BIOLOGGING: REVIEW

Navigating through the R packages for movement

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Abstract

1. The advent of miniaturized biologging devices has provided ecologists with unprecedented opportunities to record animal movement across scales, and led to the collection of ever-increasing quantities of tracking data. In parallel, sophisticated tools have been developed to process, visualize and analyse tracking data; however, many of these tools have proliferated in isolation, making it challenging for users to select the most appropriate method for the question in hand. Indeed, within the R software alone, we listed 58 packages created to deal with tracking data or 'tracking packages'.

2. Here, we reviewed and described each tracking package based on a workflow centred around tracking data (i.e. spatio-temporal locations (x, y, t)), broken down into three stages: pre-processing, post-processing and analysis, the latter consisting of data visualization, track description, path reconstruction, behavioural pattern identification, space use characterization, trajectory simulation and others.

3. Supporting documentation is key to render a package accessible for users. Based on a user survey, we reviewed the quality of packages' documentation and identified 11 packages with good or excellent documentation.

4. Links between packages were assessed through a network graph analysis. Although a large group of packages showed some degree of connectivity (either depending on functions or suggesting the use of another tracking package), one third of the packages worked in isolation, reflecting a fragmentation in the R movement-ecology programming community.

5. Finally, we provide recommendations for users when choosing packages, and for developers to maximize the usefulness of their contribution and strengthen the links within the programming community.

KEYWORDS

biologging, movement ecology, R project for statistical computing, spatial, tracking data

1 | A MOVEMENT-ECOLOGY BACKGROUND

Animal movement plays a crucial role in ecological and evolutionary processes, from the individual level to ecosystem level (Clobert,

[Correction added after online publication on 6 November 2019: Headings renumbered within section 3]

Danchin, Dhondt, & Nichols, 2001; Dingle, 1996; Nathan et al., 2008). However, studying animal movement has presented challenges to researchers, as individuals are often difficult to follow for extended time periods and over large distances. Over recent decades, decreases in the size and cost of animal-borne sensors or biologging devices have led to an exponential increase in their use. This has substantially improved our understanding of how and why animals move

(Hussey et al., 2015; Kays, Crofoot, Jetz, & Wikelski, 2015; Nathan et al., 2008). Technological advancements have also enabled a wide range of sensors to be used by ecologists, which can be integrated to remotely record a suite of metrics, including longitude and latitude (*x*, *y*), altitude or depth (*z*), acceleration, and in situ environmental conditions (Cagnacci, Boitani, Powell, & Boyce, 2010; Wilmers et al., 2015; Wilson, Shepard, & Liebsch, 2008). From these multiple sensors, fine-scale behaviours and physiological states can be inferred (Halsey, Green, Wilson, & Frappell, 2009; Rutz & Hays, 2009).

The increase in quantity and complexity of biologging data requires appropriate analytical and software tools that aid processing and interpretation of data. Those tools should be sound and transparent to allow for reproducibility of results and computation time optimization (Lowndes et al., 2017; Reichman, Jones, & Schildhauer, 2011; Urbano et al., 2010). Mainly in the last decade, many of these tools have been made available for the scientific community in the form of packages for the R software (R Core Team, 2018), which has facilitated their widespread use and contributed to make R the most dynamic programming platform in ecology. However, in order to identify the most appropriate function in R for a particular analysis, ecologists have to review and evaluate multiple functions within and between packages.

The aim of this study was to review the packages created to process or analyse a specific type of movement data: tracking data. Movement of an organism is defined as a change in the geographic location of an individual in time, so movement data can be defined by a space and a time component. Tracking data are composed of at least 2-dimensional coordinates (*x*, *y*) and a time index (*t*), and can be seen as the geometric representation (the trajectory) of an individual's path. The packages reviewed here, henceforth called tracking packages, are those explicitly developed to either create, transform or analyse tracking data (i.e. (*x*, *y*, *t*)), allowing a full workflow from raw data from biologging devices to final analytical outcome. For instance, a package that would use accelerometer, gyroscope and magnetometer data to reconstruct an animal's trajectory via dead-reckoning, thus transforming those data into an (*x*, *y*, *t*) format, would fit into the definition. However, a package analysing accelerometry series to detect changes in behaviour would not fit.

Here, we present a workflow for the study of tracking data (Figure 1) and review packages that are designed for tracking data, including their role in data processing and analysis. The workflow is composed of three stages: pre-processing, post-processing and data

analysis. Data pre-processing is the process by which data are transformed into the (*x*, *y*, *t*) format, and it would be necessary in cases where biologging devices do not provide raw data in the form of tracking data, for example for most geolocators or Global Location Sensors (GLS), only light intensity is provided. Tracking data may not be immediately usable, for example errors or outliers need to be identified, or other second- or third-order variables need to be derived for the dataset to be ready for analysis; we defined this stage of data processing as post-processing. Finally, the last stage of analysis can be divided into data visualization, track description, path reconstruction, behavioural pattern identification, space use characterization, trajectory simulation and others (e.g. population parameter estimation and interaction between individuals). In each of these subsections, we describe the tools provided by tracking packages to achieve these goals. When necessary, we also provided a short description of the biologging devices and the data they collect, since not all readers are familiar with every type of device. An additional subsection briefly describes some R packages that do not deal with tracking data (as defined above), but were developed to process and analyse data from biologging devices such as accelerometers and time-depth recorders.

Since the documentation provided in conjunction with the packages is key for rendering them accessible for users, we also review supporting documentation and, based on a survey, summarize packages based on the clarity of their documentation. The links between packages, showing how much they rely on each other and the compatibility between them, are also assessed.

This review is aimed at movement ecologists, whether they are potential users or developers of R packages. This study aimed to provide users with criteria through which they can select packages for specific analyses, and offers developers recommendations to maximize the utility of packages and strengthen the links within the R community.

2 | DATA SOURCES

Multiple sources were used to identify tracking packages, mainly (a) the spatio-temporal task view on the Comprehensive R Archive Network (CRAN) repository (https://cran.r-project.org/web/views/SpatioTemporal.html, (b) an updated list of this task on GitHub (https://bit.ly/2CWoSD6), (c) packages suggested in the description files of other packages, (d) Google search engine and (e) e-mail/Twitter

FIGURE 1 Workflow for data processing and analysis in movement ecology. Numbers in parenthesis are the number of packages dealing with each stage of the workflow. Some packages may correspond to more than one category, except for data visualization, where only packages created for that purpose are counted
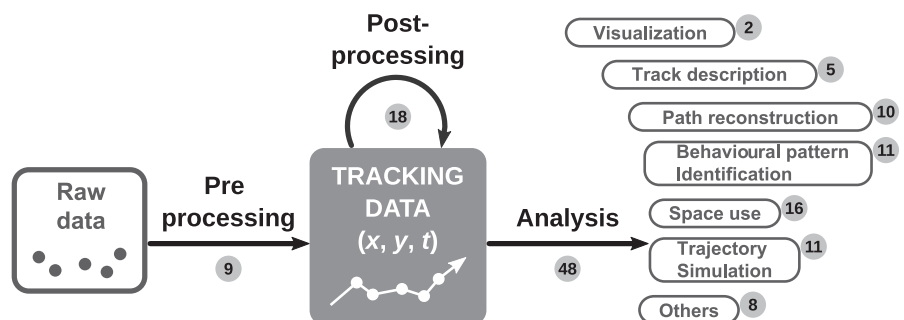
exchanges with ecologists. For the Google search, search terms were (trajectory OR movement OR spatiotemporal) AND package AND R. The combined use of these sources provided a large list of packages, from which we selected only the ones that matched the definition of a tracking package stated in the previous section (Section 1).

The package search and information gathering were done between March and August 2018. Tracking packages that were either removed from CRAN or described as in a 'very early version' on their GitHub repositories were discarded. Information on package documentation was extracted as follows. Standard documentation was categorized as existing if it was available when installing the package. A vignette had to be visible from the main page of the repository or visible as an output of *help(package)*. A peer-reviewed article had to be either mentioned on the main page of the repository, the vignette or in the citation of the package.

It should be noticed that between the period of information gathering and the time of publication of this work, new packages may have been published, and new versions of the reviewed packages containing additional functions could have been released. Information on the reviewed version of each package, and links to each package repository along with a summary of their main characteristics are included in the Zenodo repository (https://doi.org/10.5281/zenodo.3483853). In this work, package citation refers strictly to the output of *citation(package)* in R by the time of writing the manuscript and the version cited in the reference may not match the studied version.

3 | THE R PACKAGES

Fifty-eight packages were found to assist with processing and analysis of tracking data (Figure 1). Some R packages have been developed to tackle several of these stages of data processing and analysis, while others focus on only one, as shown in Table 1. To identify and classify package functions for each specific stage, our main support was the standard documentation of the packages, complemented with the additional sources of information described in Section 2 above.

