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Hidden Markov Models: Application on Identifying Seabird Foraging Areas

by

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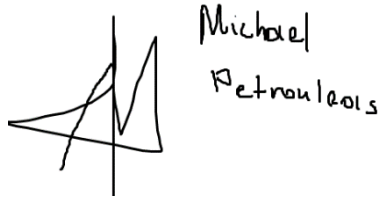
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Executive Summary

Several phenomena in nature are defined by underlying hidden states that affect their observed measurements. Hidden Markov Models (HMMs) are mathematical models that link an observed time sequence of data with an underlying/unobserved one, which describes the state of the observed phenomenon. They are usually employed to model several ecological patterns, including animal movement in terms of step-lengths and turning angles, both of which are affected by the state of the tracked animal. Throughout this analysis the properties of these models will be described and an application in temporal and spatial data will be explored by using the “moveHMM” R package. More specifically, this report serves as an introduction to how such models can be utilized in order to adequately model tern movement data and, consequently, identify their underlying states. The correct assignment and interpretability of the mentioned states will also be thoroughly discussed. Lastly, in an effort to approximate foraging areas of seabirds, the accuracy of HMM predicted states will be evaluated against the known/true ones. As it will be shown, predicted states can be classified with a relatively high accuracy.

Word Count: 3666

List of Contents

1. [Introduction](#)
2. Exploratory Data Analysis
 - 2.1. [Data](#)
 - 2.2. [Descriptive Analysis](#)
3. Methods
 - 3.1. [Model - An overview of m-Hidden Markov Models \(m-HMMs\) for movement data](#)
 - 3.2. [Selecting the number of states – m](#)
 - 3.3. [Fitting an HMM with the moveHMM package](#)
 - 3.4. [Validating the Model](#)
4. Results
 - 4.1. [Fitted moveHMM models with \$m = 2\$](#)
 - 4.2. [State interpretation via visualization methods and potential pitfalls](#)
 - 4.3. [Goodness of fit checks for the models](#)
 - 4.4. [Predictive accuracy of states](#)
5. [Discussion](#)
6. [References](#)

Appendix

List of Figures

1. [Fig.1 - Continuous behaviour - distance from colony per species](#)
2. [Fig.2 - Continuous behaviour – distance from boat per species](#)
3. [Fig. 3 -Tern tracks per behaviour for Coquet Island observed species in 2011 \(all tern journeys plotted\) – chick rearing period](#)
4. [Fig. 4 - Missing data patterns for 2010 \(left\) and 2011 \(right\) chick rearing dataframes.](#)
5. [Fig. 5 - HMM Model for Movement Data](#)
6. [Fig. 6 - Fitted 2-HMM models by species Arctis \(top-left\), Sandwich \(top-right\), Roseate \(bottom-left\), Common \(bottom-right\)](#)
7. [Fig. 7 - Summarised Boxplots of Step-length and Turning Angles per Species - based on output of prepData](#)
8. [Fig. 8 - Histograms per species and modelled states](#)
9. [Fig.9 - Time-series, qq-plots and ACF plots for the model pseudo-residuals of i\) Arctic \(top-left\), ii\) Sandwich \(top-right\), iii\) Common \(bottom-left\), iv\) Roseate \(bottom-right\)](#)
10. [Fig.10 - Confusion Matrices of states per species](#)
11. [Fig. 11 - Predicted \(Blue\) – Observed \(Orange\) Foraging Comparison per species](#)

1. Introduction

To understand the foraging patterns of seabirds and, in turn, pinpoint areas of ecological interest, possibly to aid to their preservation by simultaneously aiding the declining population of the species ([Paleczny et al., 2015](#)), an adequate method of tracking should be employed. In an effort to identify such foraging areas, different methods of sampling were utilized in the past, including the collection of observations from predefined regions or tracking bird-specific locations with the aid of technical equipment ([Perrow et al., 2006](#)). However, both methods have proven to have disadvantages that range from introducing biased results, as the foraging areas that should be covered would need to be vast and thus challenging to be monitored, to technical difficulties related to tracking equipment that can be easily damaged, produce inaccurate measures or get lost ([Perrow et al., 2006](#)).

A different approach was thus proposed ([Perrow et al., 2011](#)) that induced the visual tracking of seabirds by an inflatable boat, which contained a GPS sensor. It has been shown that terns can be adequately tracked during the duration of a foraging trip, while temporal and spatial data, referring to the boat located close to the tracked tern, can be gathered without affecting the seabird's behaviour. To gain an insight on how the movement of seabirds of interest is affected, their usual observed continuous behaviours, which are closely related to foraging patterns (feeding, transferring food, travelling etc.) can be summarised as follows ([JNCC – Wilson et al., 2014](#)):

- 1) Direct Flight (DF): Fast with minimal turns, adopted when a clear destination is set by the seabird. Terns usually adopt this mode while transferring food to their colony or travelling.
- 2) Active Search (AS): Indicates a state of constant searching for food. Can be characterized as a flight mode that incorporates a slower flight speed with steeper turns than usual. “AS” can be used to identify foraging areas of interest by the tern.
- 3) Transit Search (TS): Travelling mode with slower observed flight speed than “DF”. Direction can change and thus turns can still be observed, although at a lower scale than “AS”. Mostly resembles an opportunistic foraging – travelling hybrid mode, between the spectrum of “DF” and “AS”.

In order to detect areas where seabirds use for foraging, it would thus suffice to keep track of spatial data where the “AS” mode is observed by multiple terns. However, another method that does not require the identification of a continuous behavior by the observer, would be to check the time intervals between which a tern flies at lower speeds or, equally, forms small distances between the two successively measured points (i.e. step-lengths) to search for potential prey. Turning angles, changes of course between these successive measurements, are also expected to be higher at this foraging state. The opposite scenario (higher flight speeds or step-lengths with small turning angles) could thus indicate a non-foraging/travelling mode ([McClitock et al., 2020](#)).

The R package “moveHMM” ([Michelot et al., 2016](#)) is a tool that can convert GPS coordinate data, measured at set time intervals, to step-length and turning angles per tracked tern. Throughout this report it will be thus established how Hidden Markov Models (HMMs) can model such tern movement data, by identifying hidden states that affect the magnitude of measured values. Besides the advantages of inferring, predicting and mapping the locations of states, inferences about the species' step-length and turning angle characteristics or transition probabilities can be made. HMMs are thus more informational than simply opportunistically observing the behavioral status of tracked animals alone ([Franke, 2006](#)). The rationale for choosing the number of such states, along with their interpretability, as they usually indicate a distinct behavioral individual condition, is also explored in this report (Sections [2.2](#), [4.1](#) and [4.2](#)). Lastly, with the aid of the mentioned package, the predicted foraging areas based on these models will be evaluated against the actual/observed ones and maps of clustered foraging state points will be shown (Section [4.4](#)).

2. Exploratory Data Analysis

2.1 Data

The dataframes were constructed by the Joint Nature Conservation Committee ([JNCC – Wilson et. al, 2014](#)) and consist of spatial and temporal (Longitude/Latitude) boat-tern observations, measured at equal time intervals and gathered in 2010 and 2011 chick rearing periods, via the method of visual tracking ([Perrow et al, 2011](#)) in the colony of Coquet Island. Four species of terns (Arctic, Common, Sandwich and Roseate) were observed in both tracking sessions. Other information included is size and species of prey, straight line distances from the boat to tern (DISTKM) and the colony (DIST2COL), along with an indicator on whether the tern's path was observed in full scale, or the seabird was lost midway. Tern instantaneous and continuous behavioral characteristics are also available while the latter will form the basis of validating the models introduced in this report. In order to get a clearer picture of the variables and characteristics within the dataframes, relevant plots will be shown in the next section.

