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

Ian D. Jonsen^{1,*}, W. James Grecian², Lachlan Phillips¹, Gemma Carroll³, Clive McMahon⁴,
 Robert G. Harcourt¹, and Toby A. Patterson⁵

Department of Biological Sciences, Macquarie University, Sydney, NSW, Australia
 Scottish Oceans Institute, University of St Andrews, St Andrews, Fife, United Kingdom

 ³Environmental Defense Fund, Seattle, WA, United States
 ⁴Sydney Institute of Marine Science, Mosman, NSW, Australia
 ⁵CSIRO Ocean and Atmosphere Research, Hobart, TAS, Australia
 ^{*}corresponding author, ian.jonsen@mg.edu.au

Abstract

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17 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 20 dynamics of mobile and/or cryptic species. Additionally, the sophistication of current telemetry 21 devices enables the use of animal-borne sensors as a cost-effective approach for observing our 22 planet that compliments more traditional observing platforms (Harcourt et al., 2019; Kays et al., 23 2015; McMahon et al., 2021). In all these applications, animal biotelemetry requires rigourous 24 quality control procedures to account for common, though not universally present, data issues such as irregularly timed measurements, sensor biases and time-varying errors in location. Some 26 of these issues may be handled by a manufacturer's on-board or subsequent processing and some 27 must be dealt with by researchers using the data. 28

- ²⁹ transition paragraph focusing on analytical methods here...
- transition paragraph focusing on related R packages & defining the foieGras niche here...
- 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 much 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 location quality classes 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 observation 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.

51 2.1 | Data preparation

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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), 1c (location class), 1on (longitude), 1at (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 1c column where all 1c = "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 considered in a similar manner (see the package vignette for further details).

2 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 removed; 4) a speed filter [sda from the trip R package; Sumner et al. (2009)] is used to identify 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

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

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

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Before using fitted or predicted locations, a model fit should be checked and visualised to confirm 93 that the model adequately describes the data. In linear regression and a variety of analogous 94 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 97 forecasts of the model (Thygesen et al., 2017). The osar function computes one-step-ahead 98 (prediction) residuals and uses the oneStepPredict function from the TMB R package to make this 99 as efficient as possible. A set of residuals are calculated for the x and y values corresponding to 100 the fitted values from the SSM and returned as an fG_osar object. 101

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

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

2.4 | Behavioural estimation - fit_mpm

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

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

2.5 | Simulation - sim, simfit, sim_filter

Track simulation can be a helpful, yet informal, way of evaluating the degree to which statistical movement models capture essential features of animal movement data (Michelot et al., 2017). Michelot et al. (2016) advocate comparison of simulated tracks from fitted hidden Markov models to the observed tracks as a means of identifying potential weakness in the hidden Markov model formulation. Here, we suggest that the rw and crw state-space models and the mpm model can be fit to track data simulated from different movement processes to evaluate robustness of location and movement persistence estimates to model mis-specification. We illustrate this idea in section 3.x by drawing on flexibility in the sim function that allows a variety of movement processes to be simulated.

Simulation is also used frequently to infer habitat availability, e.g., a null model of the distribution of foraging animals in the absence of external drivers, in habitat utilization studies (Hindell et al., 2020; Raymond et al., 2015). The simfit function extracts movement parameters from a

fG_ssm fit object and simulates an arbitrary number of random tracks of the same duration from these parameters. The argument cpf = TRUE ensures that the simulated tracks start and end at approximately the same location, thereby simulating a central place forager. Something about sim_filter here...

159 3 | Examples

We illustrate the main capabilities of foieGras through a series of examples using real and simulated tracking data. These examples are for demonstration purposes and not intended as a comprehensive guide for conducting analyses with foieGras. Complete code for reproducing the examples and for gaining a deeper understanding of foieGras functions are provided as supplements.

3.1 | Southern Elephant seal - SSM validation with prediction residuals

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

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

179 3.2 | Assessing SSM robustness with simulated data

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



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.

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 per-sistence, 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 loca-tions 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 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 ($\gamma_t \to 1$) 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 travelling rapidly and directly to the Antarctic shelf region. These seals may also haulout periodically on available fast-ice to rest. This behaviour could also contribute to the higher contrast in movement persistence, relative to pelagically-foraging seals who would not have access to fast-ice.

Despite vastly different scales of movement, the time series of little penguin movement persistence estimates were broadly similar to those of the southern elephant seals (Fig. 4a-e). The little penguin foraging trips likely reflect the underlying spatial distribution of their forage-fish prey, with spatially diffuse bouts of lower movement persistence potentially indicative of foraging both within and among neighbouring discrete prey patches (Carroll et al., 2017) (Fig. 4f).

