1 ***MoveR: an R package for easy processing and analysis of animal video-tracking data***
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3 Quentin PETITJEAN[1, 2, *], Silène LARTIGUE[1], Mélina COINTE[1], Nicolas RIS[1], Vincent
4 CALCAGNO[1]
5
6 [1] Université Côte d'Azur, INRAE, CNRS, Institut Sophia Agrobiotech, Sophia Antipolis, France.
7 [2] Laboratoire Ecologie Fonctionnelle et Environnement, UMR5245 LEFE, Université de
8 Toulouse, UPS, CNRS, INP-ENSAT, Auzeville-Tolosane, France.
9 * Corresponding author: Quentin PETITJEAN, E-mail address: mailto:q.petitjean1@gmail.com;
10 quentin.petitjean@toulouse-inp.fr
11
12 **Abstract**
13
14 Animal movement and behavior are critical to understanding ecological and evolutionary
15 processes. Recent years have witnessed an increase in methodological and technological
16 innovations in video-tracking solutions for phenotyping animal behavior. Although these advances
17 enable the collection of high-resolution data describing the movement of multiple individuals,
18 analyzing and interpreting them remains challenging due to their complexity, heterogeneity, and
19 noisiness. Here, we introduce MoveR, an R package for importing, filtering, visualizing, and
20 analyzing data from common video-tracking solutions. MoveR includes flexible tools for polishing
21 data, removing tracking artifacts, subsetting and plotting individual paths, and computing different
22 movement and behavior metrics.
23 **Keywords**
24 *Video-tracking; Trajectories; Animal Movement; Behavior*
25 **Metadata**
26

Nr	Code metadata description	*Please fill in this column*
C1	Current code version	*V0.2.0*
C2	Permanent link to code/repository used for this code version	*https://github.com/qpetitjean/MoveR*
C3	Permanent link to reproducible capsule	*N.A.*
C4	Legal code license	GPL-2.0 license
C5	Code versioning system used	*git*
C6	Software code languages, tools and services used	*R*
C7	Compilation requirements, operating environments and dependencies	O.S.: Linux, OS X, Microsoft Windows Software: R (>= 3.6.2) Package dependencies : graphics*; grDevices*; hexbin; progress; R.matlab; reticulate; stats*; trajr; pracma. *Included in R v3.6.2 and above.
C8	If available, link to developer documentation/manual	https://qpetitjean.github.io/MoveR/
C9	Support email for questions	mailto:q.petitjean1@gmail.com

1. Motivation and significance
1.1. Scientific motivation

Studying animal movement patterns and behaviors is paramount to understanding ecological and evolutionary processes and developing effective species management strategies. Animal movements and behavior are often considered the first response to environmental changes or stressful conditions (e.g., pollution, climate change, introduction of non-native species) [1,2], making them valuable tools to infer underlying animal's internal states, sensory biases, and behavioral types. Therefore, changes in movement patterns and behavioral traits are increasingly considered a highly integrative and relevant endpoint to assess the effect of global changes and anthropogenic stress on organisms (e.g., ecotoxicology, conservation biology) [3–5].

In addition, behavior being at the direct interface between organisms and the environment, behavioral changes can drastically affect individual and species interactions [6] through, for instance, alterations in habitat choice, movements, foraging, social and reproductive behavior [7] with expected cascading effects on population dynamics, food webs [8], and ecosystem functions such as primary production, transport of nutrients, and hence biogeochemical cycling [9]. While animal movement and behavioral changes can directly alter ecosystem functioning, they may also prevent rapid population decline through adaptive responses, facilitating genetic adaptation through rapid evolution [1,10], or rather the opposite, resulting in population decline and even extinction when altered in a maladaptive way (*sensu* ecological & evolutionary traps; [1,11,12]). Accordingly, animal movement, migration, and dispersal may indirectly alter ecosystem functioning by affecting eco-evolutionary dynamics [13–15]. For instance, the dispersal rate among metapopulations of baker's yeast exposed to increasing concentrations of antibiotics has been shown to be an important driver of population adaptation and persistence [16].

