

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

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15 Abstract

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20 Keywords:

²¹ 1 | Introduction

²² The collection of animal-borne sensor data has become essential for understanding the
²³ movements, behaviour, social interactions, foraging ecology, physiology, habitat use and
²⁴ population dynamics of mobile and/or cryptic species (Kays et al., 2015). In addition, the
²⁵ sophistication and precision of current sensor technology now enables the use of tagged animals
²⁶ to collect in situ environmental information that complements data collected from traditional
²⁷ Earth observing platforms (McMahon et al., 2021). However, in each of these applications,
²⁸ common issues with tracking data such as irregularly timed measurements, sensor biases and
²⁹ location measurement errors must be overcome. Underlying animal movement processes must
³⁰ also be adequately characterised before robust inferences can be made about where animals
³¹ are and what they are doing when they record or transmit information.

³² State-space models (SSMs) are powerful tools for conducting quality control of and making
³³ behavioural inference from animal tracking data (Patterson et al., 2008). Within this
³⁴ framework, an animal's true location and/or behaviour in the wild are unobserved states,
³⁵ while measurements recorded by animal-borne sensors provide noisy observations. The SSM
³⁶ comprises both a movement process model (e.g., a correlated random walk) and a measurement
³⁷ model that are fit to animal tracks to estimate true location and behaviour states, thereby
³⁸ separating ecologically-meaningful signals from the noise of sensor measurements.

³⁹ Here we introduce **foieGras** (pronounced “*fwah grah*”), a package for fitting SSMs in R (R
⁴⁰ Core Team, 2021). This package has two aims: (1) to be a simple and fast implementation of
⁴¹ SSMs to quality control error-prone animal location data (Jonsen et al., 2020); and (2) for
⁴² inference of changes in behaviour along animal tracks (Jonsen et al., 2019). Although several
⁴³ implementations of SSMs for animal movement data exist, e.g. **bsam** (I. Jonsen et al., 2005),
⁴⁴ **crawl** (Johnson et al., 2008), and **ctmm** (Calabrese et al., 2016), their broad utility can be
⁴⁵ hampered by their technical complexity. **foieGras** has a more user-friendly implementation
⁴⁶ suitable for novices, yet users can exert control over many aspects of the package functions

47 via optional arguments, accommodating the needs of experienced users.

48 We describe the main features of **foieGras** and illustrate its use through a set of applications

49 drawing on Argos and GPS tracking data. Full R code and data for each of the applications

50 is provided in the Supporting Information. Additional details on package functions and use

51 can be found in the help files and package vignettes.

52 **2 | foieGras overview**

53 The workflow for **foieGras** is deliberately simple, with many of the usual track data processing

54 checks handled automatically. Here we outline the main aspects of the **foieGras** package.

55 The package's main functions are listed in Table 1 and a generalized workflow with example

56 code is depicted in Figure 1.

Table 1: Main **foieGras** functions with description and example code. In the code examples, `...` denotes optional arguments. Details on these arguments can be found in the package help files for each function.

Function	Description	Code
<code>fit_ssm</code>	Fit a State-Space Model to location data	<code>fit <- fit_ssm(data, model, time.step, ...)</code>
<code>fit_mpm</code>	Fit a Move Persistence Model to location data	<code>fmp <- fit_mpm(fit, model, ...)</code>
<code>grab</code>	Extract fitted/predicted/observed locations from a foieGras model, with or without projection information	<code>locs <- grab(fit, what = 'predicted', ...)</code>
<code>osar</code>	Estimate One-Step-Ahead Residuals from a foieGras SSM	<code>res <- osar(fit, ...)</code>
<code>map</code>	Map fitted/predicted locations with or without a defined projection	<code>map(fit, fmp, what = 'predicted', ...)</code>
<code>sim</code>	Simulate individual animal tracks with Argos LS or KF errors	<code>slocs <- sim(N, model, ...)</code>
<code>simfit</code>	Simulate animal tracks from SSM model fit objects	<code>sfit <- simfit(fit, ...)</code>
<code>sim_filter</code>	Filter simulated tracks according to similarity criteria	<code>sfit <- sim_filter(sfit, keep, ...)</code>
<code>route_path</code>	Reroute path so estimated locations are off land	<code>fit <- route_path(fit, what = 'predicted', ...)</code>
<code>plot.ssm_df</code>	Plot the fit of a foieGras SSM to data	<code>plot(fit, what = 'predicted', ...)</code>
<code>plot.osar</code>	Plot One-Step-Ahead Residuals from a foieGras SSM	<code>plot(res, type = 'ts')</code>

57 **2.1 | Data preparation**

58 Animal tracking data, consisting of a time-series of location coordinates, can be read into R
59 as a data frame using standard functions such as `read.csv`. Possible input data formats are
60 shown in Figure 1. More details on input data formats are provided in the Overview vignette
61 (<https://ianjonsen.github.io/foieGras/articles/Overview.html>).