2.2 Descriptive Analysis

The 2010 chick rearing dataframe consists of 29514 observations, whereas the 2011 one has 152411 observations. To gain an understanding of how the behaviors per species are formulated regarding each variable, it is useful to check the relationship of continuous behaviors regarding the terns' distances from the colony (Fig.1).

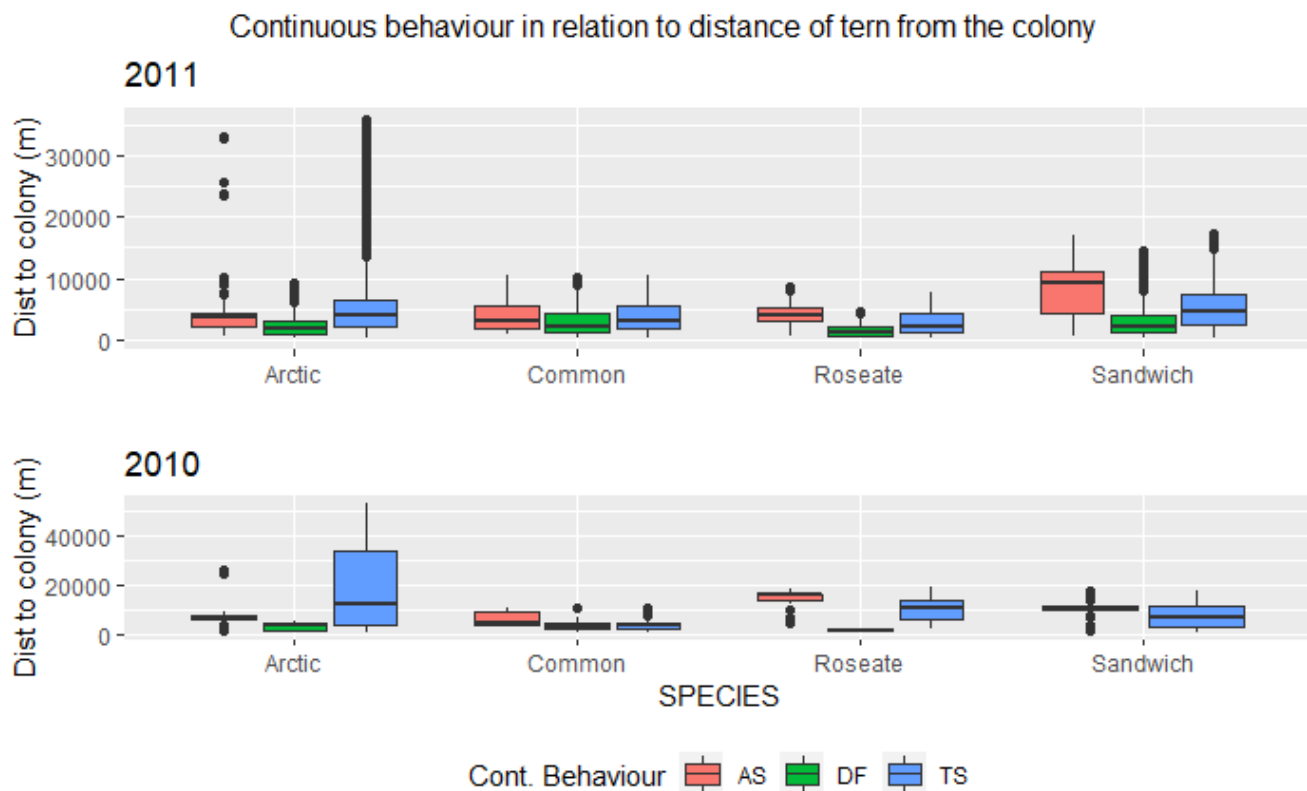


Fig.1 Continuous behaviour - distance from colony per species

All tern species seem to be engaging in direct flight (DF) in areas relatively closer to the colony, when compared to the other two behaviours. In addition, areas in which "AS" is prominent are on average 5680,017km (average among all species in the 2011 dataframe) away from the colony, a number considerably higher than the ones for the other two behavioural states ("TS": 5071,956 km, "DF": 2830,612 km). This observation can be supported by the fact that we expect seabirds to travel faster, while following a more immediate route (DF), to or from a foraging area and switch to transit (TS) or active search (AS) when close to such places of interest, that exist far from colony. In order to further

examine the links between the behavioural states and other variables, it is useful to look at additional plots.

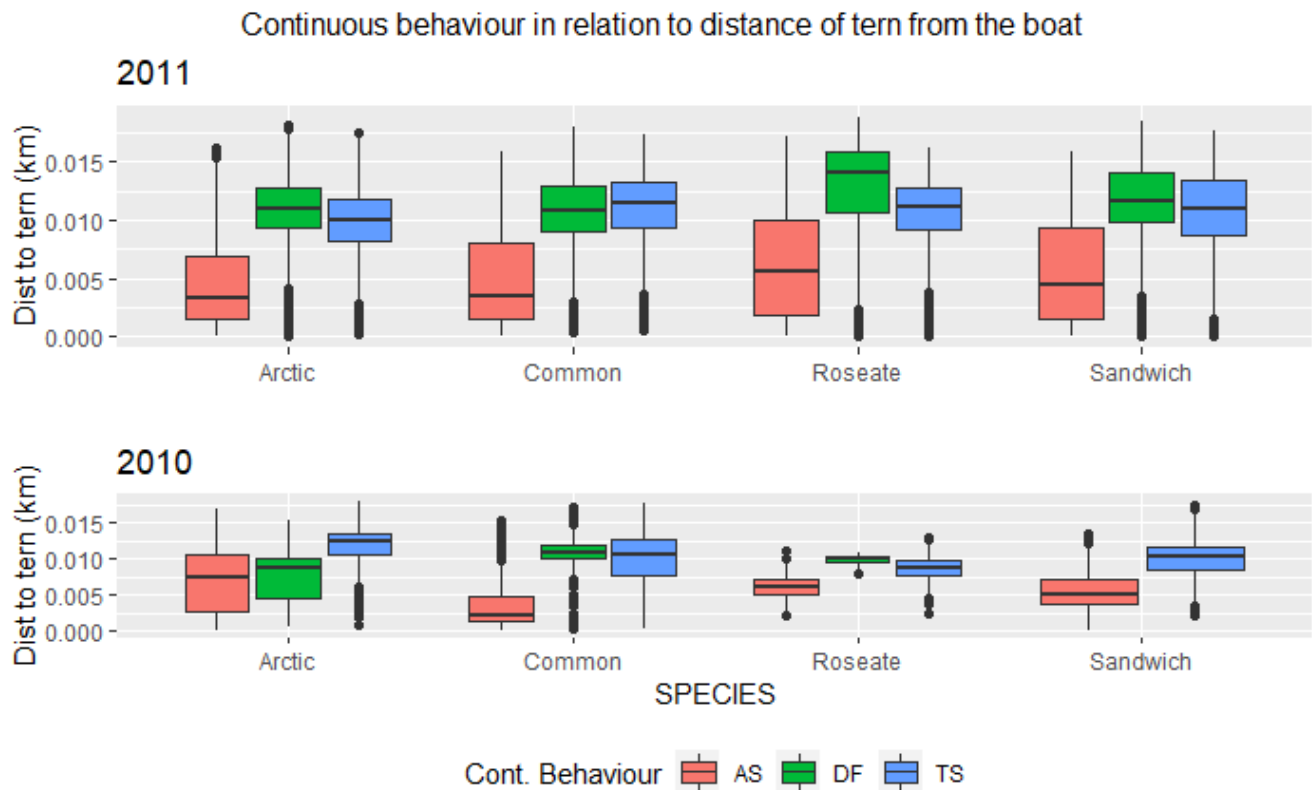


Fig.2 Continuous behaviour – distance from boat per species

As seen in Fig.2 “AS” is observed in areas closer to the boat. This can be justified as, potentially, due to lower observed tern speeds in “AS”, the boat managed to get relatively closer to these terns when they were actively searching for prey.

