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The concept of animals' trajectories from a data analysis perspective

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ABSTRACT

The Global Positioning System (GPS) has been increasingly used during the past decade to monitor the movements of free-ranging animals. This technology allows to automatically relocate fitted animals, which often results into a high-frequency sampling of their trajectory during the study period. However, depending on the objective of trajectory analysis, this study may quickly become difficult, due to the lack of well designed computer programs. For example, the trajectory may be built by several "parts" corresponding to different behaviours of the animal, and the aim of the analysis could be to identify the different parts, and thereby the different activities, based on the properties of the trajectory. This complex task needs to be performed into a flexible computing environment, to facilitate exploratory analysis of its properties. In this paper, we present a new class of object of the R software, the class "ltraj" included in the package adehabitat, allowing the analysis of animals' trajectories. We developed this class of data after an extensive review of the literature on the analysis of animal movements. This class of data facilitates the computation of descriptive parameters of the trajectory (such as the relative angles between successive moves, distance between successive relocations, etc.), graphical exploration of these parameters, as well a numerous tests and analyses developed in the literature (first passage time, trajectory partitioning, etc.). Finally, this package also contains numerous examples of animal trajectories, and a working example illustrating the use of the package.

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1. Introduction

Ecological data analysis finds its place at the intersection of three scientific fields (Chessel, 1992). On one hand, the Biology provides the data, the biological concepts underlying the study, and the questions asked for in a given analysis. On the other hand, the Mathematical theory provides general models permitting the development of statistical methods. Finally, Computer Science is at the junction of Biology and Mathematics: object classes are defined from the data provided by the biologists, and computational tools are designed from mathematical theory to manage and analyze these classes. Research in data analysis should develop new statistical methods, and organise them into a consistent approach of data analysis, to help biologists, to answer their questions. This statistical approach of data analysis should be developed into a flexible computing environment, to take into account the wide diversity of both questions and data collected by the biologists, and to allow an easy implementation.

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Animal movements provide a good example of the complexity of ecological data and of the wide variety of questions related to their analysis. There have been several studies carried out to understand how the animals' space use is related to both their internal constraints (e.g., biological rhythms) and their environment (e.g., habitat, competitors, predators). Thus, this kind of study has been carried out at the individual scale to identify the external factors affecting these movements, such as the effect of landscape heterogeneity (Johnson et al., 1992; Morales and Ellner, 2002) and of patch boundaries (Schtickzelle and Baguette, 2003), the seasonality of these movements (Bergman et al., 2000), or the orientation mechanisms of the animals (Séguinot et al., 1998). At a larger scale, several authors have used individual movements to model the spatial distribution of populations (Turchin, 1996, 1998) and the whole dynamics of a group of animal (Couzin et al., 2005).

Because of the numerous aims and data types involved in the analysis of animals' trajectories, a wide variety of mathematical tools have been developed. Several models, such as the correlated random walk (Kareiva and Shigesada, 1983) or the stochastic differential equations (Brillinger et al., 2002) have been developed to describe these movements. As well, several statistical methods relying on these models have been proposed to reach one or the other aim of trajectory analysis (e.g., Fauchald and Tveraa, 2003).

However, to our knowledge, no computing environment exists presently for the implementation of these analyses, as animals' trajectories are complex objects requiring to define new data class. Indeed, common statistical softwares generally provide only the most common data structures (e.g., data tables) and standard statistical approaches. These softwares have generally been developed for commercial use, and are poorly designed for research (Tufto and Cavallini, 2005; Calenge, 2006). Consequently, it is often difficult to manage complex ecological objects, such as animal trajectories, in these "canned" programs, which hampers the research for new statistical methods.

