths and turning angles for land animals and either depth or accelerometer data (or both) for marine animals. Each random variable in the unobserved chain X_t can take one of N possible values, and X has corresponding probability transition matrix $\Gamma \in \mathbb{R}^{N\times N}$ and initial distribution $\delta \in \mathbb{R}^N$:

$$\delta_i = Pr(X_1 = i) \qquad i=1,\ldots,N$$

$$\Gamma_{ij} = Pr(X_{t+1} = j | X_t = i) \qquad \forall t \in \{1,\ldots,T-1\}$$

Further, each random variable X_t emits an observation Y_t whose distribution depends only on the value of X_t and ~~none of the preceding observations or behavioral states:~~ $p_\theta(y_t|x_t, x_{t-1},\ldots,x_1, y_{t-1},\ldots,y_1) = p_\theta(y_t|x_t)$. ~~Note that the emission distribution depends upon parameters θ.~~ A visualization of this dependence structure can be seen in figure (2).

The probability transition matrix Γ and the parameters of the emission distributions θ can be estimated by maximizing the likelihood of the observed data y, $\mathcal{L}_{\text{HMM}}(y;\theta,\Gamma,\delta)$, with respect to Γ, δ, and θ. In addition, $\mathcal{L}_{\text{HMM}}(y;\theta,\Gamma,\delta)$ can be calculated using the *forward algorithm* as follows:

$$\mathcal{L}_{\text{HMM}}(y;\theta,\Gamma,\delta) = \delta P(y_1;\theta)\left(\prod_{t=2}^{T}\Gamma P(y_t;\theta)\right)\mathbf{1}$$

where:

$$P(y_t;\theta) = \text{diag}(p_\theta(y_t|X_t = x_1),\ldots,p_\theta(y_t|X_t = x_N))$$

and $\mathbf{1}$ is an N-dimensional column vector of ones. In order to ensure identifiability and right-stochasticity after optimizing $\mathcal{L}_{\text{HMM}}(y)$, Γ is often parameterized using $\eta \in \mathbb{R}^{N\times N}$ and the following link function:

$$\Gamma_{ij} = \frac{\exp(\eta_{ij})}{\sum_{k=1}^{N}\exp(\eta_{ik})}, \qquad \eta_{ii} = 0 \quad \forall i \in \{1,\ldots,N\}.$$

This allows for unconstrained optimization over η and removes the constraint that Γ be right-stochastic. $\mathcal{L}_{\text{HMM}}(y;\theta,\Gamma,\delta)$ can be maximized using any numerical optimizer.

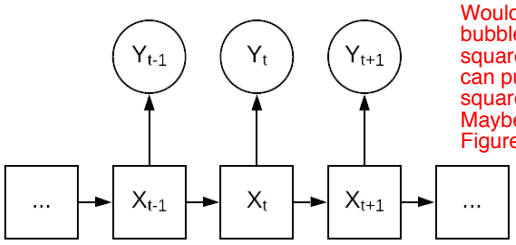


Figure 2: Graphical representation of a traditional HMM.

1.2 Hierarchical HMMs

A hierarchical hidden Markov model (or HHMM) is a variation on a hidden Markov model in which each hidden state of the original HMM X_t emits both an observation Y_t as well as another fine-scale hidden Markov model of length T_t^*. This fine-scale HMM is comprised of a fine-scale Markov chain $X_t^* = (X_{t,1}^*,\ldots,X_{t,T_t^*}^*)$ and fine-scale observations $Y_t^* = (Y_{t,1}^*,\ldots,Y_{t,T_t^*}^*)$. As before, each fine-scale observation Y_{t,t^*}^* depends only on the value of its corresponding hidden state, X_{t,t^*}^*, which can take one of N^* values. X_t^* is characterized by an initial distribution $\delta^{*(X_t)} \in \mathbb{R}^{N^*}$ and probability transition matrix $\Gamma^{*(X_t)} \in \mathbb{R}^{N^*\times N^*}$:

$$\delta_i^{*(x_t)} = Pr(X_{t,1}^* = i | X_t = x_t) \qquad i=1,\ldots,N^*$$

$$\Gamma_{ij}^{*(x_t)} = Pr(X_{t,t^*+1}^* = j | X_{t,t^*}^* = i, X_t = x_t) \quad \forall t^* \in \{1,\ldots,T_t^*-1\} \qquad i,j = 1,\ldots,N^*$$

The fine-scale emission probabilities $p_{\theta^{*(X_t)}}(y_{s,t}^*|x_{s,t}^*)$ are parameterized by $\theta^{*(X_t)}$. Note the parameters of the fine-scale hidden Markov model ($\Gamma^{*(X_t)}$, $\delta^{*(X_t)}$, and $\theta^{*(X_t)}$) all depend upon the hidden state of the *crude-scale* hidden Markov

"Discretion of researcher" - best to say something like "depending on the behaviour and responses being modelled"

I wouldn't use the term "independent" unless you mean it in the statistical sense.

