

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

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14 **Abstract**

- 15 1.
16 2.
17 3.
18 4.

19 **Keywords:**

20 **1 | Introduction**

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

32 *transition paragraph focusing on analytical methods here*

33 *transition paragraph focusing on related R packages & defining the foieGras*

34 **niche here**

35 A diverse set of software tools now exist for processing and analysis of animal telemetry
36 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
37 several more available from other publicly accessible repositories (Joo et al., 2020). Of the R
38 packages available on the CRAN repository, **crawl** (Johnson et al., 2008), **ctmm** (Calabrese
39 et al., 2016), and **bsam** (Jonsen, 2016) fill similar data quality control and analysis roles, by
40 providing continuous- or discrete-time state-space modelling tools.

42 The **foieGras**, pronounced “*fwah grah*”, package for R (R Core Team, 2021) was developed
43 to be as simple and fast to use as possible. The package implements state-space models to
44 conduct quality control on animal (re)location data collected via the Argos satellite (Service
45 Argos, 2016) and other telemetry systems. The latest stable and fully cross-platform tested
46 version of the package (currently, 1.0.0) is available on the Comprehensive R Archive Network
47 (CRAN), at <https://cran.r-project.org/package=foieGras>. The latest partially tested
48 stable and development versions are available on the lead author’s GitHub repository: <https://github.com/ianjonsen/foieGras>.

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

54 **2 | foieGras overview**

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

64 **2.1 | Data preparation**

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

71 Other types of track data can be accommodated, for example, by including the **lc** column
72 where all **lc = "G"** for GPS data. In this case, measurement error in the GPS locations is

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

Function	Description
fit_ssm	Fit a State-Space Model to location data
fit_mpm	Fit a Move Persistence Model to location data
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
map	Map fitted/predicted locations with or without a defined projection
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
route_path	Reroute path so estimated locations are off land
plot.ssm_df	Plot the fit of a foieGras SSM to data
plot.osar	Plot One-Step-Ahead Residuals from a foieGras SSM
plot.mpm_df	Plot move persistence estimates as 1-D or 2-D (along track) time-series
plot.sim	Plot simulated animal tracks

73 assumed to have a standard deviation of 0.1 x Argos class 3 locations (approximately 30 m).
74 Other types of track data can be also be considered, including those derived from light-level
75 geolocation (see the package vignette for further details).

76 **2.2 | State-space model fitting - fit_ssm**

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

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

83 The function first invokes an automated data processing stage where the following occurs:
84 1) data type (Argos Least-Squares, Argos Kalman Filter/Smoother, GPS, or General (e.g.,
85 processed light-level geolocations, acoustic telemetry, coded VHF telemetry) is determined;
86 2) datetimes are converted to POSIXt format, chronological order is ensured, and duplicate
87 datetime records are removed; 3) observations occurring less than `min.dt` seconds after a
88 prior observation are removed; 4) a speed filter [`sda` from the `trip` R package; Sumner et al.
89 (2009)] is used to identify potential outlier locations; 5) locations are projected from spherical
90 lon-lat coordinates to planar x,y coordinates in km.

91 The function then fits a state-space model to the processed data, where the process model
92 (currently, either a continuous-time `rw` or a continuous-time `crw`) is specified by the user
93 and the measurement model(s) are selected automatically (see Jonsen et al., 2020 for model
94 details). The model is fit by numerical optimization of the likelihood using either the `optim`
95 or `nlminb` R function. The R package TMB, Template Model Builder (Kristensen et al.,
96 2016), is used to compute the gradient function in C++ via reverse-mode auto-differentiation
97 and the Laplace Approximation is used to integrate out the latent states (random effects).
98 Fits to a single versus multiple individuals are handled automatically, with sequential SSM
99 fits occurring in the latter case. No hierarchical or pooled estimation among individuals is
100 currently available.

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

108 **2.3 | Model checking and visualisation - osar, plot, fmap**

109 Before using fitted or predicted locations, a model fit should be checked and visualised to
110 confirm that the model adequately describes the data. In linear regression and a variety of
111 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 the fitted values from the SSM and returned as an `fG_osar` object.