Accordingly, improving our understanding of how animals move and behave in various contexts may help to tackle critical conservation aims [17,18], including the need to stabilize or increase the numbers of small or declining populations [19,20], ensure the dispersal of biocontrol agents under various conditions [21,22] and control invasive or pest species [23,24]. For instance, a recent study has shown that combining biopesticides (i.e., essential oils) and biocontrol agents (*Trichogramma evanescens*) to mitigate pest species in agricultural fields may be counter-productive by altering biocontrol agents' fitness and behavior and hence their efficiency [21].

Overall, what appears as subtle effects on individuals' behavior may significantly affect ecosystems' functioning, evolutionary responses, and population persistence, stressing the need to study global changes' direct and indirect effects on animal behavior. In line with these needs, the increasing use of computer vision approaches, such as automated video-tracking, occurring over the past decade has enabled the collection of high-resolution movement data easily and quickly. In addition, recent methodological and technological innovations, mainly through the implementation of artificial intelligence and machine learning algorithms to video-tracking solutions, have empowered the amount of data collected, allowing, for instance, to track large groups of unmarked individuals simultaneously (e.g., idtracker.ai [26] and TRex [27]). Many open-source tracking solutions now exist and are under active development with great potential for the experimental study of animal behavior (for a recent review, see [28]). However, analyzing and

68 interpreting the data obtained through automated tracking solutions can remain challenging due
69 to their complexity, heterogeneity, and noisiness. In practice, some (possibly substantial) pre-
70 processing is required to make sense of the raw video-tracking data.

71 To address these challenges and promote the widespread use of video-tracking analyses, we
72 developed MoveR, an R package [29] for importing, filtering, analyzing, and visualizing animal
73 movement and behavior data obtained from common video-tracking solutions such as Ctrax,
74 Idtracker.ai, and TRex. MoveR includes a suite of flexible tools helping to clean data by removing
75 suspected tracking errors/artifacts and computing a range of metrics for quantifying animal
76 movement and behavior (e.g., speed, average neighbor distance). MoveR also allows the
77 computation of the mean and net square displacement values [30,31], which is helpful in inferring
78 population dispersal. In addition, the package includes an original unsupervised learning method
79 relying on density-based clustering [32] for classifying activity states (active vs. inactive) in a two-
80 dimensional space instead of the classic method, generally based on arbitrary thresholds of
81 traveled distance or speed.

82 To illustrate the utility of MoveR, we present a case study using video-tracking of a group of
83 parasitoid micro-wasps (*Trichogramma sp.)* exposed to a linear temperature ramp increasing from
84 35 to 45 degrees Celsius and then decreasing back to 35 degrees. We show how MoveR can
85 remove artifactual noise in the data, compute movement and behavior metrics, especially
86 identifying activity states, and thus estimate temperature tolerance thresholds. Our results
87 underline the utility of MoveR in improving the reproducibility and reliability of animal movement
88 and behavior data analyses and in facilitating the deployment of video-tracking techniques in an
89 era of open science.

90   1.2.   Related work

91 With the growing interest in the field of movement and behavioral studies, some proprietary
92 commercial software (e.g., Ethovision [34], LoliTrack - Loligo Systems ApS, Viborg, Denmark),
93 and more recently open source (e.g., AnimalTA [33]), video-tracking solutions have implemented
94 the possibility of running some data processing, computation, and visualization. However,
95 commercial solutions are often expensive, are based on point & click interfaces with limited
96 flexibility, and do not integrate the statistical tools that the constantly evolving R community
97 proposes.

98 On the other hand, several open-source R packages have been developed. However, they mainly
99 focus on simulating animal movement [35] or analyzing spatial data retrieved from G.P.S.
100 chipsets/collars or A.R.G.O.S. markers by investigating space use and habitat selection by wildlife
101 [36,37], or identifying behavioral states by fitting State–space [38] or hidden Markov models
102 [39,40] (for review see [41]).

