

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

[§] Ian D. Jonsen^{1,*}, W. James Grecian^{2,a}, Lachlan Phillips¹, Gemma Carroll³, Clive
McMahon⁴, Robert G. Harcourt¹, Mark A. Hindell⁵, and Toby A. Patterson⁶

⁷ ¹School of Natural Sciences, Macquarie University, Sydney, NSW, Australia

⁸ ⁹ ²Sea Mammal Research Unit, Scottish Oceans Institute, University of St Andrews, St Andrews, Fife, United Kingdom

¹⁰ ³Environmental Defense Fund, Seattle, WA, United States

¹¹ ⁴Sydney Institute of Marine Science, Mosman, NSW, Australia

¹² ⁵Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, T

¹³ ⁶CSIRO Oceans and Atmosphere, Hobart, TAS, Australia

¹⁴*corresponding author, ian.jonsen@mq.edu.au

¹⁵ ^aPresent address: Department of Geography, Durham University, Dur

16 Kingdom

17 **Abstract**

- 18 1. Animal-borne sensor and tracking data are indispensable for understanding the ecology,
19 behaviour and physiology of mobile or cryptic species. Meaningful signals in these data
20 can be obscured by noise due to imperfect measurement technologies, requiring rigorous
21 quality control as part of any comprehensive analysis.
- 22 2. State-space models are powerful tools that can separate meaningful signals from noise.
23 These tools are ideal for quality control of error-prone location data and for inferring
24 where animals are and what they are doing when they record or transmit sensor
25 information. However, they are complex statistical models that can be challenging and
26 time-consuming to fit to diverse animal tracking data sets.
- 27 3. The R package **foieGras** eases the tasks of conducting quality control on and behavioural
28 inference from animal tracking data. This is achieved via: 1) a simple but extensible
29 workflow that accommodates both novice and experienced users; 2) automated processes
30 that alleviate complexity from data processing and model specification/fitting steps; 3)
31 simple movement models coupled with a powerful numerical optimization approach for
32 rapid and reliable model fitting.
- 33 4. We highlight **foieGras**' capabilities through three applications to real animal tracking
34 data. Full R code for these and additional applications are included as Supporting
35 Information so users can gain a deeper understanding of how to use **foieGras** for their
36 own analyses.

37 **Keywords:**

- 38 animal movement, biologging, bio-telemetry, movement behaviour, move persistence, random
39 walk, simulation, state-space model

40 1 | Introduction

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

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

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

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

67 We describe the main features of **foieGras** and illustrate its use through a set of applications
68 drawing on Argos and GPS tracking data. Full R code and data for each of the applications
69 is provided in the Supporting Information. Additional details on package functions and use
70 can be found in the package help files and vignettes.

71 **2 | foieGras overview**

72 The workflow for **foieGras** is deliberately simple, with many of the usual track data processing
73 checks handled automatically. Here we outline the main aspects of the **foieGras** package.
74 The package's main functions with brief code examples are listed in Table 1, and a generalized
75 workflow with example code is depicted in Figure 1.

76 **2.1 | Data preparation**

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

81 **2.2 | State-space model fitting - fit_ssm**

82 State-space models are fit using the function `fit_ssm` (Fig. 1). The type of location data
83 is automatically detected from the location quality classes that are typical of Argos data
84 and that can be added by the user for other data types. Based on the location quality
85 classes and optional information on measurement errors contained in the data, an appropriate
86 measurement error model is selected for each observation (Jonsen *et al.*, 2020). Fits to single
87 versus multiple individuals are handled automatically, with sequential SSM fits occurring in
88 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 <- 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> |

