

**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:

## <sup>21</sup> 1 | Introduction

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

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

<sup>39</sup> Here we introduce **foieGras** (pronounced “*fwah grah*”), a package for fitting SSMs in R (R  
<sup>40</sup> Core Team, 2021). This package has two aims: (1) to be a simple and fast implementation of  
<sup>41</sup> SSMs to quality control error-prone animal location data (Jonsen *et al.*, 2020); and (2) for  
<sup>42</sup> inference of changes in behaviour along animal tracks (Jonsen *et al.*, 2019). Although several  
<sup>43</sup> implementations of SSMs for animal movement data exist, e.g. **bsam** (Jonsen *et al.*, 2005),  
<sup>44</sup> **crawl** (Johnson *et al.*, 2008), and **ctmm** (Calabrese *et al.*, 2016), their broad utility can be  
<sup>45</sup> hampered by their technical complexity. **foieGras** has a more user-friendly implementation  
<sup>46</sup> 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 with brief code examples are listed in Table 1, and a generalized  
56 workflow with example code is depicted in Figure 1.

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

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 (e.g., `?fit_ssm`).

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

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

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

75 The function first invokes an automated data processing stage where the data type and  
76 measurement error model(s) are determined, observation times are sorted and checked for  
77 duplicates, and a speed filter identifies potential extreme locations to be ignored by the  
78 SSM. The SSM is then fitted to the processed data, with the user-specified process model  
79 and automatically selected measurement error model(s). The joint likelihood is optimized  
80 numerically using either of the standard R optimizers, `optim` or `nlminb`. The R package TMB,  
81 Template Model Builder (Kristensen *et al.*, 2016), is used to compute the gradient function in  
82 C++. A fit object is returned as a nested data frame, listing the individual animal id(s), basic  
83 convergence information and a list of model output including estimated parameters and states,  
84 processed data, and diagnostic information. A simple data frame of SSM fitted (location  
85 estimates corresponding to the observation times) or predicted values (locations predicted at  
86 regular `time.step` intervals) can be extracted using the `grab` function. Parameter estimates,  
87 AIC and other model fit information can be viewed using the `summary` function.

88 **2.3 | Behavioural estimation - `fit_ssm`, `fit_mpm`**

89 Move persistence, an index of movement behaviour, can be estimated as a continuous-valued  
90 (0 - 1), time-varying latent variable that represents changes in movement pattern based  
91 on autocorrelation in speed and direction (Jonsen *et al.*, 2019). There are two approaches  
92 in `foieGras` for estimating move persistence. The first is to use `fit_ssm` with `model =`  
93 '`mp`', which fits a continuous-time move persistence model in state-space form and thereby  
94 simultaneously estimates true locations and move persistence from the error-prone telemetry  
95 data (Fig. 1). This approach is most appropriate for fitting to irregularly-timed and error-