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 (Jonsen, 2016). 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. 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 a Supplement (xx) by drawing on flexibility in the `sim` function that allows a variety of movement processes to be simulated.

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

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

2.6 | Path rerouting - `route_path`

3 | Examples

We illustrate the main capabilities of `foieGras` through a series of examples that are for demonstration purposes and not intended as a comprehensive guide for conducting analyses

193 with `foieGras`. Complete code and data for reproducing the examples and for gaining a
194 deeper understanding of `foieGras` functions are provided as supplements.

195 3.1 | Southern Elephant seal - SSM validation with prediction residuals

196 We use a sub-adult male southern elephant seal track included in `foieGras` (`sese2`, id: ct36-
197 E-09), sourced from the Australian Integrated Marine Observing System (IMOS; data
198 publicly available via imos.aodn.org.au) deployments at Iles Kerguelen in collaboration with
199 the French IPEV and SNO-MEMO programmes. The data are temporally irregular Argos
200 Least-Squares based locations, 74 % of which are in the poorest location quality classes: A
201 and B. We fit both the `rw` and `crw` models using `fit_ssm` with a speed filter threshold (`vmax`)
202 of 4 ms⁻¹ and a 12-h time step. We calculate prediction residuals using `osar`, and then use
203 the generic `plot` method for `osar` residuals to assess and compare the model fits (Fig. 1).

204 The plots of predicted states on top of the observations suggest both models yield similar
205 fits (Fig. 1a; orange vs red lines). However, corresponding predicted locations from the
206 two models differ by a median 6.62 km (range: 0.02, 53.02 km), and there are marked
207 trends in the time-series of residuals for the `rw` model fit (Fig. 1b) with significantly positive
208 autocorrelation in both the x and y directions (Fig. 1d). The `crw` prediction residuals show
209 little trend through time and have relatively little autocorrelation (Fig. 1c,e), implying that
210 the `crw` process model provides a better fit to the data.

211 3.2 | Inferring movement persistence from Argos and GPS data

212 Drawing on an expanded version of the data used in 3.1, we quality control and infer move-
213 ment persistence, γ_t , along four southern elephant seal tracks. We fitted the `mp` SSM with
214 a 24-h prediction interval using `fit_ssm`, assuming bivariate normal measurement errors
215 consistent with Argos Least-Squares-derived locations (Jonsen et al., 2020). The `mp` SSM
216 simultaneously estimates locations and γ_t , and their uncertainties. We then assess how γ_t
217 changes along the seals' tracks to infer regions where the seals spend disproportionately more
218 or less time during their foraging trips.

219 To illustrate how the method can accommodate other types of animal tracking data, we also
220 infer γ_t along four little penguin (*Eudyptula minor*) GPS tracks from Montague Island, NSW
221 Australia, described in L. Phillips et al. (2021). The data are temporally irregular GPS
222 locations, with high frequency sampling (1 - 2s) periodically disrupted by the birds' diving
223 behaviour, and are assumed to have minimal measurement error. We consequently chose to
224 fit the `crw` SSM to the GPS data and predict temporally regular locations at 5-min intervals,
225 assuming consistently small bivariate normal location measurement errors (ie. ± 10 m sd).
226 We then used `fit_mpm` to estimate γ_t from the SSM-predicted locations.

227 Movement persistence estimates along the quality-controlled southern elephant seal tracks
228 highlight some fundamental differences in movement pattern among the seals. The two seals
229 engaging in pelagic foraging trips (Fig. 2a,c and e) had less contrast in their movements
230 with consistently higher γ_t estimates compared to the two seals engaging in trips to the
231 fast-ice on the Antarctic shelf (Fig. 2b,d and e). Although γ_t 's were higher overall for the
232 pelagically foraging seals, they both spent little time making fast, highly directed movements