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

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

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

107 **2.3 | Behavioural estimation - `fit_ssm`, `fit_mpm`**

108 Move persistence, an index of movement behaviour, can be estimated as a continuous-valued
109 (0 - 1), time-varying latent variable that represents changes in movement pattern based
110 on autocorrelation in speed and direction (Jonsen *et al.*, 2019). There are two approaches
111 in `foieGras` for estimating move persistence. The first is to use `fit_ssm` with `model =`
112 '`mp`', which fits a continuous-time move persistence model in state-space form and thereby
113 simultaneously estimates true locations and move persistence from the error-prone telemetry
114 data (Fig. 1). This approach is most appropriate for fitting to irregularly-timed and error-

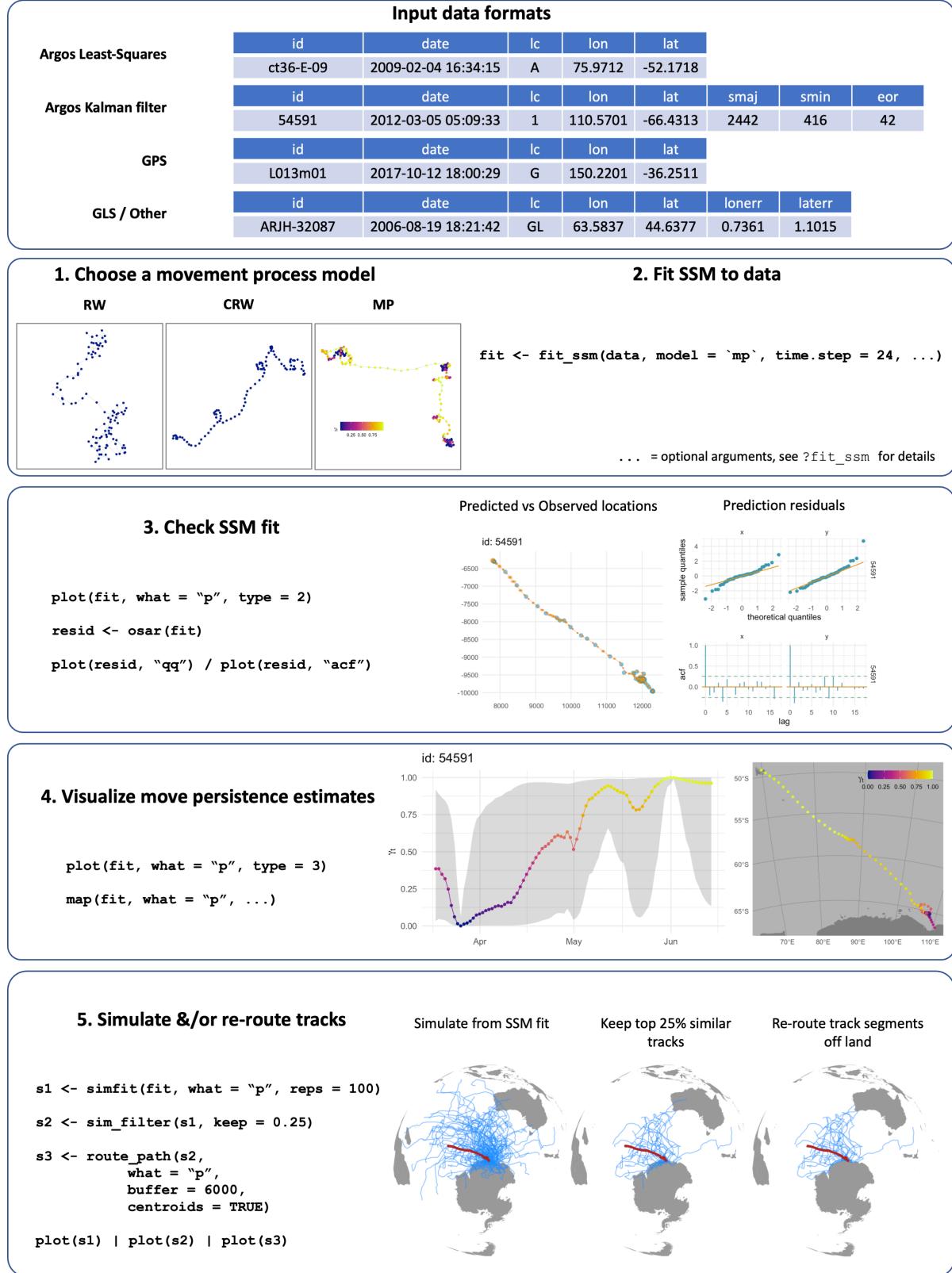


Figure 1: A generalized foieGras workflow showing required input data formats, model fitting, model checking/validation, visualisation of movement behaviour estimates, track simulation and re-routing around land. Example code is displayed for each stage.

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

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

Before using fitted or predicted locations, a `fit_ssm` model fit should be checked and visualized to confirm that the model adequately describes the data. 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 via the `oneStepPredict` function from the TMB R package (Kristensen *et al.*, 2016). A set of residuals are calculated for the `x` and `y` values corresponding to the fitted values from the SSM. A generic `plot` (`plot.osar`) method provides an easy way to visualize the prediction residuals as time-series plots, quantile-quantile plots, or autocorrelation functions (Fig. 1).

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

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

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

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

145 2.5 | Simulation - `sim`, `simfit`, `sim_filter`

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

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

159 The choice of null points can impact the performance of habitat suitability models Phillips