In this context, open source softwares offer an alternative to standard commercial softwares. In particular, the R software is especially suitable for ecological data analysis (Tufto and Cavallini, 2005; Calenge, 2006). This software, initially developed by Ross Ihaka and Robert Gentleman to provide a statistical environment to their laboratory in 1992, has been released as an open-source software in 1995. It is now increasingly used in the scientific community, and especially among ecologists. This free software relies on the programming language S, a language designed to "turn ideas into softwares" (Chambers, 1998). Because the number of users of the R software increases regularly, and because the authors of the language S have designed it to encourage the users "to slide into programming without noticing" (Chambers, 1998), more and more statistical methods are becoming available in the R environment. In addition, the R software provides simple means to define object classes, which gives it a desirable flexibility for ecological data analysis.

In this paper, we focus on the computational aspects of trajectories analysis. We present a new object class, the class "ltraj", developed for the R software, which we designed to make it closely fit to the requirements of the biologists. We first describe an overview of the existing points of view on this analysis in the ecological literature. We discuss about the biological aims, the data types, the parameters used to describe the trajectories, and the mathematical models used in trajectory analysis. We also describe how the class "ltraj" closely fits with the existing points of view in the literature. This class is available in the package adehabitat (Calenge, 2006) for the free R software (R Development Core Team, 2006).

2. A classification of trajectories

2.1. *What about the time?*

Basically, the trajectory is the curve described by the animal when it moves. Because this movement is continuous, the sampling of the trajectory implies a step of discretization, i.e., the division of this continuous curve into a number of discrete "steps" connecting successive relocations of the animal (Turchin, 1998). Depending on the sampling protocol, two main classes of trajectories can be distinguished: the trajectories of type I for which the time is not precisely known or not taken into account for the relocations of the trajectory, and the trajectories of type II for which the time is known for each relocation.

On one hand, the trajectories of type I are made of a collection of relocations characterised by their coordinates X and Y, as well as by an ordered factor G giving the order of the relocations in the trajectory. These trajectories can be obtained by sampling the tracks of the animals in the snow (Nams and Bourgeois, 2004) or in the sand (Ward and Saltz, 1994). Some more specialized techniques have also been used, such as thread trailing to monitor turtles (Claussen et al., 1997; Iglay et al., 2006), or a fluorescent powder to monitor the American Woodcock broods (Steketee and Robinson, 1995). In most cases, these trajectories are characterised by equal step lengths (Turchin, 1998). The pure geometrical analysis of such trajectories allows to derive interesting biological conclusions concerning the behaviour of an animal. For example, the tortuosity of the trajectory may bring information on the foraging strategies of an animal (Benhamou, 2004).

On the other hand, for trajectories of type II, the factor G is replaced by the time T at which relocations were collected. These trajectories are generally sampled using telemetry techniques (Johnson et al., 2002a,b; Franke et al., 2004; Frair et al., 2005) or direct observation (Root and Kareiva, 1984; Morales and Ellner, 2002). These modes of data collections often result in trajectories characterised by constant time lag, which we call "regular trajectories" in the rest of this paper.

2.2. *The class "ltraj"*

We designed the class "ltraj" in the package adehabitat (Calenge, 2006) to manage and analyze animals' trajectories in the R software. An object "ltraj" may contain data collected on several animals, with several trajectories per animal. Basically, an object of class "ltraj" is a list of tables (named "data frames" in R), each table containing: (i) the coordinates of the relocations in the trajectory (a "burst" of relocations), (ii) either their timing (type II) or a numeric variable indicating

their order (type I) in the trajectory, and (iii) several descriptive parameters of the steps (see below). Each trajectory is characterised by an attribute "ID" defining the ID of the monitored animal, and an attribute "burst" giving a unique ID for each trajectory in the object. The package adehabitat provides functions allowing to manage the content of such objects. It is easy to subset the data, keeping only given animals or given trajectories, or parts of the trajectories corresponding to specified criteria (e.g., given time limits).