When appropriate, the type of biologging devices from which the tracking data originate is described in the text, so that readers who are not familiar with these devices have a basic idea of the advantages and limitations of the devices, and why some packages focus on specific issues related to them. The description of the tracking packages also includes information on the year each package was publicly available (Figure 2), the main repository where the package is stored and whether it is actively maintained (hereafter referred to as 'active'). The official repository for R packages is the CRAN repository. CRAN enforces technical consistency, with a set of rules such as the inclusion of ownership information, cross-platform portable code (i.e. to work with Windows, Mac OS and UNIX platforms), and minimum and maximum sizes for package components. The majority of the packages reviewed in this manuscript are on CRAN; the remainder are mostly on GitHub or other repositories (e.g. R-Forge

or independent websites). Regarding package maintenance, we consider that a package hosted on GitHub is actively maintained if a 'commit' (i.e. a contribution) has been made in the last year, and for other packages (if they are not also on GitHub), that the most recent version of the package is no older than one year (analysis conducted in August 2018).

3.1 | Pre-processing

Pre-processing is required when raw biologging data are not in a tracking data format. The methods used for pre-processing depend heavily on the type of biologging device used. Among the tracking packages, 6 are focused on GLS, one on radiotelemetry and two use accelerometry and magnetometry data.

3.1.1 | GLS data pre-processing

Global Location Sensors are electronic archival tracking devices which record ambient light intensity and elapsed time. The timings of sunset and sunrise are estimated, latitude is calculated from day length, and longitude from the time of local midday relative to Greenwich Mean Time (Afanasyev, 2004). GLS can record data for several years, and their small size and low mass (<1 g) make them suitable for studying long-distance movements in a wide range of species. Several methodologies have been developed to reduce errors in geographic locations generated from the light data, which are reflected by the large number of packages for pre-processing GLS data. We classified these methods into three categories: threshold, template-fitting and twilight-free.

- *Threshold methods*. Threshold levels of solar irradiance, which are arbitrarily chosen, are used to identify the timing of sunrise and sunset. The packages that use threshold methods are GEOLIGHT (2012, CRAN, inactive) (Lisovski, Hahn, & Hodgson, 2012) and PROBGLS (2016, GitHub, inactive) (Merkel, 2019). GEOLIGHT uses astronomical equations from Montenbruck and Pfleger (2013) to derive locations from timings of sunrise and sunset, and from sun elevation angles. PROBGLS implements a probabilistic method that takes into account uncertainty in sun elevation angle and twilight events to estimate locations. Starting with the first known location (where the individual was tagged), it estimates the location of the subsequent twilight event which is replicated several times adding an error term; it then computes probabilities for each location based on the plausibility of the estimated speed or on environmental conditions (e.g. sea surface temperature SST) (Merkel et al., 2016).
- *Template-fitting methods*. The observed light irradiance levels for each twilight are modelled as a function of theoretical light levels (i.e. the template). Then, parameters from the model (e.g. a slope in a linear regression) are used to estimate the locations. The formulation of the model and the parameters used for location estimation vary from method to method (Ekstrom, 2004). The packages that use template-fitting methods are FLIGHTR

TABLE 1 Summary of the functionality of the tracking packages

Workflow stage	Categories	Method description	Data type	Package
Pre-processing		Threshold	GLS	GEOLIGHT, PROBGLS
		Template-fitting	GLS	FLIGHTR, TRACKIT, TRIPESTIMATION/SGAT
		Twilight-free	GLS	TWILIGHTFREE
		Triangulation	Radio	TELEMETR
		Dead-reckoning	Accel. + magnet	ANIMALTRACK, TRACKRECONSTRUCTION
Post-processing	Data cleaning	Filter implausible locations	PTT	ARGOSFILTER, SDLFILTER
			GPS	SDLFILTER
		Remove duplicates/speed filter	Any	T-LOCOH, TRAJDATAMINING, TRIP
	Data compression	Rediscretization	Any	ADEHABITATLT, TRAJECTORIES, TRAJR
		Interpolation	Any	ADEHABITATLT, AMT, TRAJECTORIES
		Douglas-Peucker	Any	TRAJDATAMINING, TRAJECTORIES
		Opening window	Any	TRAJDATAMINING
		Savitzky-Golay	Any	TRAJR
		Transform to pixels to link with remote sensing	Any	RSMOVE
	Metric computation	2nd- or 3rd-order variables	Any	ADEHABITATLT, AMT, BCPA, MOMENTUHMM, MOVE, MOVEHMM, RHR, SEGCLUST2D, TRAJECTORIES, TRAJR, TRIP
			Radio	FEEDR
			Acoustic	VTRACK
Visualization		Animations of tracks	Any	ANIPATHS, MOVEVIS
Track description		Summary metrics	Any	AMT, MOVEMENTANALYSIS, TRAJR, MARCHER
			GPS	TRACKER
Path reconstruction		State-space models	GLS	HMMOCE, KFTRACK, UKFSST/KFSST
			PTT	ARGOSTRACK, BSAM
			Any	CRAWL
		Functional movement model	Any	CTMCMOVE
		Continuous Markov chain in gridded space	Any	CTMM
		Bayesian Brownian bridge model	GPS + DR path	BAYESIANANIMALTRACKER
		Transformation of the space	GPS + DR path	TRACKRECONSTRUCTION
Behavioural pattern identification	Clustering techniques	Expectation-maximization binary clustering	Any	EMBC
		Random forest	Any	M2B
	Segmentation	Gueguen and Lavielle	Any	ADEHABITATLT
		Extension of Lavielle	Any	SEGCLUST2D
		Behavioural change point analysis	Any	BCPA
		Mechanistic range shift analysis	Any	MARCHER
		Net displacement models	Any	MIGRATER
	Hidden Markov-based models	Bayesian state-space model with states	PTT	BSAM
		Hidden Markov models	Any	LSMNSD, MOMENTUHMM, MOVEHMM

(Continues)

TABLE 1 (Continued)

Workflow stage	Categories	Method description	Data type	Package
Space use	Home-range estimation	Minimum convex polygon	Any	ADEHABITATHR, AMT, MOVE, RHR
		Density kernel utilization distribution	Any	ADEHABITATHR, AMT, RHR
		Movement-based utilization distribution	Any	ADEHABITATHR, AMT, BBMM, CTMM, MKDE, MOVE, MOVEMENTANALYSIS, RHR
		Local convex hull	Any	ADEHABITATHR, AMT, RHR, T-LoCoH
	Habitat use	Step selection functions	Any	AMT, HAB
		Generalized linear models	Any	CTMCMOVE
	Non-conventional approaches	(See text)	Radio	FEEDR
			Acoustic	VTRACK
			Any	MOVENT, RECURSE, RSMOVE
Trajectory simulation		Movement models fitted to data	Any	CRAWL, CTMM, MOMENTUHMM, MOVEHMM, SMAM
			PTT	ARGOSTRACK, BSAM
		Movement models with parameters defined by user	Any	ADEHABITATLT, MOVENT, SIMRIV, TRAJR
Other	Interactions	Dyad interaction metrics	Any	WILDLIFEDI
		Distance and time thresholds	Any	MOVEMENTANALYSIS, TRAJDATAMINING
	Movement similarity	Similarity measures between trajectories (e.g. Frechet)	Any	SIMILARITYMEASURES, TRAJECTORIES
	Population size	Stochastic model for abundance	Radio	CARIBOU
	Environment conditions	Likelihood maximization of airspeed model	Any	MOVEWINDSPEED
	Database management	Integrating R and PostgreSQL/PostGIS	Any	RPOSTGISLT
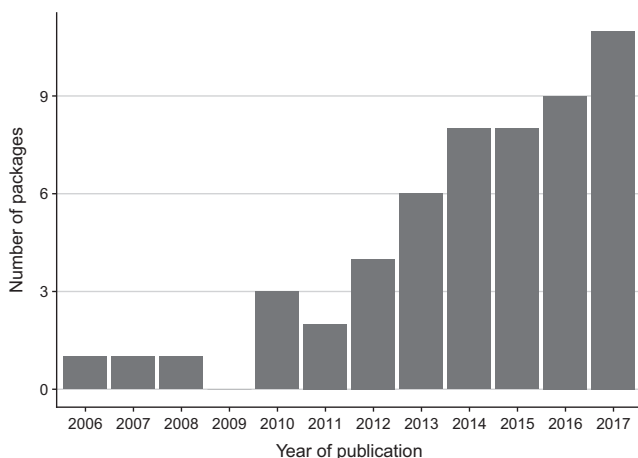
FIGURE 2 Number of packages per year of publication. Since the packages were reviewed between March and August 2018, this last year was incomplete and not included in the graph

(2015, CRAN, active) (Rakhimberdiev & Saveliev, 2019), TRACKIT (2012, GitHub, active) (Nielsen, Sibert, Ancheta, Galuardi, & Lam, 2012a) and TRIPESTIMATION (2007, GitHub, inactive) (Sumner