160 *et al.* (2009), and so the `sim_filter` function provides a tool to filter the simulated tracks
161 based on their similarity to the original path. Filtering uses one of two metrics that capture the
162 difference in the net displacement and bearing between the two paths (see `?similarity_flag`
163 for more detail). These metrics are motivated by the ‘flag value’ described in Hazen *et al.*
164 (2017). The the quantile of flag values to be retain is specified via the `keep` argument; i.e. `keep`
165 = `0.25` (the default) will return a `simfit` object containing those simulated tracks with flag

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

167 **2.6 | Path rerouting - `route_path`**

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

177 **3 | Applications**

178 We illustrate the main capabilities of `foieGras` through a set of applications that are for
179 demonstration purposes. Complete code for reproducing the applications and for gaining
180 a deeper understanding of `foieGras` functions are provided in the Supporting Information.
181 Data used in the application are available here.

182 **3.1 | SSM validation with prediction residuals**

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

190 residuals to assess and compare the model fits (Fig. 2). R code is available in Appendix S1
191 (Supporting Information).

192 Plots of predicted states on top of the observations suggest both models yield similar global
193 fits (Fig. 2a; blue versus red lines), but discrepancies are visible at a local scale (Fig. 2a,
194 inset). Predicted locations from the two models differ by a median 6.62 km (range: 0.02,
195 53.02 km), and there are marked trends in the residuals for the `rw` model fit (Fig. 2b) with
196 significantly positive autocorrelation in both the x and y directions (Fig. 2d). The `crw`
197 prediction residuals show no trend through time and have little autocorrelation (Fig. 2c,e),
198 implying the `crw` process model is a better fit to the data.

199 **3.2 | Inferring move persistence**

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

211 R code is available in Appendix S2 (Supporting Information). We provide an extra application
212 to illustrate how move persistence can be inferred from Argos data using `fit_ssm()` (Appendix
213 S3).