When trajectories of type II are under study, the class "ltra j" is mainly designed to store regular trajectories (constant time lag between relocations). Indeed, recent advances in the technics for monitoring of animal movements facilitate such designs, and it is generally more convenient for the biologist to define a constant time lag before data collection. In addition, most models used to describe animal movements (e.g., the correlated random walk, Kareiva and Shigesada, 1983) and most statistical approaches (e.g., time series analysis, Diggle, 1990) suppose this regularity. Moreover, some of the descriptive parameters of the trajectory generally used in the analysis (see below) do not have any biological meaning when the time lag varies. For example, the distribution of relative angles (angles between successive steps) depends on a given time scale; the angle between two 10-min steps of a migrating whitestork does not have the same biological meaning as the angle between two 1-day steps. If the time lag varies, the underlying process varies too. For this reason, most functions of adehabitat have been developed for "regular" trajectories. Furthermore, several functions are intended to help the user to transform an object of class "ltraj" into a regular object. Nevertheless, the class "ltraj" can be used to store irregular trajectories, which often occurs with some modes of data collection (e.g., with Argos collars).

The class "ltraj" deals with missing relocations in the trajectories. Missing values are frequent in the trajectories of animals collected using telemetry: for example, GPS collar may not receive the signal of the satellite at the time of relocation, due for example to the habitat structure obscuring the signal (Frair et al., 2004), or to the behaviour of the animal (e.g., a sleeping animal affects the position of the collar relative to the sky, D'Eon and Delparte, 2005; Graves and Waller, 2006). Because the frequency of missing values in a trajectory may sometimes be high (reaching more than 20–30% on some study areas, e.g. on the ibex in mountainous area, see the dataset ibex in the adehabitat package), and because they may be related to biologically important variables, the analysis of the patterns of missing values should be part of trajectory analysis (Graves and Waller, 2006). This preliminary analysis is allowed with the class "ltraj". For example, runs test can be used to test whether the missing values are randomly distributed over time (function runsNAltraj).

3. Description of trajectories

3.1. *Common descriptive parameters of the trajectories*

A set of parameters is needed to characterise the different aspects of the animal movement (Fig. 1). Actually, the descriptive parameters used in studies of animals' trajectories can be categorised according to the scale at which they describe the trajectory.

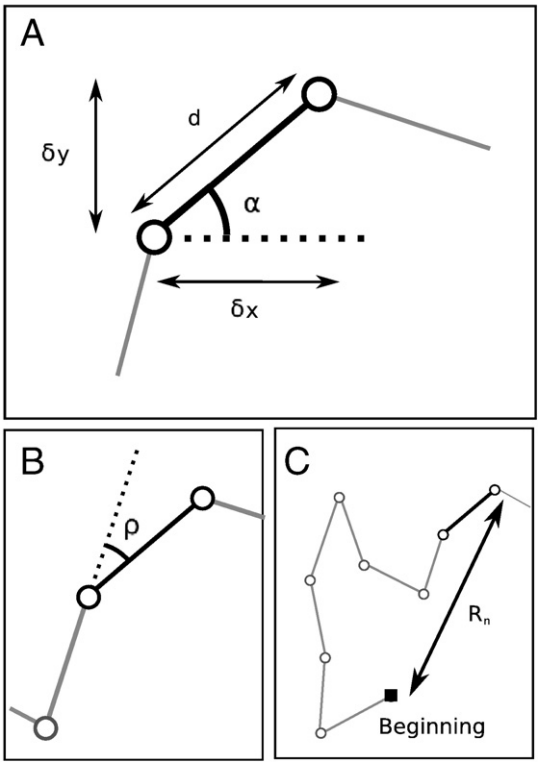

Fig. 1 – Descriptive parameters of a trajectory automatically computed by adehabitat in an object of class "ltraj": (A) parameters describing the basic unit of the trajectory — the step: increments in the *X* and *Y* directions, respectively δ*x* and δ*y*, the step length *d* and the absolute angle between the step and the *X* direction *α*; (B) the relative angle ρ measures the angle between the current step and the direction of the previous step; (C) the mean squared displacement R_n^2 is the square of the distance between the first relocation and the current relocation of the animal.