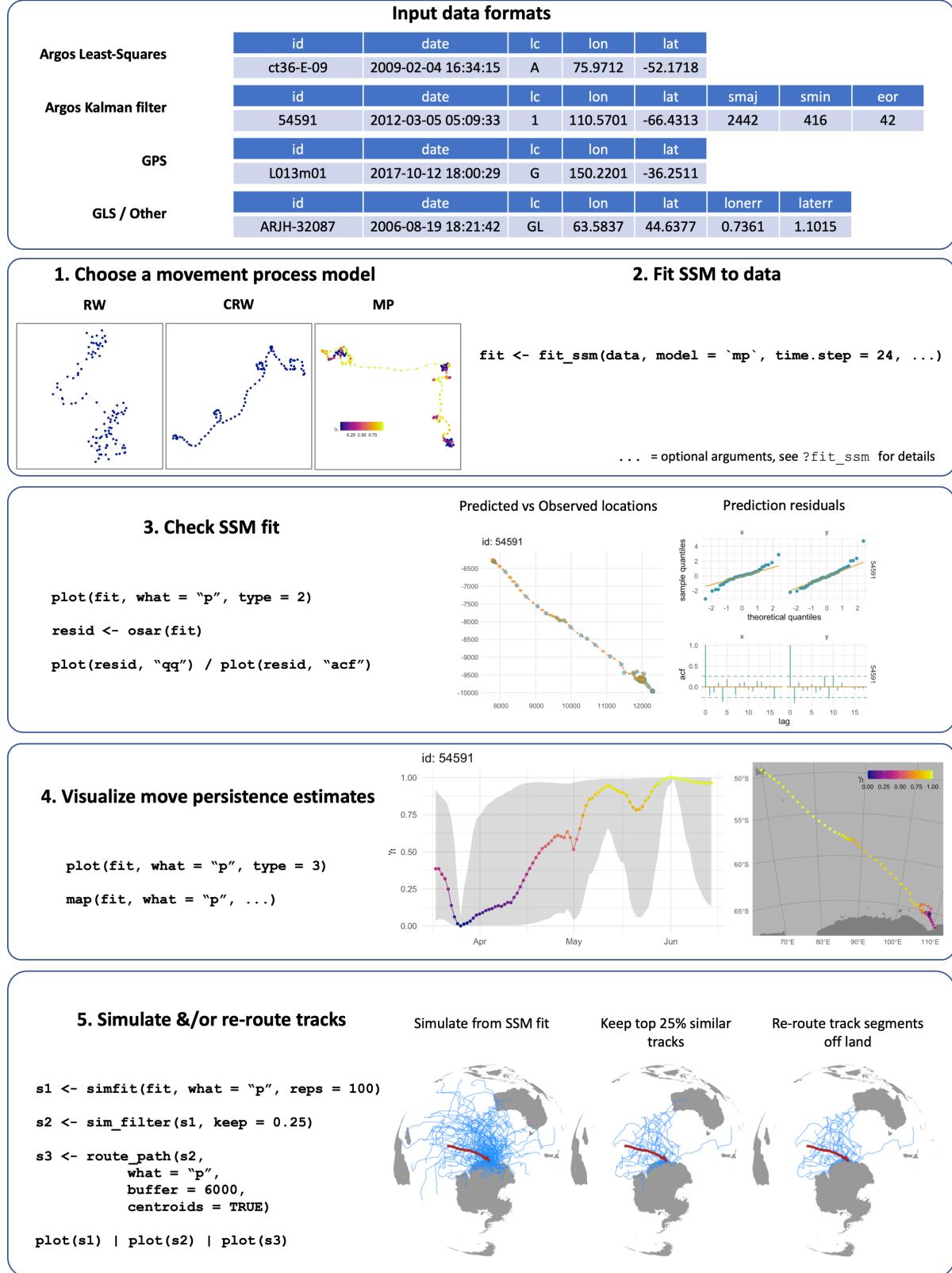


Figure 1: A generalized foieGras workflow showing required input data formats, model fitting, model checking/validation, visualisation of movement behaviour estimates, track simulation and re-routing around land. Example code is displayed for each stage.

96 prone Argos data as both aspects are taken into account explicitly. The second is to use  
97 `fit_mpm`, which can take as input either location data or SSM-estimated locations from an  
98 `fit_ssm` model fit object. This approach is generally more appropriate when the data have  
99 minimal measurement error (e.g., GPS locations; see Application 3.2).

100 **2.4 | Model checking and visualization - osar, plot, map**

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

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

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

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

122 and use of the `aes_1st` function. See code in SI for examples.

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

## 126 **2.5 | Simulation - sim, simfit, sim\_filter**

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

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

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

147 values in the top 25% of values calculated for the input `simfit` object (Fig. 1).

## 148 **2.6 | Path rerouting - `route_path`**

149 As the SSMs implemented in `foieGras` have no information about potential barriers to animal  
150 movement it is possible for locations to be estimated in implausible locations, such as on  
151 land for marine species. To overcome this, `foieGras` makes use of the `pathroutr` R package  
152 (London, 2020) to efficiently re-route locations from land back to water by using visibility  
153 graphs (Jan *et al.*, 2014). The `route_path` function can be applied to either an SSM fit  
154 object or the simulations generated by `simfit`. When the input is an SSM fit object the  
155 re-routed path can be appended to the object for visualization and use in subsequent analyses.  
156 When the input is a `simfit` object the locations within the simulation are replaced with the  
157 re-routed paths (Fig. 1). We illustrate the latter in Application 3.3.