214 The little penguin GPS tracks did not exhibit strong contrast in move persistence, with γ_t

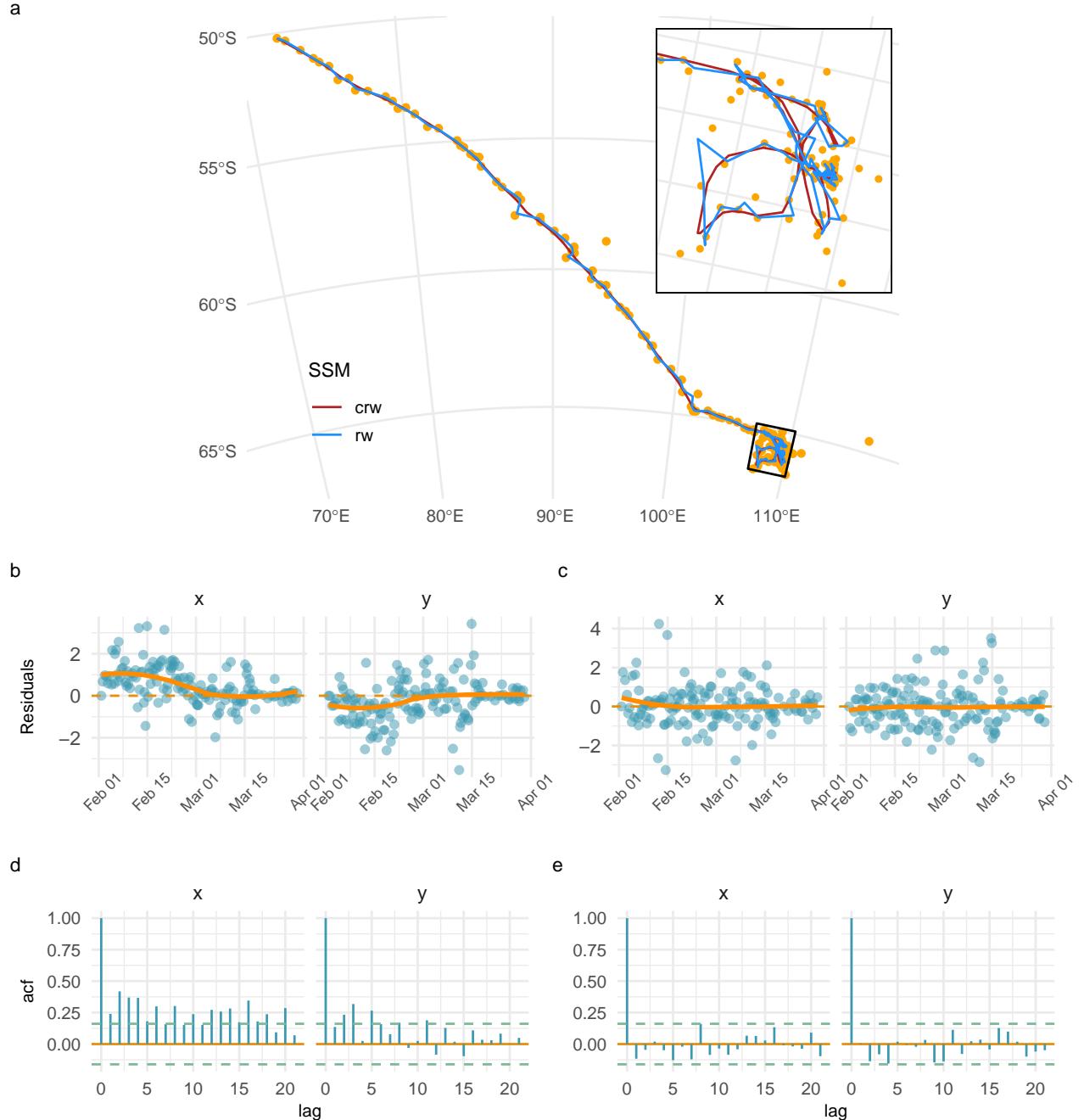


Figure 2: State-space model fits to a southern elephant seal track with finer scale detail inset (a), and diagnostic plots for assessing goodness-of-fit of the **rw** (b - prediction residual time-series; d - prediction residual autocorrelation) and **crw** (c,e) state-space models. All residual plots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