First, some parameters describe the basic unit of the trajectory — the step. These measures are calculated from the coordinates of the two relocations defining the step, to describe its length and orientation in space. These parameters include the distance between these relocations (Jones, 1977; Root and Kareiva, 1984; Marsh and Jones, 1988; Morales and Ellner, 2002; Ramos-Fernandez et al., 2004; Franke et al., 2004), the time lag (Siniff and Jessen, 1969), the speed (Siniff and Jessen, 1969; Johnson et al., 2002a; Brillinger et al., 2004), the increment in the *X* (East–West) and *Y* (North–South) directions (Brillinger et al., 2004; Wiktorsson et al., 2004), or the "absolute" angles between the step and the *X* direction (Marsh and Jones, 1988).

Moreover, some parameters describe the position of a given step relative to the other steps of the trajectory. These measures include the mean squared distance between the first relocation of the trajectory and the last relocation of the current step (Kareiva and Shigesada, 1983; Root and Kareiva, 1984; Marsh and Jones, 1988; Bovet and Benhamou, 1988;

Johnson et al., 1992; Ward and Saltz, 1994; Morales and Ellner, 2002; Ramos-Fernandez et al., 2004; Wiktorsson et al., 2004), or the "relative" angle between the current step defined by the relocations [i, (i+1)] and the next one (sometimes called "turning angles", Siniff and Jessen, 1969; Jones, 1977; Root and Kareiva, 1984; Marsh and Jones, 1988; Bovet and Benhamou, 1988; Zollner and Lima, 1999; Morales and Ellner, 2002; Ramos-Fernandez et al., 2004; Franke et al., 2004).

Finally, the above statistics are often used to derive other statistics measuring some particular features characterising the whole trajectory. In this case, it is supposed that the trajectory is statistically stationary, i.e., that the statistical distribution of these parameters is the same all along the trajectory. Thus, the tortuosity of the trajectory is an aspect reflecting the intensity of the search for food by animals, and is for this reason one of the most studied properties. It has been estimated by the fractal dimension of the trajectory (Claussen et al., 1997; Laidre et al., 2004; Nams and Bourgeois, 2004), its spectral dimension (Johnson et al., 1992), and various coefficients of tortuosity related to the variance of the circular distribution of the relative angles (Bovet and Benhamou, 1988; Benhamou, 2004; Claussen et al., 1997). For very long trajectories, home range estimators of sedentary animals can be understood as indices reflecting both the length and the tortuosity of this trajectory (Benhamou, 1998). For a given trajectory, the above statistics assume that the trajectory is stationary. When it is not, it has been advised to use them for subparts of the trajectories, e.g., using sliding windows (Benhamou, 2004).

Note that the computation of a given parameter depends on the type of available data. Thus, it does not make sense to work on the time lag between successive relocations for regular trajectories of type II. On the other hand, as noted above the computation of relative angles is not suitable for irregular trajectories of type II.

3.2. *Descriptive parameters in the objects of class "ltraj"*

Owing to Marsh and Jones (1988), a good description of the trajectory is achieved when the following criteria are fulfilled: (i) the description is achieved using a limited set of relatively easily measured parameters; (ii) the relationships between these parameters are precisely defined (with the help of a model), and (iii) the parameters and the relationships between them are sufficient to reconstruct characteristic tracks without loosing any of their significant properties. Thus, for each relocation of an object of class "ltraj", a minimum set of descriptive parameters of the steps is automatically computed and included in the table describing each burst (Fig. 1). For a given relocation i, the increment of the step in the X and Y directions (i.e., $\delta X_i = X_i - X_{i-1}$ and $\delta Y_i = Y_i - Y_{i-1}$), as well as the time lag ($\delta t = t_i - t_{i-1}$) are computed. These three parameters are sufficient to reconstruct the trajectory, and are used by several mathematical models to describe the trajectories (stochastic differential equations, Brillinger et al., 2002).

