

movedesign: Shiny R app to evaluate sampling design for animal movement studies

Inês Silva¹  | Christen H. Fleming^{2,3}  | Michael J. Noonan⁴  | William F. Fagan²  | Justin M. Calabrese^{1,2,5} 

¹Center for Advanced Systems Understanding (CASUS), Helmholtz-Zentrum Dresden-Rossendorf (HZDR), Görlitz, Germany

²Department of Biology, University of Maryland, College Park, Maryland, USA

³Smithsonian National Zoo and Conservation Biology Institute, Front Royal, Virginia, USA

⁴Department of Biology, University of British Columbia Okanagan, Kelowna, British Columbia, Canada

⁵Helmholtz Centre for Environmental Research—UFZ, Leipzig, Germany

Correspondence

Inês Silva

Email: i.silva@hzdr.de

Funding information

National Science Foundation, Grant/Award Number: NSF IIBR 1915347

Handling Editor: Edward Codling

Abstract

1. Projects focused on movement behaviour and home range are commonplace, but beyond a focus on choosing appropriate research questions, there are no clear guidelines for such studies. Without these guidelines, designing an animal tracking study to produce reliable estimates of space-use and movement properties (necessary to answer basic movement ecology questions), is often done in an ad hoc manner.
2. We developed 'movedesign', a user-friendly Shiny application, which can be utilized to investigate the precision of three estimates regularly reported in movement and spatial ecology studies: home range area, speed and distance travelled. Conceptually similar to statistical power analysis, this application enables users to assess the degree of estimate precision that may be achieved with a given sampling design; that is, the choices regarding data resolution (sampling interval) and battery life (sampling duration).
3. Leveraging the 'ctmm' R package, we utilize two methods proven to handle many common biases in animal movement datasets: autocorrelated kernel density estimators (AKDEs) and continuous-time speed and distance (CTSD) estimators. Longer sampling durations are required to reliably estimate home range areas via the detection of a sufficient number of home range crossings. In contrast, speed and distance estimation requires a sampling interval short enough to ensure that a statistically significant signature of the animal's velocity remains in the data.
4. This application addresses key challenges faced by researchers when designing tracking studies, including the trade-off between long battery life and high resolution of GPS locations collected by the devices, which may result in a compromise between reliably estimating home range or speed and distance. 'movedesign' has broad applications for researchers and decision-makers, supporting them to focus efforts and resources in achieving the optimal sampling design strategy for their research questions, prioritizing the correct deployment decisions for insightful and reliable outputs, while understanding the trade-off associated with these choices.

This is an open access article under the terms of the [Creative Commons Attribution](#) License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2023 The Authors. *Methods in Ecology and Evolution* published by John Wiley & Sons Ltd on behalf of British Ecological Society.

KEY WORDS

biologgers, experimental design, GPS sampling, GPS tracking, home range, simulations, space use

1 | BACKGROUND

Modern tracking technologies are advancing the fields of ecology and other fields of biology, with data-rich studies revealing how movement shapes ecological processes, biological interactions and behavioural responses to natural or human-induced environmental changes (Kays et al., 2015; Nathan et al., 2022). Biologging and telemetry devices, such as global positioning system (GPS) and very-high-frequency (VHF) transmitters, are common sampling methods in this field, and have been used to answer a multitude of research questions—the majority of which rely on estimates of large-scale processes, such as home ranges (Fleming & Calabrese, 2017; Horne et al., 2019), or fine-scale processes, such as speed or distance travelled (Gurarie et al., 2016; Noonan, Fleming, et al., 2019).

The technology is improving, with cheaper, less invasive tags available (Foley & Sillero-Zubiri, 2020; Gottwald et al., 2019), allowing researchers access to high-volume high-resolution movement data for an increasing number of species (Kays et al., 2015): the animal tracking data platform Movebank (www.movebank.org) already hosts 2.4 billion locations for over 1000 species. Although these data are critical for conservation, tracking devices can be costly and/or logistically difficult to deploy (Hays et al., 2016), requiring us to weigh their benefits against their costs to ensure optimal outcomes. VHF transmitters—here referring to their use in triangulation or homing of tracked animals (White & Garrott, 2012)—remain a cost-effective method for data collection on small animals, as well as most reptiles, due to constraints in weight and/or tag attachment (such as surgical implantation).

Researchers often track as many animals as possible, for as long as possible, recording new locations at regular, short sampling intervals—particularly if the goal is to identify finer movement behaviours (Nathan et al., 2022). However, although the use of GPS loggers typically allows for locations to be recorded at higher rates than VHF transmitters (which, without access to automated methods, would require triangulation/homing to be performed regularly every few seconds/minutes for high-frequency data), achieving both long battery life and high sampling frequency is challenging. Excluding other factors that may further reduce the longevity of tracking devices in the wild (e.g. additional sensors, signal acquisition time, algorithm efficiency and data recovery method), GPS battery life shortens with shorter sampling intervals (Forrest et al., 2022; Moriarty & Epps, 2015). Successfully designing an animal tracking study therefore requires a compromise between *sampling duration* (how long an animal should be tracked for) and *sampling interval* (time between which new locations are recorded; reciprocal of sampling frequency). Moreover, target analyses and sampling design are tightly linked, so we must keep specific goals in mind: there are

circumstances where we may be able to address either large-scale or fine-scale questions, but not both concurrently.

Our objective is to provide a more rigorous *a priori* approach, analogous to statistical power analysis (Steidl et al., 1997), for determining the ideal sampling duration and sampling interval of an animal tracking project. We consider three common estimates—home range area, speed and distance travelled—through the lens of continuous-time movement models and the ‘ctmm’ R package (Calabrese et al., 2016). The ‘ctmm’ methods are insensitive to the sampling schedule and deal with many of the biases present in modern movement datasets (such as those due to autocorrelation, small sample sizes, irregular or missing data or measurement error), facilitating robust comparisons across individuals, species and ecosystems (Fleming et al., 2015, 2018, 2019; Fleming & Calabrese, 2017; Silva et al., 2022). However, like many statistical tools, these methods still require adequate sample sizes to achieve high accuracy in their outputs; for example, pHREML-AKDE estimates (designed to handle small effective sample sizes) still tend to be negatively biased with effective sample sizes below 30 (Silva et al., 2022). Furthermore, like all proper estimators, statistical uncertainty decreases with increasing (effective) sample sizes. We chose to implement this in the Shiny R application, ‘movedesign’ (version 0.2.0) to facilitate adoption and accessibility to the broadest possible audience, and hope that we can contribute to the increase in comparable and reliable movement ecology studies. We note that, for most use cases, this application may require existing datasets. This application was built using the ‘golem’ framework (Fay et al., 2021), and is available as an installable R package at <https://github.com/CASUS/movedesign>.