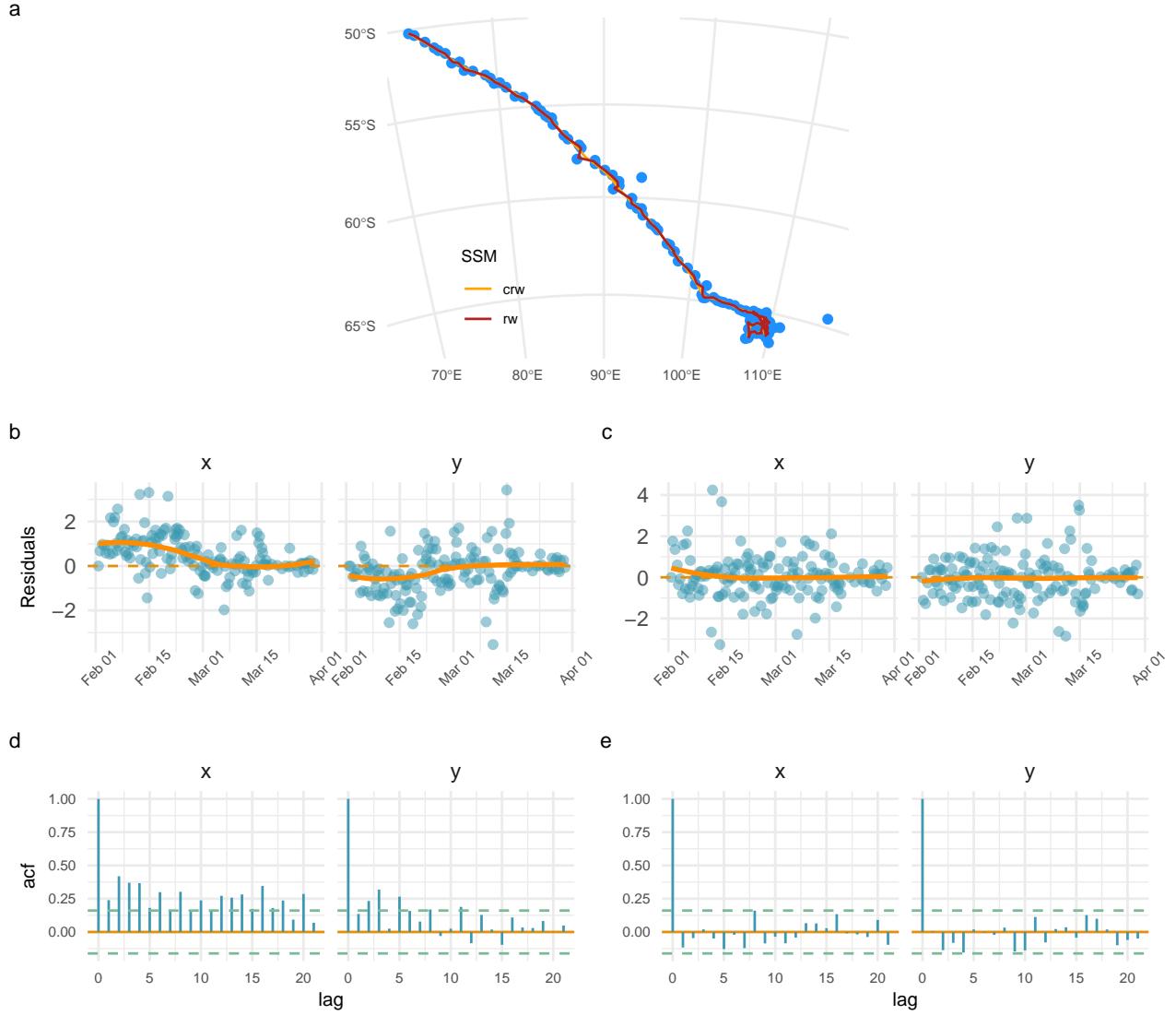


Figure 1: State-space model fits to a southern elephant seal track (a), and diagnostic plots for assessing `rw` (c - time-series of prediction residuals; e - autocorrelation of prediction residuals) and `crw` (d,f) state-space model goodness-of-fit. All residual plots generated using the `plot.fG_osar` function.