& Wotherspoon, 2016; Sumner, Wotherspoon, & Hindell, 2009). FLIGHTR was specifically developed for avian movement. In its state-space modelling framework (Patterson, Thomas, Wilcox, Ovaskainen, & Matthiopoulos, 2008), the locations are hidden states and the observation model is a physical model of light-level changes as a function of geographic location and time. A detailed description of the model and the package functions can be found in Rakhimberdiev et al. (2015) and Rakhimberdiev, Saveliev, Piersma, and Karagicheva (2017), respectively. TRACKIT was developed mainly for fish movement and light intensity around sunrise and sunset are used as inputs in a state-space model that includes solar altitude and SST as covariates (Lam, Nielsen, & Sibert, 2010). TRIPESTIMATION was developed for marine organisms. It uses a Bayesian approach modelling light level as a function of sun elevation at each plausible location, prior knowledge of the animal's movement, and complementary environmental information (e.g. SST, depth of the water column) (Sumner et al., 2009). Although TRIPESTIMATION is still available on CRAN, it is indicated in its GitHub repository that the package was deprecated in favour of SGAT (Lisovski et al., 2012; Sumner et al., 2009), which contains functions to

implement both threshold and template-fitting methods (note that the authors of TRIPESTIMATION are also the main authors of SGAT and GEOLIGHT, and that the references to cite the packages are the same). For this reason, we consider both TRIPESTIMATION and SGAT as one. Auxiliary packages also exist to detect the timing of twilight periods from light data from GLS devices (e.g. TWGEOS (Wotherspoon, Sumner, & Lisovski, 2016b) and BASTAG (Wotherspoon, Sumner, & Lisovski, 2016a)). The estimated twilight periods can be later used as inputs in the above-mentioned packages for location estimation.

- *Twilight-free methods.* It is possible to estimate locations without depending on the identification of twilight events. TWILIGHTFREE (2017, GitHub, active) (Bindoff & Wotherspoon, 2019) uses a hidden Markov model (HMM) where the hidden states are the daily geographic locations (the spatial domain is discretized as gridded cells) and the observed variable is the observed pattern of light and dark over the day (Bindoff, Wotherspoon, Guinet, Hindell, & Orme, 2017). SST and land/sea marks can be used as covariates. Parameter estimation is performed using functions from the SGAT package.

3.1.2 | Radio-tagging data pre-processing

Radio-tagging (Kenward, 2000) involves the attachment of a radiotransmitter to an animal. The radio signals transmitted (typically very-high-frequency VHF or ultra-high-frequency UHF) are picked up by an antenna and transformed into a beeping sound by a receiver. As the receiver gets closer to the transmitter, the beeps get louder. Location can then be estimated either by triangulation or with a method called homing, where the researcher moves towards the loudest beeps until the animal has been located. RFID (radio-frequency identification data) tags can also be used to record when an individual passes close to a receiver without the need to search for a signal.

TELEMETR (2012, GitHub, inactive) (Rowlingson, 2012) implements several triangulation methods as well as a maximum-likelihood procedure to estimate locations from bearing data (triangulation information). Since there are no references to the methods in the package documentation, it is aimed at users who are already familiar with the methods.

3.1.3 | Dead-reckoning using accelerometry and magnetometry data

High-frequency (e.g. >10 Hz) triaxial accelerometers measure both static (gravitational) and dynamic body acceleration (DBA). The static component is typically derived using a sliding average over short time windows of a few seconds on each axis (Shepard et al., 2008). The static component enables determining the animal's body posture. The dynamic component is calculated by subtracting the static acceleration from the raw acceleration on each axis and provides a measure of the animal's movement or velocity as a result of body motion. When coupled with time-activity budgets and validated

with empirical measurements of metabolic rate, the overall DBA can be used to estimate the animal's energy expenditure (Wilson et al., 2019). High-frequency triaxial magnetometers measure the geomagnetic field strength in the three axes and provide a measure of 3D orientation for dead-reckoning (e.g. Bidder et al., 2015) and for behavioural identification (Williams et al., 2017).

The combined use of magnetometer and accelerometer data, especially as provided by modern inertial measurement units, which solve the problem of temporal synchronization among different sensors, and optionally gyroscopes and speed sensors, allows to reconstruct sub-second fine-scale movement paths using the dead-reckoning (DR) technique (Bidder et al., 2015; Wilson, Wilson, Link, Mempel, & Adams, 1991). Given an initial known location (e.g. tagging or release location), the DR method uses speed and direction movement parameters derived from accelerometer, magnetometers and sometimes additional sensors, to reconstruct the movement path from one location to the next. Specifically, DBA derived from accelerometers can provide a useful metric of speed for terrestrial individuals (Bidder et al., 2012), though in aerial/aquatic media it may be better to use a speed sensor. Magnetometers – after appropriate calibration and correction for other sources of magnetism (Bidder et al., 2015), and in combination with accelerometers and gyroscopes when available – provide fine-scale measures of heading and direction. However, as DR is based on vectorial calculations, it accumulates errors over time, further compounded in the presence of passive movements caused by currents and drifts. Independent locations, typically collected by a GPS recording at lower frequency than the accelerometers and magnetometers, are required to correct for these errors (Bidder et al., 2015; Liu, Battaile, Trites, & Zidek, 2015); see Section 7 below for further details. Furthermore, the exact mathematical formulas for DR differ in the literature, and most of them do not account for 3D movement (see Benhamou (2018) for a comparison of movement properties in 2D and 3D). A discussion on DR per se is out of the scope of this work, but we advise users to understand the methods behind the packages performing DR before using them. ANIMALTRACK (2013, CRAN, inactive) (Farrell & Fuiman, 2013) and TRACKRECONSTRUCTION (2014, CRAN, inactive) (Battaile, 2014) implement DR to obtain tracks, though use different methods. While TRACKRECONSTRUCTION refers to Wilson et al. (2007) for DR, ANIMALTRACK cites Bowditch (1995).

3.2 | Post-processing

Post-processing of tracking data comprises data cleaning (e.g. identification of outliers or errors), compressing (i.e. reducing data resolution which is sometimes called resampling) and computation of metrics based on tracking data, which are useful for posterior analyses.

3.2.1 | Data cleaning

ARGOSFILTER (2007, CRAN, inactive) (Freitas, 2012) and SDLFILTER (2014, CRAN, active) (Shimada, Jones, Limpus, & Hamann, 2012;

Shimada et al., 2016) implement functions to filter implausible platform terminal transmitter (PTT) locations. Platform terminal (also known as Argos) transmitters send signals to polar-orbital Argos satellites, which geographically locate the source of the data. They preserve battery life by only needing to transmit signals (rather than receiving), leading them to be used for tracking of large-scale migrations, particularly marine mammals and turtles. When the tracked animals are under water, the chances of a satellite receiving PTT signals decrease, so fewer locations can be estimated, and they are likely estimated with fewer satellites, so their accuracy also diminishes. PTTs are particularly useful for individuals that cannot be recaptured, and hence, a device recovered. Along with locations, Argos provides accuracy classes (1, 2, 3, 0, A, B, Z) which are associated with different degrees of spatial error (Costa et al., 2010). ARGOSFILTER's algorithm is described in Freitas, Lydersen, Fedak, and Kovacs (2007). It essentially removes records where a location was not estimated as well as locations that required unrealistic travel speeds. SDLFILTER allows the removal of duplicates, locations estimated with a low number of satellites, biologically unrealistic locations based on speed thresholds or turning angles and locations above high tide lines. The filtering methods are described in Shimada et al. (2012), Shimada et al. (2016), and they are also adapted to GPS data. GPS loggers are perhaps the most widely used type of biologging device. Location information from GPS can be downloaded directly without any post-processing. GPS receivers collect but do not transmit information, and infer their own location based on the location of GPS satellites and the time of transmission. Four or more satellites should be visible to the receiver to obtain an accurate result (<100 m; able to reach 6 m in some cases) (Tomkiewicz, Fuller, Kie, & Bates, 2010), so when less satellites are visible, location accuracy can be reduced.

Other packages with functions for cleaning tracking data are T-LoCoH (2013, R-forge, active) (Lyons, Getz & R Development Core Team, 2018), TRAJDATAMINING (2017, CRAN, active) (Monteiro, 2018) and TRIP (2006, CRAN, active) (Sumner, 2016). They can be used for any tracking data and also contain functions to remove duplicates or records with unrealistically high speeds.

3.2.2 | Data compression

Rediscretization or getting data to equal step lengths can be achieved with ADEHABITATLT (2010, CRAN, active) (Calenge, 2006), TRAJECTORIES (2014, CRAN, active) (Pebesma, Klus, & Moradi, 2018) or TRAJR (2018, CRAN, active) (McLean & Volponi, 2018). Regular time-step interpolation can be performed using ADEHABITATLT, AMT (2016, CRAN, active) (Signer, 2018) or TRAJECTORIES. Other compression methods include Douglas-Peucker (TRAJDATAMINING and TRAJECTORIES), opening window (TRAJDATAMINING) or Savitzky-Golay (TRAJR). For a brief review on compression methods, see Meratnia and de By (2004).

RSMOVE (2017, CRAN, active) (Remelgado, 2018) provides functions to explore and transform tracking data for a posterior linkage with remote sensing data. Location fixes are transformed into pixels and grouped into regions. The spatial or temporal resolution of the tracking data can be changed to match the resolution of the remote sensing data.

