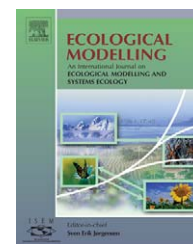


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## Short communication

# The package “adehabitat” for the R software: A tool for the analysis of space and habitat use by animals

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### ABSTRACT

The practical analysis of space use and habitat selection by animals is often a problem due to the lack of well-designed programs. I present here the “adehabitat” package for the R software, which offers basic GIS (Geographic Information System) functions, methods to analyze radio-tracking data and habitat selection by wildlife, and interfaces with other R packages. These tools can be downloaded freely on the internet. Because the functions of this package can be combined with other functions of R, “adehabitat” provides a powerful environment for the analysis of the space and habitat use.

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The study of the relationships between animals and their environment is one of the main issues in ecology. It implies the analysis of the use of space by animals, of the interactions between animals, and of the relationships between animals and their habitat. The recent development of Geographic Information Systems (GIS) has made easier this type of study, and especially the study of habitat selection, by taking into account more explicitly the spatial dimension of the data in the analyses (Manly et al., 2002). This expanded the range of possible analysis, and as a result numerous methods have been developed during the last decade in this field of Ecology (e.g. Guisan and Zimmermann, 2000).

However, the practical data analysis remains a problem. First, the analyst has to perform spatial analyses within a GIS (computation of buffers (areas containing all points located within some specified distance of a mapped feature), estimation of home ranges, etc.), and second, he needs a statistical software to analyze the data more deeply. After the analyses, he may also need to move the data back to GIS for more specifically GIS analyses. The interface between GIS and statistical software is often missing and can make the analysis long and difficult. In addition, the quality of commercial statistical program has been criticized by several authors in Ecology science (Chessel, 1992; Tufto and Cavallini, 2005). Indeed, such “canned” programs are not open enough. They provide only

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standard statistical procedures, and limit the development of new approaches.

In this framework, open-source software may be viewed as an alternative (Tufto and Cavallini, 2005). Such programs are distributed freely under a licence known as the GNU General Public Licence (GPL; Free Software Foundation and Inc., 1991), which also relies on standard copyright laws. All the source code is available, so that a user can make changes inside the program. The modified version is also free and available. This usually results in very efficient programs, because they are built and modified by their users.

Tufto and Cavallini still noted that the awareness of this phenomenon was weaker among biologists than researchers belonging to other fields of science, despite its undeniable desirable qualities. They recommended the use of free software, and listed the programs that may be of great interest, giving a special mention to the R software (R Development Core Team, 2005).

My purpose is to present, after a brief description of the R software, the package I developed to analyze the use of space and habitat selection by animals: “adehabitat”. It gathers a set of methods, through R functions, intended to provide tools for biologists.

## 1. The R software

Ross Ihaka and Robert Gentleman, from the Auckland University, developed the R software to provide a statistical envi-

ronment to their laboratory in 1992, and based this software on the S language. This one was invented at the AT&T Bell Laboratories by John Chambers and his colleagues during the mid-1970s. They wanted to encourage the user to “slide into programming, perhaps without noticing” (Chambers, 1998), and to ensure that a user can easily implement his own techniques.

With the help of Martin Mächler (working at the ETH Zürich), Ihaka and Gentleman released this software as free open-source software in 1995 (Ihaka and Gentleman, 1996). Presently, the “Comprehensive R Archive Network” (CRAN) is the core of an increasingly growing R community (Hornik and Leisch, 2001); it is the central repository for material related to R, including packages of functions (518 at the time of writing), tutorials and discussion forums (URL: <http://cran.r-project.org/>). The use of R implies the learning of a command language. At first sight, this aspect may seem to be a drawback, but it has actually numerous desirable qualities. First, this language is very intuitive (e.g. a t-test is carried out with the function `t.test()`, a generalized linear model is fitted using the function `glm()`, etc.). In addition, this language renders easier the run of repeated and batch analyses. For example, it is not necessary to repeat manually all the steps of an analysis if only one detail is to be changed in it. Numerous tutorials are available on the internet to help users quickly learn the language.