103 To our knowledge, the only R package that preceded MoveR in analyzing animal movement in
104 such a flexible way is trajr [42]. However, while implementing the possibility of computing several
105 interesting metrics (e.g., sinuosity [43,44]) to analyze animal trajectories (i.e., a set of time-specific
106 discrete locations, generally restricted to two spatial dimensions), trajr lacks some useful
107 functionalities that may help both beginners and advanced user, for instance, to import raw

108 tracking data from various tracking software and then filter/clean them into R environment.
109 Accordingly, there is no solution on the R platform to perform pre-processing steps of raw tracking
110 data through detecting and filtering potential tracking artifacts, such as spurious detections or
111 changes in individual identity, which significantly skew results interpretation. In addition, there is
112 no method to handle regions of interest (R.O.I.) or analyze temporal trends across multi-individual
113 tracking sessions, which is crucial for studying behavior in changing environments (see Illustrative
114 examples section below).

115 For these reasons, MoveR intends to fill the gaps by providing a complete workflow that allows
116 easy import, management, filtering, evaluation, analysis, and visualization of automated video-
117 tracking solutions' output in a flexible, reproducible, reliable, and open framework as required to
118 push forward the shift toward open science that has been initiated in ecology, evolution and
119 related fields of research [45–47].

120

121 **2. Software description**
122

123 The MoveR R package is developed within the R environment, an open-source platform [29]
124 continuously evolving, which has been overgrown in the past years through user-contributed
125 packages, especially in ecology [48]. MoveR is fully coded in the base R language, meaning it
126 does not need any compilation. It is highly portable (available for Linux, OS X, and Microsoft
127 Windows) and only relies on few dependencies (Table 1).

128 *Table 1.* MoveR dependencies.

Dependencies	Functions
graphics*	
grDevices*	Display graphical elements.
hexbin	
progress	Display a progress bar showing the advancement of the computations.
reticulate	Import Python formatted data.
R.matlab	Import Matlab formatted data.
stats*	Perform basic calculations
pracma	Perform advanced calculations
trajr	Compute basic movement descriptors (e.g., speed, sinuosity)

*Included in R v3.6.2 and above

129

130 As the focal object tracked through video-tracking software may be from various taxonomic
131 groups or even be a moving object, we will refer to the term "particle" to specify the focal
132 object/animal tracked hereafter.

133

134 *2.1.* **Software architecture***:*
135

136 MoveR architecture relies on six main functionalities (Figure 1), providing tools (R functions) to (i)
137 import raw data output from various video-tracking software (Figure 1, blue-green box), (ii)