Mapping the paths of all tracked terns per species can also help us validate where these continuous behaviours occur, in relation to the terns’ foraging trips. As the 2011 chick rearing dataframe has considerably more observations and a higher ratio of completely tracked tern journeys than the 2010 counterpart (37.9% vs 21.4% respectively), we will focus the rest of the analysis on the former dataframe. As is evident in [Fig. 3](#), “DF” and “TS” continuous behaviours are more prominent on areas between the “AS” ones. This indicates a process of travelling to a possible foraging point, which is identified by a change in the tern’s behaviour to “AS”.

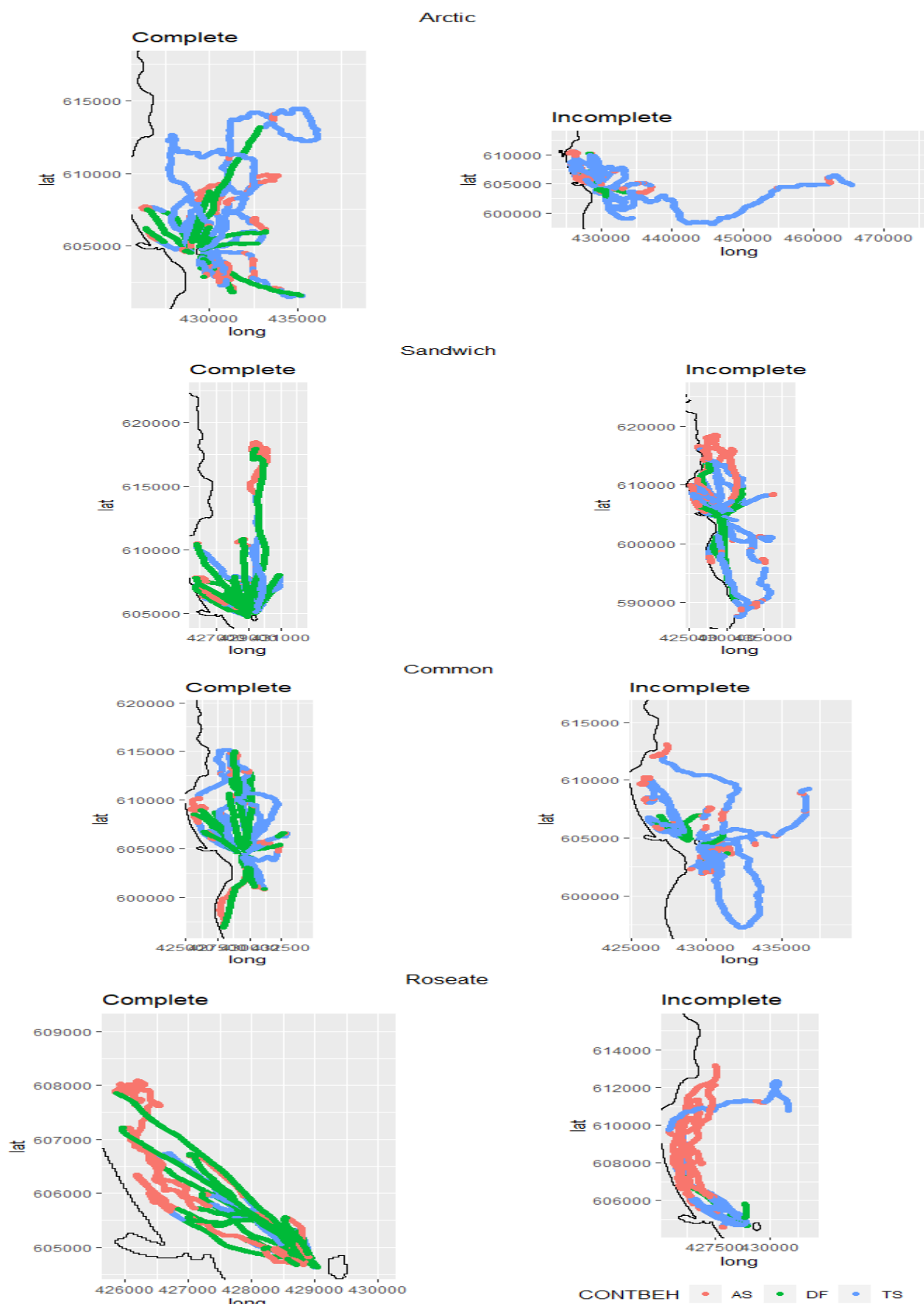


Fig. 3 Tern tracks per behaviour for Coquet Island observed species in 2011 (all tern journeys plotted) - chick rearing period