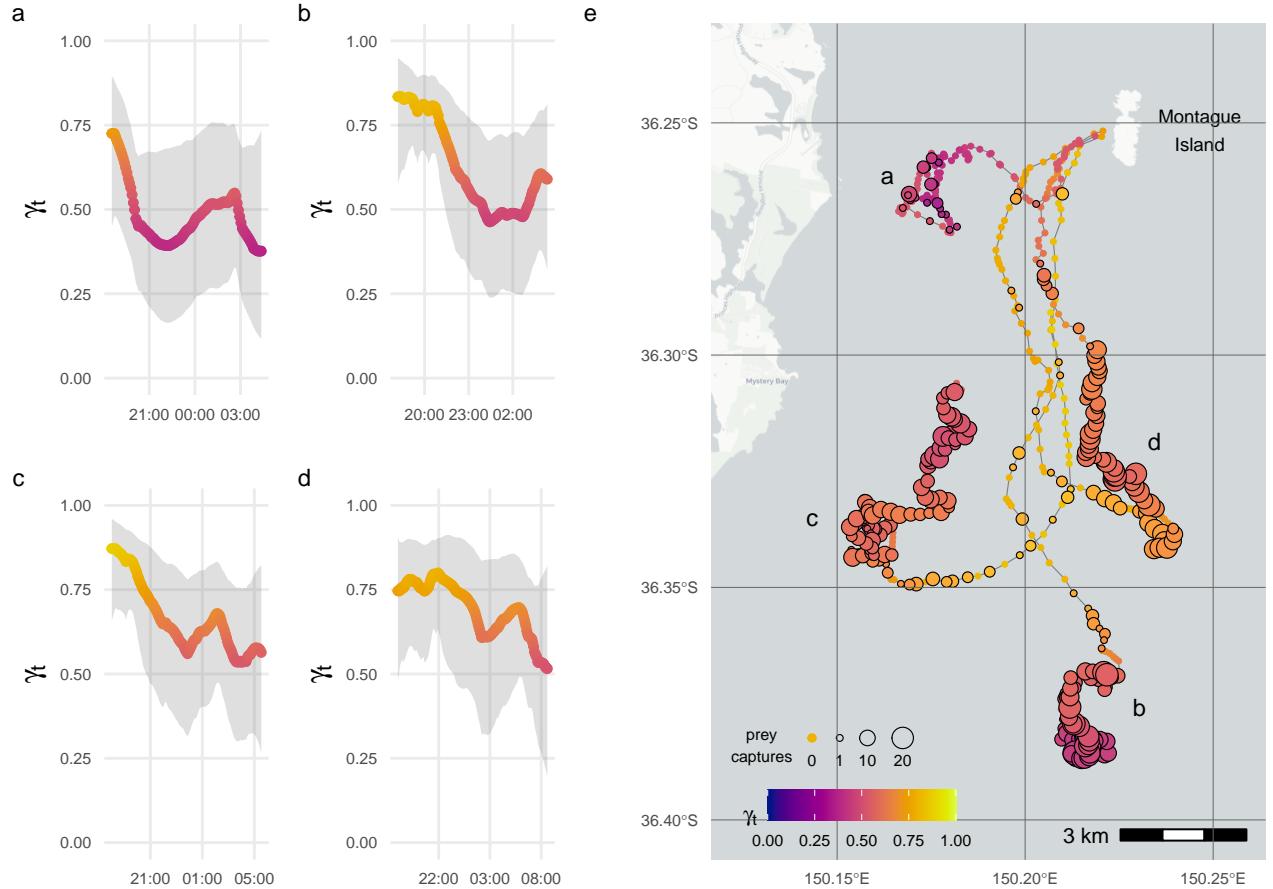


Figure 3: Inferred move persistence, γ_t , 1-D time-series (a-d; grey envelopes are 95 % CI's) and along SSM-predicted little penguin tracks (e). Location symbol sizes are proportional to the number of prey capture events, inferred from accelerometry data, at 5-min intervals corresponding to the SSM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