138 visualize pre- and post-processed tracklets (i.e., fragments of the track/trajectory followed by a
139 moving particle), (iii) manage regions of interest (R.O.I), (iv) evaluate the detection rate over the
140 tracking process using particles' positions manually annotated, (v) clean/filter potential tracking
141 artifact due to the experimental design, the study system (i.e., the focal species) or the tracking
142 algorithm based on user-defined filters (Figure 1, blue boxes). Finally, (vi) the MoveR workflow
143 enables the analysis of particles' tracklets through the computation of basic or more advanced
144 metrics describing animal movements (Figure 1, purple boxes). For example, advanced
145 functionalities allow the unsupervised classification of activity states, the computation of sociability
146 index or population dispersal (i.e., MSD and Dcoef), the computation of temporal trends, and the
147 identification of particular motifs of behavioral states or changes in areas' locations. In addition,
148 the resulting output is compatible with various R packages to conduct further statistical tests and
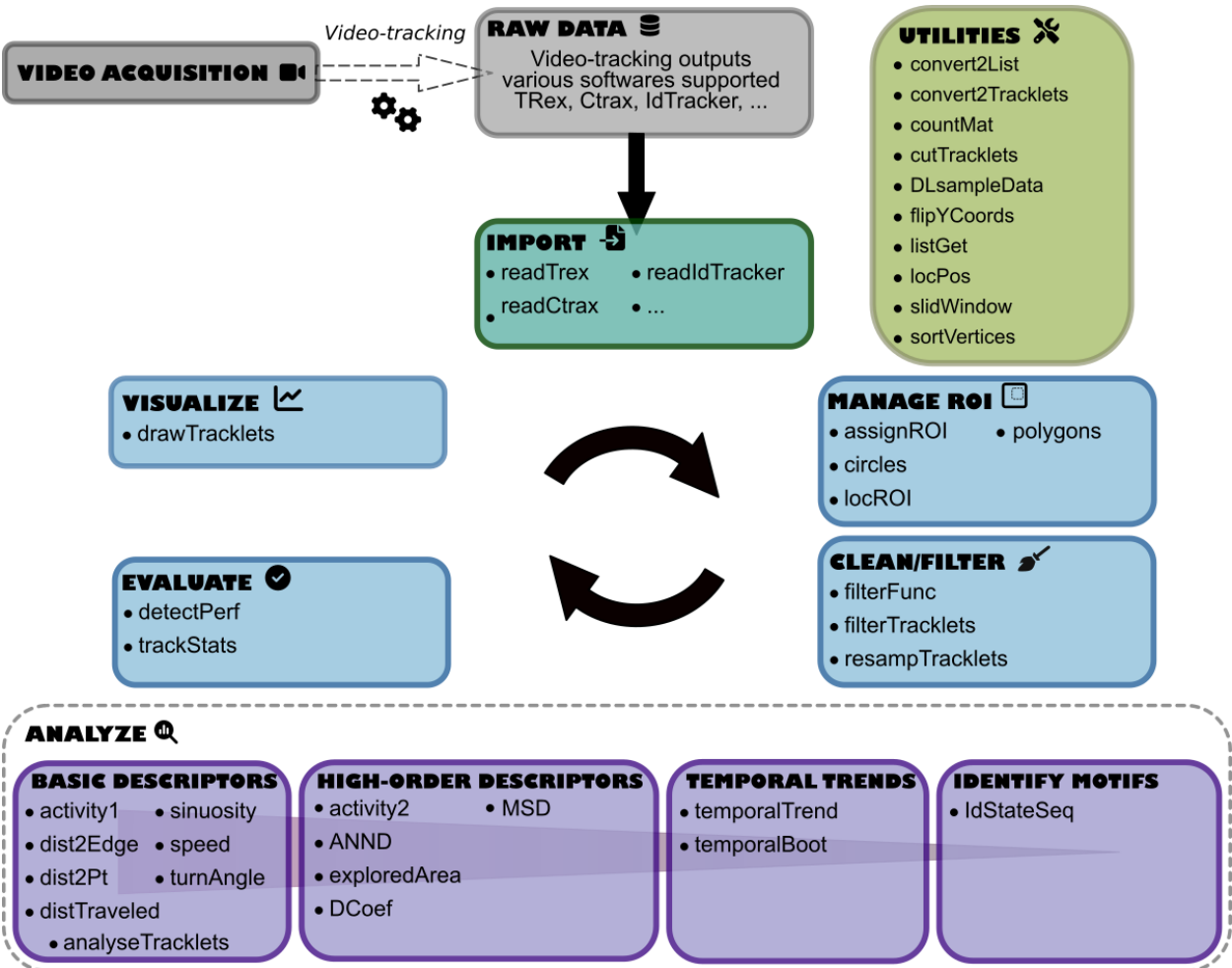149 modeling classically used in ecology and evolution (e.g., [49]).

150

151
152 **Figure 1.** *MoveR package workflow and six main functionalities: import, visualize, manage ROI, evaluate,*
153 *clean/filter, and analyze.*
154

| 155 | *2.2.* **Software** functionalities*:* |
| 156 | |

157 MoveR provides a highly flexible and unified environment relying on six main functionalities,
158 including explicitly named functions using camelCase programming conventions (see Figure 1
159 and Table 2).