Another family of models (see below) characterise the step defined by the relocations [(i−1),i] by its length and either the "absolute" angle between this step and the X direction (e.g., biased random walk, Marsh and Jones, 1988), or the "relative" angle between this step and the previous step defined by the relocations [i,(i+1)] (e.g., correlated random walk). The increment in X and Y can be used to derive the length of the step, and both the relative and absolute angles are automatically computed when an object of class "ltraj" is created.

Finally, for each relocation, the squared net displacement between the current relocation and the first relocation of the trajectory is also automatically computed, as a large amount of research has been performed on this measure during the last decades and theoretical values are available for several models, for example for the correlated random walk (Kareiva and Shigesada, 1983; Bovet and Benhamou, 1988), or the Brownian motion (Jammalamadaka and SenGupta, 2001).

4. Statistical analyses

4.1. *Models describing animals' trajectories*

Most often the analysis implies the use of models to identify the patterns in the trajectories, or to summarise the trajectory with a small set of parameters. Two broad classes of trajectory models have been used by ecologists until now.

The first class includes models developed by physicians to describe the movement of particles. They generate theoretical trajectories sequentially, using the last step of the trajectory as a reference to build an additional step. These models generally describe a step of the trajectory by the relative angle between the step and the preceding step (randomly drawn from a circular distribution), and by the length of this step. Note that trajectories of type II are supposed to be regular (as the relative angle only has a sense at a given time scale). Several models developed in physics are used for a long time in ecology, such as the correlated random walk (Kareiva and Shigesada, 1983), or the biased random walk (Marsh and Jones, 1988). The main quality of these models is their simplicity, which explains their success (Ward and Saltz, 1994). Note that other models used in physical science have been introduced more recently in ecology, such as the Lévy flight (Viswanathan et al., 1996, 1999; Ramos-Fernandez et al., 2004). Actually, several authors have noted that advances in physics can be of use for ecologists (e.g., Johnson et al., 1992).

The second class of models has been developed in probability, and especially in the field of random processes analysis. Such models have been widely used in financial sciences to model economic processes (e.g., Osborne, 1972). In ecology, they are intended to model trajectories of type II (time known), and do not make any assumption on the regularity of the trajectories (continuous time). The position of the relocation at time t is generally determined by adding to the relocation collected at time $t-1$ a bivariate vector describing the increment in X and Y of the trajectory. The Ornstein–Uhlenbeck process is probably the first model belonging to this class that has been used in ecology to describe animals' movements (Dunn and Gipson, 1977; Blackwell, 1997). Other models, such as state-space models (Bayesian approach of trajectory analysis, Jonsen et al., 2003) or stochastic differential equations (Brillinger et al., 2002, 2004; Preisler et al., 2004) have also been proposed. Their complexity makes them more difficult to use, but they are generally highly parametrizeable, allowing to take into account a wide variety of patterns.

No model will ever allow to take into account the whole complexity of the animal behaviour. However, all the above models can be used as reference to which the observed trajectories are compared (i.e., null models). For example do the studied trajectory exhibit smaller relative angles than theoretical trajectories generated by this model (indicating some autocorrelation in the direction chosen by the animal from one step to the next)? Are the relative angles auto-correlated in the trajectory, indicating possible changes in behaviour?

4.2. *Analysis of trajectories in adehabitat*

Many approaches have been used in the literature to analyze animals' trajectories. However, as noted above the questions of the biologists are various and the types of data are even more diverse. Consequently, each study is particular, and no universal recipe to analyze animals' trajectories can be given. However, a set of tools is provided by the package adehabitat to help the biologist to build an analytic approach, given the data at hand (Fig. 2).

First, the package adehabitat contains functions allowing a dynamical exploration of the trajectory (function trajdyn). The graphical exploration of the statistical distribution of the descriptive parameters is also facilitated by functions of the powerful R environment (histograms, quantile plots, etc., Cleveland, 1993).