## 158 **3 | Applications**

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

### 163 **3.1 | SSM validation with prediction residuals**

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

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

179 **3.2 | Inferring move persistence**

180 To illustrate how move persistence ( $\gamma_t$ ) can be estimated from GPS data, we use four little  
181 penguin (*Eudyptula minor*) tracks of daily foraging trips during the chick-rearing period from  
182 Montague Island, NSW, Australia (described in Phillips *et al.*, 2022). The data are temporally  
183 irregular GPS locations, with high frequency sampling (mean 15 s) intermittently disrupted  
184 by the birds' diving behaviour, and are assumed to have minimal measurement error. We  
185 fitted the `crw` SSM to the GPS data to predict temporally regular locations at 5-min intervals,  
186 and assumed consistently small bivariate normal location measurement errors (ie.  $\pm 30$  m  
187 sd). We then used `fit_mpm()` to estimate  $\gamma_t$  from these regularized locations. Finally, we  
188 visually compared  $\gamma_t$  estimates with prey capture events inferred from accelerometry data  
189 (see Carroll *et al.*, 2014, for details) to ascertain whether reduced  $\gamma_t$  is indicative of active  
190 foraging by these penguins.

191 We provide an extra application to illustrate how move persistence can be inferred from Argos  
192 data using `fit_ssm()` (Appendix S4).

193 The little penguin GPS tracks did not exhibit strong contrast in move persistence, with  $\gamma_t$   
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