2 | CONCEPTUALIZATION

2.1 | Parameters

Explicitly modelling all the complex interactions between internal states, biophysical constraints, environmental cues and social dynamics that determine animal movement is generally considered impossible (Codling et al., 2008). However, by interpreting movement as a continuous-time stochastic process (Calabrese et al., 2016; Fleming et al., 2014a; Gurarie & Ovaskainen, 2011), we can efficiently summarize behaviour using characteristic timescales, including the position autocorrelation (τ_p) and velocity autocorrelation (τ_v) timescale parameters, and describe long-term dispersal behaviour and short-term movement behaviour across levels of data resolution and duration. The autocorrelation timescales indicate the time required for the correlations in the focal quantity (here position or velocity) to decay by a factor of $1/e$ —conventionally, the data are considered effectively

independent when 5% or less autocorrelation remains (Gurarie & Ovaskainen, 2011). These timescales impose constraints on the sampling design that must be met in order to evaluate both small-scale (speed and distance) and large-scale phenomena (home range) (Fleming et al., 2014b). If these constraints are not met, it could lead to biases and estimate uncertainty.

The position autocorrelation parameter (τ_p) can be interpreted as the home range crossing time, or the time taken on average for an animal to cross the linear extent of its range (Silva et al., 2022). As τ_p increases, we can expect an animal to take longer to travel this linear extent. Range-resident animals tend to travel away from their point of origin at a rate controlled by the location variance parameter (σ_p) while simultaneously reverting back to it at a rate driven by τ_p (Péron et al., 2017). As $\tau_p \rightarrow \infty$, movement becomes endlessly diffusive ($\sigma_p \rightarrow \infty$) with no range residency behaviour; for range-resident species, σ_p is asymptotically constant and proportional to home range area (Calabrese et al., 2016; Fleming et al., 2014a).

The velocity autocorrelation parameter (τ_v) describes how velocity persists through time (directional persistence; Fleming et al., 2014a). Animals with strong directional persistence—longer bouts of constant speed and constant direction—will tend to have a large τ_v parameter (such as a migratory species), while animals with more tortuous movement—less linear, more diffusive—tend towards smaller τ_v . Speed and distance travelled are two of the properties of an animal's velocity process, with variance $\sigma_v = \sigma_p / (\tau_p \times \tau_v)$ for stationary processes (Noonan, Fleming, et al., 2019). For any value of σ_v , as $\tau_v \rightarrow \infty$, the movement process approximates ballistic motion.

2.2 | Sampling design

Study design optimization requires clearly defined research questions and objectives (Fieberg & Börger, 2012), and an understanding of existing constraints, both those related to the study species (characterized by τ_p , τ_v , σ_p and σ_v) and the sampling parameters (duration and interval).

Our choice of sampling parameters largely determines our ability to detect the characteristic timescales of the movement process: it is the sampling duration and interval relative to characteristic timescales that determine whether there will be any signature of the animal's range crossing time (τ_p), or its directional persistence (τ_v). Typically, sampling duration (T) should be at least as long as τ_p (and ideally many times longer) for home range estimation (Fleming et al., 2019; Fleming & Calabrese, 2017; Silva et al., 2022). For estimating speed and distance, the sampling interval (Δt) needs to be less than or equal to the velocity autocorrelation timescale for distance and speed estimation, that is, $\Delta t \leq \tau_v$ (Noonan, Fleming, et al., 2019). If $\Delta t > 3\tau_v$ then no statistically significant signature of the animal's velocity will remain (Noonan, Fleming, et al., 2019).

We can evaluate how much information is present in an animal tracking dataset by considering the *effective sample size* (N). This concept, while well-discussed in statistical literature, is frequently

ignored in movement ecology studies. *Effective sample sizes* are the number of independent locations that provide the same information as the nonindependent data under consideration (Fieberg & Börger, 2012; Fleming et al., 2019; Silva et al., 2022)—and differ depending on the parameter in question. For the purposes of home range estimation, if an animal crosses its home range once per day and we collect locations for 100 days, our effective sample size (N) will be roughly 100. This equivalence is irrespective of sampling interval Δt (provided that $\Delta t < 1$ day), as N here is driven by the number of days sampled, and not by the number of samples per day. Simply put, the information present in this autocorrelated tracking dataset will not change if we collected new locations once a day (for an absolute sample size, n , of 100 locations), every hour ($n=2400$ locations), or every minute ($n=144,000$ locations). Considering that recorded locations are frequently autocorrelated in modern tracking datasets (and that most species take longer than a day to cross their home range; Calabrese et al., 2016; Patterson et al., 2017), obtaining a satisfactory effective sample size ($N > 30$) can be challenging but is essential for a reliable movement metric or space-use estimate. For example, if the study species takes months to cross its home range, as is the case of the Mongolian Gazelle (average τ_p of 6.6 months; Fleming et al., 2014b), achieving an $N = 30$ could require an individual to be tracked for over 16 years, which is substantially longer than their average lifespan.

The choice between tracking devices further complicates sampling design. For GPS/satellite loggers, as sampling is automated and conducted by satellite systems, battery life is inherently linked to both sampling duration and frequency—that is, choosing a higher fix rate (shorter intervals between recorded locations) leads to lower battery life (and, therefore, shorter sampling durations); excluding self-charging models such as solar tags, researchers are required to choose one over the other. For VHF transmitters, battery life is decoupled from any specific sampling interval, and depends only on the sampling duration specified by the manufacturer—that is, researchers choose a transmitter based on its battery life, but the interval between new locations is subject only to the data collection employed manually in the field (locating the animal every hour, or every day, has no influence on the battery life).

In contrast with conventional radio-telemetry, GPS loggers have a higher potential to resolve fine-scale movements; however, the trade-off between battery life and resolution is more conspicuous, and with a greater impact on potential outputs. To facilitate sampling design within 'movedesign', we visualize this trade-off (sampling duration vs. sampling interval) by simulating GPS battery life as a three-parameter log-logistic function (Appendix S1), based on the battery life-resolution trade-off of several GPS models of animal tracking devices.

2.3 | Analytic scope

Our evaluation of sampling design focuses on the precision of three estimates at two different scales—large scale (*home range area*) and

fine scale (speed and *distance travelled*). As the choice of statistical estimator can further obscure estimate interpretation and comparison (Fieberg & Börger, 2012; Fleming et al., 2015), we leverage the 'ctmm' package to develop a reliable inferential framework for sampling design evaluation, generating comparable estimates with confidence intervals (Calabrese et al., 2016; Fleming et al., 2018, 2019; Fleming & Calabrese, 2017).

Home range area is one of the core outputs of movement or spatial ecology studies and provides information on the long-term space-use requirements, which are invaluable for conservation policies and protected area delimitation (Bartoń et al., 2019; Lambertucci et al., 2014). Here, we follow the definition of home range as the area repeatedly used throughout an animal's lifetime for all its normal behaviours and activities, excluding the occasional exploratory excursions (Burt, 1943; Calabrese et al., 2016; Silva et al., 2022), and estimate it using the autocorrelated kernel density estimator (AKDE; Calabrese et al., 2016), which accounts for the autocorrelation present in tracking data.