model. However, depending upon the discretion of the researcher, it is possible to force any of these parameters to be independent of the crude-scale hidden state X_t. A visualization of the full structure of the HHMM can be seen in figure (3). Due to the nested structure of a hierarchical hidden Markov model, the likelihood of an HHMM is still easy to calculate using the forward algorithm:

$$\mathcal{L}_{\text{HHMM}}(y, y^*; \theta, \theta^*, \Gamma, \Gamma^*, \delta, \delta^*) = \delta P(y_1, y_1^*; \theta, \theta^*, \Gamma^*, \delta^*) \prod_{t=2}^{T} \Gamma P(y_t, y_t^*; \theta, \theta^*, \Gamma^*, \delta^*)\mathbf{1}$$

where: confusing notation in the conditioning statement. Do you mean x_t=s_1, x_t=s_N? we have x_1,..., x_T

$$P(y_t, y_t^*; \theta, \theta^*, \Gamma^*, \delta^*) = \text{diag}\left[p_\theta(y_t|x_t = x_1)\mathcal{L}_{\text{HMM}}\left(y_t^*; \theta^{*(x_1)}, \Gamma^{*(x_1)}, \delta^{*(x_1)}\right), ..., \right.$$
$$\left. p_\theta(y_t|x_t = x_N)\mathcal{L}_{\text{HMM}}\left(y_t^*; \theta^{*(x_N)}, \Gamma^{*(x_N)}, \delta^{*(x_N)}\right)\right]$$

Note that this formulation assumes that the crude-scale observations at a given time Y_t and the fine-scale observation time series Y_t^* are independent of one another when conditioned on X_t. For more information on specific considerations for HHMMs such as incorporating covariates into the probability transition matrix, model selection and model checking, see Adam et al [1].

The word "coarse" is good, "crude" not so good, because of its other meanings.

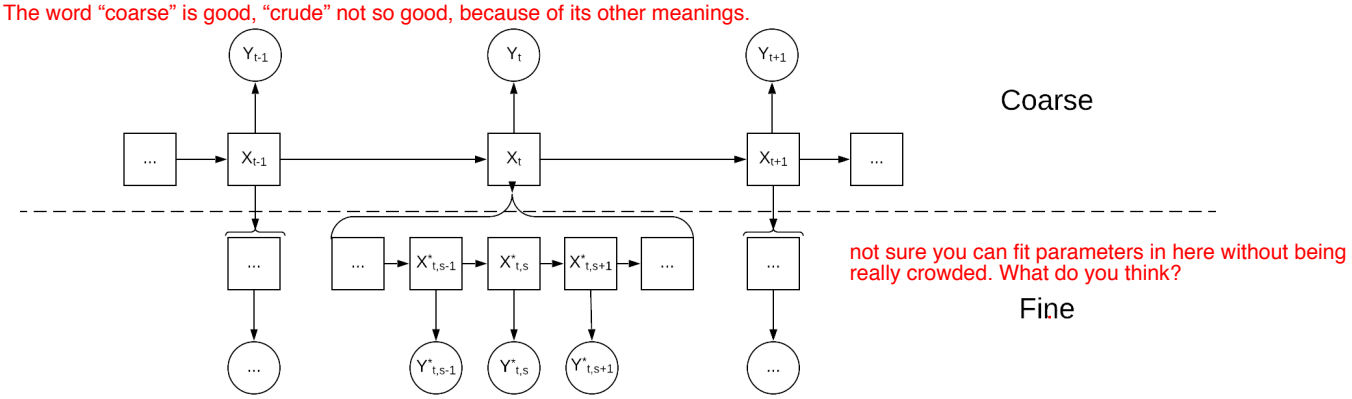


Figure 3: Graphical representation of a traditional HHMM.

1.3 Conditionally auto-regressive HMMs

One of the key assumptions of both HMMs and HHMMs is *conditional Independence* between observations at both the crude and fine scale. Namely, given the state X_t or X_{t,t^*}^*, Y_t or Y_{t,t^*}^* (respectively) is assumed to be independent from all other observations. Therefore, traditional HMMs and HHMMs can fail when the observation sequence Y exhibits significant auto-correlation in time. Examples include fluking in marine mammals in Vancouver, BC (see the results section) and the swimming behavior of horn sharks off the coast of Southern California [1].

One way to deal with auto-correlation in fine-scale behavioral processes is to use a state-switching continuous model such as the one introduced by Michelot et al [5], which models the movement of an animal as an Ornstein-Uhlenbeck process with parameters that depend upon the underlying behavioural state of the animal. Continuous time models are advantageous because of their flexibility: they can be built up from arbitrarily complex stochastic differential equations and they allow for uneven step lengths in the observations sequence Y. However, most continuous time models require MCMC algorithms to perform inference over and as a result are not easily incorporated into the HHMM structure.

Another option is to use the CarHMM, or *conditionally auto-regressive hidden Markov model*, introduced by Lawler et al [4]. The CarHMM explicitly models auto-correlation into the emission distributions of the HMM while maintaining the structure needed to run the forward algorithm. In particular, if the emission distribution of observation Y_t is parameterized by its mean and variance, i.e. $\theta_{x_t} = \{\mu_{x_t}, \sigma_{x_t}^2\}$, the CarHMM assumes that an observation Y_t has mean $(1-\phi_{x_t}) \cdot \mu_{x_t} + \phi_{x_t} \cdot y_{t-1}$ rather than μ_{x_t}. This introduces one new parameter, ϕ_{x_t}, which represents the auto-correlation of y_t and depends upon the behavioral state of the animal. This model easily fits into the HHMM structure, but seems to lack the natural

interpretation of continuous-time models. However, we prove in the following section that under certain conditions these two models are in fact equivalent.