62 **2.2 | State-space model fitting - `fit_ssm`**

63 State-space models are fit using the function `fit_ssm`. The type of location data is automati-
64 cally detected from the location quality class designations that are typical of Argos data
65 and that can be added to the data by the researcher for other types of location data (Fig.
66 1). Based on the location quality classes and optional information on measurement errors
67 contained in the data, an appropriate measurement error model is selected for each observation
68 (Jonsen et al., 2020). Fits to single versus multiple individuals are handled automatically,
69 with sequential SSM fits occurring in the latter case. No hierarchical or pooled estimation
70 among individuals is currently available.

71 There are a large number of optional arguments that can be specified in `fit_ssm`, and these
72 are explained in the documentation. We focus only the essential arguments here:

- 73 • `data` the input data structured as illustrated in Fig. 1
74 • `model` the process model to be used (one of `rw`, `crw`, or `mp`)
75 • `time.step` the prediction time interval (expressed in hours)

76 The function first invokes an automated data processing stage where the data type and
77 measurement error model(s) are determined, observation times are sorted and checked for
78 duplicates, and a speed filter identifies potential extreme locations to be ignored by the
79 SSM. The SSM is then fit to the processed data, with the user-specified process model and
80 automatically selected measurement error model. The likelihood is optimized numerically
81 using either of the standard R optimizers, `optim` or `nlminb`. The R package `TMB`, Template

