`foieGras` an R package for animal movement data: rapid quality control, behavioural estimation and simulation

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Abstract

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Keywords:

1 | Introduction

Animal biotelemetry as a discipline has matured, with telemetry data now virtually essential for understanding behaviour and social interactions, foraging ecology, habitat use and population dynamics of mobile and/or cryptic species. Additionally, the sophistication of current telemetry devices enables the use of animal-borne sensors as a cost-effective approach for observing our planet that compliments more traditional observing platforms (Harcourt et al., 2019; Kays et al., 2015; McMahon et al., 2021). In all these applications, animal biotelemetry requires rigourous quality control procedures to account for common, though not universally present, data issues such as irregularly timed measurements, sensor biases and location measurement error. Some of these issues may be handled by a manufacturer's on-board or subsequent processing and some must be dealt with by researchers using the data.

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transition paragraph focusing on related R packages & defining the foieGras niche here

A diverse set of software tools now exist for processing and analysis of animal telemetry data. The CRAN Task View: Processing and Analysis of Tracking Data (https://CRAN.R-project.org/view =Tracking) lists 42 R packages available on CRAN, including foieGras, and several more available from other publicly accessible repositories (Joo et al., 2020). Of the R packages available on the CRAN repository, `crawl` (Johnson et al., 2008), `ctmm` (Calabrese et al., 2016), and `bsam` (Jonsen, 2016) fill similar data quality control and analysis roles, by providing continuous- or discrete-time state-space modelling tools.

The `foieGras`, pronounced "*fwah grah*," package for R (R Core Team, 2021) was developed to be as simple and fast to use as possible. The package implements state-space models to conduct

quality control on animal (re)location data collected via the Argos satellite (Service Argos, 2016) and other telemetry systems. The latest stable and fully cross-platform tested version of the package (currently, 1.0.0) is available on the Comprehensive R Archive Network (CRAN), at https://cran.r-project.org/package=foieGras. The latest partially tested stable and development versions are available on the lead author's GitHub repository: https://github.com/ianjonsen/foieGras.

Here, we describe the main features of `foieGras` and illustrate its use through examples using both real and simulated data. Full R code for each of the examples is provided in the Supporting Information. Additional details on package functions and their use can be found in their help files and in the package's vignettes.

2 | `foieGras` overview

The workflow for `foieGras` is deliberately simple, with many of the usual track data processing checks and formatting handled automatically. The main functions are listed in Table 1. When fitting a model, `foieGras` automatically detects the type of tracking data from the location quality class designations that are typical of Argos data and that can be added to the data by the researcher for other types of track data. Based on the location quality classes and other, optional information on measurement errors contained in the data, `foieGras` chooses an appropriate measurement error model for each observation. This capability allows for combinations of different tracking data types, e.g., Argos and GPS, in a single input data frame and to be fit in a single state-space model.

2.1 | Data preparation

Animal tracking data, consisting of a time-series of location coordinates, can be read into R as a data frame using standard functions such as `read.csv`. The canonical data format for Argos tracks consists of a data frame with 5 columns corresponding to the following named variables: `id` (individual id), `date` (date and time), `lc` (location class), `lon` (longitude), `lat` (latitude). Optionally, an additional 3 columns, `smaj` (semi-major axis), `smin` (semi-minor axis), `eor` (ellipse orientation), providing Argos error ellipse information may be included.

Other types of track data can be accommodated, for example, by including the `lc` column where all `lc = "G"` for GPS data. In this case, measurement error in the GPS locations is assumed to have a standard deviation of 0.1 x Argos class 3 locations (approximately 30 m). Other types of track data can be also be considered, including those derived from light-level geolocation (see the package vignette for further details).