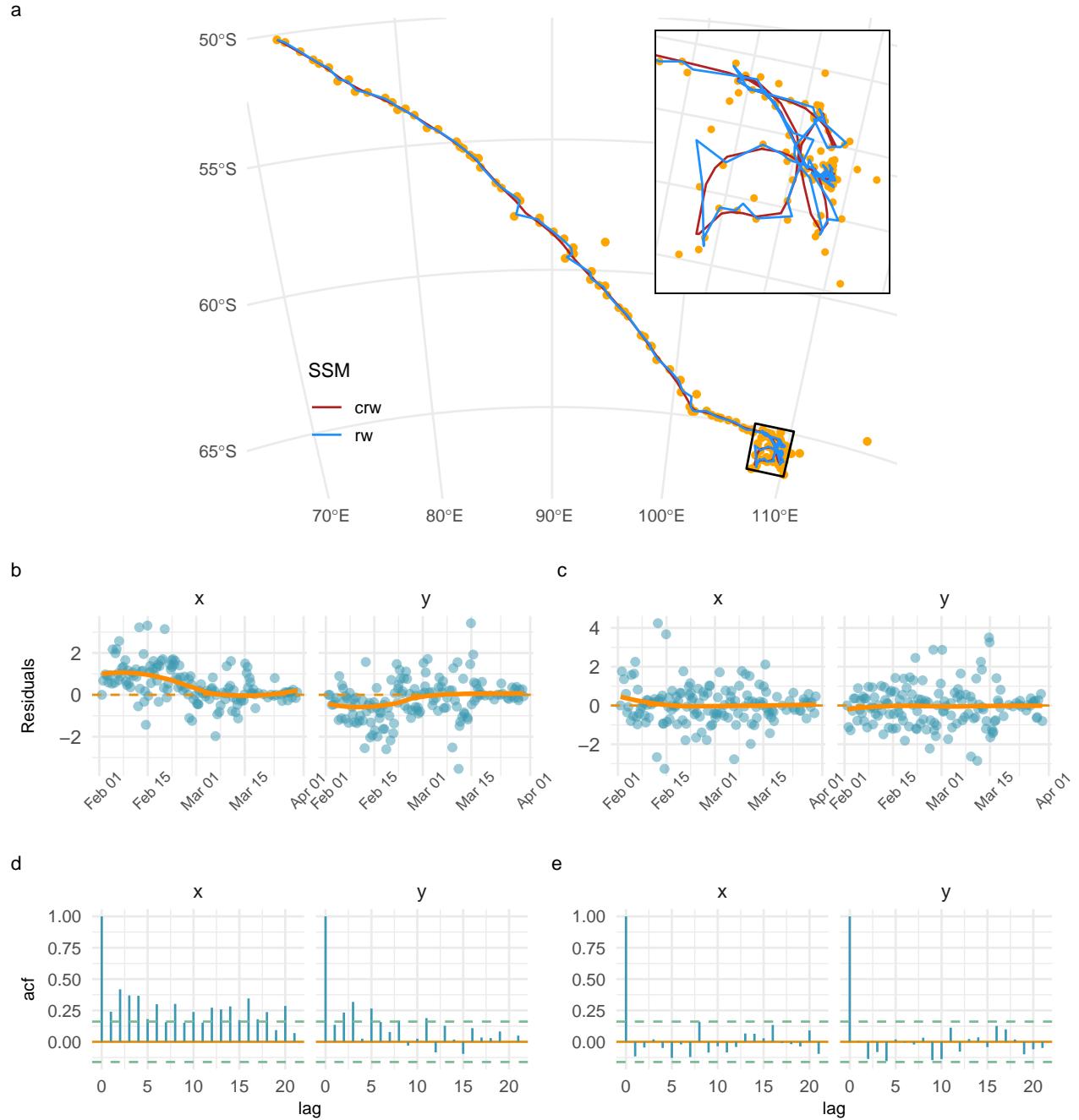


Figure 2: State-space model fits to a southern elephant seal track with finer scale detail inset (a), and diagnostic plots for assessing goodness-of-fit of the **rw** (b - prediction residual time-series; d - prediction residual autocorrelation) and **crw** (c,e) state-space models. All residual plots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