Both speed and *distance travelled* provide quantifiable links between behaviour and energetics, as demographic outcomes and population dynamics are affected by how far and how fast animals must travel to meet their nutritional and reproductive needs (Morales et al., 2010; Noonan, Fleming, et al., 2019). *Distance travelled* is usually equated with the sum of the straight-line displacement (SLD) between all subsequent locations, while *speed* is the sum of SLD divided by time. Here, we use the continuous-time speed and distance (CTSD) estimator instead, as it overcomes important limitations of SLD estimation (Noonan, Fleming, et al., 2019). Specifically, SLD tends to overestimate speed and *distance travelled* at small sampling intervals and underestimates these quantities at large sampling intervals (see Noonan, Fleming, et al., 2019).

There are two objective metrics that quantify the performance of these estimators: the effective sample size for home range estimation (N_{area}), or how many independent location fixes would be required to calculate the same quality home range estimate, and the effective sample size for speed estimation (N_{speed}), or how many independent velocity fixes would be required to calculate the same quality mean speed estimate.

In addition, the accuracy and precision of the estimates above—calculated from any sampling design—is judged by the relative error of both point estimates compared to the exact expectation values from simulations, and their confidence intervals. For home range areas, we derive the exact expectation value of the true 95% area based on the model from which data are simulated (see Fleming et al., 2014b; Noonan, Tucker, et al., 2019; Silva et al., 2022). For speed and *distance travelled*, the expected values are extracted from a fine-scale error-free trajectory simulated for 10 days at a sampling interval of $\tau_v/10$ (Noonan, Fleming, et al., 2019), functioning as a Riemann sum approximation of the path length that achieves a relative error of $\mathcal{O}(10^{-3})$ while reducing computation time.

3 | WORKFLOW

The main goal of 'movedesign' is to determine if a particular sampling design is sufficient to answer an a priori defined research question, following the conceptual workflow presented in Figure 1. First, users should consider a proxy dataset (typically the same species, or one with similar movement behaviours; see below for further details) from which to extract the aforementioned measures: characteristic timescales (τ), location variance (σ_p) and velocity variance (σ_v). These measures are extracted during automated model fitting and selection (Fleming et al., 2019)—a step that allows users to proceed with study design experimentation without requiring prior knowledge of the underlying movement process. If known a priori, users can also directly input these measures and skip the extraction step. Second, we input sampling design parameters—duration (T) and interval (Δt)—to generate simulated datasets conditional on the previously fitted model. Third, we run estimators for home range and/or speed/*distance travelled* on the simulated data, while calculating the expected values in the background, from the model and parameters used in the simulation. Finally, we compare the estimates with the expected values ('truth') and with simulation results from previous studies (Noonan, Fleming, et al., 2019; Silva et al., 2022), providing an overview of the reliability of that sampling design for estimating home range areas or speed and *distance travelled*.

The application consists of four main sections, organized as easy-to-navigate tabs seen in the left sidebar. Once the user has set their data source and research question(s), the sidebar will automatically subset to only the required steps. We advise users to follow along the guided tutorial available in the 'Home' tab, until they feel confident with the application's workflow. Each run-through of the entire workflow may take a few minutes up to several hours to run; computation bottlenecks arise from the `ctmm::ctmm.select()` and `ctmm::speed()` functions, particularly if the absolute sample size exceeds 10^3 locations, or for very short sampling intervals.

3.1 | Importing movement data

There are three data source options available in 'movedesign': (1) Import data, (2) Select data and (3) Simulate data. For the first option, and prior to using 'movedesign', users should find an animal tracking dataset for their intended study species (e.g. from Movebank, published studies, requesting directly from data owners), preferably in a similar environment to the focal study site (e.g. natural vs. human-dominated environment); if this is not available, search for species with a similar physiological and behavioural phenotype (e.g. the same genus or family, occupying the same ecological niche, similar body size). As the outputs from 'movedesign' depend heavily on the extracted species parameters from pre-existing datasets, this step is crucial to ensure the interpretability and reliance of all