2.2 | State-space model fitting - `fit_ssm`

State-space models are fit using `fit_ssm`. There are a large number of options that can be set in `fit_ssm` (see Suppl for details). We focus only the essential options here:

- `data` the input data structured as described in **2.1**
- `vmax` a maximum threshold speed (ms^{-1}) to help identify potential outlier locations
- `model` the process model to be used
- `time.step` the prediction time interval (h)

The function first invokes an automated data processing stage where the following occurs: 1) data type (Argos Least-Squares, Argos Kalman Filter/Smoother, GPS, or General (e.g., processed light-level geolocations, acoustic telemetry, coded VHF telemetry) is determined; 2) datetimes are converted to POSIXt format, chronological order is ensured, and duplicate datetime records are removed; 3) observations occurring less than `min.dt` seconds after a prior observation are re-moved; 4) a speed filter [`sda` from the `trip` R package; Sumner et al. (2009)] is used to identify

Table 1: Main functions for the R package `foieGras`

Function	Description
`fit_mpm`	Fit a Move Persistence Model to location data
`fit_ssm`	Fit a State-Space Model to location data
`fmap`	Plot fitted/predicted locations on a map with or without a defined projection
`grab`	Extract fitted/predicted/observed locations from a foieGras model, with or without projection information
`osar`	Estimate One-Step-Ahead Residuals from a foieGras SSM
`sim`	Simulate individual animal tracks with Argos LS or KF errors
`simfit`	Simulate animal tracks from 'fG_ssm' fit objects
`sim_filter`	Filter tracks simulated with 'simfit' according to similarity criteria
`plot.fG_ssm`	Plot the fit of a foieGras SSM to data
`plot.fG_osar`	Plot One-Step-Ahead Residuals from a foieGras SSM
`plot.fG_mpm`	Plot move persistence estimates as 1-D or 2-D (along track) time-series
`plot.fG_sim`	Plot simulated animal tracks

potential outlier locations; 5) locations are projected from spherical lon-lat coordinates to planar x,y coordinates in km.

The function then fits a state-space model to the processed data, where the process model (currently, either a continuous-time `rw` or a continuous-time `crw`) is specified by the user and the measurement model(s) are selected automatically (see Jonsen et al., 2020 for model details). The model is fit by numerical optimization of the likelihood using either the `optim` or `nlminb` R function. The R package `TMB`, Template Model Builder (Kristensen et al., 2016), is used to compute the gradient function in C++ via reverse-mode auto-differentiation and the Laplace Approximation is used to integrate out the latent states (random effects). Fits to a single versus multiple individuals are handled automatically, with sequential SSM fits occurring in the latter case. No hierarchical or pooled estimation among individuals is currently available.

`fit_ssm` returns a `foieGras` fit object (a nested data frame with class `fG_ssm`). The outer data frame lists the individual id(s), basic convergence information and a list with class `ssm`. This list contains dense information on the model parameter and state estimates, predictions, processed data, optimizer results, and other diagnostic and contextual information. Users can extract a simple data frame of SSM fitted (location estimates corresponding to the, typically irregular, observation times) or predicted values (locations predicted at regular `time.step` intervals) using the `grab` function.

2.3 | Model checking and visualisation - `osar`, `plot`, `fmap`

Before using fitted or predicted locations, a model fit should be checked and visualised to confirm that the model adequately describes the data. In linear regression and a variety of analogous methods, goodness-of-fit can be assessed by calculating standard residuals such as Pearson or deviance residuals. There is no simple way to calculate residuals for latent variable models that have non-finite state-spaces and that may be nonlinear, but they can be computed based on iterative forecasts of the model (Thygesen et al., 2017). The `osar` function computes one-step-ahead (prediction) residuals and uses the `oneStepPredict` function from the `TMB` R package to make this as efficient as possible. A set of residuals are calculated for the `x` and `y` values corresponding to

110 the fitted values from the SSM and returned as an `fG_osar` object.

111 A generic `plot` method provides an easy way to visualise the `fG_osar` residuals. Time-series plots
112 of the prediction residuals can be used to detect temporal changes in goodness-of-fit. Quantile-
113 quantile plots of residuals against standard normal quantiles can be used to detect departures
114 from normality. Sample autocorrelation function plots of the residuals are useful for detecting auto-
115 correlation not accounted for by the model. Assessing residual autocorrelation can be particularly
116 important as Argos locations, for example, are themselves derived from a time-series model (Lopez
117 et al., 2015) which can introduce additional autocorrelation in the location errors.