215 declining below 0.5 for only two of the birds (Fig. 3a-d). Nonetheless, the move persistence
216 estimates highlight change in movement pattern over the course of the penguins' daily foraging
217 trips (Fig. 3e). The penguins departed Montague Is. with relatively fast movements, three
218 directed southward (Fig. 3 tracks b-d in e) and one less directed and remaining close to the
219 island (track a), before slowing down and engaging in meandering movements (orange - red in
220 Fig. 3e). Lower γ_t was associated with consistently higher and more frequent prey captures,
221 implying that low move persistence is indicative of foraging activity by these penguins (Fig.
222 3e). The spatially diffuse bouts of lower move persistence may reflect the fine-scale patchiness
223 of the penguins' forage-fish prey with search and prey-capture occurring both within and
224 among discrete neighbouring prey aggregations (Carroll *et al.*, 2017).

225 **3.3 | Simulating tracks from foieGras model fits**

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

231 We simulate 50 animal movement paths from the **crw** process model using **simfit**, and apply
232 a potential function using the **grad** and **beta** arguments to constrain the simulated paths
233 to largely remain in water. These tracks are then filtered based on their similarity to the
234 original path using **sim_filter** and the top 10% retained (**keep = 0.1**) (Fig. 4a,b). As the
235 potential function does not guarantee all locations remain off land, we re-route any remaining
236 simulated locations from land back to water using **route_path** (Fig. 4c). In combination,
237 these functions provide a pragmatic, non-statistical method to generate and objectively filter
238 pseudo-tracks for use in movement or habitat modelling applications. R code is available in
239 Appendix S4 (Supporting Information).