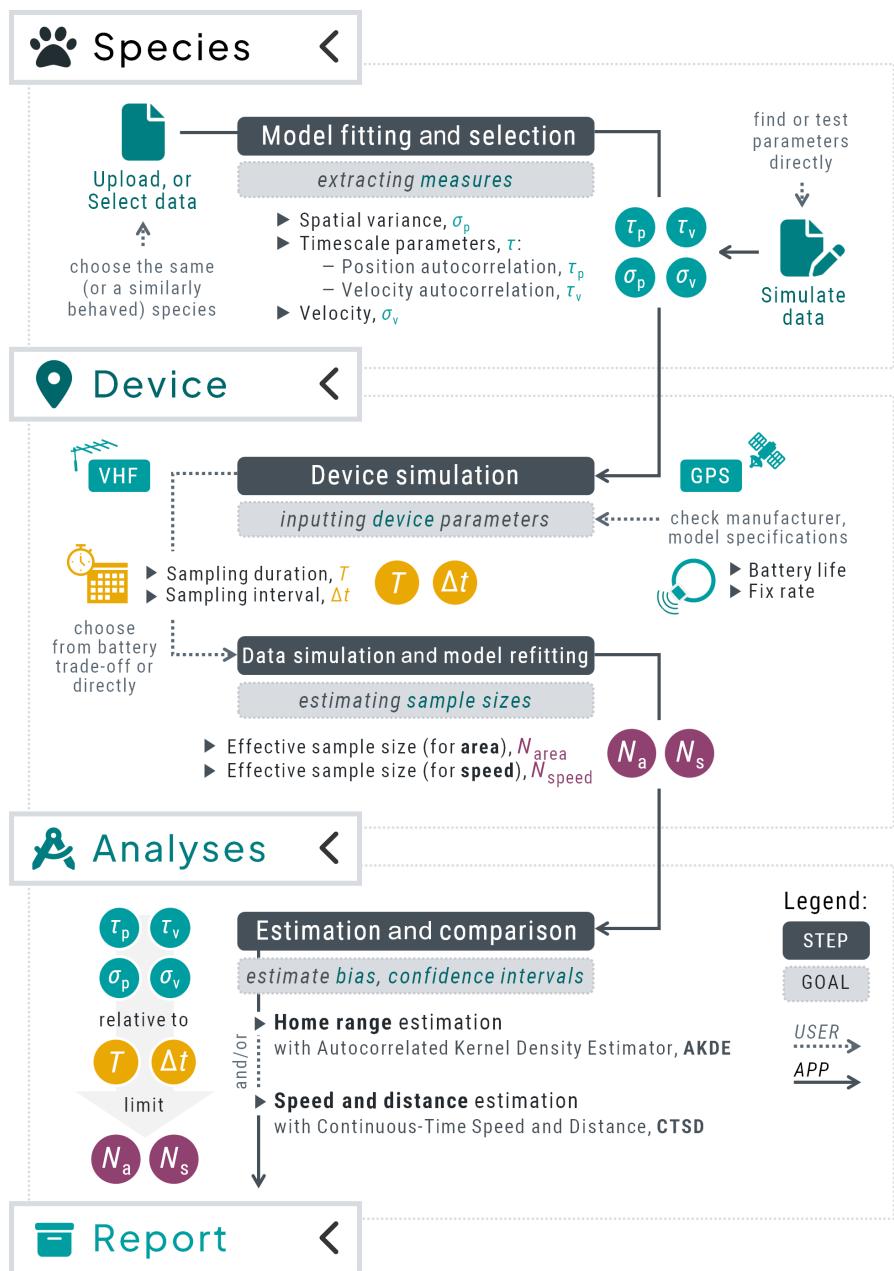


FIGURE 1 Conceptual workflow of the key elements of the 'movedesign' application, providing a R/Shiny-powered user interface to test different sampling designs for specified tracking projects. The application is divided into four main sections: 'Species' (where data are uploaded, selected or simulated to extract relevant parameters and measures), 'Device' (where users input device parameters, visualize potential trade-offs and evaluate effective sample sizes), 'Analyses' (where users can estimate home range areas, and speed and distance travelled, using the 'ctmm' R package) and 'Report' (a summary page of all inputs, outputs and final recommendations).

subsequent steps. Correctly importing data into the 'movedesign' application requires that datasets conform to Movebank naming conventions (<http://www.movebank.org/>). We recommend that users first upload their datasets (privately if needed) to Movebank, as this will facilitate data preparation. For the second option, the user can select one of the seven example species available within the 'ctmm' package and extract their parameters, which serve as worked examples, but may also help inform animal tracking studies of species with similar movement behaviours to those listed. For the third option, the user can simulate an animal tracking dataset from scratch by inputting model parameters (τ_p, τ_v) and associated measures (σ_p, σ_v) directly; if chosen, this option requires previous knowledge of the study species' movement behaviour, and an educated guess regarding their species parameters. For range-resident species, τ_p is generally on the order of days to weeks, while

τ_v is generally on the order of minutes to hours (Noonan, Tucker, et al., 2019); however, these parameters are likely to differ between species, populations and individuals.

For options 1 and 2 ('Import data' and 'Select data'), the application checks if datasets are valid: specifically, if there is still a signature of the animal's position or velocity autocorrelation parameter. For example, if the user is interested in speed estimation but provides only a coarsely sampled tracking dataset ($\Delta t \gg \tau_v$) then the property of continuous velocities is not supported by the data and the resulting movement model is fractal (i.e. we cannot proceed with speed estimation). Data visualization boxes are also available to assist in additional validation steps that cannot be done automatically, such as variograms to confirm range residency if the goal is home range estimation (Fleming et al., 2014a), or plots to identify outliers (which should be removed and the data re-uploaded before proceeding).

FIGURE 2 Initial steps in the 'movedesign' Shiny application workflow ('Home' and 'Species' tabs). For the case study presented here, set a fixed seed to reproduce all outputs, the correct data source, both research questions, and the stated species and individual from the list (before validation and extraction).

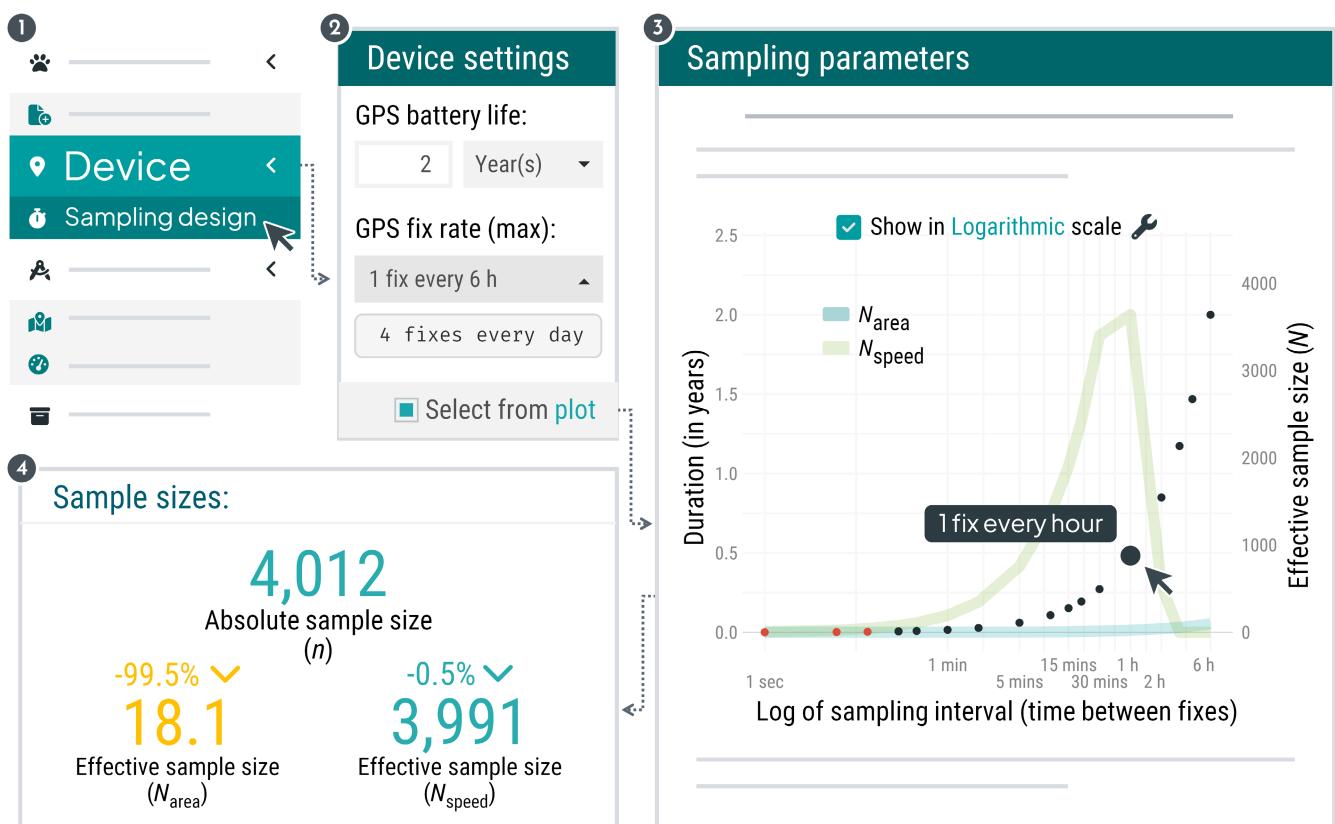
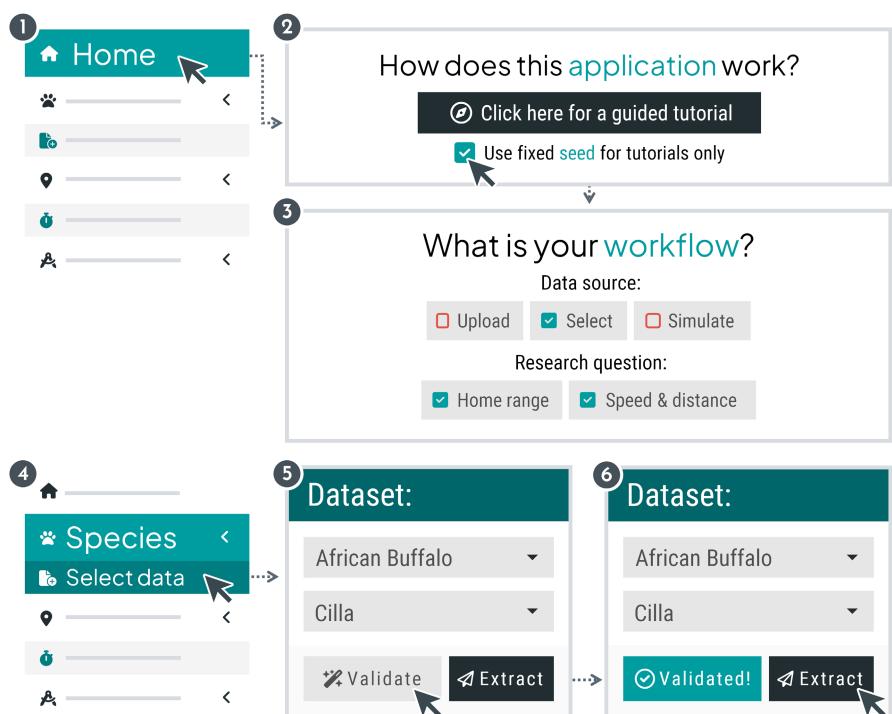