118 State-space model fits to data can also be visualised by using the generic `plot` function on an
119 `fG_ssm` data frame. Options exist to plot fitted or predicted values along with observations as
120 either paired, 1-D time-series or as 2-D tracks with confidence intervals or ellipses, respectively.
121 These plots provide a more intuitive and rapid method for assessing SSM fits to data, however,
122 they do not replace the residual diagnostics. Fitted `fG_ssm` data frames can be mapped using the
123 `fmap` function for single or multiple individuals. Estimated tracks can be displayed with or without
124 confidence ellipses, observations, and/or a projection and maps of single tracks can be coloured
125 by date.

2.4 | Behavioural estimation - `fit_mpm`

127 The `fit_mpm` function fits a simple move persistence model to estimate a continuous-valued, time-
128 varying latent variable that indexes changes in movement behaviour (Jonsen et al., 2019). This
129 variable measures the autocorrelation in speed and direction between consecutive pairs of move-
130 ments such that high values correspond to fast, directed movements at one end of the continuum
131 and low values correspond to slow, tortuous movements at the other end. It's important to note
132 that this approach is unlike hidden Markov models (McClintock & Michelot, 2018; Michelot et al.,
133 2016) and some state-space models (Jonsen, 2016) as there is no notion of discrete behavioural
134 states that animals periodically switch between. Nonetheless, move persistence can be used to
135 identify objectively places where animals spend disproportionately more or less time, and with
136 extensions be correlated with environment or other covariates (See Examples 3.x).

137 The move persistence model assumes that locations are absent of measurement error and can
138 occur either irregularly or regularly in time. `fit_mpm` takes either a `fG_ssm` data frame as input or a
139 data frame with the follow variables: `id`, `date`, `x`, `y`, where `x` and `y` coordinates can be planar `x,y`
140 or spherical `long,lat`. This latter input format allows the model to be fit easily to GPS or other
141 tracking data with negligible measurement error. When the data contain multiple individuals, the
142 default model is fit jointly by assuming all individuals share the same move persistence variance
143 parameter (Jonsen, 2016). There is an option to fit the model separately to each individual. The
144 time-series of estimated move persistence with confidence intervals can be visualized by using
145 the generic `plot` function with the resulting `fG_mpm` data frame. Visualization of move persistence
146 along the 2-D tracks can be plotted or mapped by using the `plot` or `fmap` functions, respectively,
147 and supplying both the `fG_mpm` and `fG_ssm` nested data frames. When using `fit_mpm` on, for
148 example, GPS tracking data that do not require state-space filtering, the movement persistence
149 estimates can be extracted from the `fG_mpm` data frame using the `grab` function and subsequently
150 merged with the observed track data for visualization.

2.5 | Simulation - `sim`, `simfit`, `sim_filter`

152 Track simulation can be a helpful, yet informal, way of evaluating the degree to which statistical
153 movement models capture essential features of animal movement data (Michelot et al., 2017).
154 Michelot et al. (2016) advocate comparison of simulated tracks from fitted hidden Markov models
155 to the observed tracks as a means of identifying potential weakness in the hidden Markov model

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156 formulation. Here, we suggest that the `rw` and `crw` state-space models and the `mpm` model can be
157 fit to track data simulated from different movement processes to evaluate robustness of location
158 and movement persistence estimates to model mis-specification. We illustrate this idea in section
159 3.x by drawing on flexibility in the `sim` function that allows a variety of movement processes to be
160 simulated.

161 Simulation is also used frequently to provide a measure of habitat availability (Aarts et al., 2012)
162 by providing a source of 'pseudo-absence' points representing a null model of the distribution of
163 foraging animals in the absence of external drivers (Hindell et al., 2020; S. J. Phillips et al., 2009;
164 Raymond et al., 2015). The `simfit` function extracts movement parameters from a `fG_ssm` fit
165 object and simulates a user defined number of random tracks of the same duration from these
166 parameters. The argument `cpf = TRUE` allows the user to simulate a central place forager by
167 ensuring that the simulated tracks start and end at approximately the same location.

168 The choice of null points can have a large impact on the performance of habitat suitabillity models
169 (Lobo et al., 2010; S. J. Phillips et al., 2009), and so the `sim_filter` function provides a tool to
170 filter the simulated tracks based on their similarity to the original path. The filtering is based on one
171 of two metrics that capture the difference in the net displacement and bearing between the two
172 paths (see `similarity_flag` for more detail). This metric is motivated by the 'flag value' described
173 in Hazen et al. (2017). The user can also specify the quantile of flag values to retain; i.e. `keep =`
174 `0.25` (the default) will return a `simfit` object containing those simulated tracks with flag values in
175 the top 25% of values calculated for the input `simfit` object.