3. Methods

3.1 Model - An overview of m-Hidden Markov Models (m-HMMs) for movement data

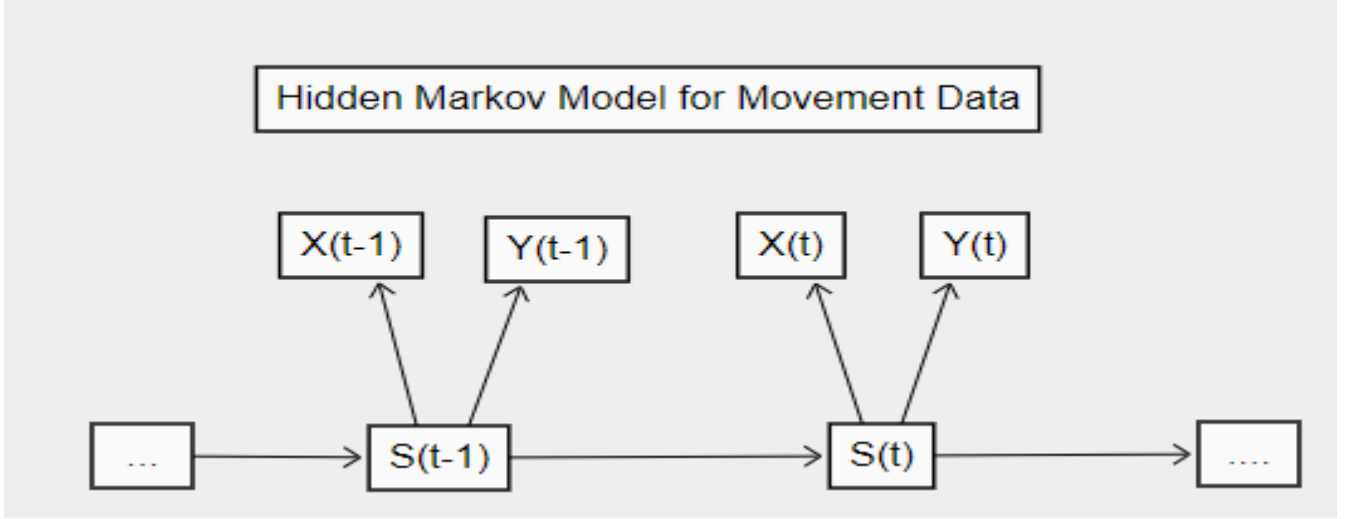


Fig. 5 HMM Model for Movement Data

The Hidden Markov Model that is going to be explored in this analysis consists of two stochastic processes. The first one is an unobserved hidden sequence $S(t) \in \{1, 2, \dots, m\}$, where m is the predefined number of hidden states in the model, and an observed bivariate state-dependent one, expressed by the step length $X(t) \in [0, \infty)$ and turning angle $Y(t) \in (-\pi, \pi]$ at a set discrete time $t \in \mathbb{N}^*$ defined by equal time intervals/sequential measurements. Before one should apply HMMs they need to firstly define the following assumptions/properties that can further simplify them. It should be thus noted at this point that i) “conditional independence” is assumed and ii) the Markov property for the states sequence is satisfied. This means that the joint distribution of $(X(t), Y(t))$ depends only on the current hidden state $S(t)$ at time $t = \mathbb{N}^*$, while the past and future states in the model do not affect it in any way. The following conditions are thus satisfied:

- **Conditional Independence**

$$f(x_t, y_t | S_t = i) = f(x_t, y_t | X_{t-1}, \dots, X_1, Y_{t-1}, \dots, Y_1, S_t = i, S_{t-1} = j, \dots, S_1 = k) =$$

$$= f(x_t | S_t = i) * f(y_t | S_t = i), \quad i, j, k = \{1, 2, \dots, m\}, t = \{1, 2, \dots\} \quad (1)$$

- **Markov property for state sequence**

$$P(S_t | S_{t-1}, S_{t-2}, \dots, S_1) = P(S_t | S_{t-1}) \quad (2)$$

where f refers to the distributions used to model the variables X or Y , which are independent given a hidden state S at time t . Although several choices for f exist for each variable, in this analysis the step length X will be modelled with a Gamma distribution, while the turning angle Y with a Von Mises distribution, usually employed to model circular data ([Zucchini, 2016](#)). A visual representation of the model can be seen in Fig.5 presented above.

By using these assumptions, we can now discuss about the building blocks that define an HMM. These are:

- 1) **The initial distribution δ :** Describes the probabilities of the modelled system being in each of the m states, at the start of the sequence (i.e. $t=1$). In mathematical notation, this can be written as a $1 \times m$ probability vector: $\delta = (\Pr(S_1 = 1), \dots, \Pr(S_1 = m))$.

- 2) **The state dependent distributions** $f(x_t|S_t = i)$: Define the probabilities of an observation belonging to each state at time t . They can be represented with a $m \times m$ diagonal matrix $P(x_t) = \text{diag}(f(x_t|S_t = 1), \dots, f(x_t|S_t = m))$.
- 3) **The state transition probabilities** $\gamma_{ij} = \Pr(S_{t+1} = j | S_t = i)$: Specifies the probabilities of switching from state i to j , at times t and $t+1$ respectively. They can also be defined as an $m \times m$ transition probability matrix, notated as Γ .

By using these three components, we can evaluate the likelihood of the model $L(\theta|x_1, x_2, \dots, x_T)$ by implementing the forward algorithm, a process of matrix multiplications through the whole observed sequence: $L(\theta|x_1, x_2, \dots, x_T) = \delta * P(x_1) * \Gamma * P(x_2) * \Gamma * \dots * P(x_T) * \Gamma * I$, with I being a $m \times 1$ ones vector. Maximising the likelihood function means that the vector of unknown parameters θ (that define the distributions set on each variable) needs to be estimated. This involves the process of “fitting” the HMM model to the observed data, something that can be accomplished by either employing frequentist or Bayesian methods. Throughout this analysis the former are employed.

3.2 Selecting the number of states – m

Setting m , the number of possible hidden states, is thus the last component that should be defined. Usually, when analysing movement data, the number of states is reduced to two (indicating “exploration” or “encampment”) for interpretability reasons ([Pohle et al., 2017](#); [Patterson et al., 2017](#)). In this particular setting, indications from the background tern behavioral information ([Wilson et al., 2014](#)) and exploratory data analysis (i.e. Fig.1-3) already suggest that modes “TS” and “DF” can be modelled as one travelling state (perceived as State 2), while “AS” alone as a completely different foraging one (State 1). Therefore, with evidence that will also be established in the results section, it is sensible to set m as equal to 2 in this analysis. For consistency reasons, observations with a continuous behaviour equal to “End”/“END” (Arctic: 48 (0.11%), Sandwich: 71 (0.13%), Common: 42 (0.12%), Roseate: 9 (0.17%)) were removed from the dataset before the model fitting process.

3.3 Fitting an HMM with the moveHMM package

In this analysis, the moveHMM package will be used. Through the prepData function, the coordinates in the given dataframe can be transformed into step-lengths and turning angles for each tern, identified with a unique ID and time-point per measurement. This will form the observed sequence (X_t, Y_t) as described above. The underlying states, whose number is already pre-defined, will be evaluated during the fitting process.