The likelihood of CarHMM is still compatible with the forward algorithm:

$$\mathcal{L}_{\text{CarHMM}}(y) = \delta \prod_{t=2}^{T} \Gamma P(y_t;\theta)\mathbf{1} \tag{1}$$

where:

$$P(y_t;\theta) = \text{diag}(p_\theta(y_t|y_{t-1}, X_t = x_1), ..., p_\theta(y_t|y_{t-1}, X_t = x_N)), \qquad t > 1$$

and the first observation y_1 is assumed to be fixed as an initial value. The graphical model associated with the structure of a CarHMM is shown in figure (4).

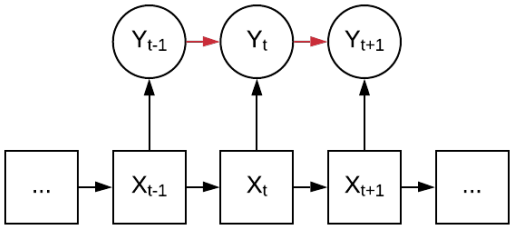


Figure 4: Graphical representation of a traditional CarHMM. The additional arrows representing auto-correlation between observations are shown in red for emphasis.

1.4 State decoding

Once an HMM, HHMM, or CarHMM model is fit using by maximizing ~~their~~ its respective likelihoods with respect to ~~their~~ parameters, it is common to find the most likely sequence of hidden states $\hat{X}$. This is often done using a dynamic programming algorithm called the Viterbi algorithm [6]. In the case of HHMMs, after running the Viterbi algorithm on the coarse-scale process X, it can be run again on each fine-scale process X_t^* to find the mostly likely sequence of fine-scale hidden states $\hat{X}_t^*$ conditioned on the estimated crude-state value $\hat{X}_t$. Note that while $\hat{X}$ is a maximum likelihood estimate of X, $\hat{X}_t^*$ is *not* necessarily a maximum likelihood estimate of $\hat{X}_t^*$ because it is conditioned on the value of $\hat{X}_t$.

While the Viterbi algorithm is the de-facto standard in the current ecology literature, we suggest to instead find the *probability* of each crude-level state (conditioned on the learned parameters) using the *forward-backward algorithm*. The forward-backward algorithm has the same time complexity as the forward algorithm and is also used to find the *psuedoresiduals* of a given model, which is an important tool for model validation. In addition, for HHMMs the forward-backward algorithm can be used recursively to find the probability of the fine-level states $X_{s,t}^*$ exactly by marginalizing out X_t:

$$P(X_{s,t}^* = x_{s,t}^*) = \sum_{n=1}^{N} P(X_t = x_n) P(X_{s,t}^* = x_{s,t}^* | X_t = x_n)$$

where $P(X_t = x_n)$ can be found using the forward-backward algorithm on the crude-level Markov chain and $P(X_{s,t}^* = x_{s,t}^* | X_t = x_n)$ can be found by running the forward-backward algorithm on the fine-level HMM for every possible value of X_t.

2 Results regarding CarHMMs and the Ornstein-Uhlenbeck process

2.1 Equivalence of CarHMM and OU process

Once the CarHMM is fit by maximizing the likelihood in equation (1), the emission distributions can be interpretted as the solution of a state-switching Ornstein-Uhlenbeck process similar to the one introduced by Michelot et al [5]. In order for this to be the case, however, the following two conditions must be met:

1. The underlying behavioral state of the continuous-time model must follow a Markov chain rather than a Markov process.
2. The emission distributions of the CarHMM must be normal.

If this is the case, then the CarHMM is equivalent to a state-switching Ornstein-Uhlenbeck process. This gives new interpretation to the learned parameters of the CarHMM in the context of continuous-time model.

2.1.1 Proof

You need to call something a theorem in order to use the word "proof".

A one-dimensional state-switching Ornstein-Uhlenbeck process y is the solution to the following stochastic differential equation:

$$dy_t = \beta_{x_t}(\gamma_{x_t} - y_t)dt + \omega_{x_t}dW_t$$

where x_t is the fine-scale behavior of the animal at time t, β_{x_t} relates to rate at which the process returns to its mean value, γ_{x_t} is the long-term mean value of the process, ω_{x_t} is related to short-term variance, and W is a Wiener process. x_t is described by an unobserved Markov process. Here, $t \in \mathbb{R}$ is a continuous time stamp rather than an index. If the behavioral state x_t does not change between observations (i.e. x_t follows a Markov chain), the solution to this equation is known to be the following [5]:

$$y_{t+\Delta t}|x_{t:t+\Delta t} \sim \mathcal{N}\left((1 - e^{-\beta_{x_t}\Delta t})\gamma_{x_t} + e^{-\beta_{x_t}\Delta t}y_t, \quad \frac{\omega_{x_t}^2}{2\beta_{x_t}}(1 - e^{-2\beta_{x_t}\Delta t})\right)$$

Now, suppose that Δt is constant for all observations, as is the case for hidden Markov models. In addition, introduce the following transformations:

$$\mu_{x_t} = \gamma_{x_t}, \qquad \phi_{x_t} = e^{-\beta_{x_t}\Delta t}, \qquad \sigma_{x_t}^2 = \frac{\omega_{x_t}^2}{2\beta_{x_t}}(1 - e^{-2\beta_{x_t}\Delta t}) \tag{2}$$

Then, almost immediately we can see the following:

$$y_{t+\Delta t}|x_{t:t+\Delta t} \sim \mathcal{N}\left((1 - \phi_{x_t})\mu_{x_t} + \phi_{x_t}y_t, \quad \sigma_{x_t}^2\right)$$

If Δt is fixed and x_t is adjusted to follow a Markov chain rather than a Markov process, then this model is equivalent to the CarHMM with normal emission probabilities. Note that all of the parameter transformations above are one-to-one, so it is easy to go from the CarHMM to the continuous model and back again. This allows for the principled construction of the continuous-time model to be combined with the computational convenience of the CarHMM.