176 3 | Examples

177 We illustrate the main capabilities of `foieGras` through a series of examples using real and sim-
178 ulated tracking data. These examples are for demonstration purposes and not intended as a
179 comprehensive guide for conducting analyses with `foieGras`. Complete code for reproducing the
180 examples and for gaining a deeper understanding of `foieGras` functions are provided as supple-
181 ments.

182 3.1 | Southern Elephant seal - SSM validation with prediction residuals

183 We use a subadult male southern elephant seal track included in `foieGras` (`sese1`), sourced
184 from from the Australian Integrated Marine Observing System (IMOS; data publicly available via
185 imos.aodn.org.au) deployments at Iles Kerguelen in collaboration with the French IPEV and SNO-
186 MEMO programmes. The data are temporally irregular Argos Least-Squares based locations, 73
187 % of which are in the poorest location quality classes: A and B. We fit both the `rw` and `crw` models
188 using `fit_ssm` with a speed filter threshold (`vmax`) of 4 ms^{-1} and a 12-h time step. We calculate
189 prediction residuals using `osar`, and then use the generic `plot` method for `osar` residuals to assess
190 and compare the model fits (Fig. 1).

191 The plots of predicted states on top of the observations suggests both models yield similar fits
192 (Fig. 1a,b), however, there are marked trends in the time-series of residuals for the `rw` model fit
193 (Fig. 1c) and the `rw` ACF's reveal consistent positive autocorrelation in the prediction residuals (Fig.
194 1e). The corresponding `crw` prediction residuals show no apparent trends through time and have
195 relatively little autocorrelation (Fig. 1d,f), implying that the `crw` provides a better fit to the data.

196 3.2 | Assessing SSM robustness with simulated data

197 Using the `sim` function, we simulate animal movement tracks with a variety of plausible movement
198 patterns. We use these simulated data to examine the accuracy of SSM fits to data generated
199 by processes that differ from the `rw` and `crw` process models use in `fit_ssm`. While we regard

Figure 1: Selected diagnostic plots for assessing `rw` (a,c,e) and `crw` (b,d,f) state-space model fits to a southern elephant seal track. Top panels (a,b) are plots of predicted states (red; regular 12-h time intervals) and observations (blue) with pre-filtered observations (orange; ignored by the SSM), using the `plot.fG_ssm` function. Panels c,d are time-series plots of the prediction residuals for the x and y coordinates of each fitted state. Panels e,f are autocorrelation functions of the prediction residuals. All residual plots generated using the `plot.fG_osar` function.

this example as an atypical use of the track simulation function, it nonetheless illustrates one of the many possible uses of such a simulation tool. Another, more common application of track simulation as a preparatory step for a habitat usage analysis is highlighted in example 3.4.

We used `sim` to generate 50 animal tracks from each of the following 3 process models: 1) the same `crw` process used in `fit_ssm`; 2) a 2-state `crw` with stochastic switching between movement states; 3) the movement persistence model, where persistence in directionality and speed varies as a random walk. All tracks were simulated for 300 regular, 6-h time steps and a randomly selected Argos Kalman Filter error ellipse was assigned to each simulated location independent of the movement process. Further details on the track simulations are in Supplement xx. Representative simulated tracks for each movement process are shown in (Fig. 2a-c). We then used `fit_ssm` to fit both the `rw` and `crw` SSM's to these simulation tracks and calculated the Root Mean Squared Error of the SSM fits using the Euclidean distance between each SSM-estimated location and the corresponding simulated location (without Argos error). As the spatial scale of the simulated tracks differed among the 3 movement processes, we normalized RMSE values by the mean step length calculated across all tracks within each movement process type.