FIGURE 3 Example outputs shown in the 'Device' tab, including the simulated trade-off between sampling duration and sampling interval (shown in logarithmic scale) for the specified device settings, with the chosen interval selected from the plot (1 fix every hour), and the absolute and effective sample sizes extracted from the new model fit.

For option 3 ('Simulate data'), the application will simulate autocorrelated tracking data using an isotropic Ornstein–Uhlenbeck with foraging (OUF) Gaussian process, which incorporates both

correlated velocities and constrained space use. This OUF model is also the most frequently selected across modern GPS tracking datasets (Noonan, Tucker, et al., 2019).

3.2 | Choosing sampling design

The Device section allows for the simulation of a new dataset, conditioned upon previously extracted parameters, and based on the sampling design of the user's choice. First, users are prompted to input their desired device type (GPS/Satellite loggers or VHF transmitter) as appropriate sampling design is dependent on the device's battery life: for GPS/Satellite loggers, battery life depends on both duration and frequency, while for VHF transmitters, battery life depends only on duration. For the GPS option, if users do not intend to visualize the trade-off curve and already have a specific sampling design in mind, they can uncheck the 'Select from plot' to 'Set regime manually' located in the footer of the Device settings box (this is equivalent to setting VHF transmitter as the device of choice).

The application will once again validate all current inputs, and inform the user of the expected run time of the simulation step. For home range estimation, we recommend that the user check the range residency assumption through the variogram in the data visualization boxes. The user can also check the effective sample sizes extracted from the new model fit, which will assist in decision making (to continue with the current sampling design, or to make further adjustments before proceeding).

3.3 | Running estimators and building the report

In the Analyses section, there will be one or two tabs available to the user, based on the chosen outputs: (1) Home range and/or (2)