3.2.3 | Computation of metrics

Some packages automatically derive second- or third-order movement variables (e.g. distance and angles between consecutive fixes) when transforming the tracking data into the package's data class (most packages define their own data classes; see file in Zenodo, https://doi.org/10.5281/zenodo.3483853). These packages are ADEHABITATLT, MOMENTUHMM (2017, CRAN, active) (McClintock & Michelot, 2018), MOVEHMM (2015, CRAN, active) (Michelot, Langrock, Patterson, & McInerny, 2016), RHR (2014, GitHub, inactive) (Signer, 2016) and TRAJECTORIES. BCPA has a function to compute speeds, step lengths, orientations and other attributes from a track. AMT, MOVE (2012, CRAN, active) (Kranstauber, Smolla, & Scharf, 2018), SEGCLUST2D (2018, CRAN, active) (Patin, Etienne, Lebarbier, & Benhamou, 2018), TRAJR and TRIP also contain functions for computing those metrics, but the user needs to specify which ones they need to compute.

FEEDR (2016, GitHub, active) (LaZerte, 2019) works specifically with RFID data (described in Section 3.3 above). Raw RFID data typically contain an individual line of data for each read event made by each RFID logger. FEEDR contains functions to read raw data from several RFID loggers, and to transform the data of logger detection into movement data for each individual, computing statistics such as the time of arrival and departure from each logger station, and how much time was spent near a station at each visitation.

VTRACK (2015, CRAN, active) (Campbell, Watts, Dwyer, & Franklin, 2012) handles acoustic telemetry data. Acoustic telemetry uses high-frequency sound (between 30 and 300 kHz) to transmit information through water. Tags (transmitters) emit a pulse of sound, which is detected by a hydrophone (or an array of hydrophones) with an acoustic receiver. The distance at which a transmitter can be detected depends on the power and frequency of the tag, and the characteristics of the surrounding environment (e.g. background noise, water turbidity and temperature) (DeCelles & Zemeckis, 2014). VTRACK was created to deal with VEMCO© data, which has a similar structure than RFID; it is composed of transmitter ID, receiver ID, datetime stamps and the location of receiver. Like FEEDR for RFID, VTRACK can compute statistics such as the time of arrival and departure from each receiver, and how much time was spent near a receiver at each visitation.

3.3 | Visualization

In this section, we focus on the packages mainly developed for visualization purposes. Those are ANIPATHS (2017, CRAN, active) (Scharf, 2018) and MOVEVIS (2017, CRAN, active) (Schwalb-Willmann, 2018).

They were both conceived for producing animations of tracks. ANIPATHS relies on the ANIMATION package (Xie, 2013; Xie, Mueller, Yu, & Zhu, 2017). Users can specify time steps and seconds per frame for animation, add a background map (e.g. Google Maps) and an

individual-level covariate (e.g. migrant and stationary), among others. Consecutive fixes are joined via a spline-based interpolation and a confidence interval for the interpolation of the path for animation can be shown.

MOVEVIS is based on a GGPLOT2 (Wickham, 2016) plotting architecture and works with MOVE data class objects. Users can choose between 'true time' which displays the animation respecting the time stamps provided, or 'simple' animations where time is not taken into account and all individuals are displayed together as if their tracks started at time 0. Consecutive fixes are joined via linear interpolation. As in ANIPATHS, users can specify the number of frames per second and personalize the background map. Statistics related to the background layer (e.g. temperature and land cover) can also be shown as animated lines or bar plots. For both packages, animations can be saved in many different formats such as mpeg, mp4 and gif.

3.4 | Track description

AMT, MOVEMENTANALYSIS (2013, GitHub, inactive) (Sijben, 2013) and TRAJR compute summary metrics of tracks, such as total distance covered, straightness index and sinuosity. It should be noted that MOVEMENTANALYSIS depends on ADEHABITAT, which was officially removed from CRAN in 2018, as it was superseded by ADEHABITATLT, ADEHABITATHR (2010, CRAN, active) (Calenge, 2006) and ADEHABITATMA (Calenge, 2006) in 2010.

TRACKER (2015, CRAN, active) (Frick & Kosmidis, 2017) was created to analyse running, cycling and swimming data from GPS-tracking devices for humans. TRACKER computes metrics summarizing movement effort during each track (or workout effort per session). Those metrics include total distance covered, total duration, time spent moving, work-to-rest ratio, averages of speed, pace and heart rate.

3.5 | Path reconstruction

Whether it is for the purposes of correcting for sampling errors, or obtaining finer data resolutions or regular time steps, path reconstruction is a common goal in movement analysis. Here, we mention methods available; however, before choosing a method, users should be aware that every method is constructed under unique movement assumptions (either inherent to the mathematical model or constructed for a particular species or type of data), and users should refer to the literature on the methods first. Packages available for path reconstruction are HMMOCE (2017, CRAN, active) (Braun, Galuardi, Thorrold, & Parrini, 2017), KFTRACK (2011, GitHub, active) (Sibert, Nielsen, Ancheta, Galuardi, & Lam, 2012), UKFSST/KFSST (2012, GitHub, active) (Nielsen, Sibert, Ancheta, Galuardi, & Lam, 2012b), ARGOSTRACK (2014, GitHub, active) (Albertsen, 2018; Albertsen, Whoriskey, Yurkowski, Nielsen, & Flemming, 2015), BSAM (2016, CRAN, active) (Jonsen, 2016; Jonsen, Flemming, & Myers, 2005), BAYESIANANIMALTRACKER (2014, CRAN, inactive) (Liu, 2014), TRACKRECONSTRUCTION, CRAWL (2008, CRAN, active) (Johnson & London, 2018; Johnson, London, Lea, & Durban, 2008),

CTMCMOVE (2015, CRAN, active) (Hanks, 2018) and CTMM (2015, CRAN, active) (Fleming & Calabrese, 2019). While the first three focus on GLS data, BSAM is intended for PTT data, BAYESIANANIMALTRACKER and TRACKRECONSTRUCTION combine GPS data and DR, and the last three could be used with any tracking data.

3.5.1 | Improving location estimation from GLS data

KFTRACK, KFSST and UKFSST were developed by the same team of TRACKIT, described in Section 3.1 above. As TRACKIT, they are mainly focused on fish movement. KFTRACK, UKFSST and KFSST use already estimated positions, either by the threshold method or given by the provider, and improve those estimations using a 2-dimensional random walk model (Sibert, Musyl, & Brill, 2003). Because of the generality of this modelling framework, KFTRACK could actually be used for any tracking data. In addition to the random walk model, KFSST includes SST as a covariate in the model (Nielsen, Bigelow, Musyl, & Sibert, 2006), but it has been superseded by UKFSST, which implements an optimized parameter estimation. For that reason, we consider KFSST and UKFSST as one package.

HMMOCE, also adapted to fish movement and working with already estimated/provided locations, uses HMMs (like TWILIGHTFREE) and incorporates depth-temperature profiles and SST as covariates in the observed model (Braun et al., 2017).

3.5.2 | Improving location estimation from PTT data

BSAM estimates locations by fitting Bayesian state-space models to the data. They offer the possibility of accounting for different movement patterns using 'switching models' or HMMs; if this is opted out, first-difference correlated random walk models (DCRWs) are used. It is possible to estimate some of the model parameters for each individual and others at the population level (see Jonsen et al. (2013); Jonsen (2016) for more details). The ARGOSTRACK package fits several types of movement models to PTT data (Albertsen et al., 2015), such as correlated random walks (CRWs) in discrete and continuous versions, and Ornstein-Uhlenbeck (OU) models, using Laplace approximation via Template Model Builder.

3.5.3 | Combining dead-reckoning and GPS data

Dead-reckoning is based on vectorial calculations; thus, even small errors in speed and/or direction accumulate over time. This can be further compounded in the presence of passive movements caused by currents and drifts. Independent locations, typically collected by a GPS recording at lower frequency than the accelerometers and magnetometers, are required to correct for these errors. TRACKRECONSTRUCTION provides a function that, after computing DR, forces the estimated locations to go through the known GPS points via space transformation, which returns a path with good shape but with biased length and orientation. BAYESIANANIMALTRACKER does not assume GPS to give the 'true locations'. Instead, it implements a Bayesian approach to correct for biases, assuming a Brownian bridge

prior and using GPS points and an already estimated DR path to obtain a posterior of the sequence of locations. The posterior mean can be used as an estimate of the track, and the posterior standard error provides a measure of uncertainty about the estimated path (Liu, Zidek, Trites, & Battaile, 2016).

In Bidder et al. (2015), the speed component is expressed as a linear equation, where the values of the coefficients are corrected iteratively until the dead-reckoned paths and ground-truth positions (e.g. GPS data) match. They also propose computing a correction factor for the heading vector. This method allows for correcting within the DR procedure, but has not been implemented in any R package so far.