160 **Table 2.** *Main functions provided by the MoveR package and quick description of what they help*
161 *to achieve.*

Functions	What it does	Details/Equations
IMPORT		
readAnimalTA()	Import AnimalTA tracking output .csv file.	http://vchiara.eu/index.php/animalta
readCtrax()	Import Ctrax tracking output .mat file.	https://ctrax.sourceforge.net/
readIdtracker()	Import idtracker.ai tracking output .npy file.	https://idtracker.ai/en/latest/index.html
readPlain()	Import plain tracking output from a table.	
readTrackR()	Import TrackR tracking output .csv file.	https://swarm-lab.github.io/trackR/index.html
readTrex()	Import Trex tracking output .npz files.	https://trex.run/
VISUALIZE		
drawTracklets()	Display tracklets on a plot.	
MANAGE ROI		
assignROI()	Assign ROI(s) identity to a particle's position.	
circles()	Generate points located on a circle's contour and draw circle(s).	
locROI()	Locate ROI.	
polygons()	Generate points located on polygon vertices and draw polygon(s).	
CLEAN/FILTER		
filterFunc()	Create and test a custom filter on tracklets.	
filterTracklets()	Apply a custom filter on tracklets.	
mergeFilters()	Merge condition tests (i.e., filterFunc outputs).	
resampTracklets()	Resampling tracklets.	
EVALUATE		
detectPerf()	Compute sensitivity index for particles detection.	
trackStats()	Summary statistics of the tracking data.	
ANALYSE: BASIC DESCRIPTORS		
activity1()	Determine active or inactive states according to the speed of particles along its trajectory.	
analyseTracklets()	Perform custom computation over a tracklet list.	
dist2Edge()	Compute the distance from the particle to the edge of an object (e.g., the arena) over its trajectory.	User can specify its own formula, although, a solution for circular arena is already implemented as follow: $$r = mean\left(\sqrt{(x_c - x_e)^2 + (y_c - y_e)^2}\right)$$ $$d_{jc} = \sqrt{\left(x_c - x_j\right)^2 + \left(y_c - y_j\right)^2}$$ $$d_e = d_{jc} - r$$
dist2Pt()	Compute euclidean distance between a particle and object(s).	$$d_{ij} = \sqrt{\left(x_j - x_i\right)^2 + \left(y_j - y_i\right)^2}$$
distTraveled()	Compute the distance traveled by a particle over a trajectory.	$$d_j = \sqrt{\left(x_j + P - x_j\right)^2 + \left(y_j + P - y_j\right)^2}$$
sinuosity()	Compute corrected rediscretized sinuosity index for a given tracklet.	$$S = 2\left[p\left(\frac{1+c}{1-c} + b^2\right)\right]^{-0.5}$$
speed()	Compute particle's speed over a trajectory.	$$s(t) = |v(t)| = \sqrt{\left(\frac{dx(t)}{dt}\right)^2 + \left(\frac{dy(t)}{dt}\right)^2}$$
turnAngle()	Compute particle's turning angle over a trajectory.	$$\theta = tan^{-1}\left(\frac{r}{i}\right)$$ $$\alpha_i = \theta_i - \theta_{i-1}$$
ANALYSE: HIGH-ORDER DESCRIPTORS		
activity2()	Determine active or inactive states according to density-based clustering method.	
ANND()	Compute the Average Nearest Neighbour Distance (ANND) among tracklets.	

exploredArea()	Compute the total surface explored and display the corresponding heatmap.	
MSD()	Compute the mean square displacement according to Kareiva & Shigesada (1983) or Turchin (2015). The Turchin's equation is a simplified version of the Kareiva & Shigesada' equation, assuming symmetric turning angles.	Kareiva & Shigesada: $$\alpha = \tan^{-1}\left(\frac{s}{\varphi}\right)$$ $$\gamma = ((1-\varphi)^2 - s^2)\cos(\alpha(n+1)) - 2s(1-\varphi)\sin(\alpha(n+1))$$ $$MSD = m_2 n + 2m_1^2\left(\frac{n(\varphi - s^2 - \varphi^2) - \varphi}{s^2 + (1-\varphi^2)} + \frac{(s^2+\varphi)^{\frac{n+1}{2}} + 2s^2}{(s^2+(1-\varphi)^2)^2}\gamma\right)$$ Turchin: $$MSD = m_2 n + 2m_1^2 \frac{\varphi}{(1-\varphi)^2}\left[\varphi^{n/2} - n\varphi + n - 1\right]$$
DCoef()	Compute the net square displacement (population spread) according to Kareiva & Shigesada (1983) or Turchin (2015). Turchin's equation is a simplified version of Kareiva & Shigesada' equation, assuming symmetric turning angles.	Kareiva & Shigesada: $$var(m) = m_2 - m_1^2$$ $$D\infty = \frac{a}{4}\left[var(m) + m_1^2\left(\frac{1 + \varphi - \frac{s^2}{1-\varphi}}{1 - \varphi - \frac{s^2}{1-\varphi}}\right)\right]$$ Turchin: $$D\infty = a\frac{m_2 + 2m_1^2\frac{\varphi}{1-\varphi}}{4}$$
ANALYSE: TEMPORAL TRENDS		
temporalTrend()	Perform analysis across tracklets and time.	
temporalBoot()	Compute 95% studentized CI across tracklets and time.	
ANALYSE: IDENTIFY MOTIFS		
IdStateSeq()	Identify and extract specified patterns/sequences from tracklets.	Use regular expressions (regex) to identify and capture patterns over tracklets.