Several packages are available for the analysis of ecological data. Among them, the “ade4” package allows the analysis of ecological and environmental data in the framework

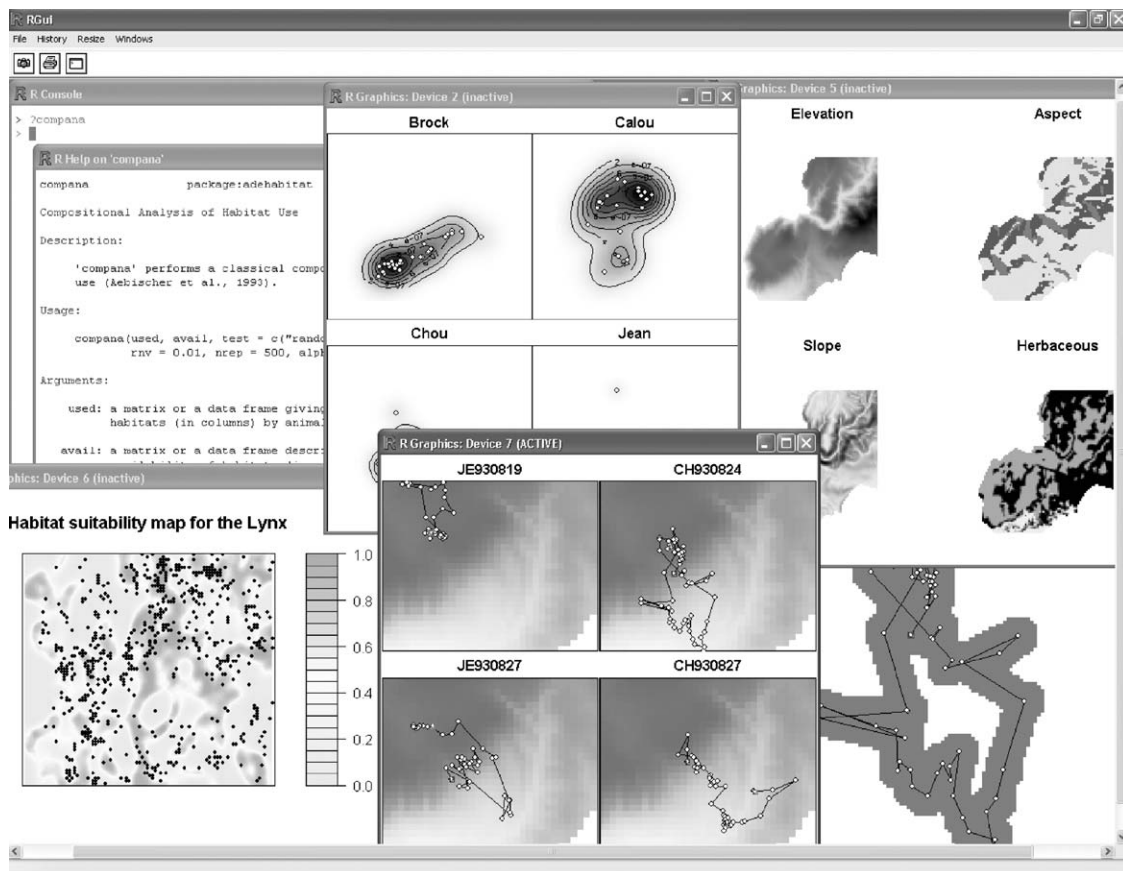


Fig. 1 – Capture screen of one session with R and the package “adehabitat”.

of Euclidean Exploratory methods (Chessel et al., 2004), the “vegan” package is intended for the vegetation and community analysis, and the “GRASP” package aims at building predictive models of the distribution range of species in biogeography, using generalized regression and spatial prediction (Lehmann et al., 2002).

## 2. The “adehabitat” package

I have developed the “adehabitat” package to study the space use and habitat selection by wildlife. It contains about 100 functions giving tools frequently used in this field of research. The graphical possibilities of this package (Fig. 1), and the combination of the “adehabitat” functions with the powerful analysis environment provided by R allow the users to design a large diversity of analyses of the relationships between animals and their environment. A quick learning can be carried out with the tutorial included in the package.