3.5.4 | Modelling movement of general tracking data

CRAWL reconstructs paths by fitting continuous-time CRW models (called CTCRWs) (Johnson et al., 2008) to tracking data. Though it can be used for any tracking data, CRAWL can account for the accuracy classes of PTT data to model the error associated with locations. CTMCMOVE fits a functional movement model (Buderman, Hooten, Ivan, & Shenk, 2016) to the data and a set of probable true paths can be generated. CTMM fits several continuous movement models such as Brownian motion and OU-based models, selects the best models via AIC and allows for prediction (thus path reconstruction) with the selected model.

3.6 | Behavioural pattern identification

Another common goal in movement ecology is to get a proxy of the individual's behaviour through the observed movement patterns, based on either the locations themselves or second-/third-order variables such as distance, speed or turning angles. Covariates, mainly related to the environment, are frequently used for behavioural pattern identification.

We classify the methods in this section as follows: (a) non-sequential classification or clustering techniques, where each fix in the track is classified as a given type of behaviour, independently of the classification of the preceding or following fixes (i.e. independently of the temporal sequence); (b) segmentation methods, which identify change in behaviour in time series of movement patterns to cut them into several segments; and (c) hidden Markov models, centred upon a hidden state Markovian process (representing the sequence of non-observed behaviours) that conditions the observed movement patterns (Langrock et al., 2012).

3.6.1 | Non-sequential classification or clustering techniques

EMBC (2015, CRAN, active) (Garriga, Palmer, Oltra, & Bartumeus, 2018) implements the expectation-maximization binary clustering method (Garriga, Palmer, Oltra, & Bartumeus, 2016). M2B (2017, CRAN, inactive) (Dubroca & Thiebault, 2017) implements a random

forest (a wrapper for the RANDOMFOREST (Liaw & Wiener, 2002) package functions) to classify behaviours using a supervised training dataset; thus, a dataset of both tracking data and known behaviours is needed to train the model.

3.6.2 | Segmentation methods

ADEHABITATLT, BCPA (2013, CRAN, inactive) (Gurarie, 2014), SEGCLUST2D, MARCHER (2017, CRAN, active) (Gurarie & Cheraghi, 2017) and MIGRATER (2016, GitHub, active) (Spitz, 2018) implement segmentation methods. ADEHABITATLT presents two of these methods: Guéguen (2001) and Lavielle (1999, 2005). BCPA implements the behavioural change point analysis (Gurarie, Andrews, & Laidre, 2009). SEGCLUST2D implements a bivariate extension of Lavielle and is also described as an extension of Picard, Robin, Lebarbier, and Daudin (2007) by its authors, but there was no documentation on the method by the time of the review. Both MARCHER and MIGRATER are suited for the analysis of migratory behaviour. MARCHER enables the mechanistic range shift analysis method (Gurarie et al., 2017) that identifies changes in locations of focal ranges, so migration and resident behaviours can be distinguished. The ranging models available in the package can take into account autocorrelation in location and in velocity. MIGRATER uses net displacement models to identify migratory, residency and nomadic behaviour (Spitz, Hebblewhite, & Stephenson, 2017). The models can incorporate factors such as elevation, sensitivity to starting date in the series and minimum time out of residence zone, among other features.

3.6.3 | Hidden Markov models

In this category, we consider standard HMMs as well as more complex versions of these models, for example adding hierarchical structures, a second observation process for locations (state-space modelling), covariates affecting different components in the model, autoregressive processes or a spatial covariance structure. BSAM, LSMNSD (2016, GitHub, active) (Bastille-Rousseau, 2019a), MOVEHMM and MOMENTUHMM implement methods that fall in the HMM category. BSAM, for PTT data, implements Bayesian state-space models as described in Section 7 above and may incorporate a layer of two switching states into the model: one state representing directed fast movement and the other representing relatively undirected slow movement (Jonsen et al., 2013). LSMNSD uses an HMM approach where the observed variable is net-squared displacement and its mixture model distribution is conditioned on three hidden states that would correspond to two encamped and one exploratory mode (Bastille-Rousseau et al., 2016); the time spent in each mode and the transition probabilities are used to classify the track as migration, dispersal, nomadic or sedentary.

MOVEHMM and MOMENTUHMM are not restricted to two or three states. MOVEHMM implements HMMs incorporating covariates and allowing for state sequence reconstruction, for example sequences of the behavioural proxies, via the Viterbi algorithm. In MOVEHMM, the variables modelled in the observed process are

step length and turning angles, or two variables that statistically behave as step length and turning angles. ᴍᴏᴍᴇɴᴛᴜHMM implements generalized hidden Markov models (McClintock et al., 2012) with great flexibility for the choice of observed variables and their probability distributions, and covariate incorporation in the models. Since HMMs require regular time steps, ᴍᴏᴍᴇɴᴛᴜHMM offers a multiple imputation method (McClintock, 2017): it fits a CTCRW (from ᴄʀᴀᴡʟ) to the data obtaining regular time-step realizations and then fits an HMM to those realizations; all of this is done multiple times. Even if the data classes and model formulation in the package differ from ᴍᴏᴠᴇHMM, many of the HMM-related functions are based on ᴍᴏᴠᴇHMM. ᴍᴏᴠᴇHMM is more user-friendly than ᴍᴏᴍᴇɴᴛᴜHMM, but ᴍᴏᴍᴇɴᴛᴜHMM offers greater modelling possibilities.

3.7 | Space and habitat use characterization

Multiple packages implement functions to help answer questions related to where animals spend their time and what role environmental conditions play in movement or space use decisions, which are typically split into two categories: home-range calculation and habitat selection.

3.7.1 | Home range

Several packages allow the estimation of home ranges: ᴀᴅᴇʜᴀʙɪᴛᴀᴛHR, ᴀᴍᴛ, ʙʙᴍᴍ (2010, CRAN, inactive) (Nielson, Sawyer, & McDonald, 2013), ᴄᴛᴍᴍ, ᴍᴋᴅᴇ (2014, CRAN, inactive) (Tracey, Sheppard, Zhu, Sinkovts, et al., 2014), ᴍᴏᴠᴇᴍᴇɴᴛAnalysis, ᴍᴏᴠᴇ, ʀʜʀ and T-LoCoH. They provide a variety of methods, from simple minimum convex polygons (MCP) (Mohr, 1947) to more complex probabilistic utilization distributions (UD) (Van Winkle, 1975), potentially accounting for the temporal autocorrelation in tracking data, as detailed below.

- ᴀᴅᴇʜᴀʙɪᴛᴀᴛHR contains a comprehensive list of methods to estimate home ranges: convex hull methods such as MCP, clustering techniques, local convex hulls (LoCoH) (Getz et al., 2007) and the characteristic hull method Downs and Horner (2009); UD methods such as kernel home ranges, also with the modification from Benhamou and Cornélis (2010) to account for boundaries, and methods to account for temporal autocorrelation between locations (Brownian bridge kernel method) (Bullard, 1991); biased random bridge kernel method also known as movement-based kernel estimation (Benhamou, 2011; Benhamou & Cornélis, 2010); and product-kernel algorithm, Horne, Garton, Krone, and Lewis (2007).
- ᴀᴍᴛ also allows the estimation of home ranges using three common approaches not based on movement (MCP, LoCoh and kernel UD), as well as movement-based UDs from fitted step selection functions (SSFs, Fortin et al., 2005, see below).
- ʀʜʀ (Signer & Balkenhol, 2015) provides a graphical user interface to estimate home ranges using several non-movement-based methods, such as parametric home ranges, MCP, kernel UD or

local convex hulls, as well as the Brownian bridge kernel method (as a wrapper to the ᴀᴅᴇʜᴀʙɪᴛᴀᴛHR function). Complementary analyses include time to statistical independence, site fidelity test (against random permutation of step lengths and angles), among others.

- T-LoCoH is focused on constructing home-range hulls (Lyons, Turner, & Getz, 2013). A time-scale distance metric and a set of different nearest-neighbour criteria are available to choose which points to consider in a same hull. Hull metrics for space use, such as number of revisitations (repeated visits of an individual to the same hull) and their durations, are also computed. Although the package was originally implemented for GPS data, it can be used for tracking data in general.
- ʙʙᴍᴍ, ᴍᴏᴠᴇᴍᴇɴᴛAnalysis and ᴍᴋᴅᴇ use Brownian bridge movement models to obtain UDs. ᴍᴋᴅᴇ allows for a 3D extension of the Brownian bridges (Tracey, Sheppard, Zhu, Wei, et al., 2014).
- ᴍᴏᴠᴇ, in turn, calculates UDs of tracking data via dynamic Brownian bridge modelling (Kranstauber, Kays, Lapoint, Wikelski, & Safi, 2012) or uses MCP for home-range estimation; for the latter, it imports functions from ᴀᴅᴇʜᴀʙɪᴛᴀᴛHR.
- ᴄᴛᴍᴍ fits several candidate continuous-time movement models via a variogram regression approach (Fleming et al., 2014), which can account for spatial autocorrelation in locations and periodicity in space use (Péron, Fleming, Paula, & Calabrese, 2016). UDs are computed via an autocorrelated kernel estimator, where the autocorrelation term comes from the movement model previously fitted (Fleming et al., 2015).