2.2 Generalization to unequal time steps

Using this intuition, we generalize the CarHMM to data with unequal time steps Δt. First, it is necessary to assume that the behavioral state x_t only changes once between observations, which is a fair assumption if each time step Δt is sufficiently small. Next, the following definitions are introduced:

$$\Gamma_{\Delta t,\Lambda} = \begin{pmatrix} 1 - e^{-\lambda_1\Delta t} & p_{12}e^{-\lambda_1\Delta t} & \dots & p_{1N}e^{-\lambda_1\Delta t} \\ p_{21}e^{-\lambda_2\Delta t} & 1 - e^{-\lambda_2\Delta t} & \dots & p_{2N}e^{-\lambda_2\Delta t} \\ \vdots & \vdots & \ddots & \vdots \\ p_{N1}e^{-\lambda_N\Delta t} & p_{N2}e^{-\lambda_N\Delta t} & \dots & 1 - e^{-\lambda_N\Delta t} \end{pmatrix}$$

where $\Lambda = \{p, \lambda\}$, p_{ij} is the probability that the animal moves from state i to state j given that it left state i, and λ_i is the rate at which the animal leaves behavioral state i. Finally, we just note that the parameters in equation (2) become functions of the time step between observations Δt:

$$\mu_{x_t} = \gamma_{x_t}, \qquad \phi_{x_t}(\Delta t) = e^{-\beta_{x_t}\Delta t}, \qquad \sigma_{x_t}^2(\Delta t) = \frac{\omega_{x_t}^2}{2\beta_{x_t}}(1 - e^{-2\beta_{x_t}\Delta t})$$

Then the likelihood of the CarHMM with unequal time steps is the following:

$$\mathcal{L}_{\text{CarHMM}}(y; \theta, \Lambda, \delta) = \delta \prod_{t=2}^{T} \Gamma_{\Delta t,\Lambda} P(y_t; \theta)\mathbf{1}$$

You can't assume that's true in a mathematically rigorous proof. It's just not true. You'd have to split off a set where there is more than one state change and show that probability of that set goes to zero as delta t goes to zero. Then you'd have to worry about the calculations on the set where there is only one state change. I don't know how challenging it would be to have a rigorous proof. But what you have here is not appropriate for CJS.

where:

$$P(y_t;\theta) = \text{diag}(p_\theta(y_t|y_{t-1},\Delta t, X_t = x_1), ..., p_\theta(y_t|y_{t-1},\Delta t, X_t = x_N)), \qquad t > 1$$

and:

$$p_\theta(y_t|y_{t-1},\Delta t, X_t = x_t) = \mathcal{N}\left((1-\phi_{x_t}(\Delta t))\mu_{x_t} + \phi_{x_t}(\Delta t)y_{t-1}, \quad \sigma^2_{x_t}(\Delta t)\right).$$

now $\mathcal{L}_{\text{CarHMM}}(y;\theta,\Lambda,\delta)$ is simply maximized with respect to $\theta = \{\beta,\omega,\gamma\}$, $\Lambda = \{p,\lambda\}$, and δ to find the maximum likelihood estimate of the CarHMM with uneven time steps.

3 Model Formulation

3.1 Short-time Fourier Transform on Fine-scale process

One issue with the CarHMM is that it assumes Markovian dynamics conditioned on the hidden state, i.e. that any observation Y^*_{t,t^*} depends only on the behavioral state X^*_{t,t^*} and Y^*_{t,t^*-1} (here we focus on the fine-scale process). However, there are many animal movement processes which violate this Markov property on very fine scales. For example, swimming behaviour of marine mammals can be periodic since the animal repeatedly flukes to propel itself forward. Work has been done in the past to model non-Markovian dynamics in the *behavioural* process X^*_t [3], but addressing non-Markovian dynamics within the observation process Y^*_t is still a relatively unstudied area (MAYBE?). With improvements in tagging technology allowing for data collection at very high frequencies, data exhibiting noisy and non-Markovian fine scale behavior is likely to persist.

To address this issue, we recommend borrowing techniques from the signal processing literature to compress the data and summarize its essential elements. In particular, we suggest performing the discrete-time Short-time Fourier Transform (STFT) over each observed fine-scale process Y^*_t:

$$STFT\{Y^*_{t,t^*:t^*+w-1}\}(n) := \hat{Y}^{*(n)}_{t,t^*} = \sum_{n=0}^{w-1} Y^*_{t,t^*+n} e^{-i\frac{2\pi k}{w}n} \qquad \forall n \in \{0,\dots,w-1\}, \quad t^* \in \{1, w+1, 2w+1, \dots, w\left(\lfloor T^*_t/w \rfloor - 1\right)+1\}.$$

The STFT slides a moving window of length w across the time series Y^*_t with a step size of w and transforms the domain of each window from time to frequency. This allows the spectrum of Y^*_t at time t^* to be summarized by a w-dimensional vector of Fourier coefficients. While other step sizes can be used for the sliding window, we select w to avoid serial dependence between windows.