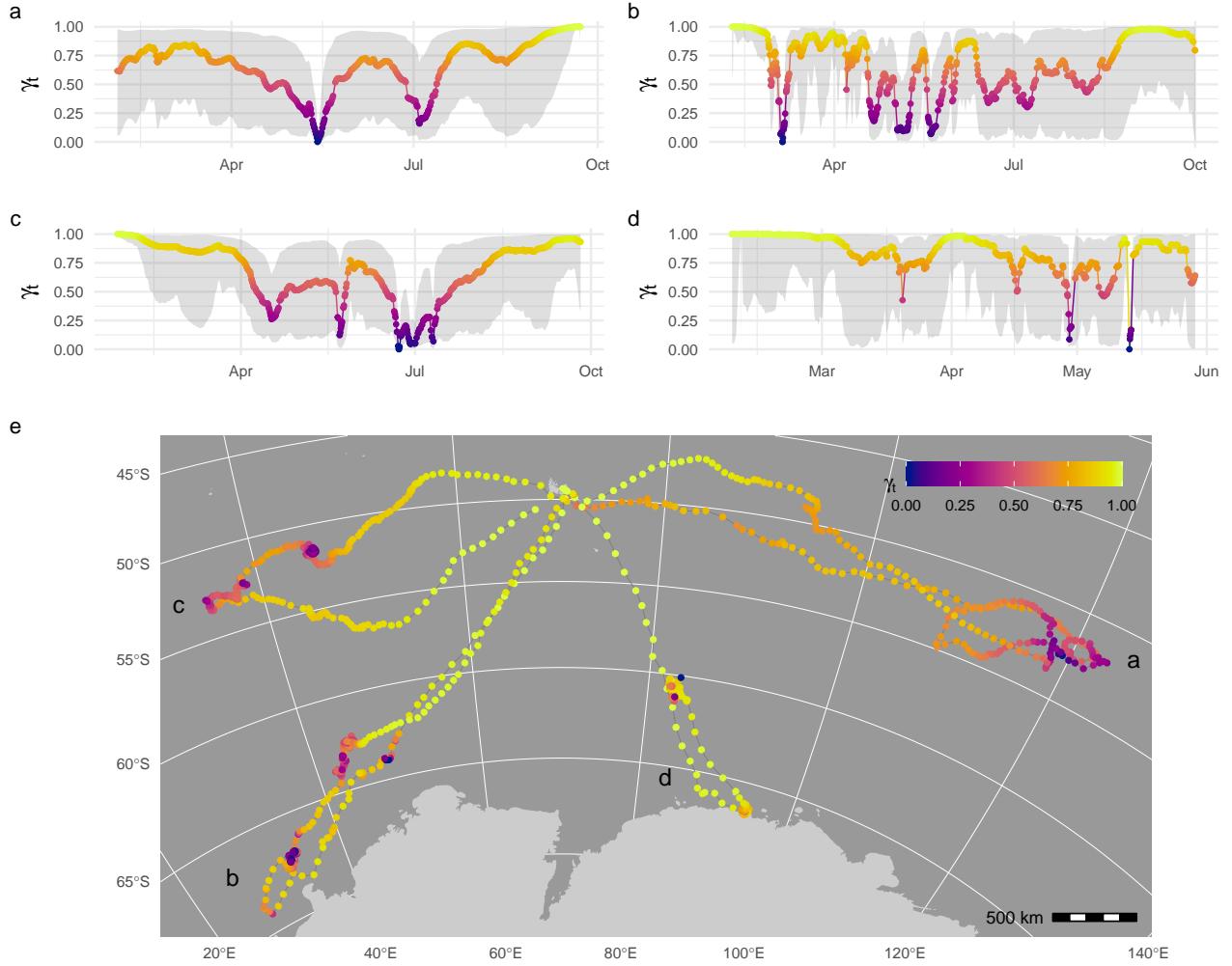


Figure 2: Inferred move persistence, γ_t , 1-D time-series for four southern elephant seals (a-d; grey envelopes are 95 % CI's) and along their 2-D tracks (e; track labels, a-d, correspond to the 1-D time-series plots). Locations associated with low move persistence (purple) are indicative of slow, undirected movements, whereas high move persistence (yellow) is indicative of faster, directed movements.

($\gamma_t \rightarrow 1$) relative to the shelf-foraging seals (2a,c vs b,d). 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.