3.7.2 | Habitat use

The role of habitat features on animal space use, or habitat selection, can be investigated with any of the following four packages.

- ʜᴀʙ (2015, GitHub, inactive) (Basille, 2015) enhances several utility functions of ᴀᴅᴇʜᴀʙɪᴛᴀᴛHS (Calenge, 2006), ᴀᴅᴇʜᴀʙɪᴛᴀᴛHR and ᴀᴅᴇʜᴀʙɪᴛᴀᴛLT, and provides core functions to prepare, fit and evaluate SSFs while relying on ᴀᴅᴇʜᴀʙɪᴛᴀᴛLT classes to handle trajectories. SSFs essentially investigate habitat selection along the trajectory, by comparing habitat features at observed step locations with those at alternative random steps taken from the same starting point (Thurfjell, Ciuti, & Boyce, 2014).
- ᴀᴍᴛ contains functions and wrappers to streamline the process of fitting SSFs from pairs of coordinates defining locations, to the conditional logistic regression model. It also allows fitting of integrated step selection functions (iSSFs), in which both movement behaviour and resource selection are modelled, and the role of environmental variables on each of these processes is investigated (Avgar, Potts, Lewis, & Boyce, 2016).
- In ᴄᴛᴍᴄᴍᴏᴠᴇ, the role of habitat features is investigated through a generalized linear model framework, for which these features are rasterized, and the animal track is first imputed via functional movement modelling and then discretized in a gridded space (more details in Hanks, Hooten, and Alldredge (2015)).

3.7.3 | Non-conventional approaches for space use

Other non-conventional approaches for investigating space use from tracking data can be found in MOVENT (2017, GitHub, active) (Bastille-Rousseau, 2019b), RECURSE (2017, CRAN, active) (Bracis, Bildstein, & Mueller, 2018), RSMOVE, FEEDR and VTRACK.

- MOVENT tackles space use analysis via network graph theory (Bastille-Rousseau, Douglas-Hamilton, Blake, Northrup, & Wittemyer, 2018). The procedure could be summarized as follows: (a) tracking data are represented over a gridded map and the number of transitions between pixels is counted; (b) the adjacency matrix, that is the counts of transitions, is then used to compute some network metrics at the pixel level; and (c) a Gaussian mixture model is fitted to one of the metrics (user choice) to cluster values in two groups potentially representing patches and inter-patch movement.

- RSMOVE implements a procedure to identify feeding sites from tracking data as a function of environmental variables (remote sensing data). It uses a random forest classification model from the CARET package (Kuhn, 2018); however, there is no information about how to fix the parameters of the model, so users should go through the documentation of CARET to understand and calibrate the model. An application of the method can be found in Remelgado et al. (2017), but the parametrization is not described in the manuscript.

- RECURSE aims at computing number of revisitations to predefined areas and their duration. These areas can be defined by the user by entering their centre of gravity (by default, the fixes in the track) and a radius. The vignette gives important criteria to use the functions and interpret the results, though there are no citations of scientific publications. FEEDR and VTRACK, for radio and acoustic telemetry data, respectively, provide statistics on animal visits to given logger stations/receivers.

3.8 | Trajectory simulation

Simulating trajectories can be useful to test hypotheses concerning movement, by comparing the patterns of simulated movement from several alternative theoretical models, or the patterns in the simulated movement to those of real observed tracks. In addition, simulation allows the quantification of estimator uncertainty by parametric bootstrapping (e.g. Michelot et al. (2016)). As with other types of data analysis, simulations highly depend on the model used by the researcher. The tracking packages implement trajectory simulation mainly based on hidden Markov models, correlated random walks, Brownian motions, Lévy walks or Ornstein-Uhlenbeck processes.

Packages that allow simulation of trajectories from movement models fitted to tracking data (i.e. parameters are estimated by the models) are MOVEHMM, MOMENTUHMM (HMMs), BSAM (DCRWs), CRAWL (CTCRWs), ARGOSTRACK (discrete and continuous CRWs, and OU processes) and CTMM (several continuous-time movement

models). These packages have been described in previous sections, and the simulations are presented as additional features after model fitting in their documentation. Another package for model fitting and simulation is SMAM (2013, CRAN, inactive) (Pozdnyakov, Elbroch, Hu, Meyer, & Yan, 2018; Pozdnyakov, Elbroch, Labarga, Meyer, & Yan, 2019; Pozdnyakov, Meyer, Wang, & Yan, 2014; Yan et al., 2014; Yan, Pozdnyakov, & Hu, 2018). It can fit and simulate two types of movement models: Brownian motions with measurement error (Pozdnyakov et al., 2014) and moving-resting processes with Brownian motion for the moving stage (Yan et al., 2014).

Other packages implement simulation functions when there is no previous model fitting to tracking data (i.e. movement parameters are known or simulations concern hypothetical mobile organisms). ADEHABITATLT proposes trajectory simulation using Brownian motion-based models, Lévy walks, CRWs and bivariate OU motion. TRAJR allows for CRWs, directed random walks (direction is equal to a constant plus a small noise), Brownian motion and Lévy walks. MOVENT enables simulation of movement within and between patches. Movement within patches can follow an OU process (wrapping functions from ADEHABITATLT) or a two-states movement model (wrapping functions from MOVEHMM). Movement between patches is simulated via a Brownian bridge movement model (from ADEHABITATLT).

SIMRIV (2016, CRAN, active) (Quaglietta & Porto, 2018) is another package created for simulation, and it can take into account environmental constraints. It allows simulating random walks, correlated random walks, multistate movement and constraining the area by an environmental resistance variable – defined by the user – that conditions the direction of the movement. The available documentation gives a detailed explanation of the simulation process.

3.9 | Other analyses of tracking data

3.9.1 | Interactions

Interactions between individuals can be assessed using metrics from WILDLIFEDI (2014, CRAN, active) (Long, 2014), which quantifies the dynamic interaction between two tracks of distinct individuals through several metrics (see Long, Nelson, Webb, and Gee (2014) for details). The package relies on 'Itraj' objects (ADEHABITATLT data class for trajectories). Other packages that include functions investigating interaction are TRAJDATAMINING and MOVEMENTANALYSIS: TRAJDATAMINING can identify potential partners based on distance and time thresholds fixed by the user and MOVEMENTANALYSIS computes the expected duration of encounters at each location for every pair of IDs, based on a Brownian bridge movement model fitted to the tracking data.

3.9.2 | Movement similarity

SIMILARITYMEASURES (2015, CRAN, inactive) (Toohey, 2015) assesses similarity between trajectories using metrics such as the longest common subsequence (LCSS), Fréchet distance, edit distance and

dynamic time warping (DTW). Magdy, Sakr, Mostafa, and El-Bahnasy (2015) provides a brief review on trajectory similarity measures. TRAJECTORIES also computes the Fréchet distance for two trajectories.

3.9.3 | Population size

CARIBOU (2011, CRAN, inactive) (Crepeau, Rivest, Couturier, & Baillargeon, 2012) was specifically created to estimate population size from Caribou tracking data, but can also be used for wildlife populations with similar home-range behaviour. The methods implemented here are described in Rivest, Couturier, and Crépeau (1998). The user needs to specify parameters concerning the size of each detected group, the number of collars in each of these groups and the detection model to use.

3.9.4 | Inferring environmental conditions

Using tracking data to infer an environmental variable is the objective of MOVEWINDSPEED (2016, CRAN, active) (Kranstauber & Weinzierl, 2019).. It uses avian tracking data to estimate wind speed via a maximum-likelihood approach (Weinzierl et al., 2016). The estimation is only performed for segments where the bird is circling in a thermal, so a function in the package identifies those segments. Speed is modelled as a mean with an autocorrelated drift.

3.9.5 | Database management

Finally, RPOSTGISLT (2016, CRAN, active) (Dukai, Basille, & Bucklin, 2016) handles database management for trajectory data by integrating R and the 'PostgreSQL/PostGIS' database system. The package relies on ADEHABITATLT, and allows users to seamlessly transfer 'ltraj' objects from R to the database, and vice versa, using the corresponding 'pgtraj' data structure in the database.

3.10 | Analysis of biologging but not tracking data

Time-depth recorders (TDRs) collect data on depth, velocity and other parameters as animals move through the water. These biologging data by themselves do not allow obtaining tracking data (*x*, *y*, *t*) and thus comparable analyses to the ones presented above; however, we briefly describe the R packages that could be used to analyse TDR and accelerometer data. DIVEMOVE (Luque, 2007) and RBL, the latter also for accelerometer data, are the two packages implementing TDR data analysis. DIVEMOVE contains functions to identify wet and dry periods in the series, calibrate depth and speed sensor readings, identify individual dives and their phases, summarize statistics per dive and plot the data. With RBL, accelerometry data are used for identifying prey catch attempts (Viviant, Trites, Rosen, Monestiez, & Guinet, 2010) and swimming effort from frequency and magnitude of tail movement (Bras, Jouma'a, Picard, & Guinet, 2016). Other functions allow the extraction of summary statistics from dives (e.g. maximum depth), fitting broken stick models (i.e. piecewise linear regression) to dive series and identifying dive phases.