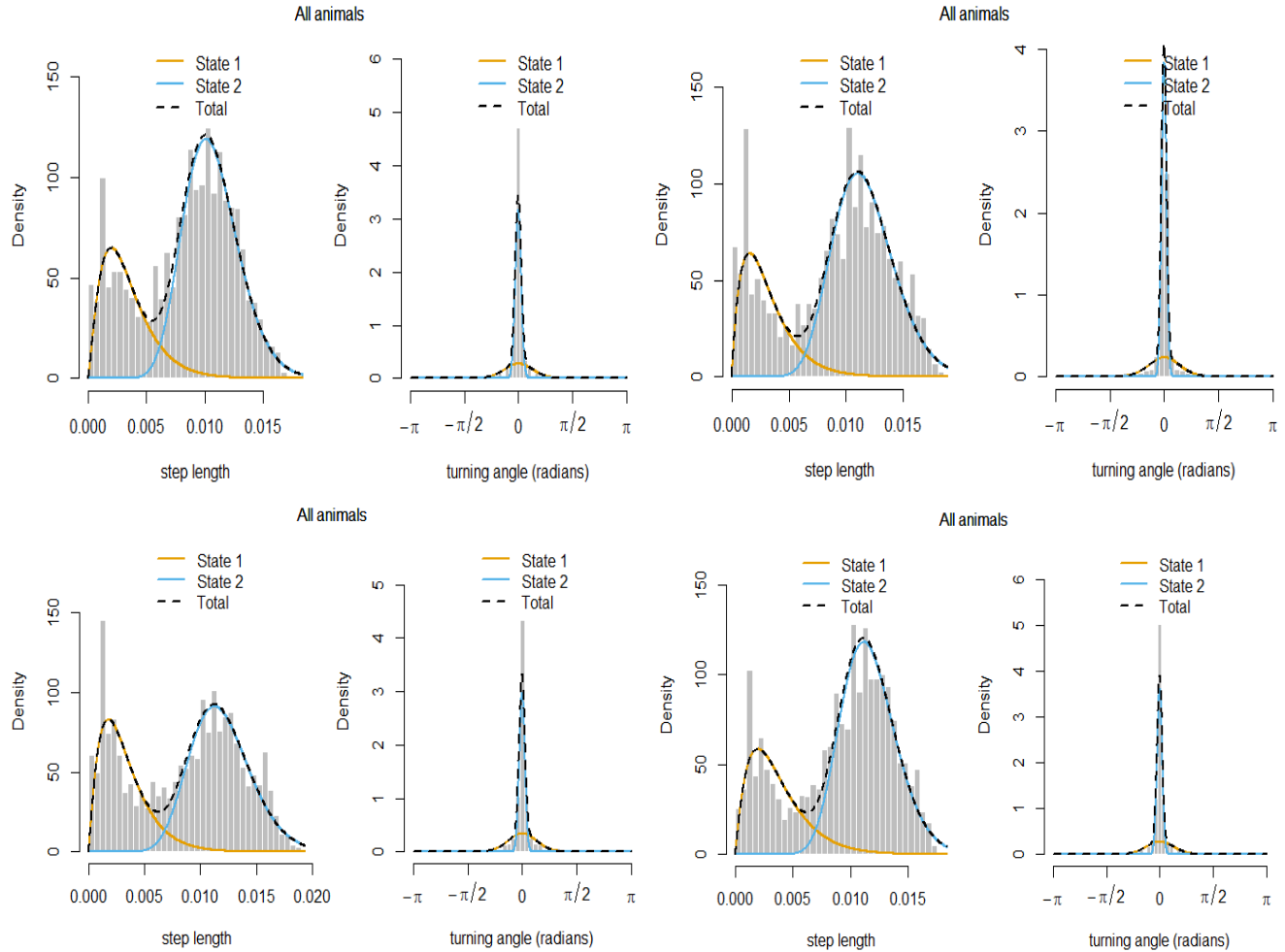
The model fitting can be also easily performed with the fitHMM function, which implements the forward algorithm to evaluate, and the “nlm” function to maximize the likelihood function of the data. Since initialization of the starting values in the optimization process is needed to reach the global maximum, the maximized value of the likelihood will be evaluated through a 5-iteration optimization process with randomized starting values (a seed = 1 is set to ensure reproducibility). Due to each tern species demonstrating potentially a different behaviour, a unique HMM was fitted per tern species data. Furthermore, adding covariates have produced a higher AIC score compared to a baseline, no-covariate HMM. Hence, no additional variables have been used in this analysis during the fitting process.

3.4 Validating the Model

Given a fitted HMM model, the Viterbi algorithm can be used to compute the most probable hidden states (S_t) , under the observation sequence (X_t, Y_t) ([Patterson et al., 2017](#)). Hence, employing the viterbi() function from the moveHMM package can give us the “fitted states” that can be validated against the true behavioural ones from the original dataframe. A heatmap, providing the accuracy of each predicted state against the true one will be thus constructed with accuracy being the evaluation metric.

4. Results

4.1 Fitted moveHMM models with $m = 2$



In [Fig. 6](#) it is evident that the fitted step-lengths and training angles can be adequately described by a 2-state HMM. State 1 indicates small step-lengths and large turning angles (orange line), while State 2 portrays a large-step length/low turning angle. The 2 modes in the step-length plots indicate that fitting a 3-state HMM would most likely inadequately model the existing data, as a meaningful and interpretable local maximum that refers to a third state would prove hard to be found.

Since the model output correctly identified the two states, the next step would be to find a meaningful interpretation of them. By taking into account the information regarding the tern behaviours, which are available within the dataframe, one can look for patterns in this unsupervised setting and assign a physical underlying behavioural mode to these states. The extracted step-lengths and turning angles will be thus examined in the following section.

4.2 State interpretation via visualization methods and potential pitfalls

As it can be interpreted by the boxplots of the step-length and turning angles per species ([Fig.7](#)), the choice of a 2-state HMM is indeed sensible for this analysis. “AS”, being positioned lower in the y step-length axis while simultaneously having a higher spread of turning angle values, describes smaller step-length measurements with possibly higher turning angles (similar to State 1 – [Fig.6](#)) than “DF” and “TS”, both of which are described by larger step-lengths with small turning angles (State 2 – [Fig.6](#)).

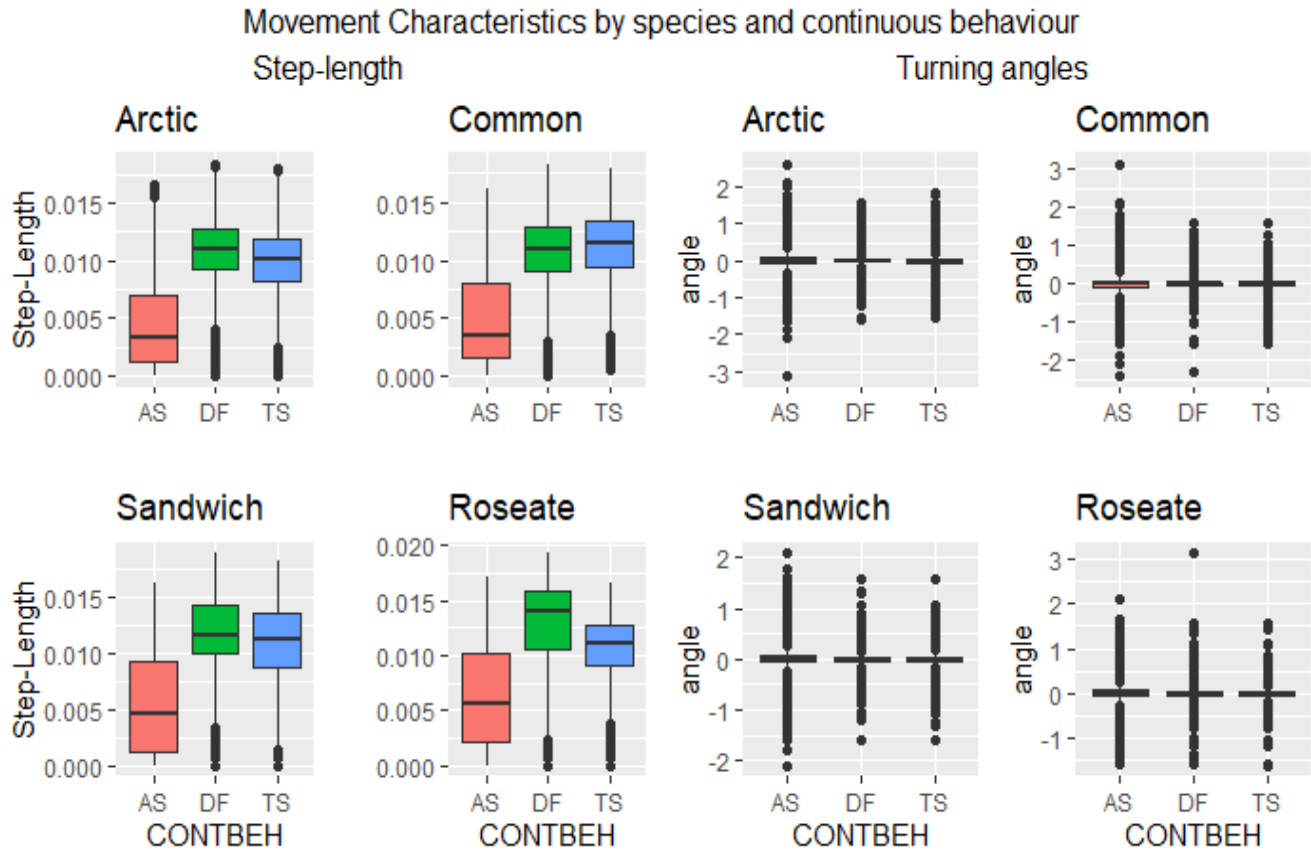


Fig. 7 Summarised Boxplots of Step-length and Turning Angles per Species - based on output of prepData