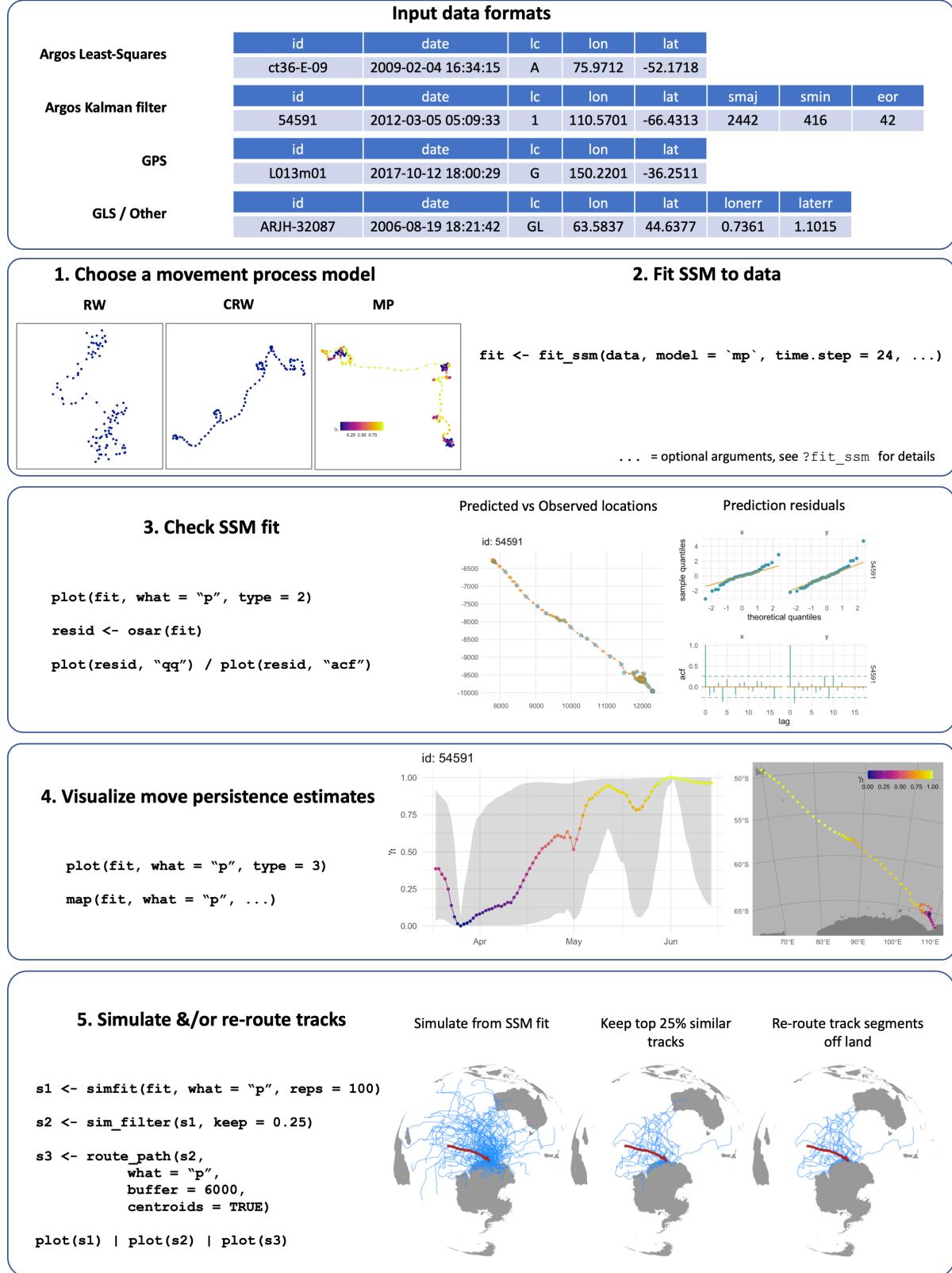


Figure 1: A generalized foieGras workflow showing required input data formats, model fitting, model checking/validation, visualisation of movement behaviour estimates, track simulation and re-routing around land. Example code is displayed for each stage.

82 Model Builder (Kristensen et al., 2016), is used to compute the gradient function in C++.
83 A fit object is returned as a nested data frame, listing the individual animal id(s), basic
84 convergence information and a list of model output including estimated parameters and states,
85 processed data, and diagnostic information. A simple data frame of SSM fitted (location
86 estimates corresponding to the observation times) or predicted values (locations predicted at
87 regular `time.step` intervals) can be extracted using the `grab` function. Parameter estimates,
88 AIC and other model fit information can be viewed using the `summary` function.

89 **2.3 | Behavioural estimation - `fit_ssm`, `fit_mpm`**

90 Move persistence, an index of movement behaviour, can be estimated as a continuous-valued
91 (0 - 1), time-varying latent variable that represents changes in movement pattern based
92 on autocorrelation in speed and direction Jonsen et al. (2019). There are two approaches
93 in `foieGras` for estimating move persistence. The first is to use `fit_ssm` with `model =`
94 '`mp`', which fits a continuous-time move persistence model in state-space form and thereby
95 simultaneously estimates true locations and move persistence from the error-prone telemetry
96 data. This approach is most appropriate for fitting to irregularly-timed and error-prone Argos
97 data as both aspects are taken into account explicitly. The second is to use `fit_mpm`, which
98 can take as input either location data or SSM-estimated locations from an `ssm_df` fit object.
99 This approach is generally more appropriate when the data have minimal measurement error
100 (e.g., GPS locations).

101 **2.4 | Model checking and visualization - `osar`, `plot`, `map`**

102 Before using fitted or predicted locations, a `fit_ssm` model fit should be checked and visualized
103 to confirm that the model adequately describes the data. There is no simple way to calculate
104 residuals for latent variable models that have non-finite state-spaces and that may be nonlinear,
105 but they can be computed based on iterative forecasts of the model (Thygesen et al., 2017).
106 The `osar` function computes one-step-ahead (prediction) residuals via the `oneStepPredict`

107 function from the `TMB` R package (Kristensen et al., 2016). A set of residuals are calculated
108 for the `x` and `y` values corresponding to the fitted values from the SSM. A generic `plot`
109 (`plot.osar`) method provides an easy way to visualize the prediction residuals as time-series
110 plots, quantile-quantile plots, or autocorrelation functions (Fig. 1).

111 State-space model fits to data can also be visualised by using the generic `plot` (`plot.ssm_df`)
112 function on a model fit object. Options exist to plot fitted or predicted values along with
113 observations as either paired, 1-D time-series (using the `type = 1` argument), or as 2-D tracks
114 (`type = 2`) with 95% confidence intervals or ellipses. These plots provide a rapid check on
115 SSM fits to data. Additionally, when the fitted SSM is the move persistence model (i.e.,
116 `model = 'mp'`), 1-D time-series (`type = 3`) or 2-D track plots (`type = 4`) of move persistence
117 estimates can be displayed (Fig. 1).