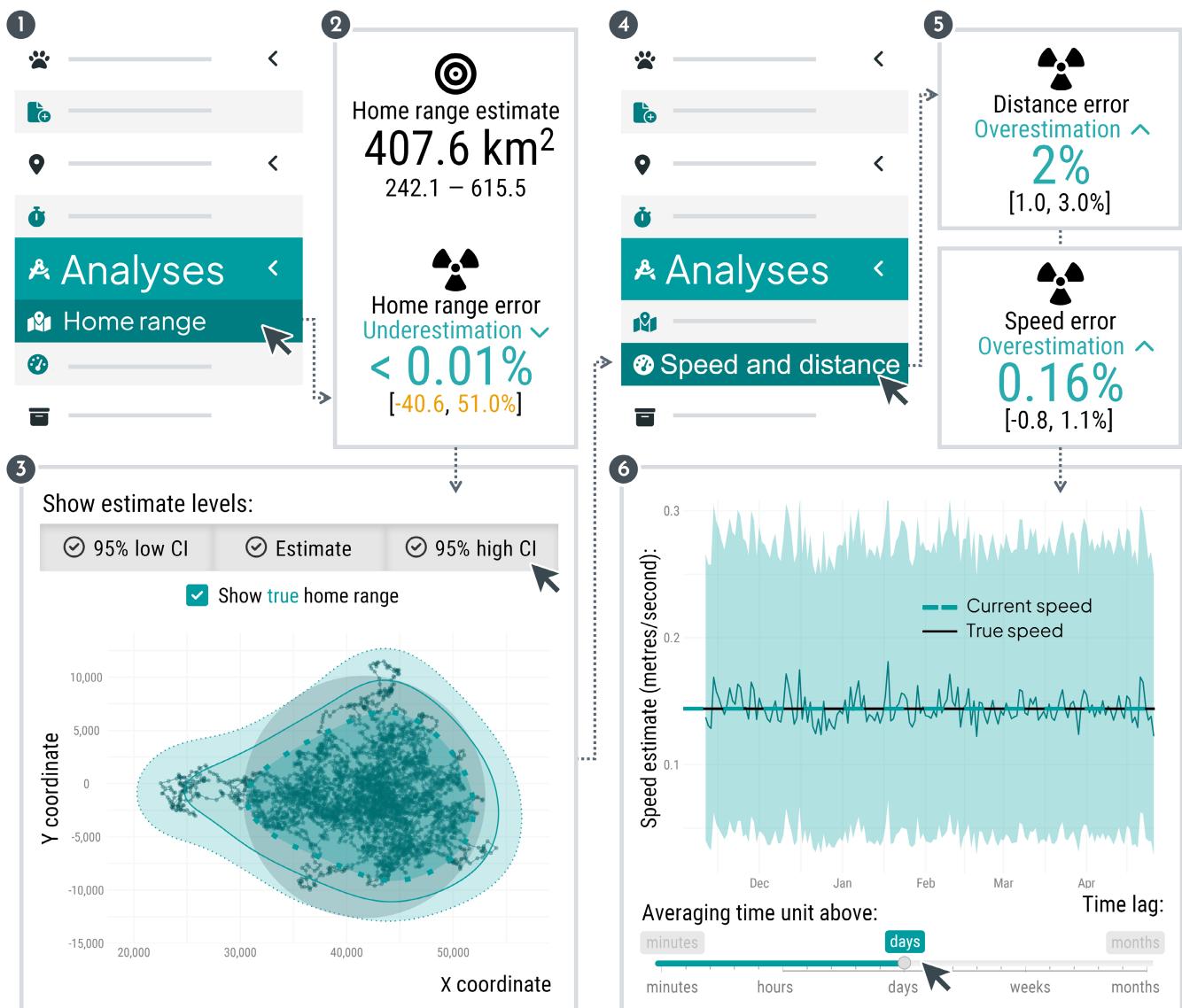


FIGURE 4 Example outputs shown in the 'Analyses' tabs, including the point estimates (and corresponding confidence intervals below the point estimate in small, black text) and/or expected errors associated with both home range and speed/distance. We can also visualize the home range estimate (with the true 95% area for comparison), and the instantaneous speed estimates at different timescales—other visualizations (such as those related to distance) are not shown here but are available within the app.

Speed and distance. Each tab will run an estimator on the simulated dataset, created during the previous section. For each output, there will be two sets of values in the main output box: 'Estimate', which is the point estimate followed by the 95% confidence intervals (CIs), and 'Expected error', which is the relative error (in %) of the point estimate (and of the 95% CIs) in relation to the expected values. The user can utilize these outputs (as well as effective sample sizes) to plan an appropriate sampling duration and interval so the confidence intervals are sufficiently narrow and relative errors acceptably low: typically, a more reliable home range estimate requires a longer sampling duration than the one specified, while a more reliable speed and distance estimation requires shorter sampling intervals. However, we advise caution in two scenarios for speed and distance estimation: (1) producing a CTSD estimate at $\Delta t > 3\tau_v$ does not guarantee a meaningful output, and (2) $\Delta t \ll \tau_v$ may only yield a marginal benefit over $\Delta t < \tau_v$ while markedly increasing computation time (see Noonan, Fleming, et al., 2019 for more details). Users can then navigate to the last section, the 'Report' tab, to see a summary of all previous inputs and outputs, and the final recommendations regarding home range and/or speed and distance estimation.

4 | CASE STUDY

To present the application's key features, we used the African Buffalo (*Syncerus caffer*) data available within the 'ctmm' R package as a case study. These individuals were tracked in Kruger National Park, South

Africa (Cross et al., 2009). Our objectives were to reliably estimate home range area and speed/distance travelled (Figure 2) using GPS loggers for a hypothetical tracking project with the same species in a similar study site. We choose a GPS model with a maximum lifespan of 2 years if four new locations were collected every day ($\Delta t = 1$ fix every 6 h; Figure 3).

We selected the individual 'Cilla' for parameter extraction; once validated, we extracted parameters from the fitted OUF anisotropic model for a τ_p of approximately 7.5 days (CI: 4.4–12.7), and a τ_v of 42 min (39.6–44.7). We plotted our sampling design options based on the chosen tracking device parameters (Figure 3), which revealed that a rough estimate of N_{area} for any sampling interval was substantially smaller the N_{speed} (as expected, since $\tau_p \gg \tau_v$). As our focus was both home range and speed/distance estimation, we wanted to maximize N_{area} and N_{speed} , so we selected a sampling interval of 1 h (which sets our sampling duration to 5.7 months, due to the battery/resolution trade-off discussed earlier). Once we successfully validated and ran our new simulation, our sample sizes were $n = 4012$, $N_{area} = 18.1$ and $N_{speed} = 3991$.

With an appropriate movement model available, the next step was to estimate home range area, mean speed and total distance travelled (Figure 4). Once the final report was built, the AKDE estimates showed high uncertainty, while the CTSD estimates did not. Based on these results and the effective sample sizes, we determined that our sampling design was adequate for speed/distance estimation, but could be insufficient for home range (Figure 5). After exploring further sampling designs for our choice of GPS model, we

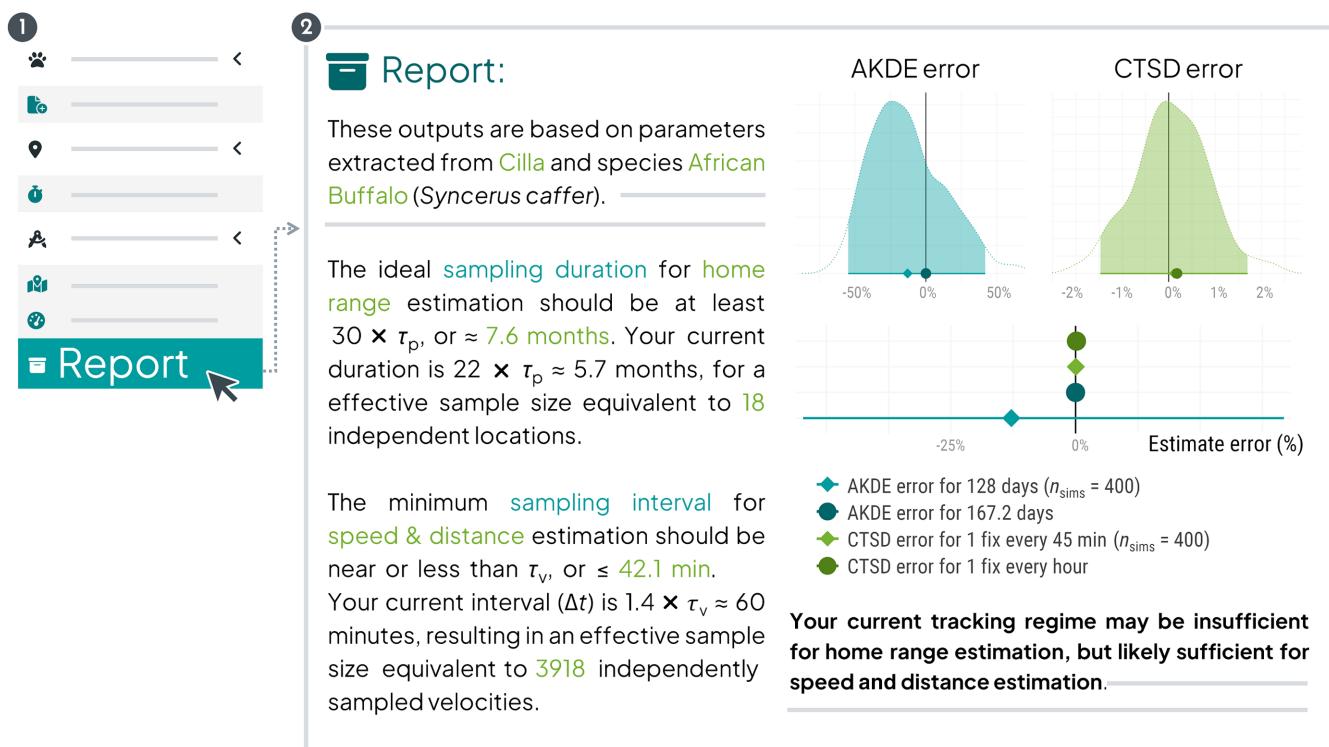


FIGURE 5 Final report for a workflow that requested both home range and speed/distance as the research questions, for a hypothetical tracking study of the African buffalo *Syncerus caffer* species with a sampling duration of 5.7 months and a sampling interval of 1 h—based on a GPS model with a maximum battery life of 2 years if the sampling interval was set to 6 h.

decided upon one fix every 2 h for a sampling duration of 11 months, reducing the uncertainty associated with home range area—although at the cost of increased uncertainty in speed/distance estimation (follow along the guided tutorial in the 'Home' tab for this particular workflow).