If $Y^*_t \in \mathbb{R}^{T^*_t}$, then $\hat{Y}^*_t \in \mathbb{C}^{\lfloor T^*_t/w \rfloor \times w}$. Although this allows Y^*_t to be represented in a way that eliminates obvious periodic behavior, the data set itself is still approximately as large as Y^*_t itself. To reduce the size of $\hat{Y}^*_t$, we propose taking summary statistics of each window as follows:

$$Z^{*(1)}_{t,t^*} = \mathcal{R}\left(\hat{Y}^{*(0)}_{t,t^*}\right) \qquad Z^{*(2)}_{t,t^*} = \frac{1}{w}\sum_{n=1}^{\tilde{f}} |\hat{Y}^{*(n)}_{t,t^*}|^2$$

$Z^{*(1)}_{t,t^*}$ is equal to the average value of $Y^*_{t,t^*:t^*+w-1}$, and $Z^{*(2)}_{t,t^*}$ is equal to the squared 2-norm of the component of $Y^*_{t,t^*:t^*+w-1}$ that can be attributed to frequencies in the signal between 1 and $\tilde{f}$ periods per window length. Both the window length w and the max frequency $\tilde{f}$ are tuning parameters that should be tuned in a problem-specific way. w should be long enough to capture the periodic behavior of the underlying process (at least as long as the length of a period), but short enough to avoid over-smoothing of the data and to maintain high resolution in the behavioral process X^*. $\tilde{f}$ should be selected such that the maximum frequency of Y^*_t that makes biological sense is $\tilde{f}$ per window length. Note that these summary statistics are just one possible choice, and future studies can adjust the definitions as needed. A visualization of transforming a one-dimensional sequence Y^* to Z^* can be seen in figure (5).

Finally, note that it is possible to accomodate for unequal time steps within each window by using the **non-uniform discrete Fourier transform (NDFT)**. We do not describe the details of this method in this work, but the generalization is straightforward. Refer to Bagchi et al [2] for details.

3.2 Model Structure: combining the HHMM and CarHMM

Hierarchical hidden Markov models can be used to jointly model simultaneous coarse-scale and fine-scale processes taking place simultaneously. However, as mentioned before, the fine-scale process Y^* can often exhibit autocorrelation and intricate structure. Transforming Y^*_t to Z^*_t removes fine-scale periodic behavior, but Z^*_t can still exhibit autocorrelation, especially in the window averge, $Z^{*(1)}_{t,t^*}$. Therefore, we replace the fine-scale HMM within the Hierarchical HMM with a CarHMM according to figure (6).