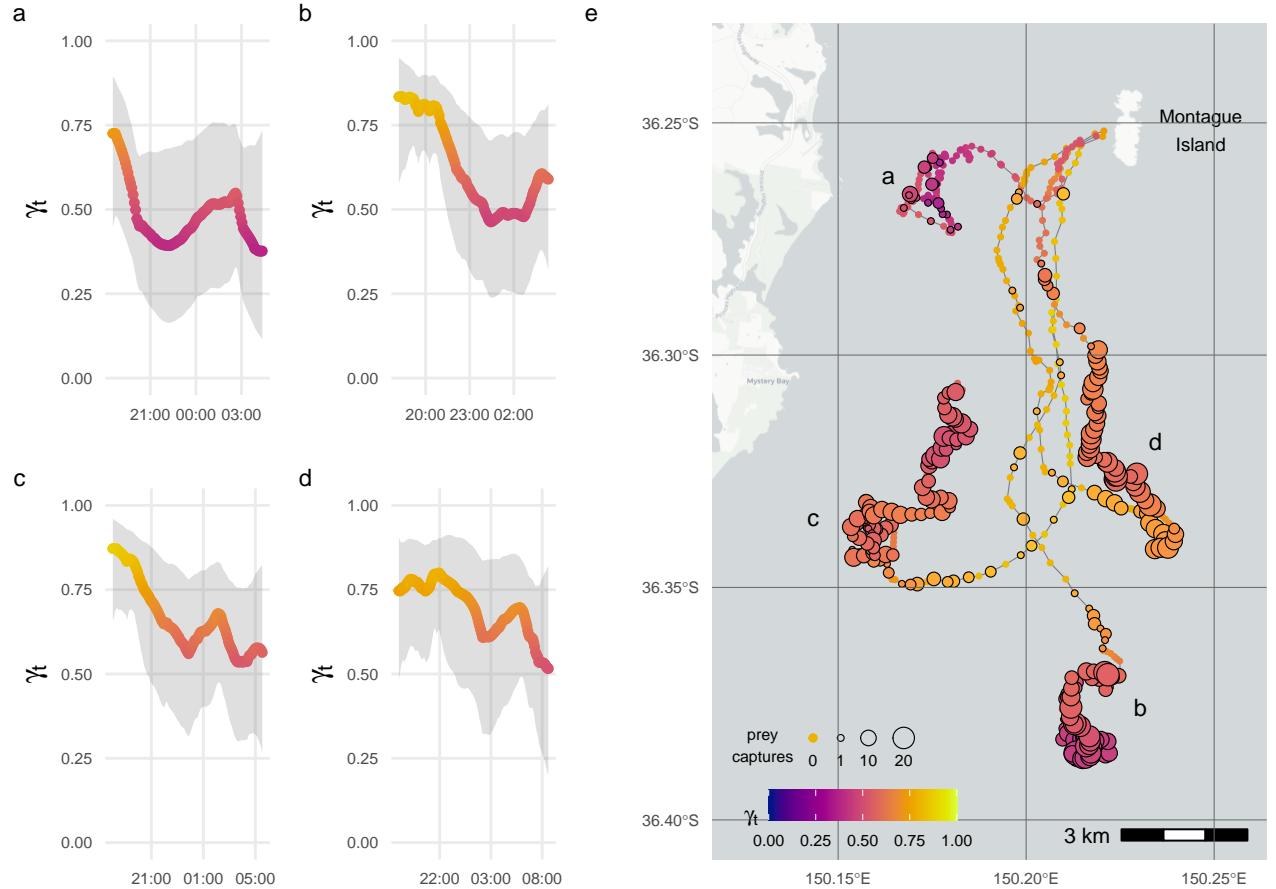


Figure 3: Inferred move persistence,  $\gamma_t$ , 1-D time-series (a-d; grey envelopes are 95 % CI's) and along SSM-predicted little penguin tracks (e). Location symbol sizes are proportional to the number of prey capture events, inferred from accelerometry data, at 5-min intervals corresponding to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

trips (Fig. 3e). The penguins departed Montague Is. with relatively fast movements, three directed southward (Fig. 3 tracks b-d in e) and one less directed and remaining close to the island (track a), before slowing down and engaging in meandering movements (orange - red in Fig. 3e). Lower  $\gamma_t$  was associated with consistently higher and more frequent prey captures, implying that low move persistence can be indicative of foraging activity by these penguins. The spatially diffuse bouts of lower move persistence may reflect the fine-scale patchiness of the penguins' forage-fish prey with search and prey-capture occurring both within and among discrete neighbouring prey aggregations (Carroll *et al.*, 2017).

### 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  $4 \text{ ms}^{-1}$  speed filter threshold (`vmax`) and a 12-h prediction interval (`time.step`).