By recoding the three behaviours into two, as described above, we can assign a meaning to the two states of the HMM output. However, it is clear by [Fig. 8](#) that the two new interpretable states, although distinguishable, overlap with each other in some areas of the histogram. Namely, in TS & DF (State 2) histograms, continuous behaviours that indicate travelling, close to 0 step-length observations occur far more frequently than desired and are clearly under-evaluated by the fitted distributions in [Fig.6](#). In the same sense, “AS” step-length distributions have a heavier right tail than anticipated. This can potentially create areas of uncertainty for the model, making the correct classification of the two states (through the viterbi algorithm) much more inaccurate ([Lawler et al., 2019](#)). A notable example is the Roseate species, where a mixture-bimodal distribution is observed in both states. It is thus expected that HMMs fitted and evaluated under such overlapping states will produce a lower accuracy metric.

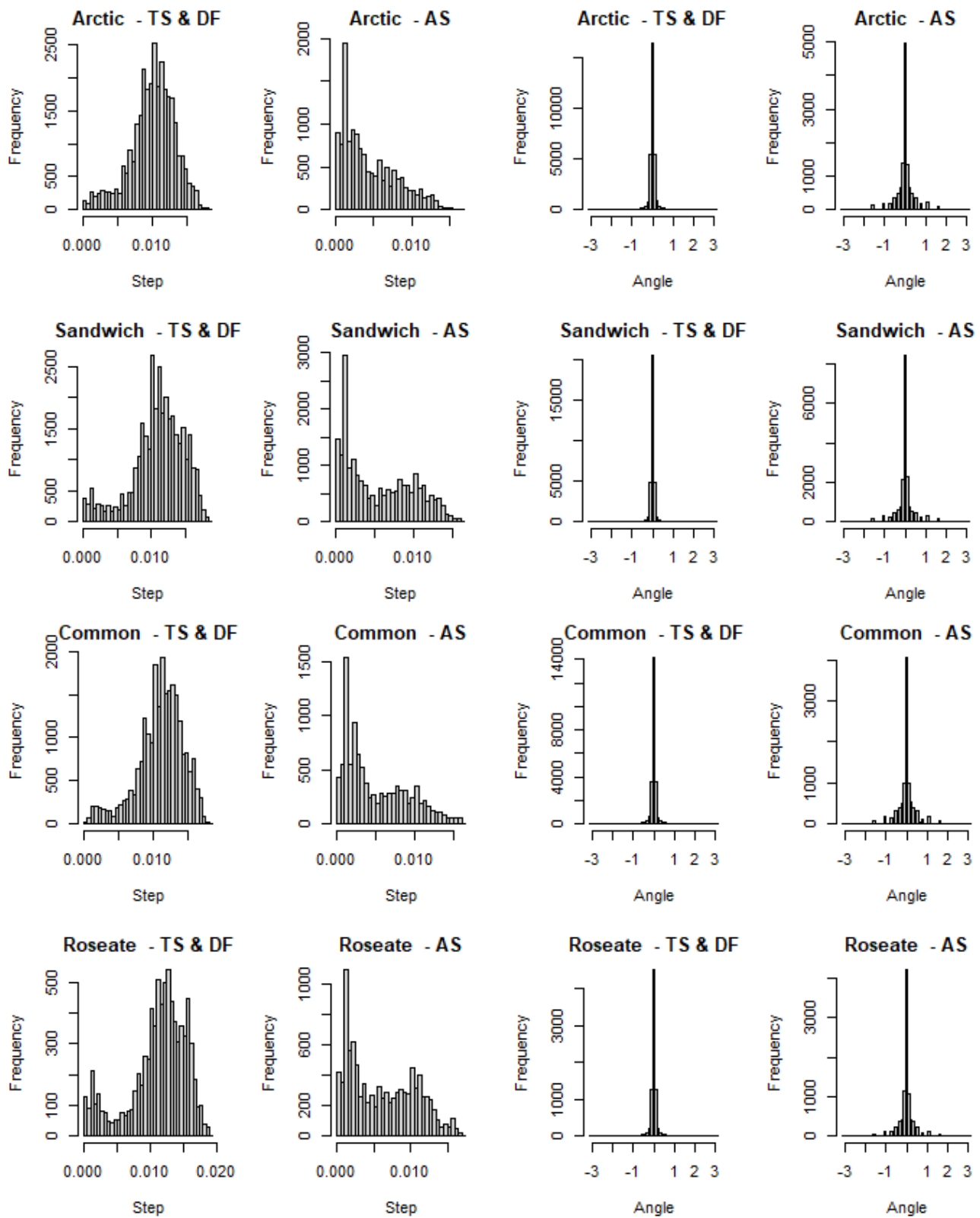


Fig. 8 Histograms per species and modelled states

4.3 Goodness of fit checks for the models

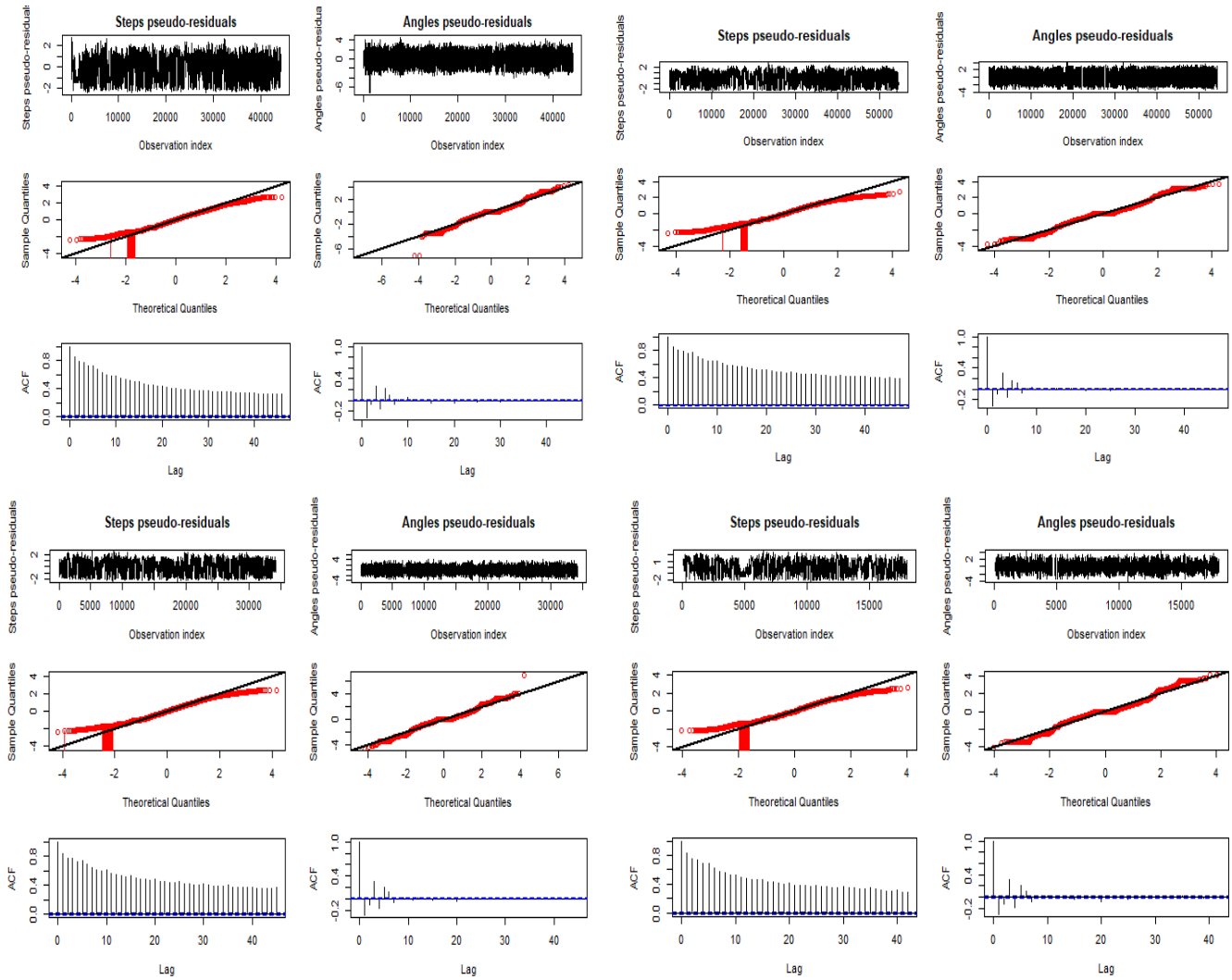


Fig.9 Time-series, qq-plots and ACF plots for the model pseudo-residuals of i) Arctic (top-left), ii) Sandwich (top-right), iii) Common (bottom-left), iv) Roseate (bottom-right)

To determine if the models were adequately fitted to the data, pseudo-residuals can be evaluated on their goodness of fit to the standard Normal distribution ([Zucchini, 2016](#)) and the existing serial correlation. For turning angle there does not seem to be an indication for a violation of the normality assumption and the autocorrelation drops to 0 by lag 10 for all cases. Both factors indicate that the model adequately described this variable.