118 `fit_ssm` model fits can be mapped using the `map` function for single or multiple individuals.
119 By default, `map` uses the coastline data from the `rnatuarlearth` R package (South, 2022) at
120 medium or high resolution, but can also use tiled maps for finer-scale detail, via the `rosm`
121 (Dunnington, 2019) and `ggspatial` (Dunnington, 2021) R packages. Mapping aesthetics (e.g.,
122 plot symbols, sizes, colours, fills) can be customized via the `aes` argument and use of the
123 `aes_lst` function (Fig. 1). See code in SI for examples.

124 All `foieGras` visualizations draw on the `ggplot2` R package (Wickham, 2016), with multi-
125 panel plots also using the `patchwork` R package (Pedersen, 2020), and generally can be
126 modified through additive calls in the usual `ggplot2` manner. See code in SI for examples.

127 **2.5 | Simulation - `sim`, `simfit`, `sim_filter`**

128 Track simulation can be a helpful, yet informal, way of evaluating the degree to which
129 statistical movement models capture essential features of animal movement data (Michelot et
130 al., 2017). The `sim` function can simulate a variety of movement process, including the `rw`,
131 `crw`, and `mp` process models, as well as simple multiple movement state switching processes.

132 Simulation is also used frequently in habitat usage modelling to provide a measure of habitat
133 availability (Aarts et al., 2012) by generating a source of ‘background’ points representing a
134 null model of the distribution of foraging animals in the absence of external drivers (Raymond
135 et al., 2015). The **simfit** function extracts movement parameters from an SSM fit object
136 and simulates random tracks of the same duration from these parameters. The argument **cpf**
137 = TRUE allows simulation of central place foragers by ensuring that tracks start and end at
138 approximately the same location. Movements can also be constrained to remain mostly in
139 water via a potential function (Preisler et al., 2013), using included gradient rasters and the
140 **grad** and **beta** arguments. These are illustrated in the code for Application 3.3.

141 The choice of null points can impact the performance of habitat suitability models (S. J.
142 Phillips et al., 2009), and so the **sim_filter** function provides a tool to filter the simulated
143 tracks based on their similarity to the original path. Filtering uses one of two metrics
144 that capture the difference in the net displacement and bearing between the two paths (see
145 **?similarity_flag** for more detail). These metrics are motivated by the ‘flag value’ described
146 in Hazen et al. (2017). The the quantile of flag values to be retain is specified via the
147 **keep** argument; i.e. **keep** = 0.25 (the default) will return a **simfit** object containing those
148 simulated tracks with flag values in the top 25% of values calculated for the input **simfit**
149 object (Fig. 1).

150 **2.6 | Path rerouting - route_path**

151 As the SSMs implemented in **foieGras** have no information about potential barriers to animal
152 movement it is possible for locations to be estimated in implausible locations, such as on
153 land for marine species. To overcome this, **foieGras** makes use of the **pathroutr** R package
154 (London, 2020) to efficiently re-route locations from land back to water by using visibility
155 graphs (Jan et al., 2014). The **route_path** function can be applied to either an SSM fit
156 object or the simulations generated by **simfit**. When the input is an SSM fit object the
157 re-routed path can be appended to the object for visualization and use in subsequent analyses.

158 When the input is a `simfit` object the locations within the simulation are replaced with the
159 re-routed paths (Fig. 1). We illustrate the latter in Application 3.3.

160 3 | Applications

161 We illustrate the main capabilities of `foieGras` through a set of applications that are for
162 demonstration purposes. Complete code and data for reproducing the applications and for
163 gaining a deeper understanding of `foieGras` functions are provided in the Supplementary
164 Information.

165 3.1 | SSM validation with prediction residuals

166 We used a sub-adult male southern elephant seal (*Mirounga leonina*) track included as example
167 data in `foieGras` (`sese2`, id: ct36-E-09), sourced from from the Australian Integrated Marine
168 Observing System (IMOS; data publicly available via imos.aodn.org.au) deployments at Iles
169 Kerguelen in collaboration with the French IPEV and SNO-MEMO programmes. The data
170 are temporally irregular Argos Least-Squares locations. We fitted both the `rw` and `crw` models
171 using `fit_ssm()` with a speed filter threshold (`vmax`) of 4 ms^{-1} and a 12-h time step. We
172 calculated prediction residuals using `osar()`, and then used the generic `plot` method for `osar`
173 residuals to assess and compare the model fits (Fig. 2).

174 Plots of predicted states on top of the observations suggest both models yield similar global
175 fits (Fig. 2a; blue versus red lines), but discrepancies are visible at a local scale (Fig. 2a,
176 inset). Predicted locations from the two models differ by a median 6.62 km (range: 0.02,
177 53.02 km), and there are marked trends in the residuals for the `rw` model fit (Fig. 2b) with
178 significantly positive autocorrelation in both the x and y directions (Fig. 2d). The `crw`
179 prediction residuals show no trend through time and have little autocorrelation (Fig. 2c,e),
180 implying the `crw` process model is a better fit to the data.