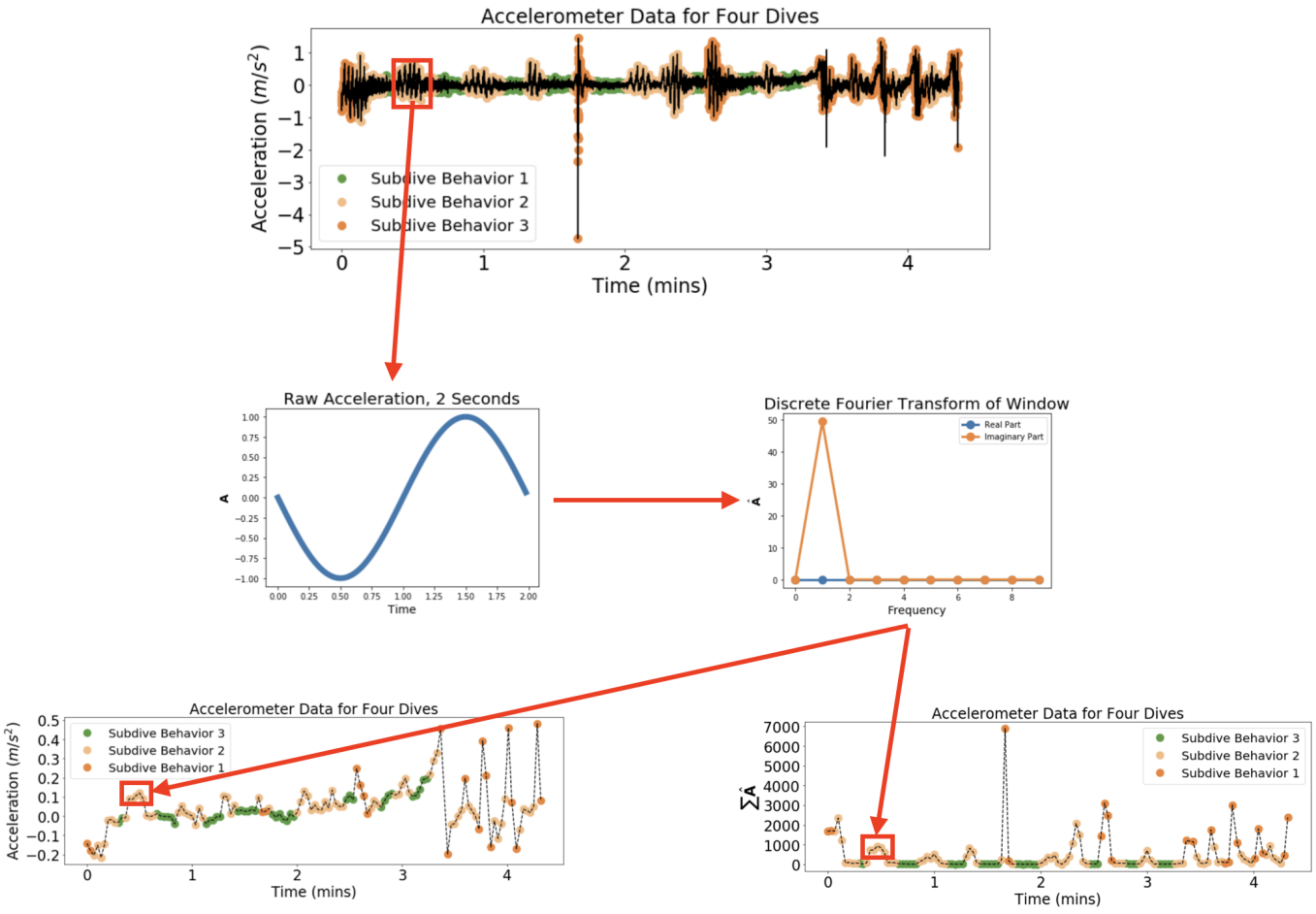


Figure 5: Visualization of transforming Y_t^* into Z_t^* using a sliding window and fourier transform.

The likelihood of this model is still easy to calculate using the forward algorithm:

$$\mathcal{L}_{\text{CarHHMM}}(y, z^*; \theta, \theta^*, \Gamma, \Gamma^*, \delta, \delta^*) = \delta P(y_1, z_1^*; \theta, \theta^*, \Gamma^*, \delta^*) \prod_{t=2}^{T} \Gamma P(y_t, z_t^*; \theta, \theta^*, \Gamma^*, \delta^*) \mathbf{1}$$

where:

$$P(y_t, z_t^*; \theta, \theta^*, \Gamma^*, \delta^*) = \text{diag}\left[p_\theta(y_t | X_t = x_1)\mathcal{L}_{\text{CarHMM}}\left(z_t^*; \theta^{*(x_1)}, \Gamma^{*(x_1)}, \delta^{*(x_1)}\right), ..., \right.$$
$$\left. p_\theta(y_t | x_t = x_N)\mathcal{L}_{\text{CarHMM}}\left(z_t^*; \theta^{*(x_N)}, \Gamma^{*(x_N)}, \delta^{*(x_N)}\right)\right]$$

4 Simulation Study

4.1 Data Simulation

mammal?

To test the CarHHMM with STFT, a sequence of 100 marine-animal dives were simulated. The coarse-scale observations Y were set as the duration of each dive, and the fine-scale observations Y^* were set as one dimensional acceleration readings simulated at 50 hertz. Specifically, the following procedure was followed:

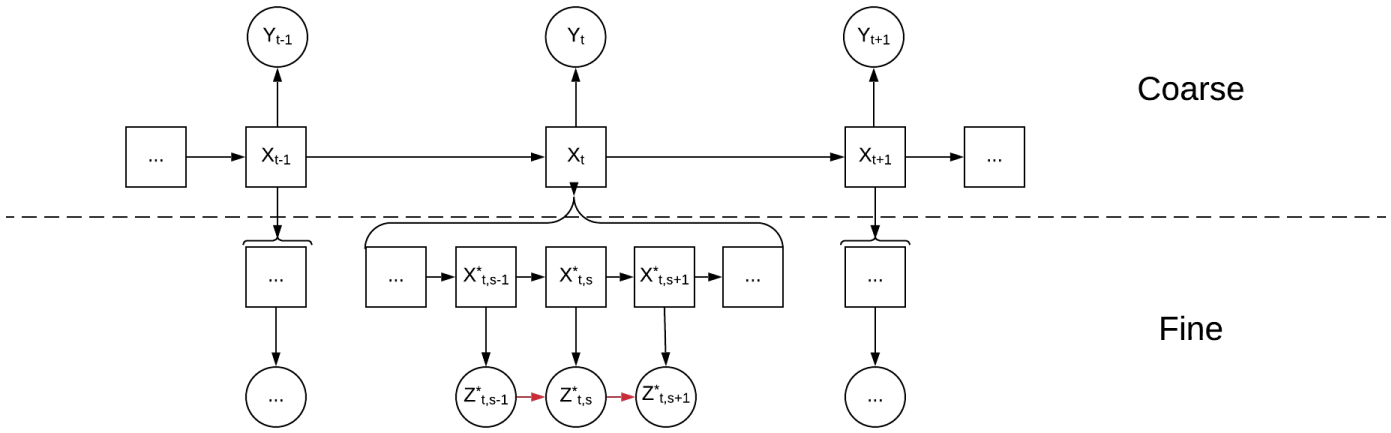


Figure 6: Graphical representation of a CarHHMM. The additional arrows representing autocorrelation between observations are shown in red for emphasis.

you will want to refer back to the definition of the HMM model - by either equation numbers or section numbers

1. 100 dive durations were simulated using an HMM generative model with the following parameters:

$$\Gamma = \begin{pmatrix} 0.4 & 0.6 \\ 0.6 & 0.4 \end{pmatrix}$$

$$Y_t|X_t \sim Gamma$$ use {\rm{ Gamma}}

$$\mathbb{E}(Y_t|X_t = 1) = 15s, \quad \mathbb{E}(Y_t|X_t = 2) = 60s$$
$$\mathbb{V}(Y_t|X_t = 1) = 25s^2, \quad \mathbb{V}(Y_t|X_t = 2) = 100s^2$$

you will want to refer back to this model definition too

2. Once the dive durations were calculated, for each $t \in \{1, \ldots, 100\}$, dive t was broken into $\lfloor Y_t/2 \rfloor$ 2-second segments (the end of the dive sequence was discarded). Further, each 2-second segment was assigned a behaviour according to a fine-scale Markov chain X_t^*, where $X_{t,t^*}^* \in \{1, 2\}$ and $t^* \in \{1, 101, 201, \ldots, 100 * \lfloor Y_t/2 \rfloor + 1\}$. The parameters of the fine-scale behaviour Makov chain were set to be as follows:

$$\Gamma^{*(1)} = \begin{pmatrix} 0.25 & 0.75 \\ 0.75 & 025 \end{pmatrix} \qquad \Gamma^{*(2)} = \begin{pmatrix} 0.75 & 0.25 \\ 0.25 & 0.75 \end{pmatrix}$$

where $\Gamma^{*(1)}$ was used for dives where $X_t = 1$ and $\Gamma^{*(2)}$ was used for dives where $X_t = 2$