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

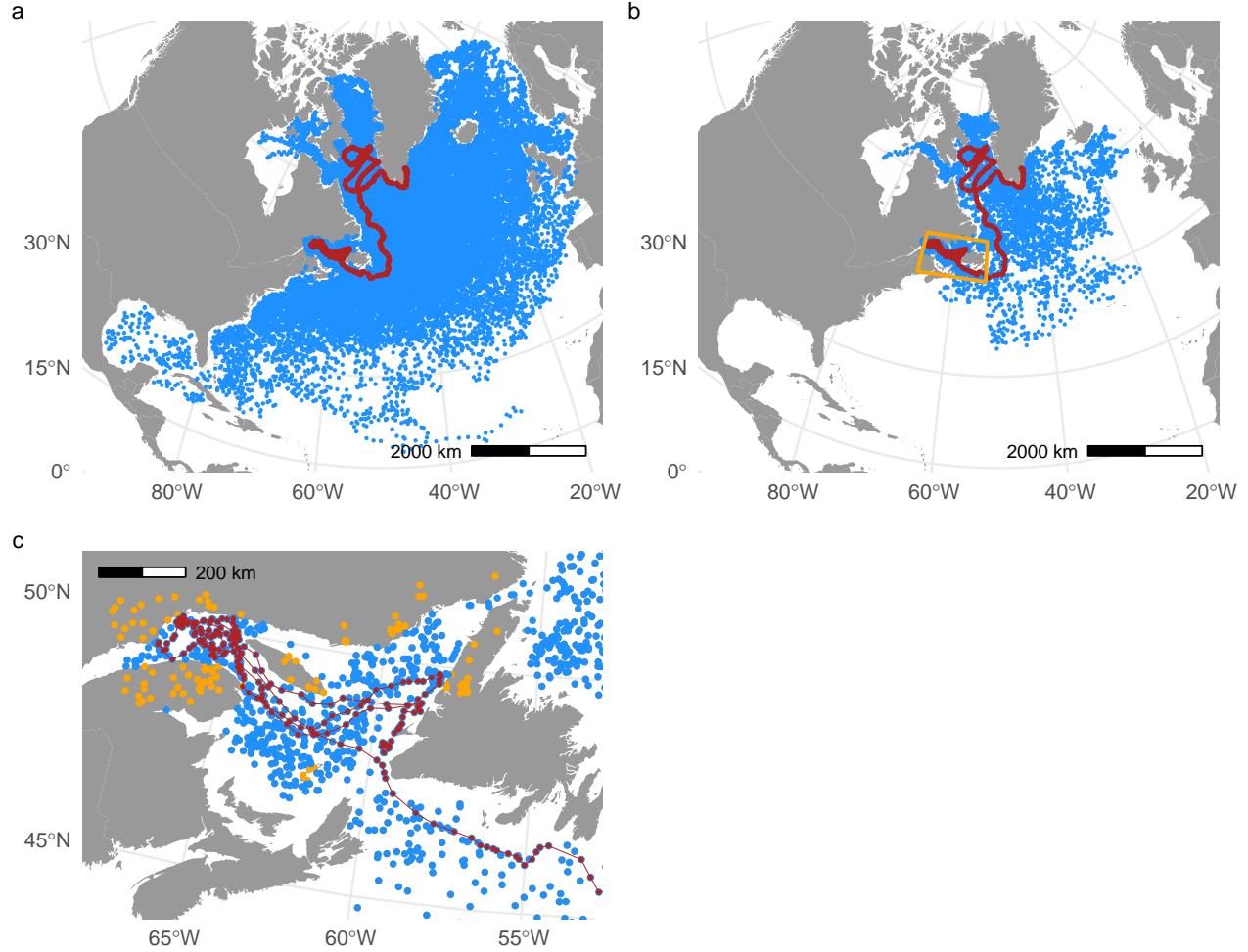


Figure 4: Simulating (a) 100 movement paths from a correlated random walk process model; (b) filtering those tracks to select the top 10% based on their similarity to the original SSM-predicted track (red); and (c) re-routing simulated locations on land (orange) back to ocean (blue). The orange box in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

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  
228 objectively identifying changes in movement behaviour along animal tracks without any  
229 required *a priori* knowledge or decisions about the kind or number of behavioural states  
230 potentially hidden within the data. Subsequent analysis could entail use of a hidden Markov  
231 model to infer potential drivers of observed movements (e.g., Michelot *et al.*, 2016; McClintock  
232 & Michelot, 2018). Alternatively, move persistence - covariate relationships among multiple  
233 individuals can be inferred rapidly in a mixed-effects model framework using the **mpmm** package  
234 (Jonsen *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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<sup>264</sup> (little penguins), and University of St Andrews (harp seals).

<sup>265</sup> **Author's Contributions**

<sup>266</sup> IDJ developed the R package; WJG contributed harp seal data and to the R package; LP,  
<sup>267</sup> GC, and RGH contributed little penguin data; CRM, RGH and MAH contributed Southern

268 elephant seal data; IDJ and TAP developed the state-space models; IDJ wrote an initial  
269 draft of the manuscript with contributions from WJG; all authors contributed to the final  
270 manuscript.

271 **Data Accessibility**

272 All code and data used here are provided in the **foieGras** package for R or in the Supplemen-  
273 tary Information. The latest stable and cross-platform tested version of the package (currently,  
274 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  
275 GitHub repository: <https://github.com/ianjonsen/foieGras>. An older version of **foieGras**  
276 (0.7-6) remains on CRAN at <https://CRAN.R-project.org/package=foieGras>, however, we  
277 recommend users upgrade to the latest R-universe version for full access to the functionality  
278 presented here.  
279

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