5 | FINAL CONSIDERATIONS

Data collection and sampling design optimization allows researchers to better address key ecological questions, as conclusions drawn from lower-resolution data may not be appropriate to detect fine-scale movement properties, while higher-resolution datasets may still be unsuitable to detect patterns at larger spatial or temporal scales (e.g. space use), if the sampling duration is too short (Nathan et al., 2022). Our workflow allows users to evaluate a wide range of potential sampling designs, which can then serve as a solid foundation for future tracking projects, or even the evaluation of on-going and published studies. One limitation of our study is that our GPS simulations do not consider the case of solar tags. As a workaround, users can test the minimum expected battery life or the duration of the entire tracking study. Our application also assumes, for the purposes of home range estimation, that the intended study species is range resident; if users plan to track migratory species, they should consider assessing resident periods (before and/or after migration, if applicable) as separate study design scenarios, each requiring their own assessment. We recommend that users employ the same methods during the study planning phase (facilitated here through the 'movedesign' application) and the final analyses after data collection to ensure similar effective sample sizes. We are continuously working to improve the application's code, and have plans to explore new use cases and address more challenging sampling design questions.

AUTHOR CONTRIBUTIONS

Inês Silva, Christen Fleming, Michael Noonan and Justin Calabrese conceived the ideas; Inês Silva designed and developed the application; Justin Calabrese and Inês Silva led the drafting the manuscript; Inês Silva, Christen Fleming, Michael Noonan, William Fagan and Justin Calabrese edited the draft. All authors reviewed the application, contributed critically to the manuscript and gave final approval for publication.

ACKNOWLEDGEMENTS

This work was partially funded by the Center of Advanced Systems Understanding (CASUS), which is financed by Germany's Federal Ministry of Education and Research (BMBF) and by the Saxon Ministry for Science, Culture and Tourism (SMWK) with tax funds on the basis of the budget approved by the Saxon State Parliament. C.H.F. and J.M.C. were supported by NSF IIBR 1915347. Open Access funding enabled and organized by Projekt DEAL.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

PEER REVIEW

The peer review history for this article is available at <https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/2041-210X.14153>.

DATA AVAILABILITY STATEMENT

The empirical dataset used in the manuscript is openly accessible: the African buffalo tracking data are archived in the MoveBank Data Repository (Cross et al., 2016) and partially included in the ctmm package (Fleming & Calabrese, 2022). Source code of the 'movedesign' application is available on GitHub (<https://github.com/CASUS/movedesign>), and version 0.2.0 has been archived on Zenodo (Silva, 2023).

ORCID

Inês Silva  <https://orcid.org/0000-0003-4850-6193>
 Christen H. Fleming  <https://orcid.org/0000-0002-9356-6518>
 Michael J. Noonan  <https://orcid.org/0000-0003-4512-0535>
 William F. Fagan  <https://orcid.org/0000-0003-2433-9052>
 Justin M. Calabrese  <https://orcid.org/0000-0003-0575-6408>

REFERENCES

Bartoń, K. A., Zwijacz-Kozica, T., Zięba, F., Sergiel, A., & Selva, N. (2019). Bears without borders: Long-distance movement in human-dominated landscapes. *Global Ecology and Conservation*, 17, e00541. <https://doi.org/10.1016/j.gecco.2019.e00541>

Burt, W. H. (1943). Territoriality and home range concepts as applied to mammals. *Journal of Mammalogy*, 24(3), 346–352. <https://doi.org/10.2307/1374834>

Calabrese, J. M., Fleming, C. H., & Gurarie, E. (2016). ctmm: An R package for analyzing animal relocation data as a continuous-time stochastic process. *Methods in Ecology and Evolution*, 7(9), 1124–1132.

Codling, E. A., Plank, M. J., & Benhamou, S. (2008). Random walk models in biology. *Journal of the Royal Society Interface*, 5, 813–834. <https://doi.org/10.1098/rsif.2008.0014>

Cross, P. C., Bowers, J. A., Hay, C. T., Wolhuter, J., Buss, P., Hofmeyr, M., Toit, J. T., & Getz, W. M. (2016). Data from: Nonparametric kernel methods for constructing home ranges and utilization distributions. Movebank Data Repository, <https://doi.org/10.5441/001/1.j900f88t/1>

Cross, P. C., Heisey, D. M., Bowers, J. A., Hay, C. T., Wolhuter, J., Buss, P., Hofmeyr, M., Michel, A. L., Bengis, R. G., & Bird, T. L. F. (2009). Disease, predation and demography: Assessing the impacts of bovine tuberculosis on African buffalo by monitoring at individual and population levels. *Journal of Applied Ecology*, 46(2), 467–475. <https://doi.org/10.1111/j.1365-2664.2008.01589.x>

Fay, C., Guyader, V., Rochette, S., & Girard, C. (2021). Golem: A framework for robust shiny applications. R package version 0.3. 1.

Fieberg, J., & Börger, L. (2012). Could you please phrase 'home range' as a question? *Journal of Mammalogy*, 93(4), 890–902.

Fleming, C. H., & Calabrese, J. M. (2017). A new kernel density estimator for accurate home-range and species-range area estimation. *Methods in Ecology and Evolution*, 8(5), 571–579.

Fleming, C. H., & Calabrese, J. M. (2022). Ctmm: Continuous-time movement modeling. R package version 1.1.0. <https://CRAN.R-project.org/package=ctmm>

Fleming, C. H., Calabrese, J. M., Mueller, T., Olson, K. A., Leimgruber, P., & Fagan, W. F. (2014a). From fine-scale foraging to home ranges:

A semivariance approach to identifying movement modes across spatiotemporal scales. *The American Naturalist*, 183(5), E154–E167.