3. For each 2-second segment, the Fourier modes $\hat{Y}_{t,t^*}^*$ were simulated using the following procedure. Note that the n^{th} Fourier mode of $\hat{Y}_{t,t^*}^*$ is denoted as $\hat{Y}_{t,t^*}^{*(n)}$:

$$\hat{Y}^{*(0)}_{t,1} \sim \mathcal{N}\left(\mu = 1, \sigma^2 = 0.01\right)$$
$$\hat{Y}^{*(0)}_{t,t^*} \sim \mathcal{N}\left(\mu = 0.9Y^{*(0)}_{t,t^*-100} + 0.1, \sigma^2 = 0.01\right), \qquad t^* \in \{101, 201, \ldots, 100 * \lfloor Y_t/2 \rfloor + 1\}$$
$$\hat{Y}^{*(n)}_{t,t^*} = a^{(n)}_{t,t^*} i\sqrt{b^{(n)}_{t,t^*}}, \qquad n \in \{1, \ldots, 49\}$$

$$a^{(n)}_{t,t^*} \sim \begin{cases} -1 & w.p.\ 1/2 \\ 1 & w.p.\ 1/2 \end{cases}$$
$$(b^{(n)}_{t,t^*} | X^*_{t,t^*} = 1) \sim Gamma(1/n^2, 1)$$
$$(b^{(n)}_{t,t^*} | X^*_{t,t^*} = 2) \sim \begin{cases} Gamma(1/n^2, 1) & \text{for } n \neq 2 \\ Gamma(100, 1) & \text{for } n = 2 \end{cases}$$

$$\hat{Y}^{*(50)}_{t,t^*} = 0$$
$$\hat{Y}^{*(n)}_{t,t^*} = -\hat{Y}^{*(100-n)}_{t,t^*}, \qquad n \in \{51, \ldots, 99\}$$

Finally, $Y^*_{t,t^*:t^*+99}$ is set using the inverse discrete fourier transform of $\hat{Y}^*_{t,t^*}$:

does the subscript need brackets? it's not clear what you mean. say t=1, t^*=3, this looks like Y^* is a vector made up of Y*_{1,3}, Y*_{1,4}..., Y*_{1,102}
no no - Y*_{1,3+99} (since t*:t* + 99 = (t*+99):(t*+99)
Please don't make me think so hard to figure out what you mean!

$$Y^*_{t,t^*:t^*+99} = IDFT\left(\hat{Y}^*_{t,t^*}\right)$$

This gives a strong periodic component to acceleration when the subdive state $X^*_{t,t^*} = 2$. There are several practical reasons behind this construction:

(a) $\hat{Y}^*_{t,t^*}$ is anti-symetric about $\hat{Y}^{*(50)}_{t,t^*}$ so that its inverse fourier transform is real-valued.

(b) $\hat{Y}^{*(n)}_{t,t^*}$ decays like $1/n^2$ to facilitate continutity.

Note that this process idoes not result in a continuous sequence Y^*_t since the average values of consecutive 2-second segments jump. However, note that these average values are highly autocorrelated, so the jumps are not too severe. See figure (7) for details. In addition, Y^*_t has the following desirable properties:

1. $Z^{*(1)}_{t,t^*+1} | Z^{*(1)}_{t,t^*} \sim \mathcal{N}\left(\mu = 0.9Z^{*(1)}_{t,t^*} + 0.1, \sigma^2 = 0.01\right)$
2. $$Z^{*(2)}_{t,t^*} \sim \begin{cases} \text{Gamma}(\sum_{n=1}^{\tilde{w}} \frac{1}{n^2}, 1) & \text{for } X^*_{t,t^*} = 1 \\ \text{Gamma}(20 + \sum_{n=2}^{\tilde{w}} \frac{1}{n^2}, 1) & \text{for } X^*_{t,t^*} = 2 \end{cases}$$

So we can directly compare the results of the CarHHMM with the ground truth.

I still need to put in the actually results from the simulation study- I had to rethink how to do the simulation in the first place since enforcing continuity was REALLY hard to do in a principled way.

5 Results

so this is the data analysis, yes? A good title would be something like "Analysis of Killer Whale Data"

Results will go here. I have some stuff on CarHMMs and HHMMs from STAT 548 but I need to put it together still.

6 Discussion

THE FOLLOWING IS FROM THE STAT 548 PAPER:

While incorporating autocorrelation within a hidden Markov model to analyze animal movement is not new, Lawler et al. introduce a new formulation of this model in the CarHMM. They also review several useful preprocessing tools such as the lag plot and a method for interpolation that includes dividing the data into separate groups if observations are far apart.