Regardless of the simulated movement process, the `crw` SSM consistently provided more accurate fits than the `rw` SSM (Fig. 2d-f). Although fits to the simulated 2-state `crw` and `mpm` tracks were less accurate than to the `crw` tracks, the differences were not large and goodness-of-fit based on prediction residuals were reasonable (Supplement xx). We advocate that in most cases the `crw` SSM should be preferred for quality-control of Argos tracking data, however the `rw` SSM may converge more reliably when fitting to problematic data (e.g., tracks with frequent and relatively large temporal data gaps).

3.3 | Inferring movement persistence as an index of behaviour from Argos and GPS data

Drawing on an expanded version of the data used in 3.1, we quality control and infer movement persistence, γ_t, along five southern elephant seal tracks. We fitted the `crw` SSM with a 24-h prediction interval using `fit_ssm` and assuming bivariate normal location measurement errors consistent with Argos Least-Squares-derived locations (Jonsen et al., 2020). We used the SSM-predicted locations to estimate movement persistence jointly among the 5 seals using `fit_mpm` and visualise the behavioural index along the seals' tracks. The data can be accessed in `foieGras` via `data(sese, package = 'foieGras')`. As the estimation of γ_t is sensitive to choice of time scale, we examined the influence of different prediction intervals (1 - 20 min) on the ability of the movement persistence model to resolve changes in movement pattern along the penguin tracks.

To illustrate how the method can accommodate other types of animal tracking data, we also infer γ_t along six little penguin (*Eudyptula minor*) GPS tracks from Montague Island, NSW Australia, described in L. Phillips et al. (2021). The data are temporally irregular GPS locations that are assumed to have minimal measurement error. We fitted the `crw` SSM to predict temporally regular locations at 5-min intervals, assuming consistently small bivariate normal location measurement errors (ie. $\pm$ 10 m sd).