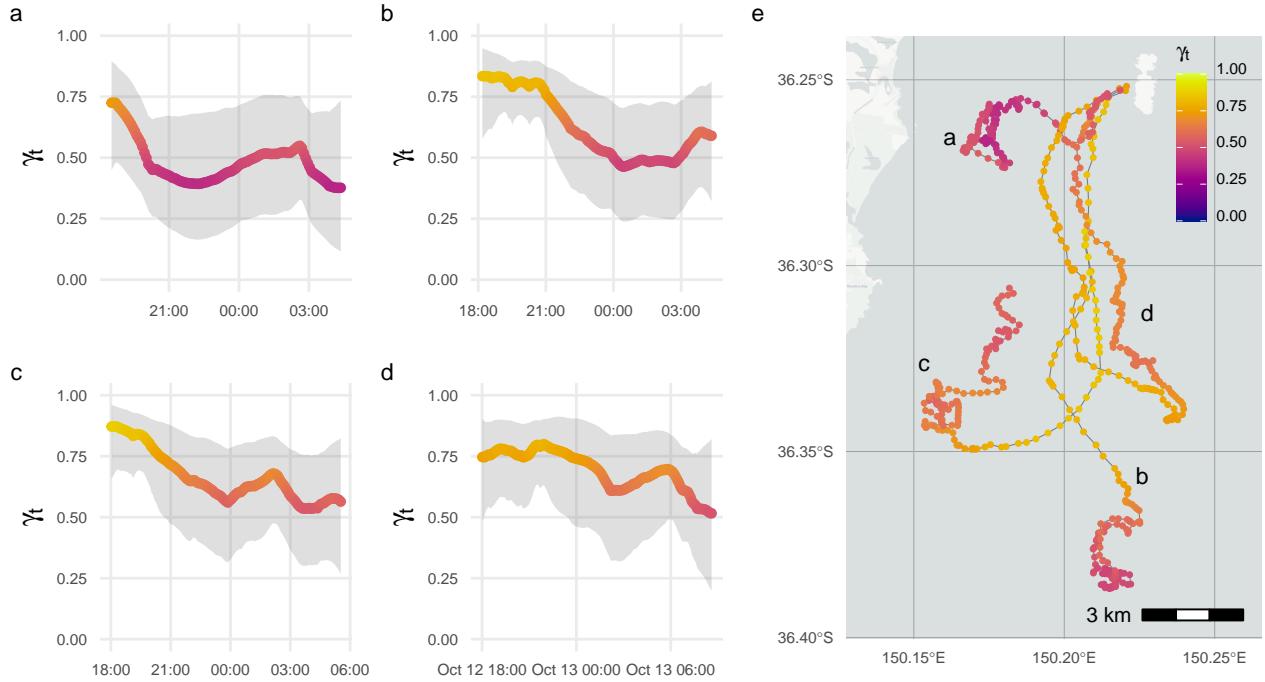


Figure 3: Inferred move persistence, γ_t , 1-D time-series (a-d; grey envelopes are 95 % CI's) and along little penguin GPS tracks (e).

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. 3a-d). 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. 3e).

3.3 | Simulating tracks from foieGras model fits

To illustrate how to simulate tracks from **foieGras** model fits we use a juvenile harp seal (*Pagophilus groenlandicus*) tracked from the Gulf of St Lawrence, Canada, and described in Grecian et al. (2022). The data are temporally irregular Argos locations including error ellipse information. We fit the **crw** model using **fit_ssm** with a 4 ms^{-1} speed filter threshold (**vmax**) and a 12-h prediction interval (**time.step**).

- 252 We simulate 50 animal movement paths from the `crw` process model using `simfit`, and apply
 253 a potential function using the `grad` and `beta` arguments to constrain the simulated paths
 254 to largely remain in water. These tracks are then filtered based on their similarity to the
 255 original path using `sim_filter` and the top 10% retained (`keep = 0.1`) (Fig. 4a,b).
 256 As the potential function does not guarantee all locations remain off land, we re-route any
 257 remaining simulated locations from land back to water using `route_path` (Fig. 4c).
 258 In combination, these functions provide a simple, pragmatic method to generate and objec-
 259 tively filter pseudo-tracks for use in movement or habitat modelling applications.