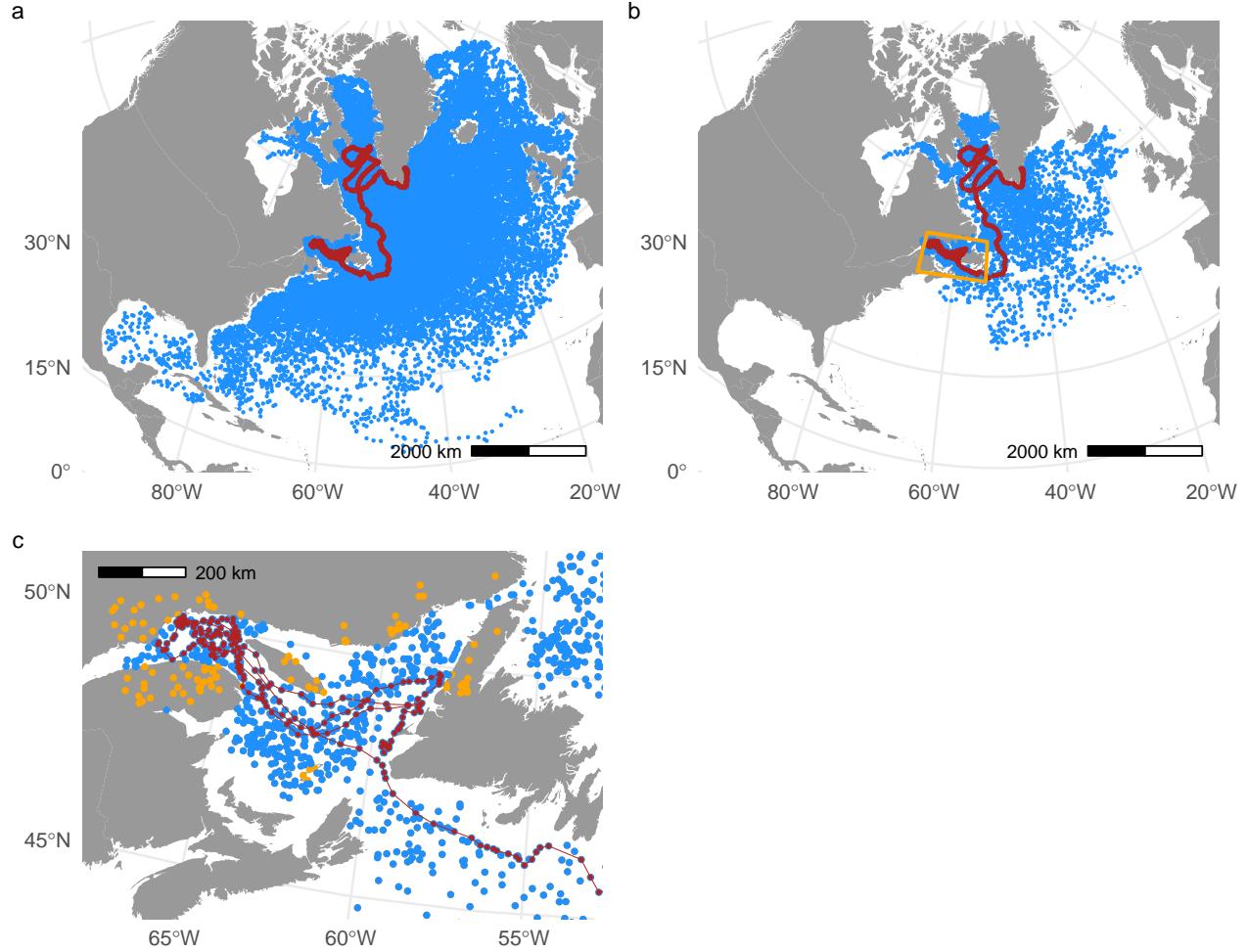


Figure 4: Simulating (a) 100 movement paths from a correlated random walk process model; (b) filtering those tracks to select the top 10% based on their similarity to the original SSM-predicted track (red); and (c) re-routing simulated locations on land (orange) back to ocean (blue). The orange box in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

240 **4 | Conclusions**

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

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

257 The **foieGras** package will undergo further development, expanding the range of available
258 SSM's via new movement process models and/or enhanced measurement models for other
259 electronic tracking data types. Additionally, we will seek to enhance integration with other
260 R packages for processing and analysis of animal movement data, where feasible. Feedback
261 from users is invaluable and encouraged. Users may submit bug reports and enhancement
262 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
264 directly.

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285 Committee guidelines of the University of Tasmania (elephant seals), Macquarie University
286 (little penguins), and University of St Andrews (harp seals).

287 **Author's Contributions**

288 IDJ developed the R package; WJG contributed harp seal data and to the R package; LP,
289 GC, and RGH contributed little penguin data; CRM, RGH and MAH contributed Southern

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

293 **Data Accessibility**

294 All code used here is provided in the `foieGras` package for R or in the Supporting Information.
295 Data will be made publicly available on Dryad here. For review purposes, the example
296 application data and associated .Rmd files can be accessed here: <https://github.com/ianjonsen/foieGras.paper/tree/main/SI>.
297
298 The latest stable and cross-platform tested version of the package (currently, 1.0-7) is available
299 via ROpenSci's R-universe, at <https://ianjonsen.r-universe.dev/ui#package:foieGras>. The
300 latest partially tested stable and development versions are available on the GitHub repository:
301 <https://github.com/ianjonsen/foieGras>. An older version of `foieGras` (0.7-6) remains on
302 CRAN at <https://CRAN.R-project.org/package=foieGras>, however, we recommend users
303 upgrade to the latest R-universe version for full access to the functionality presented here.

304 **ORCID**

305 *Ian D Jonsen* <https://orcid.org/0000-0001-5423-6076>
306 *W James Grecian* <https://orcid.org/0000-0002-6428-719X>
307 *Lachlan Phillips* <https://orcid.org/0000-0002-7635-2817>
308 *Gemma Carroll* <https://orcid.org/0000-0001-7776-0946>
309 *Clive R McMahon* <https://orcid.org/0000-0001-5241-8917>
310 *Robert G Harcourt* <https://orcid.org/0000-0003-4666-2934>
311 *Mark A Hindell* <https://orcid.org/0000-0002-7823-7185>
312 *Toby A Patterson* <https://orcid.org/0000-0002-7150-9205>

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