The “adehabitat” package includes functions that create an interface with GIS commonly used in Ecology, such as Arcview GIS (ESRI, 1996), the free program GRASS (available at: <http://grass.itc.it/>) or the free software Landserf (available at: [www.soi.city.ac.uk/~jwo/landserf/](http://www.soi.city.ac.uk/~jwo/landserf/)). Single maps can be imported within R, and then combined into multilayer maps; these maps are grids of pixels on which several variables are measured, allowing multivariate analysis of habitat use by animals. Several basic GIS functions are also available in “adehabitat”. It is for example possible to compute buffers around lines or points, to determine the habitat composition at given points, to select sub-areas on a map, to define masks, to reduce the resolution of a map, and so on. In addition, several functions provide an interface with the spatial classes of the “sp” package which is itself an interface toward other R packages dealing with spatial data (Pebesma and Bivand, 2005), another efficient way to analyze data.

Common analyses of habitat selection may also be carried out using “adehabitat”. Thus, several functions allow the computation of selection ratios (Manly et al., 2002), compositional analysis (Aebischer et al., 1993), K-select analysis (Calenge et al., 2005) or Ecological Niche Factor Analysis (ENFA, Hirzel et al., 2002). Moreover, habitat suitability maps can be computed using Mahalanobis distances (Clark et al., 1993), the DOMAIN algorithm (Skov, 2000), or the ENFA (Hirzel et al., 2002). Resource selection functions may also be fitted, using the spatial classes of “adehabitat” and the powerful modelling capabilities of R. To take into account the multivariate aspect of habitat (Hall et al., 1997), this package also provides an interface with the package “ade4” (Chessel et al., 2004).

“Adehabitat” also includes several tools suitable for the analysis of radio-tracking data. Home range estimators include the minimum convex polygon (Mohr, 1947) the kernel estimator (Worton, 1989), the nearest neighbor convex hull (Getz and Wilmers, 2004), or the grid method (Siniff and Tester, 1965). And so, the estimates can be used in the analyses of spatial interactions between animals, habitat selection, etc. Schoener’s ratio can be computed to detect temporal autocor-

relation in the relocations (Swihart and Slade, 1985), and basic statistics to analyze animal movements such as speed or turning angles (Turchin, 1998).

## 3. Discussion

The main objective of the “adehabitat” package is to provide tools for analyzing the relationships between animals and their environment. Because the R community is very active, the package is improved frequently, making new functions available to other users. Thus, since its first release in September 2004, two additional versions of the package have been submitted on CRAN as a result of the suggestions made by the users concerning the methods that would find their place in “adehabitat”. For instance, the recent development of GPS (Global Positioning System) to monitor space use by animals has raised a number of questions among ecologists (autocorrelation, how to analyze such trajectories, etc.). In view of this situation, Paolo Cavallini (working at Faunalia, Italy) created a discussion forum to make the communication easier between scientists of various fields interested by the analysis of animal movement (URL: [www.faunalia.com/animov/](http://www.faunalia.com/animov/)). Several functions of the package have been added or modified following discussions that arose on this forum, e.g. the kernel Brownian bridge estimator of the home range (Bullard, 1991) or the nearest neighbor convex hull estimator of the home range (Getz and Wilmers, 2004).

The functions of “adehabitat”, and more generally, the R functions are well documented on the help pages. These pages describe the arguments and options needed by the functions, give examples of use, and sometimes the context in which they were developed and the context in which they are to be used. Examples of syntax for some standard analyses are available at the URL: [www.faunalia.com/animov/howto.php](http://www.faunalia.com/animov/howto.php). Thus, R is more than a simple technical tool, and becomes integral part of the development of methods. This illustrates well the philosophy behind the S language, which is, owing to the nice expression of Chambers (1998), “to turn ideas into software”. R is therefore the biometrical tool par excellence. As the interdisciplinarity emerges today as an important aspect of science (e.g. Morillo et al., 2003), the R software and the “adehabitat” package will be of major use to wildlife biometricians who are concerned by the use of space and habitat selection by animals.

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