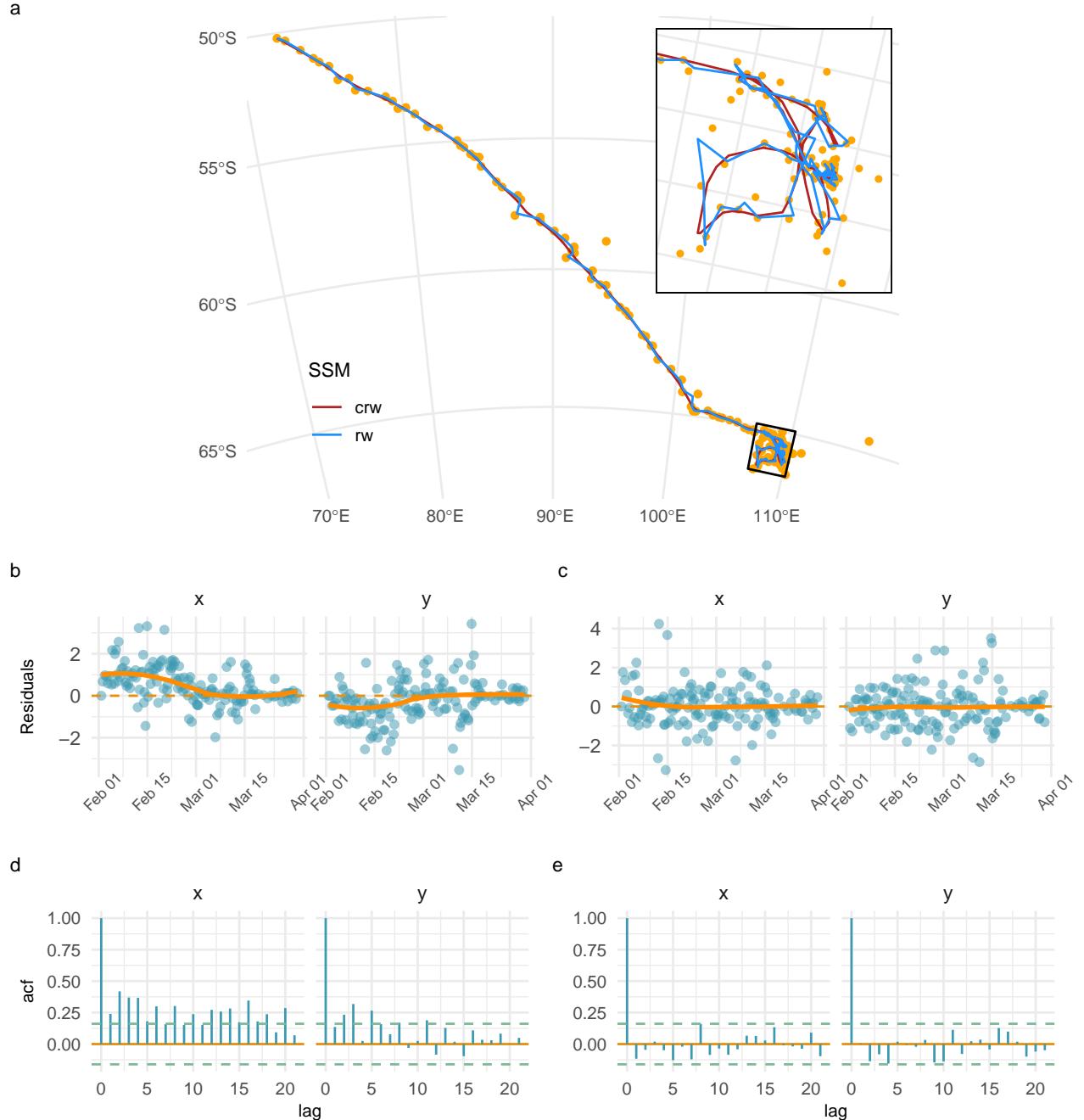


Figure 2: State-space model fits to a southern elephant seal track with finer scale detail inset (a), and diagnostic plots for assessing goodness-of-fit of the **rw** (b - prediction residual time-series; d - prediction residual autocorrelation) and **crw** (c,e) state-space models. All residual plots generated using the `plot.osar` function.