An important aspect of trajectory analysis is the question of the independence of the descriptive parameters within the trajectory (Root and Kareiva, 1984). For example, under the hypothesis that the trajectory has been generated by a correlated random walk, the relative angles associated to the steps should be independently distributed within the trajectory. If there is a positive autocorrelation of the relative angles (i.e., a small angle is followed by a small angle), this indicates that some parts of the trajectories are characterised by linear movements (between-patch movements) and others by more sinuous movements (e.g., foraging movements inside a patch of resource): the trajectory is not stationary. Dray et al. (in preparation) provided criteria to test the independence of each one of the parameters (function testang.ltraj for the absolute and relative angles, indmove for a simultaneous test of the independence of increment in the X and Y directions, testdist.ltraj for the step length, and wawotest for separate tests in the X and Y directions). Based on these criteria, they also developed methods allowing to identify the degree of the autocorrelation of these parameters, i.e. whether a given step i is dependent only on the step $i-1$, or also of the step $i-2$, $i-3$, etc. (functions acfdist.ltraj

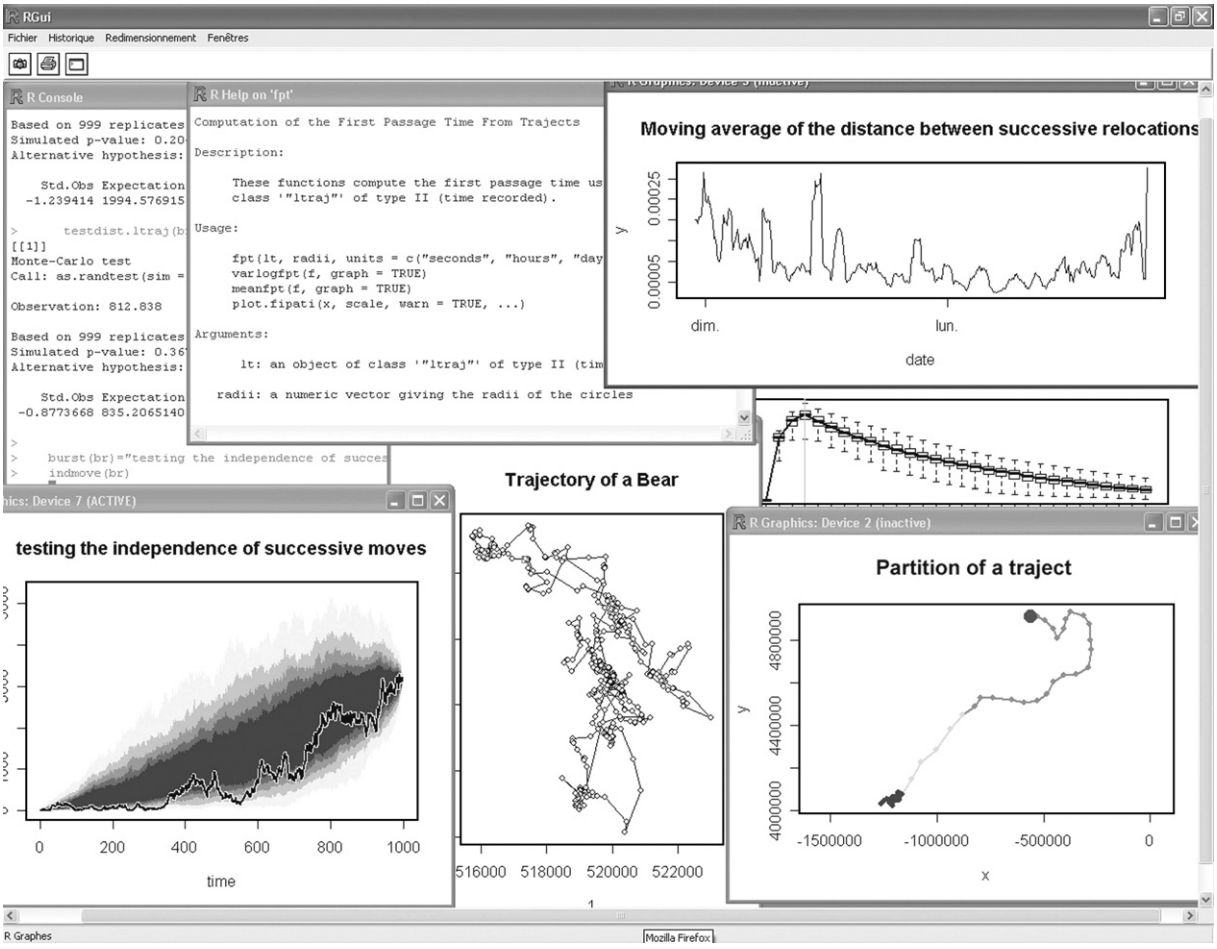

Fig. 2 – Capture screen of one R session with adehabitat, showing a small portion of the analysis possibilities with the class "ltraj".

and acfang.ltraj). Note that, under certain models, some parameters are expected to be independent, whereas they are expected to be autocorrelated under other models. For example, the increments in the *X* direction are expected to be independent under the Brownian process, whereas they are expected to be autocorrelated with the Ornstein–Uhlenbeck process (Royer-Carenzi et al. in preparation).

The issue of the non-stationarity of the trajectories raises the question of the identification of these behavioural bouts based on the shape of the trajectory (Fauchald and Tveraa, 2003; Schwager et al., 2007), and of their organisation according to the environment and the internal constraints (seasonal or circadian rhythms) of the animal (Johnson et al., 2002a; Morales and Ellner, 2002; Franke et al., 2004). As noted by Morales and Ellner (2002), "the main challenge for scaling up movement patterns resides in the complexities of individual behavior rather than in the spatial structure of the landscape". The package adehabitat provides functions allowing to investigate the non-stationarity of the