Accelerometry data are also used in human studies, primarily to assess levels of physical activity. Six R packages focus on the analysis of human accelerometry data, mainly to describe periodicity and levels of activity. ACCELEROMETRY (Van Domelen, 2018), GGIR (van Hees et al., 2014, 2015, 2019) and PhysicalActivity (Choi, Beck, Liu, Matthews, & Buchowski, 2018) identify wear and non-wear time of the accelerometers. NPARACT computes descriptive statistics such as interdaily stability, intradaily variability and relative amplitude of activity (Blume, Santhi, & Schabus, 2016). ACC (Song & Cox, 2016), GGIR and PAWACC (Geraci, 2017; Geraci et al., 2012) classify wear data into different levels of activity (e.g. sedentary, moderate and vigorous) using thresholds given by the user and offer some functions for visual representation of the data and descriptive statistics on the types of activities. Additionally, ACC allows for activity simulation via Hidden Markov modelling.

4 | PACKAGE DOCUMENTATION

Documentation in the form of manuals, vignettes (long-form documentation), tutorials or published articles is key to guide the use of a package's features, especially if the package contains a large number of functions and tools. Without proper user testing and peer editing, package documentation can lead to large gaps of understanding and limited usefulness of the package. If functions and workflows are not explicitly defined, a package's capacity to help users is undermined. Vignettes can act as road maps for the user, and published articles pertaining to the package help provide context and guidance on the internal workings of functions. Moreover, since packages make specific methods available for R users, the documentation should not only explain how to use the packages but also describe or provide references for the methods.

To assess package documentation, an online survey was conducted between August and October 2018. The survey got Institutional Review Board exemption (IRB201802319). Questions in the survey regarded helpfulness of package documentation and the frequency of package use; it was completed by 225 people. The exact formulation of each question in the survey, detailed results and a discussion on the representativity of the survey are accessible in https://doi.org/10.5281/zenodo.3483853.

Among 26 packages with at least 10 respondents, we identified 10 packages as having 'adequate documentation', meaning that more than 75% of the respondents expressed that the documentation was either good (allowing the user to do everything they wanted and needed to do with the package) or excellent (allowing users to do even more than what they initially planned because of the excellent quality of the information). These are as follows: MOMENTUHMM (93.8%), MOVEHMM (89.5%), ADEHABITATLT (88.6%), ADEHABITATHR (83.2%), EMBC (81.8%), WILDLIFEDI (81.3%), CTMM (80.0%), GeoLight (77.8%), MOVE (76.6%) and RECURSE (76.5%) (see Figure 3). From this group of packages, MOVE offers manuals and vignettes, while all the others offer in addition scientific articles centred on the package.
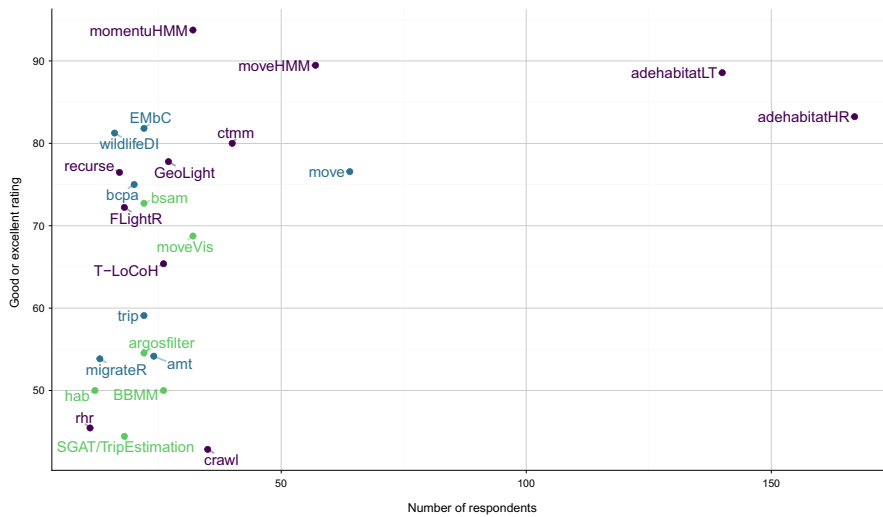
FIGURE 3 Packages with good and excellent documentation (survey results). Text colour in green corresponds to packages with standard documentation only, blue is for packages with vignettes, and purple is for packages that also have peer-reviewed articles published. Only results for packages with at least 10 respondents are shown

The results of this survey should be used by package developers as guidance to decide on whether to improve the documentation of their packages so more researchers can use them.

5 | LINKS BETWEEN THE PACKAGES

We analysed the links between tracking packages. If a package needs functions that have already been created by another package, the developer(s) can use those functions by declaring this dependency in the description file of the package under 'Depends on', 'Imports' or 'Linking to' categories. Theoretically, there are some differences between the three, but in practice developers mix those groups, so we consider them as part of the same concept: dependency. A package can also suggest using other packages; for instance, a package focused on data analysis can recommend, in the case data have to be cleaned first, the use of a package that allows post-processing.

Developers usually define their own data classes for their packages. A data class allows them to predefine the minimum requirements that data should have (e.g. dimensions and variables) and guarantee that the functions in the package will work if the data are in the predefined format. Similarly, if a package uses functions from other packages or the developer wants to facilitate the use of other packages along with their own, the latter should also provide coercion methods, that is functions that allow compatibility with data classes from these other packages.

The dependency and suggestion information (collected in August 2018) was used for a graph analysis of package links (Figure 4). Thirty-nine packages in total showed some level of connections among them (30 in the form of one large group and three other small groups), while 19 (32%) of the packages worked in isolation. ADEHABITATLT and MOVE were the most suggested/depended on packages with 14 and 8 links to them, respectively (8 and 2, respectively, were dependencies). Indeed, many packages use functions compatible with the 'ltraj' data class from ADEHABITATLT and some others with the 'move' class from MOVE. AMT suggests more

packages than any other (6), and it provides coercion methods for data classes from the packages it suggests.

6 | DISCUSSION

As the quantity and diversity of biologging data increase, so does the need for suitable statistical techniques and software resources. These tools are essential to convert collected data into ecologically meaningful measures and analyse outputs to test hypotheses. Through a systematic search, we identified 58 R packages aimed at processing or analysing tracking data. The packages offer tools for data processing, visualization, computation of statistics for track description, path reconstruction, behavioural pattern identification, space use characterization and trajectory simulation. All the stages of the movement-ecology workflow are covered by the reviewed packages. In some cases, there is even function overlapping, with more than one package implementing the same type of analysis with the same or very similar approaches (e.g. ANIMALTRACK and TRACKRECONSTRUCTION for DR, BBMM, MOVEMENTANALYSIS and MKDE for Brownian bridge movement models). A type of analysis that was poorly covered was collective motion: mainly WILDLIFEDI and, to a lesser degree, TRAJDATAMINING and MOVEMENTANALYSIS allow computing descriptive metrics on encounters between individuals, periods of proximity or other metrics of interaction. The lack of R functions to analyse collective movement beyond descriptive statistics is most likely a reflection of the early stages of this field regarding the use of tracking data; collective behaviour has mostly relied on controlled laboratory-based studies and theoretical models (Westley, Berdahl, Torney, & Biro, 2018). Overall, the review not only highlighted the abundance of analytical tools available, but also identified a need to improve visibility and accessibility (i.e. documentation) to existing packages more than developing new packages.