181 **3.2 | Inferring move persistence**

182 To illustrate how move persistence (γ_t) can be estimated from GPS data, we use four little
183 penguin (*Eudyptula minor*) tracks of daily foraging trips during the chick-rearing period from
184 Montague Island, NSW, Australia (described in L. Phillips et al. (2021)). The data are
185 temporally irregular GPS locations, with high frequency sampling (mean 15 s) intermittently
186 disrupted by the birds' diving behaviour, and are assumed to have minimal measurement error.
187 We fitted the `crw` SSM to the GPS data to predict temporally regular locations at 5-min
188 intervals, and assumed consistently small bivariate normal location measurement errors (ie. \pm
189 30 m sd). We then used `fit_mpm()` to estimate γ_t from these regularized locations. Finally,
190 we visually compared γ_t estimates with prey capture events inferred from accelerometry data
191 (see Carroll et al. (2014) for details) to ascertain whether reduced γ_t is indicative of active
192 foraging by these penguins.

193 The little penguin GPS tracks did not exhibit strong contrast in move persistence, with γ_t
194 declining below 0.5 for only two of the birds (Fig. 3a-d). Nonetheless, the move persistence
195 estimates highlight change in movement pattern over the course of the penguins' daily foraging
196 trips (Fig. 3e). The penguins departed Montague Is. with relatively fast movements, three
197 directed southward (Fig. 3 tracks b-d in e) and one less directed and remaining close to the
198 island (track a), before slowing down and engaging in meandering movements (orange - red in
199 Fig. 3e). Lower γ_t was associated with consistently higher and more frequent prey captures,
200 implying that low move persistence can be indicative of foraging activity by these penguins.
201 The spatially diffuse bouts of lower move persistence may reflect the fine-scale patchiness of
202 the penguins' forage-fish prey with search and prey-capture occurring both within and among
203 discrete neighbouring prey aggregations (Carroll et al., 2017).

204 **3.3 | Simulating tracks from `foieGras` model fits**

205 To illustrate how to simulate tracks from `foieGras` model fits we use a juvenile harp seal
206 (*Pagophilus groenlandicus*) tracked from the Gulf of St Lawrence, Canada, and described