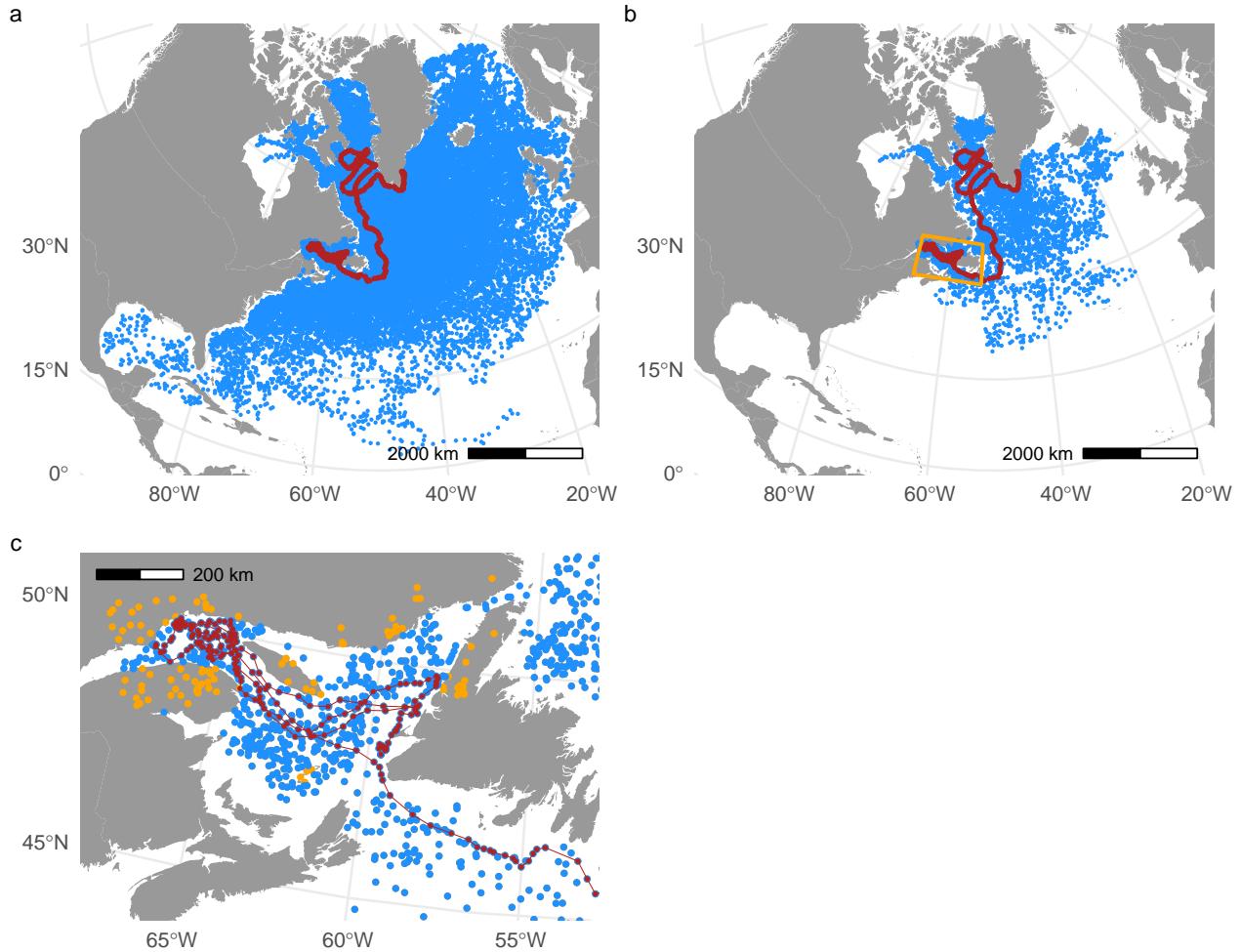


Figure 4: Simulating (a) 100 movement paths from a correlated random walk process model; (b) filtering those tracks to select the top 10% based on their similarity to the original SSM-predicted track (red); and (c) re-routing simulated locations on land (orange) back to ocean (blue). The orange box in (b) indicates region magnified in (c). SSM-predicted track (red) overlaid in all panels for context.

260 **4 | Discussion**

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

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280 **Author's Contributions**

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

285 **Data Accessibility**

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

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