Fleming, C. H., Calabrese, J. M., Mueller, T., Olson, K. A., Leimgruber, P., & Fagan, W. F. (2014b). Non-Markovian maximum likelihood estimation of autocorrelated movement processes. *Methods in Ecology and Evolution*, 5(5), 462–472. <https://doi.org/10.1111/2041-210X.12176>

Fleming, C. H., Fagan, W. F., Mueller, T., Olson, K. A., Leimgruber, P., & Calabrese, J. M. (2015). Rigorous home range estimation with movement data: A new autocorrelated kernel density estimator. *Ecology*, 96(5), 1182–1188. <https://doi.org/10.1890/14-2010.1>

Fleming, C. H., Noonan, M. J., Medici, E. P., & Calabrese, J. M. (2019). Overcoming the challenge of small effective sample sizes in home-range estimation. *Methods in Ecology and Evolution*, 10(10), 1679–1689.

Fleming, C. H., Sheldon, D., Fagan, W. F., Leimgruber, P., Mueller, T., Nandintsetseg, D., Noonan, M. J., Olson, K. A., Setyawani, E., & Sianipar, A. (2018). Correcting for missing and irregular data in home-range estimation. *Ecological Applications*, 28(4), 1003–1010.

Foley, C. J., & Sillero-Zubiri, C. (2020). Open-source, low-cost modular GPS collars for monitoring and tracking wildlife. *Methods in Ecology and Evolution*, 11(4), 553–558.

Forrest, S. W., Recio, M. R., & Seddon, P. J. (2022). Moving wildlife tracking forward under forested conditions with the SWIFT GPS algorithm. *Animal Biotelemetry*, 10(1), 19. <https://doi.org/10.1186/s40317-022-00289-9>

Gottwald, J., Zeidler, R., Friess, N., Ludwig, M., Reudenbach, C., & Nauss, T. (2019). Introduction of an automatic and open-source radio-tracking system for small animals. *Methods in Ecology and Evolution*, 10(12), 2163–2172. <https://doi.org/10.1111/2041-210X.13294>

Gurarie, E., Bracis, C., Delgado, M., Meckley, T. D., Kojola, I., & Wagner, C. M. (2016). What is the animal doing? Tools for exploring behavioural structure in animal movements. *Journal of Animal Ecology*, 85(1), 69–84.

Gurarie, E., & Ovaskainen, O. (2011). Characteristic spatial and temporal scales unify models of animal movement. *The American Naturalist*, 178(1), 113–123.

Hays, G. C., Ferreira, L. C., Sequeira, A. M. M., Meekan, M. G., Duarte, C. M., Bailey, H., Bailleul, F., Bowen, W. D., Caley, M. J., Costa, D. P., Eguíluz, V. M., Fossette, S., Friedlaender, A. S., Gales, N., Gleiss, A. C., Gunn, J., Harcourt, R., Hazen, E. L., Heithaus, M. R., ... Thums, M. (2016). Key questions in marine megafauna movement ecology. *Trends in Ecology & Evolution*, 31(6), 463–475. <https://doi.org/10.1016/j.tree.2016.02.015>

Horne, J., Fieberg, J., Börger, L., Rachlow, J. L., Calabrese, J. M., & Fleming, C. H. (2019). Animal home ranges. In D. L. Murray & B. K. Sandercock (Eds.), *Population ecology in practice* (pp. 315–332). Wiley-Blackwell.

Kays, R., Crofoot, M. C., Jetz, W., & Wikelski, M. (2015). Terrestrial animal tracking as an eye on life and planet. *Science*, 348(6240), aaa2478. <https://doi.org/10.1126/science.aaa2478>

Lambertucci, S. A., Alarcón, P. A., Hiraldo, F., Sanchez-Zapata, J. A., Blanco, G., & Donázar, J. A. (2014). Apex scavenger movements call for transboundary conservation policies. *Biological Conservation*, 170, 145–150.

Morales, J. M., Moorcroft, P. R., Matthiopoulos, J., Frair, J. L., Kie, J. G., Powell, R. A., Merrill, E. H., & Haydon, D. T. (2010). Building the bridge between animal movement and population dynamics. *Philosophical Transactions of the Royal Society, B: Biological Sciences*, 365(1550), 2289–2301.

Moriarty, K. M., & Epps, C. W. (2015). Retained satellite information influences performance of GPS devices in a forested ecosystem. *Wildlife Society Bulletin*, 39(2), 349–357. <https://doi.org/10.1002/wsb.524>

Nathan, R., Monk, C. T., Arlinghaus, R., Adam, T., Alós, J., Assaf, M., Baktoft, H., Beardsworth, C. E., Bertram, M. G., & Bijleveld, A. I. (2022). Big-data approaches lead to an increased understanding of the ecology of animal movement. *Science*, 375(6582), eabg1780.

Noonan, M. J., Fleming, C. H., Akre, T. S., Drescher-Lehman, J., Gurarie, E., Harrison, A.-L., Kays, R., & Calabrese, J. M. (2019). Scale-insensitive estimation of speed and distance traveled from animal tracking data. *Movement Ecology*, 7(1), 1–15. <https://doi.org/10.1186/s40462-019-0177-1>

Noonan, M. J., Tucker, M. A., Fleming, C. H., Akre, T. S., Alberts, S. C., Ali, A. H., Altmann, J., Antunes, P. C., Belant, J. L., & Beyer, D. (2019). A comprehensive analysis of autocorrelation and bias in home range estimation. *Ecological Monographs*, 89(2), e01344.

Patterson, T. A., Parton, A., Langrock, R., Blackwell, P. G., Thomas, L., & King, R. (2017). Statistical modelling of individual animal movement: An overview of key methods and a discussion of practical challenges. *AStA Advances in Statistical Analysis*, 101(4), 399–438.

Péron, G., Fleming, C. H., de Paula, R. C., Mitchell, N., Strohbach, M., Leimgruber, P., & Calabrese, J. M. (2017). Periodic continuous-time movement models uncover behavioral changes of wild canids along anthropization gradients. *Ecological Monographs*, 87(3), 442–456. <https://doi.org/10.1002/ecm.1260>

Silva, I. (2023). ecoisilva/movedesign: movedesign v0.2.0. Zenodo, <https://doi.org/10.5281/zenodo.7963190>

Silva, I., Fleming, C. H., Noonan, M. J., Alston, J., Folta, C., Fagan, W. F., & Calabrese, J. M. (2022). Autocorrelation-informed home range estimation: A review and practical guide. *Methods in Ecology and Evolution*, 13(3), 534–544.

Steidl, R. J., Hayes, J. P., & Schauber, E. (1997). Statistical power analysis in wildlife research. *The Journal of Wildlife Management*, 61, 270–279. <https://doi.org/10.2307/3802582>

White, G. C., & Garrott, R. A. (2012). *Analysis of wildlife radio-tracking data*. Elsevier.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Appendix S1: Description of GPS battery trade-off function.

How to cite this article: Silva, I., Fleming, C. H., Noonan, M. J., Fagan, W. F., & Calabrese, J. M. (2023). movedesign: Shiny R app to evaluate sampling design for animal movement studies. *Methods in Ecology and Evolution*, 14, 2216–2225. <https://doi.org/10.1111/2041-210X.14153>