descriptive parameters of the trajectories: functions allow to draw time plots (function plotltr), to apply a smoothing function to the parameters describing the trajectory in a sliding window (function sliwinltr). Further studies may imply the partition of a trajectory into segments corresponding to a stationary behaviour of the animal, e.g., using the *K*-means algorithm (as recommended by Schwager et al., 2007, function *k* means). The study of the non-stationarity can also be done using time series analysis (Diggle, 1990), easily implemented in the R environment (e.g., functions spectrum for the periodogram, acf for the autocorrelation function, etc.).

Note that it can be useful to compare the distribution of descriptive parameters computed for one trajectory with the distribution expected with theoretical models for the trajectory, using simulations. Therefore, we also implemented several models of animal trajectories in adehabitat. Thus, the function simm.brown simulates a Brownian motion. The function simm.mba simulates the arithmetic Brownian process (takes into account a potential drift in the move, and/or a correlation structure between the increments in the *X* and *Y* directions, Royer-Carenzi et al. in preparation). The function simm.mou simulates a bivariate Ornstein–Uhlenbeck process (Blackwell, 1997; Dunn and Gipson, 1977). These three functions simulate special cases of process belonging to the family of the stochastic differential equation (Brillinger et al., 2002, 2004; Preisler et al., 2004). We also included a function named simm.crw to simulate the correlated random walk (takes into account a unimodal distribution of the relative angles between successive steps). Finally, the function simm.levy implements an algorithm to simulate the Levy walk (Viswanathan et al., 1999; Bartumeus et al., 2005) a family of models taking into account an exponential distribution of the steps length).

In case of stationarity, if an acceptable model has been chosen for the trajectory, then the whole trajectory can be summarised by the parameters of the model, and a study at a larger scale can be carried out to compare the value of these parameters with those of trajectories sampled in different conditions (different animals, different time period, etc.). The R environment contains numerous functions facilitating this study. For example, the R package CircStats contains several functions implementing tests for circular data, so that it is straightforward to compare the concentration parameters of the distribution of relative angles between two or more trajectories.