This paper summarizes the CarHMM and provides intuition behind the interpolation scheme laid out by Lawler et al. In addition, it shows that if the emission distributions are normal for the sequence of step-sizes **D**, then the CarHMM models **D** as a one dimensional Ornstein-Uhlenbeck process.

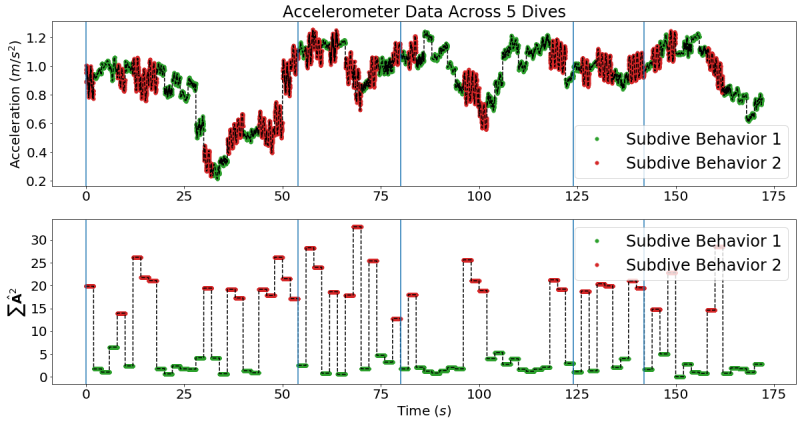


Figure 7: Simulated Acceleration Data.

Finally, the CarHMM is adapted to dive data and used to model the behavior of a killer whale off the coast of British Columbia, Canada. In particular, that whale exhibited auto-correlated velocities in the z-direction as well as sinusoidal behavior in dynamic body acceleration. The adjusted CarHMM is able to capture within-dive behaviors of active swimming and passive gliding, but more analysis is necessary to determine the exact number of within-dive behaviors and generalize the method to a larger number of dive types.

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Appendix

A Dimension Reduction on $\hat{Y}_t^*$

First, we simply use down-sampling and only record every w^{th} time step of $\hat{Y}_t^*$. This both reduces the space of $\hat{Y}_t^*$ to $\mathbb{C}^{\lfloor S_t^*/w \rfloor \times w}$ and ensures that none of the sliding windows overlap when taking the STFT. This is important because HMMs assume temporal independence between observations. Next, the dimension of $\hat{Y}_t^*$ can be cut in half by recognizing that the Y_t^* is real-valued, and therefore $\hat{Y}_{t,k}^*$ is equal to the complex-congugate of $\hat{Y}_{t,w-k-1}^*$. Finally, by Parseval's Thereom we have that:

$$\sum_{n=0}^{w-1} |Y_{t+n}^*|^2 = \sum_{n=0}^{w-1} |\hat{Y}_{t,n}^*|^2$$

B Equivalency of CarHMM and one-dimensional state-switching Ornstein-Uhlenbeck process

If it is the case that (1) the underlying behavioral state of the continuous-time model must follow a Markov chain rather than a Markov process, and (2) the emission distributions of the CarHMM are gaussian, then the CarHMM and the state-switching continuous model are equivalent. This allows the theoretically grounded continuous-time state-switching model to be used in the computational convieneint HMM (and therefore HHMM) framework. In addition, it gives new intpretation to the learned parameters of the CarHMM in the context of an Ornstein-Uhlenbeck process.

A one-dimensional state-switching Ornstein-Uhlenbeck process y^* is the solution to the following stochastic differential equation:

$$dy_t^* = \beta_{x_t^*}(\gamma_{x_t^*} - y_t^*)dt + \omega_{x_t^*} dW_t$$

where x_t^* is the fine-scale behavior of the animal at time t, $\beta_{x_t^*}$ relates to rate at which the process returns to its mean value, $\gamma_{x_t^*}$ is the long-term mean value of the process, $\omega_{x_t^*}$ is related to short-term variance, and W is a Wiener process. As before, x_t^* is described by an unobserved Markov process. The solution to this equation is known to be the following [5]:

$$y_{t+\delta}^* \sim \mathcal{N}\left((1 - e^{-\beta_{x_t^*}\delta})\gamma_{x_t^*} + e^{-\beta_{x_t^*}\delta} y_t^*, \quad \frac{\omega_{x_t^*}^2}{2\beta_{x_t^*}}(1 - e^{-2\beta_{x_t^*}\delta})\right)$$

Now, suppose that δ is constant for all observations, as is the case for hidden Markov models. In addition, introduce the following transformations:

$$\mu_{x_t^*} = \gamma_{x_t^*}, \qquad \phi_{x_t^*} = e^{-\beta_{x_t^*}\delta}, \qquad \sigma_{x_t^*}^2 = \frac{\omega_{x_t^*}^2}{2\beta_{x_t^*}}(1 - e^{-2\beta_{x_t^*}\delta})$$

Then, we have the following:

$$y_{t+\delta}^* \sim \mathcal{N}\left((1 - \phi_{x_t^*})\mu_{x_t^*} + \phi_{x_t^*} y_t^*, \quad \sigma_{x_t^*}^2\right)$$

If δ is fixed and x_t^* is adjusted to follow a Markov chain rather than a Markov process, then this model is equivalent to the CarHMM with normal emission probabilities. Note that all of the parameter transformations above are one-to-one, so it is easy to go from the CarHMM to the continuous model and back again. This allows for the pricipled construction of the continuous-time model to be combined with the computational convienence of the CarHMM.