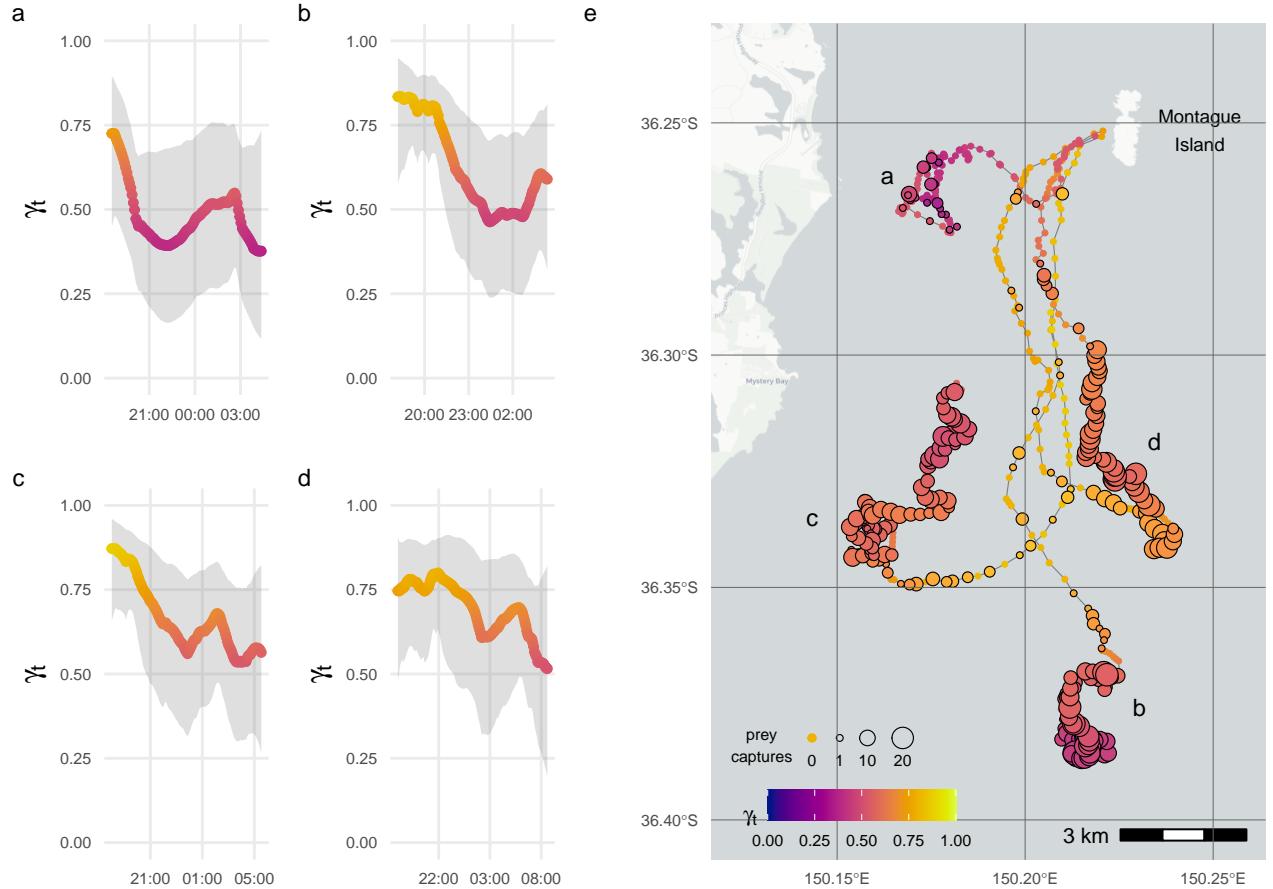


Figure 3: Inferred move persistence, γ_t , 1-D time-series (a-d; grey envelopes are 95 % CI's) and along SSM-predicted little penguin tracks (e). Location symbol sizes are proportional to the number of prey capture events, inferred from accelerometry data, at 5-min intervals corresponding to the SSM predicted location times.

207 in Grecian et al. (2022). The data are temporally irregular Argos locations including error
208 ellipse information. We fit the `crw` model using `fit_ssm` with a 4 ms^{-1} speed filter threshold
209 (`vmax`) and a 12-h prediction interval (`time.step`).