More complex cases can however arise, for example when several trajectories of an animal show a significant autocorrelation of a given parameter, whereas others do not. It might be, for example, because the biological constraints differ between the two trajectories (some trajectories might have been collected during the rutting period and the other during rearing-young period). It is difficult to give here any universal recipe to deal with such cases: The decision should be taken case-by-case according to the data and the biological aims.

Note that several functions have been implemented in adehabitat to facilitate the study of the effect of the time or spatial scale of the study on the descriptive parameters of the trajectories. Thus, the function subsample allows to change the time lag between successive relocation for regular trajectories of type II (e.g., to compute a trajectory sampled every 20 min instead of 10 min). When trajectories of type I are under study, the function redisltraj can be used to rediscretize the trajectory into steps of specified length, as recommended by several authors (Bovet and Benhamou, 1988; Turchin, 1998; Benhamou, 2004). The function fpt (for regular trajectories of type II) can be used to identify the scale at which animals concentrate their search when they forage (Fauchald and Tveraa, 2003).

Finally, other functions of adehabitat may be used to manage vector or raster maps of environmental variables (Calenge, 2006). Several basic operations can be performed with this package: a buffer can be computed around the trajectories (i.e., identify the area comprised within a specified distance of the trajectory), an operation sometimes needed to compute some descriptive parameters of the trajectories not automatically computed in the object of class "ltraj" (Doerr and Doerr, 2005). The value of mapped environmental variables can be determined for each relocation, allowing analyses of habitat selection.

5. Discussion

For a long time, animals' trajectories have been mainly studied on insects, which are easy to monitor visually (Jones, 1977; Root and Kareiva, 1984; Johnson et al., 1992; Schultz, 1998). However, for large and "shy" species such as ungulates, direct observation of the animals was not possible, and the study of movements often relied on radio-tracking (e.g., Maillard, 1996). However, the collection of relocations at short time lags on several animals requires an important staff and a heavy protocol, so that these studies were rather scarce in the ecological literature. The recent development of GPS (Global Positioning System) has facilitated this type of study. Indeed, GPS collars allow the automatic collection of animals' relocations, so that the movements are often sampled at regular and short time lag. The increasing use of GPS collars now renders possible the study of movement on species for which this kind of study was difficult before (Johnson et al., 2002a,b; Franke et al., 2004; Frair et al., 2005).

In this paper, we presented a new class of data, the class "ltraj", intended to manage and analyze animals' trajectories

in the R software. Designing a class of object for R is interesting from a methodologist perspective: the structure of the class reflects a point of view of the programmer on the biological object and on its analysis. Thus, we had to identify the different types of trajectories that can be encountered (time recorded or not, regular or not, etc.); numerous decisions had to be made concerning the class itself — for example, we did not allow additional variables (e.g., environmental variables, or measures of precision of the relocations) to be included in the object "ltraj" with other descriptive parameters of the steps, as this class is intended to store only purely geometrical properties of the trajectory.

This point of view was developed after an extensive review of the ecological literature on trajectory analysis, which we summarised in this paper. We also based our reflexion on a large amount of trajectories collected on a large diversity of species (bears, wild boars, albatross, hooded seals, porpoise, roe deer, mouflons, ibex, etc.), monitored mainly using telemetry modes of data collection (GPS, Argos, radio-tracking). For this reason, the package adehabitat contains a large number of example trajectories, which shows the large diversity of data that can be encountered in biological studies. All the functions are documented in help files, which present examples of their use in the context they are to be used. Note also that typing demo(managltraj) in the R console performs a sample session giving examples of use of the package for management of trajectories, and typing demo(analysisltraj) provides a working example of trajectory analysis.

This class was developed within a group of researchers composed of numerous biologists, methodologists and mathematicians. The discussions between specialists of these three fields allowed to develop this class, which in turn was discussed to develop an approach of statistical analysis of animal trajectories (Dray et al. in preparation; Royer-Carenzi et al. in preparation). We hope that the present approach will serve as a basis for future methodological developments.

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