6.1 | Integration over proliferation

Transparency in science is facilitated by the sharing of data and analytical tools, including code. This has resulted in a general tendency
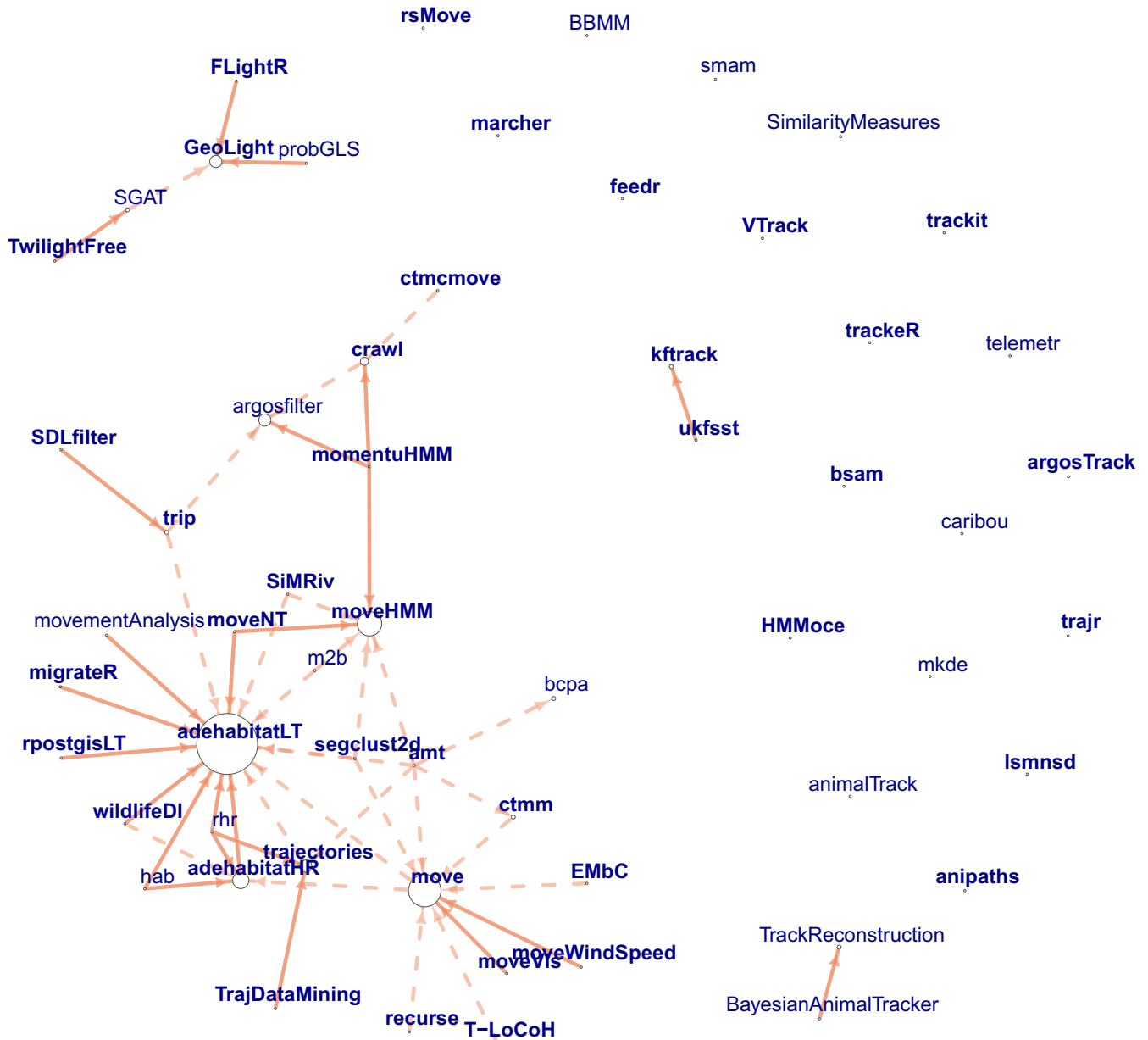
FIGURE 4 Network representation of the dependency and suggestion between tracking packages. The arrows go towards the package the others suggest (dashed arrows) or depend on (solid arrows). Bold font corresponds to active packages. The size of the circle is proportional to the number of packages that suggest or depend on this one

in the scientific community to convert functions into publicly available packages. In movement ecology, this has translated into a proliferation of R packages dealing with tracking data, many of them, isolated from all other packages (Figure 4) despite having similar goals and methods. While a large number of packages reflect that the field is active and that codes for several types of analyses are available for the community, such independent proliferation of packages makes it hard to maintain an overview of their functionality and availability. Here, we presented a list of 58 packages, but the number is expected to keep increasing steadily associated with an increased possibility of unnecessary redundancy and disconnection between the packages. Due to the already overwhelming number of tracking packages, we suggest developers only create new packages in the

future when they represent a new and complementary contribution to the scientific and programming community.

While package necessity is not assessed through any repository, there is a peer-review process available for packages through rOpenSci, a non-profit initiative founded in 2011 with the goal of making scientific data more retrievable and reproducible (http://ropensci. org). Packages submitted to rOpenSci are reviewed by two independent reviewers for readability, usability, usefulness and redundancy. The rOpenSci community checks that developers adhere to coding 'best practices' such as unit testing (i.e. testing whether individual units of code work correctly), continuous integration (i.e. all changes made by developers are immediately tested and reported when added to the mainline code base), minimizing code duplication and

strong documentation. This open review process improves packages as it helps developers strengthen their package and coding, while gaining additional technical support from rOpenSci's volunteer staff. In addition, a couple of journals have partnered with rOpenSci: the Journal of Open Source Software (JOSS, https://joss.theoj.org) and Methods in Ecology and Evolution (MEE, methodsinecologyandevolution.org). JOSS is an open-access journal for research software packages that adheres to similar standards as rOpenSci, and if the submitted package has already been accepted to rOpenSci, they can be submitted for fast-track publication at JOSS, in which JOSS editors may evaluate based on rOpenSci's reviews alone. MEE can publish articles on new R packages and gives authors the option of a joint rOpenSci-MEE review in which the package is reviewed by rOpenSci, followed by fast-tracked review of the manuscript by MEE. The R Journal (https://journal.r-project.org/) and, for packages concerning statistical analysis, the Journal of Statistical Software (https://besjournals.onlinelibrary.wiley.com/journal/2041210x) are other choices of journal that adhere to similar standards as rOpenSci.

6.2 | Recommendations

This work is not intended to tell ecologists exactly which packages to use, but to provide them an exhaustive catalog of tracking packages, a description of their functions, and show the similarities and differences between them. We suggest researchers use packages with good documentation that are actively maintained and that have a large number of users. Good documentation facilitates the initial use of a package. A regularly maintained package means that there is a person or team behind it and that, when an error arises in the package, it will likely be fixed rapidly and a new version will be available. A package that has a large number of users means greater opportunity to (a) identify bugs in the package, calling the attention of the maintainer for a rapid fix, and thus improving functionality, and to (b) obtain additional guidance on package use from other users. Regarding the methods available in the packages, while we previously stated the importance of describing them and citing references, it is the responsibility of the researchers to select and apply a method if they correctly understand it, and not only because it is available in a package. Also, with a critical use of packages, researchers should feel encouraged to report bugs when they see them, to contribute to their improvement.

When developers are working on new packages, we recommend they submit to rOpenSci and consider the following criteria:

- Contribution: Does your package fill a gap or need? Does a function within the package perform a novel task that does not already exist in another published package? Can those functions be instead added to an existing package? Developers should contemplate the possibility (and appropriateness) of contacting authors of existing and actively maintained packages to incorporate new functions. We also suggest the authors of existing packages to be open to integration of new functions (and new collaborators) within their package.

- Data class coercion: Does the package handle commonly used data classes (e.g. spatial classes from sp or 'ltraj' from ADEHABITATLT), so that it is compatible with the use of other packages? Since tracking packages deal with spatial data, most of them use georeferenced data classes. SP data classes (Bivand, Pebesma, & Gomez-Rubio, 2013; Pebesma & Bivand, 2005) are the most popular spatial data classes (40 out of the 58 packages use them). The recent SF package (Pebesma, 2018) aims at providing a simpler and standard implementation of geographic objects in R; handling SF objects is as easy as handling non-spatial objects in R, and computationally more efficient than using SP. Only one package (CRAWL) was compatible with SF at the time our research was done. Because of its functionalities, we encourage developers to provide coercion methods to SF. Regarding data classes for trajectories, ltraj (from ADEHABITATLT) is one of the oldest and most used data classes, but others exist (e.g. trip from TRIP or track from TRAJECTORIES). Ideally, the community of tracking-package developers should unite to discuss the best data class for a trajectory, and, once a consensus is reached, provide coercion methods to that class.

- Documentation: Is the documentation clear, exhaustive on the functions, with method description or references available? The latter is even more important if the package implements a new method of analysis. Worked examples and vignettes can enable researchers to navigate through the package and learn what it does more easily, minimizing the need for additional support.

- Maintenance: Who will maintain the package over time? Specific people are required to maintain the continuity of packages. Typically, laboratory PIs or members of a working group/collaboration could take this role in view of the long-term commitment. On CRAN, non-maintained packages are considered 'orphaned' if they are not actively maintained and 'archived' if they do not pass 'R CMD check' anymore (https://cran.r-project.org/src/contrib/Orphaned/README).

7 | CONCLUSIONS

This review has served as a road map of the tools implemented by the packages for data analysis in movement ecology. In recent years, programmers have responded to the need for advanced statistical tools to analyse movement data by developing at least 58 R tracking packages. However, we emphasize that increased accessibility and understanding of existing packages (in which documentation plays a fundamental role), and more integration for package development will help the advancement of research in this field, allowing researchers to continue to address novel and exciting questions.

AUTHORS' CONTRIBUTIONS

R.J. conceived the ideas of the review and reviewed the R packages. R.J. and M.B. worked on the workflow for the manuscript. R.J. and M.E.B. gathered the information on the packages. R.J. led the survey and analysed the results; M.E.B. and M.B. implemented it in an online platform. R.J., M.E.B. and M.B. worked in the Zenodo repository. R.J. led the writing of the manuscript. All authors contributed critically to the drafts and responses to the reviewers and gave final approval for publication.

DATA AVAILABILITY STATEMENT

The data collected on all the packages and used for the review and the anonymous data from the survey, as well as R codes and additional files to reproduce Figures 2–4 are available on Zenodo: https://doi.org/10.5281/zenodo.3483853. (Joo et al., 2019).

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