Movement persistence estimates along the quality-controlled southern elephant seal tracks highlight some fundamental differences in movement pattern among the seals. The two seals engaging in pelagic foraging trips (Fig. 3a,c and f) had less contrast in their movements with consistently higher γ_t estimates compared to the three seals engaging in trips to the fast-ice on the Antarctic shelf (Fig. 3b,d-e and f). Although γ_t's were higher overall for the pelagically foraging seals, they both spent little time making fast, highly directed movements ($\gamma_t \rightarrow 1$) relative to the shelf-foraging seals (3a,c vs b,d-e). This suggests the pelagically-foraging seals may spend considerable time searching for suitable foraging habitat in the highly variable eddy fields between the Subantarctic and Polar Fronts (Jonsen et al., 2019), whereas foraging habitat may be more predictable for seals
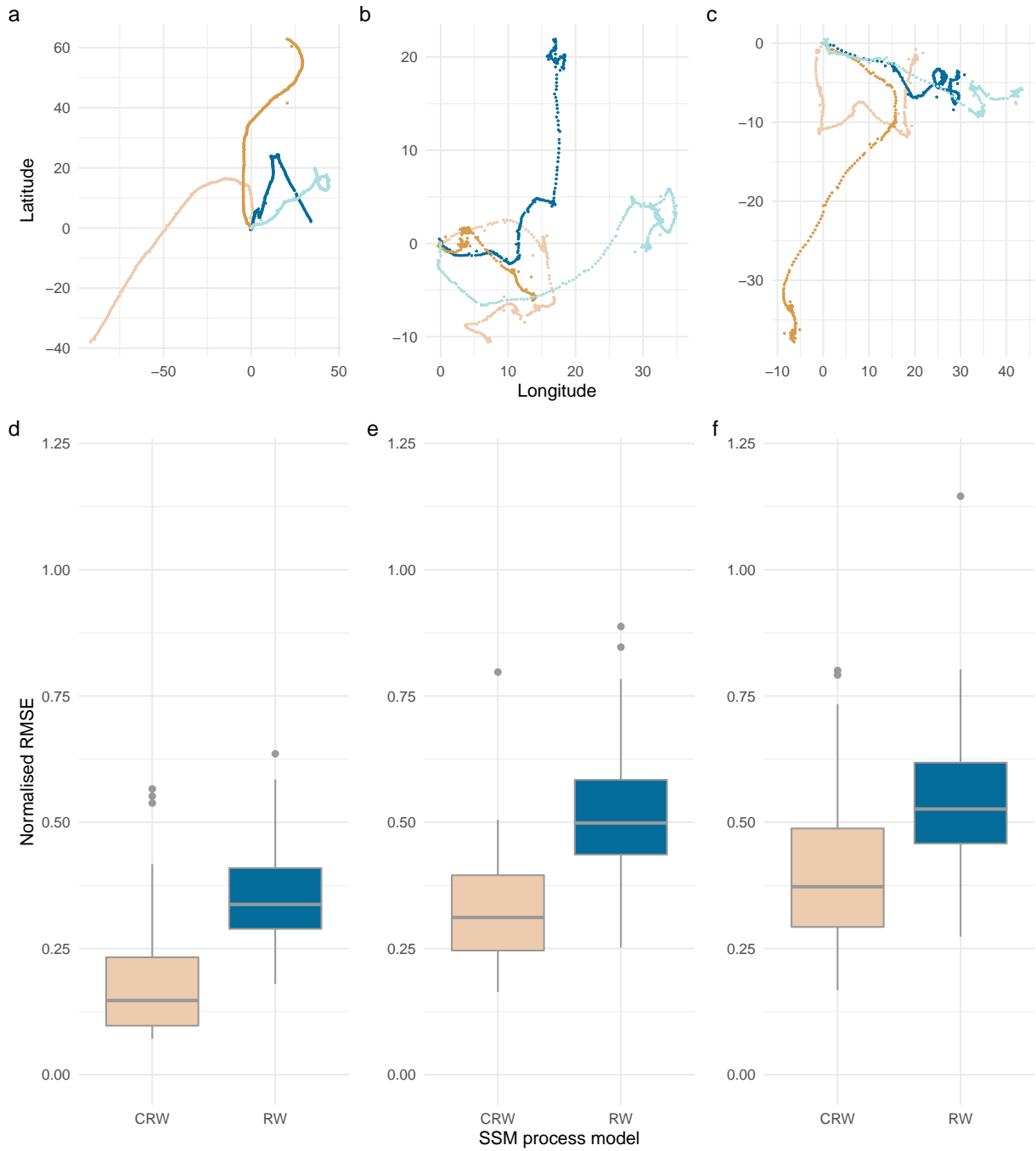
Figure 2: Four example tracks simulated from the correlated random walk process model (`crw`, a), a 2-state `crw` model (b), and the movement persistence model (`mpm`, c). Normalised Root Mean Squared Errors of state-space models fit with either the `crw` or random walk (`rw`) process model to 50 simulated `crw` tracks (d), 50 simulated `2-state crw` tracks (e), and 50 simulated `mpm` tracks (f). The SSM fits using the `crw` process model were consistently more accurate than those using the `rw` process model, regardless of the type of movements simulated.

247 travelling rapidly and directly to the Antarctic shelf region. These seals may also haulout periodically
248 on available fast-ice to rest. This behaviour could also contribute to the higher contrast in move-
249 ment persistence, relative to pelagically-foraging seals who would not have access to fast-ice.