However, when it comes to the step-length pseudo-residuals, the upper and lower percentiles of the data indicate a slight deviation from the standard normal distribution. What is more, high serial correlation is observed, with ACF values being close to 0.4 even at lag 40. This could indicate a violation of the first-order state-sequence Markov property ([Section 3 – \(2\)](#)) or that a larger number of states might be needed to model that data ([Michelot et al., 2016](#)). Nevertheless, high ACF among the pseudo-residuals does not generally indicate that the underlying model is not the true one and inference should not be done at this observation alone ([Zucchini, 2016](#)). As evident by the exploratory data analysis in sections [2.2](#) and [4.2](#), two states can potentially explain this phenomenon well enough and other measures need to be taken in order to remedy the high autocorrelation of the pseudo-residuals within the sample.

4.4 Predictive accuracy of states

As it can be inferred by Fig.10, the accuracy of the fitted models remains relatively high, attaining values close to 80% for the Arctic, Sandwich and Common species. Notable is the Roseate case, where the accuracy metric only managed to reach a value of 69,81%, possibly due to the pitfalls introduced in the previous section (4.2). A higher relative percentage of misclassifications seems to occur in State 1 cases that are more usually assigned as State 2 ones. In particular, the average State 1 - false discovery rate ($FDR = \{\text{Number of False State 1}\} / \{\text{Total State 1}\}$) is 28% for Arctic and Common species and 40% for the Sandwich and Roseate species.

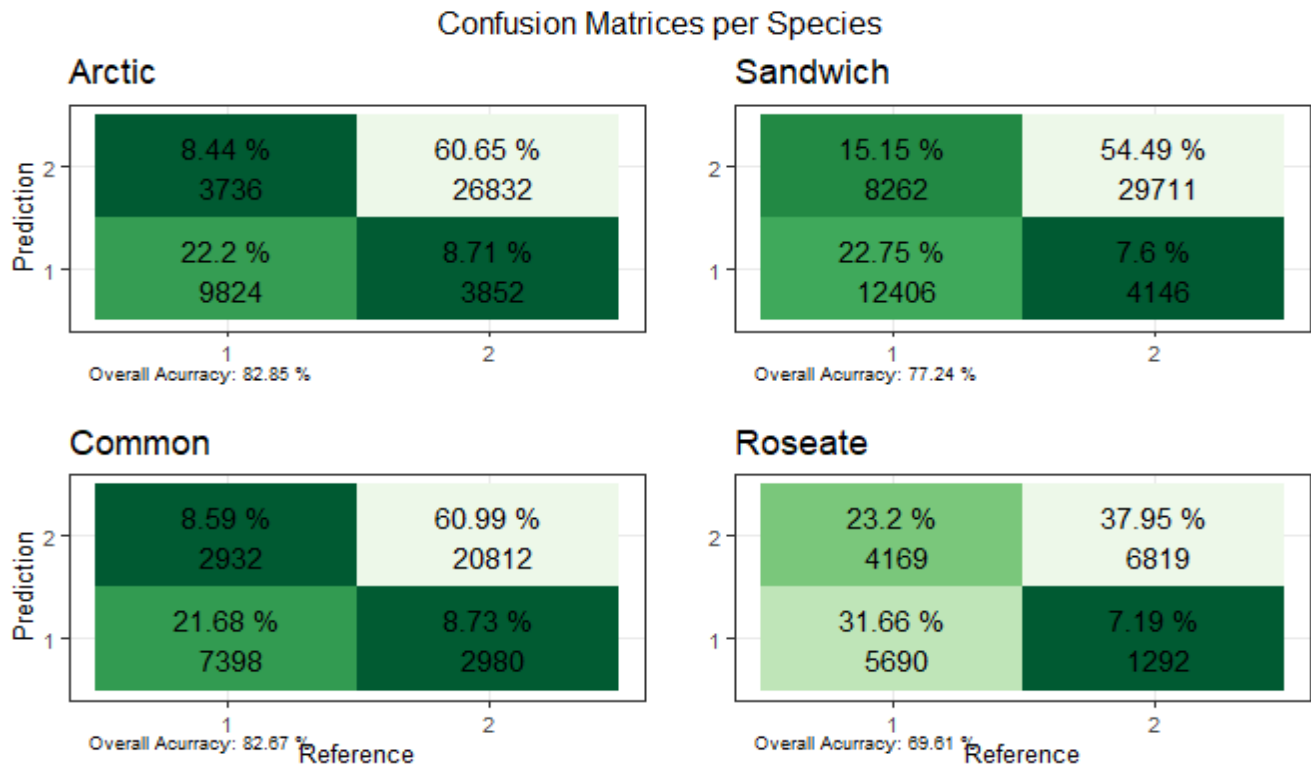


Fig.10 Confusion Matrices of states per species

Such misclassifications will thus mostly underevaluate State 1 points on the map, which are of prime interest to this analysis, as they are the ones that can indicate foraging spots. False State 1 locations also contribute to lower accuracy, while simultaneously assigning travelling points as misleading foraging ones. The overall comparison between the true “AS” versus the predicted “State 1” clustered points can be visually evaluated in [Fig.11](#). As it can be seen, although the two maps closely resemble each other, even in lower observed FDR species’ models, they are still far from being identical.