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

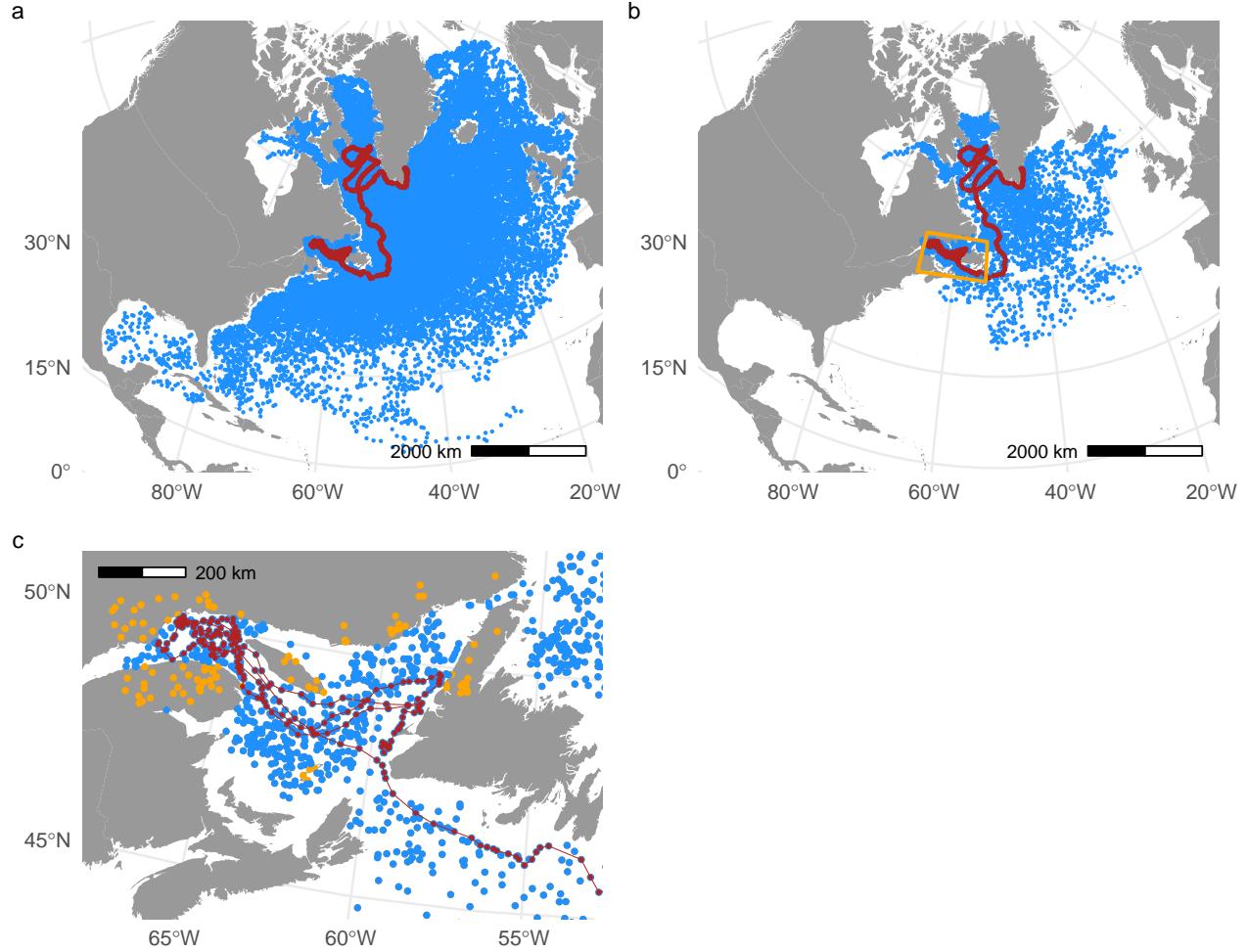


Figure 4: Simulating (a) 100 movement paths from a correlated random walk process model; (b) filtering those tracks to select the top 10% based on their similarity to the original SSM-predicted track (red); and (c) re-routing simulated locations on land (orange) back to ocean (blue). The orange box in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

218 **4 | Conclusions**

219 The **foieGras** package was developed to ease fitting state-space models for quality control
220 of animal location data and for inference of behavioural change along animal tracks. We
221 achieve these primarily through a simple yet extensible workflow, model parsimony, and
222 computational speed. Combined, these traits accommodate both novice or occasional and
223 advanced users, and facilitate use in automated, operational quality-assurance/quality-control
224 processes for animal-borne ocean observations (McMahon et al., 2021).

225 The **foieGras** package is an intermediate analysis toolbox where location quality control
226 typically occurs after some initial data processing but prior to any comprehensive, final
227 analysis. In this vein, the move persistence model tools provide a rapid approach for objectively
228 identifying changes in movement behaviour along animal tracks without any required *a priori*
229 knowledge or decisions about the kind or number of behavioural states potentially hidden
230 within the data. Subsequent analysis could entail use of a hidden Markov model to infer
231 potential drivers of observed movements (e.g., Michelot et al. (2016); McClintock & Michelot
232 (2018)). Alternatively, move persistence - covariate relationships among multiple individuals
233 can be inferred rapidly in a mixed-effects model framework using the **mpmm** package (Jonsen
234 et al. (2019); <https://github.com/ianjonsen/mpmm>).

235 The **foieGras** package will undergo further development, expanding the range of available
236 SSM's via new movement process models and/or enhanced measurement models for other
237 electronic tracking data types. Additionally, we will seek to enhance integration with other
238 R packages for processing and analysis of animal movement data, where feasible. Feedback
239 from users is invaluable and encouraged. Users may submit bug reports and enhancement
240 suggestions via the foieGras GitHub issues page ([https://github.com/ianjonsen/foieGras/is
sues/new/choose](https://github.com/ianjonsen/foieGras/issues/new/choose)). More general feedback is always welcome by contacting the lead author
242 directly.

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²⁵⁹ Macquarie University (little penguins), and . . . **University (harp seals) - JAMES, need**
²⁶⁰ **input here.**

²⁶¹ **Author's Contributions**

²⁶² IDJ developed the R package; WJG contributed harp seal data and to the R package; LP,
²⁶³ GC, and RGH contributed little penguin data; CRM, RGH and MAH contributed Southern
²⁶⁴ elephant seal data; IDJ and TAP developed the state-space models; IDJ wrote an initial
²⁶⁵ draft of the manuscript with contributions from WJG; all authors contributed to the final
²⁶⁶ manuscript.

267 **Data Accessibility**

268 All code and data used here are provided in the `foieGras` package for R or in the Supplemen-
269 tary Information. The latest stable and cross-platform tested version of the package (currently,
270 1.0-7) is available via ROpenSci’s R-universe, at <https://ianjonsen.r-universe.dev/ui#package:foieGras>. The latest partially tested stable and development versions are available on the
271 GitHub repository: <https://github.com/ianjonsen/foieGras>. An older version of `foieGras`
272 (0.7-6) remains on CRAN at <https://CRAN.R-project.org/package=foieGras>, however, we
273 recommend users upgrade to the latest R-universe version for full access to the functionality
274 presented here.
275

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