3.4 | Simulating tracks from foieGras model fits

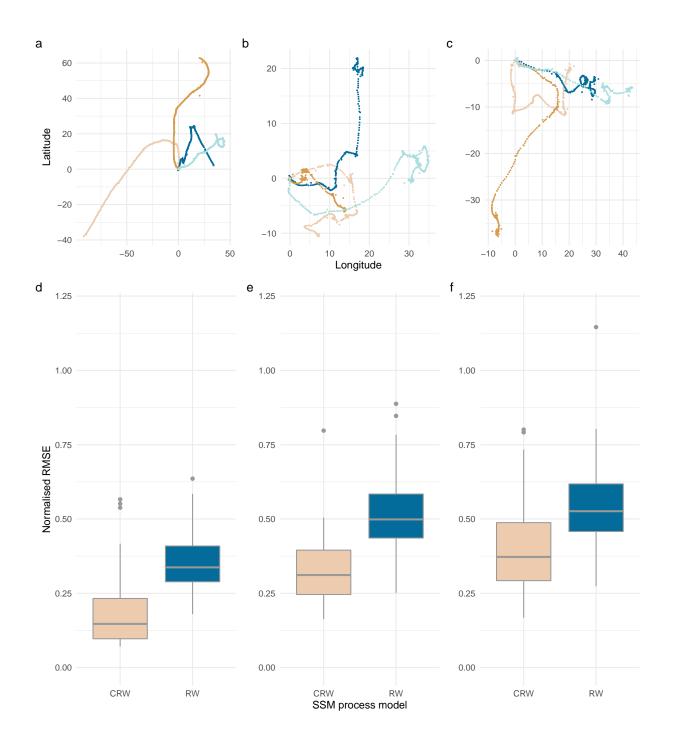


Figure 2: Four example tracks simulated from the correlated random walk process model (crw, a), a 2-state crw model (b), and the movement persistence model (mpm, c). Normalised Root Mean Squared Errors of state-space models fit with either the crw or random walk (rw) process model to 50 simulated crw 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.

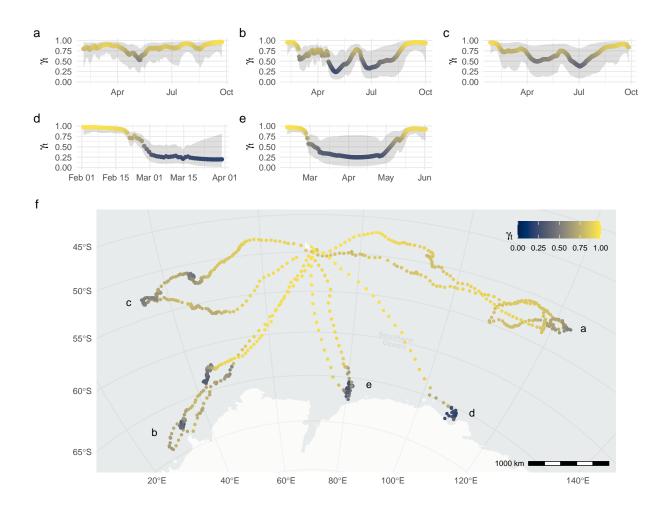


Figure 3: Inferred move persistence, γ_t , 1-D time-series for five southern elephant seals (a-e; grey envelopes are 95 % Cl's) and along their 2-D tracks (f; track labels, a-e, correspond to the 1-D time-series plots). Locations associated with low move persistence (blue) are indicative of slow, undirected 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 lles 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.

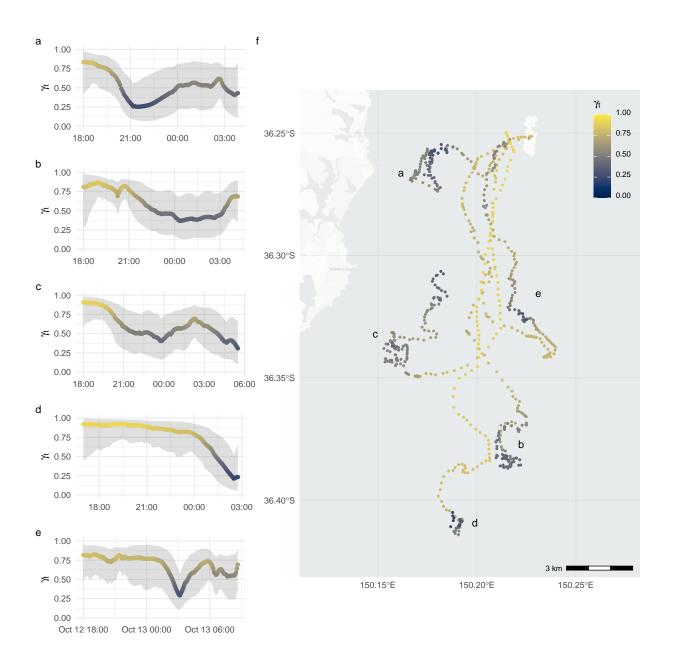


Figure 4: Inferred move persistence, γ_t , 1-D time-series (a-f; grey envelopes are 95 % Cl's) and along little penguin GPS tracks (g). Colour palette as in 3. Movement persistence was estimated from SSM-predicted locations with a regular 5-min interval.

239 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

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258 Author's Contributions

²⁵⁹ IDJ developed the R package; WJG contributed harp seal data and to the R package; LP, GC, and RGH contributed little penguin data; IDJ and TAP developed the state-space models; IDJ wrote an initial draft of the manuscript with a contribution from WJG; all authors edited the manuscript.

262 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...

266 ORCID

- 267 Ian D Jonsen https://orcid.org/0000-0001-5423-6076
- ²⁶⁸ W James Grecian https://orcid.org/0000-0002-6428-719X
- ²⁶⁹ Lachlan Phillips https://orcid.org/0000-0002-7635-2817
- ²⁷⁰ Gemma Carroll https://orcid.org/0000-0001-7776-0946
- 271 Robert G Harcourt https://orcid.org/0000-0003-4666-2934
- ²⁷² Toby A Patterson https://orcid.org/0000-0002-7150-9205

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