Therefore, although predicted states derived from fitted HMM models can provide a good approximation of foraging points, further improvement methods must be considered for the models.

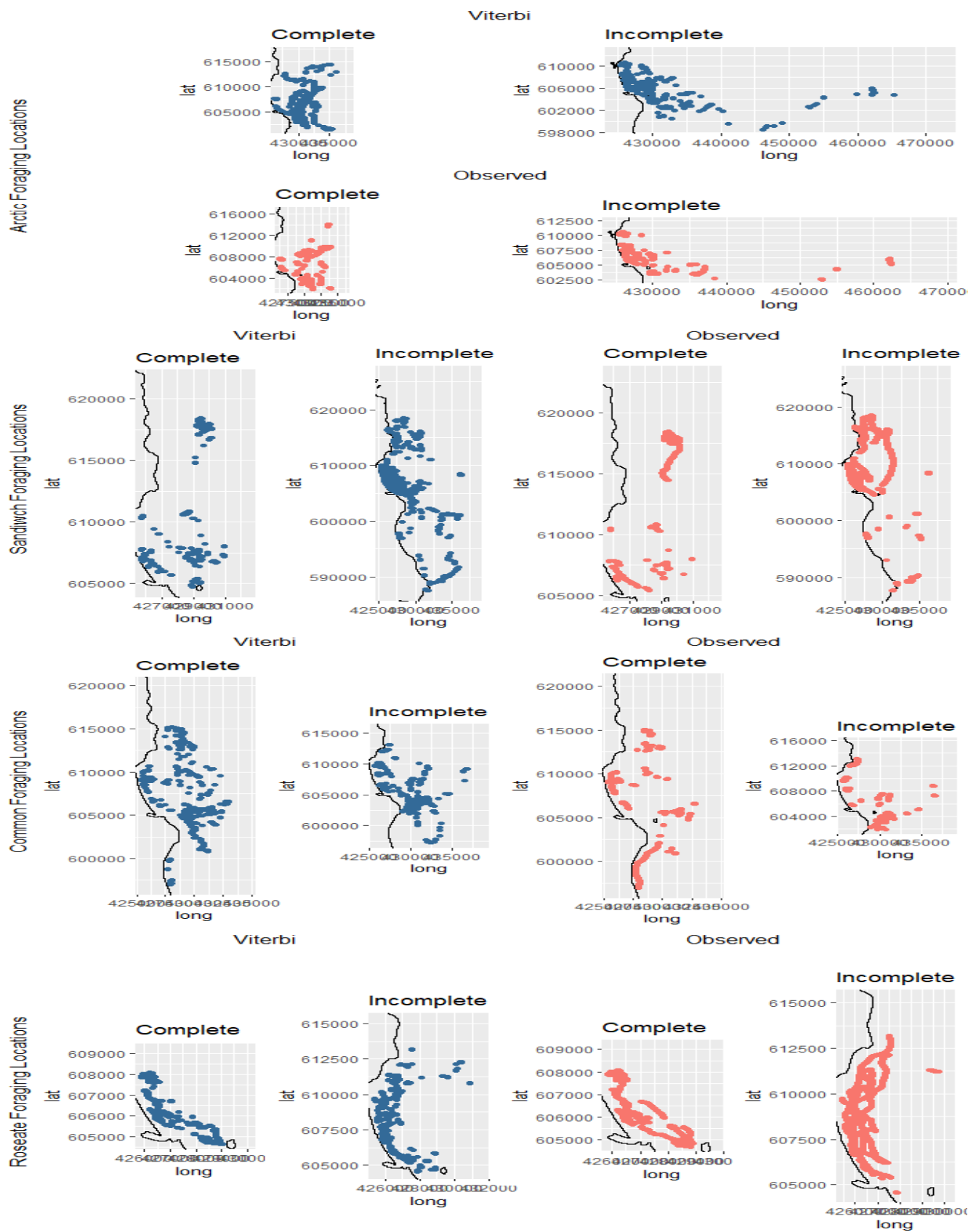


Fig. 11 Predicted (Blue) – Observed (Orange) Foraging Comparison per species

5. Discussion

Throughout the analysis, it has been shown that an HMM can be used to adequately identify hidden states by temporal and spatial collected data that refers to terns. Also, methods of interpretability of the said states were discussed and a validation procedure of the predicted versus the true states was performed.

Findings reported that the models managed to correctly classify the two states with a relatively high accuracy in most species. However, possibly to overlapping step-length/angle distributions between the continuous behaviours within the data and the high autocorrelation within the step-length variable, these models are prone to further improvement.

Firstly, as the GPS coordinates are subject to the boat used for visual tracking, thinning the data could potentially improve the step-length/turning angle measurements in the models plus contribute to a lower overall autocorrelation in the pseudo-residuals. The analysis would have to be repeated and the viterbi “fitted” states against the true ones would need to be reevaluated in order to investigate the effect of this phenomenon. Otherwise, a conditionally autoregressive HMM (CarHMM; [Lawler, 2019](#)) that serves as a generalization of the base HMM model might be more appropriate for this scenario.

Secondly, a gamma distribution was used for modelling the step-lengths in each state. Considering a gamma mixture, to allow for each state to account for the overlapping areas between the two states would also possibly lead to model improvements and a more correct definition of the states. A measure to assess the confidence of the viterbi assigned states on each occasion would be also a useful tool to evaluate predicted foraging areas based on that metric.

Lastly, it would be interesting to investigate how transforming the boat coordinates to tern ones, (by finding a projection of new coordinates referring to where the tern is located) would possibly affect the models. Given that the linear distance from the boat to tern is known (DISTKM), if the bearing from boat to tern was also available, aviation equations could thus be used even in a flat earth model scenario (given that observed DISTKM are small enough to allow it) to gain a new coordinate approximation and fit a new HMM based on this data. Otherwise, when there is such error in tracking data, State Space Models (SSMs) might be a viable alternative to HMMs ([Patterson et al., 2017](#)).

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APPENDIX

Directed Acrylic Graph creation - code (<http://www.dagitty.net/dags.html>)

```
dag {  
  bb="-6.711,-6.758,7.784,6.856"  
  "Hidden Markov Model for Movement Data" [pos="-2.821,-2.175"]  
  "S(t)" [pos="-1.869,0.491"]  
  "S(t-1)" [pos="-3.671,0.506"]  
  "X(t)" [pos="-2.238,-1.082"]  
  "X(t-1)" [pos="-4.029,-1.082"]  
  "Y(t)" [pos="-1.490,-1.082"]  
  "Y(t-1)" [pos="-3.190,-1.052"]  
  ... [pos="-4.879,0.491"]  
  .... [pos="-0.375,0.476"]  
  "S(t)" -> "X(t)"  
  "S(t)" -> "Y(t)"  
  "S(t)" -> ....  
  "S(t-1)" -> "S(t)"  
  "S(t-1)" -> "X(t-1)"  
  "S(t-1)" -> "Y(t-1)"  
  ... -> "S(t-1)"  
}
```