250 Despite vastly different scales of movement, the time series of little penguin movement persis-
251 tence estimates were broadly similar to those of the southern elephant seals (Fig. 4a-e). The little
252 penguin foraging trips likely reflect the underlying spatial distribution of their forage-fish prey, with
253 spatially diffuse bouts of lower movement persistence potentially indicative of foraging both within
254 and among neighbouring discrete prey patches (Carroll et al., 2017) (Fig. 4f).
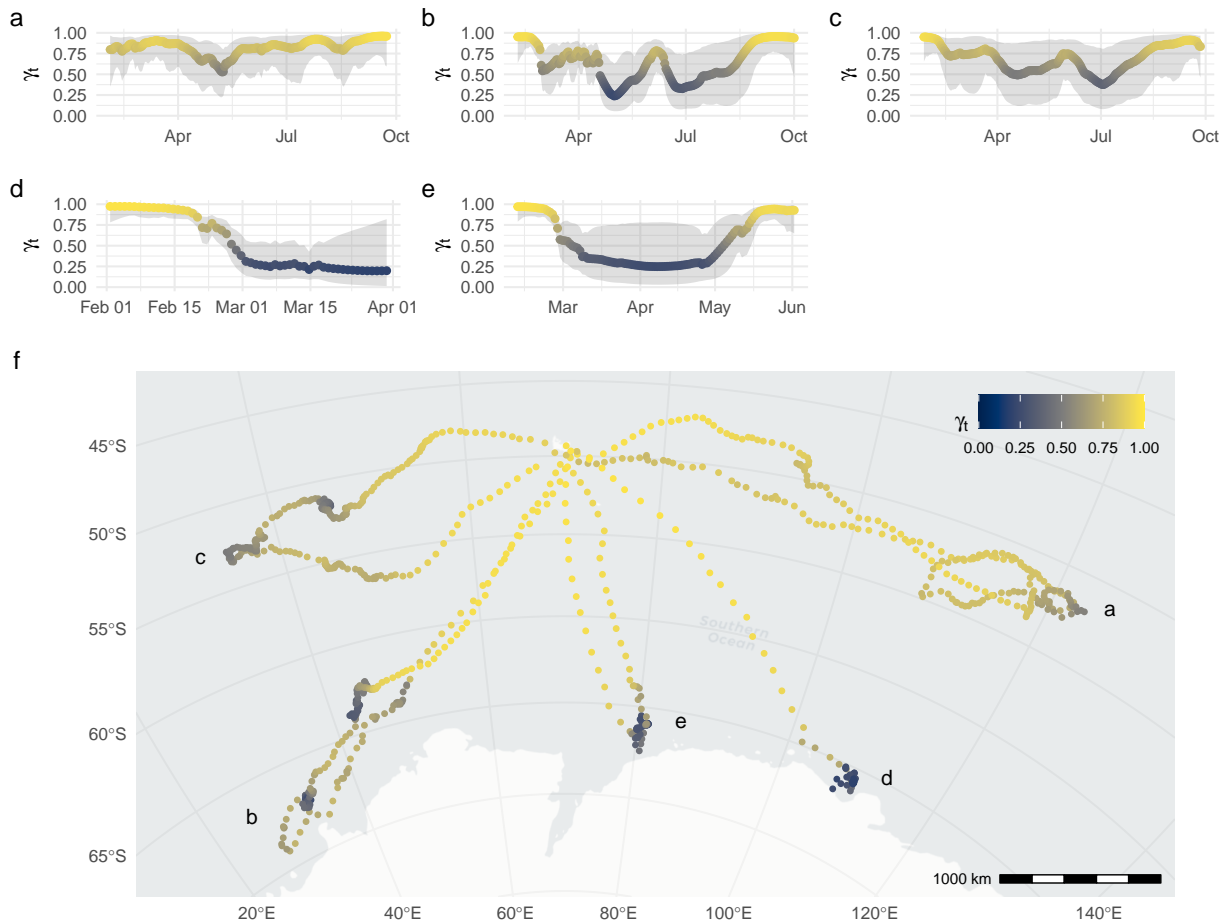
Figure 3: Inferred move persistence, γ_t, 1-D time-series for five southern elephant seals (a-e; grey envelopes are 95 % CI's) and along their 2-D tracks (f; track labels, a-e, correspond to the 1-D time-series plots). Locations associated with low move persistence (blue) are indicative of slow, undirected movements, whereas high move persistence (yellow) is indicative of faster, directed movements. The lowest move persistence tends to occur at the distal end of foraging trips from the colony at Iles Kerguelen, suggesting these bouts of low movement persistence are associated with foraging activity. Due to the stereographic projection used and huge area covered in (f), the scale bar is not accurate in all regions and is indicative only.

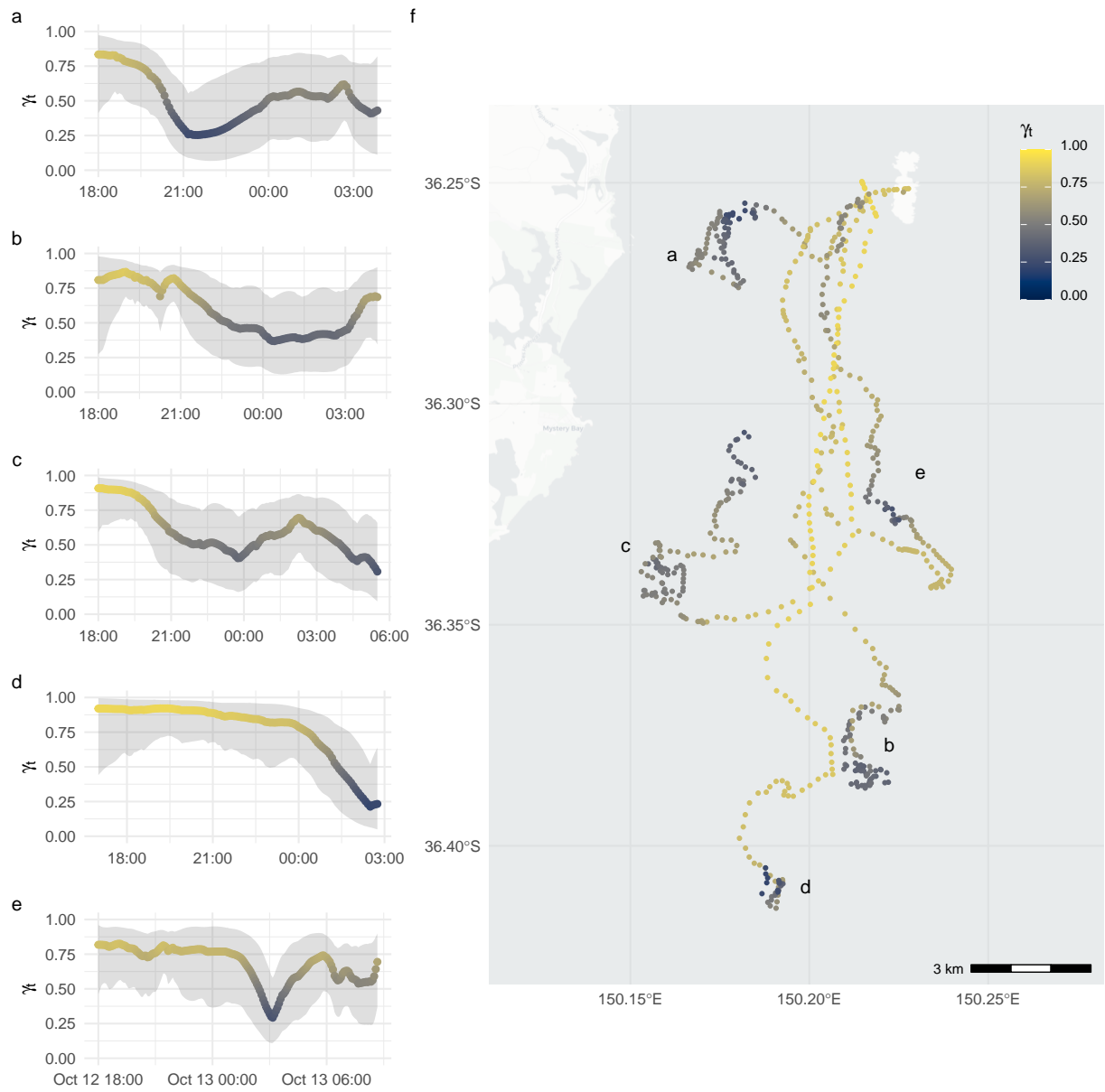255 ### 3.4 | Simulating tracks from `foieGras` model fits

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Figure 4: Inferred move persistence, γ_t, 1-D time-series (a-f; grey envelopes are 95 % CI's) and along little penguin GPS tracks (g). Colour palette as in 3. Movement persistence was estimated from SSM-predicted locations with a regular 5-min interval.

4 | Discussion

Ex 3.2 In a limited way, this provides information on the robustness of the `foieGras` SSM's to different kinds plausible animal movements

Author's Contributions

IDJ developed the R package; WJG contributed harp seal data and to the R package; LP, GC, and RGH contributed little penguin data; CRM and RGH contributed Southern elephant seal data; IDJ and TAP developed the state-space models; IDJ wrote an initial draft of the manuscript with contributions from WJG; all authors edited the manuscript.

Data Accessibility

All code mentioned here is provided in the `foieGras` package for R available on CRAN at https://CRAN.R-project.org/package=foieGras. The development version of the package is available on GitHub at https://github.com/ianjonsen/foieGras. Data used in the examples are available at…

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