r radius of the (circular) arena.

d_{jc} distance between the point j (particle) and the center of the (circular) arena.

x_i & y_i x and y coordinates of point i (an object).

x_j & y x and y coordinates of point j (a particle).

x_c & y_c x and y coordinates of the arena center (a circle).

x_e & y_e x and y coordinates of the arena edge (a circle).

$x_j + P$ & $y_j + P$ x and y coordinates of point j plus the step between consecutive points.

b step length coefficient of variation.

c measure of tortuosity.

p mean step length.

$x(t)$ & $y(t)$ x and y-coordinates as a function of time.

$\frac{dx(t)}{dt}$ & $\frac{dy(t)}{dt}$ rate of change of x and y-coordinates.

θ angle for a given complex number.

m_1 average displacement per step.

m_2 average square displacement per step.

a mean activity rate.

s average sine of turning angle per step.

φ average cosine of turning angle per step.

162

Briefly, **import** functionality allows raw data integration from software like Ctrax and idtracker.ai using intuitive read functions (e.g., readCtrax).

The visualize functionality allows displaying pre- or post-processed tracklets using `drawTracklets` function, which supports various customizations, including adding elements like R.O.I. or arena boundaries.

The manage R.O.I. functionality allows importing the location of area edges from a distance matrix generated using an image processing program (e.g., [50]) through the `locROI` function or by specifying it from scratch using `circles` or `polygons` functions. Once R.O.I.s are specified, the `assignROI` function can retrieve the particles' location among them.

172   **The clean/filter** functionality allows filtering the data according to user-defined functions
173   using the `filterFunc` function and passed to `filterTracklets`. Indeed, potential tracking artifacts
174   or identity switching may depend on experimental design or a particular system/focal species. A
175   quantitative summary of filtered data is also provided at the end of the filtering process.

176   **The evaluate** functionality allows computing a quantitative summary of the video and
177   tracking statistics (e.g., video duration, the number of tracklets, and their length and duration)
178   through the call to the `trackStats` function. It also allows to assess video-tracking and filtering
179   process accuracy by comparing manual and automated detections using the `detectPerf` function
180   (i.e., check the amount of true and false detection compared to manual annotation).

181   **The analyze** functionality is versatile and enables a wide range of calculations, either pre-
182   set (e.g., speed) or user-defined on tracklets, time, or space (e.g., across areas) and behavioral
183   state (e.g., among activity states) using functions like `analyseTracklets` and `temporalTrends`
184   and `idStateSeq`. Here, four types of functions can be described:

185   -   Basic descriptors can help to compute classic metrics over tracklets, such as speed and
186   sinuosity.
187   -   High-order descriptors can help to characterize activity states (i.e., active vs. inactive
188   states) using unsupervised learning methods with the `activity2` function according to the
189   density-based clustering method reported in [32] and implemented by [51]. Alternatively,
190   it also makes possible to compute the expected diffusion coefficient, a proxy of population
191   dispersal, assuming a correlated random walk model using the `Dcoef` function according
192   to [30,31].
193   -   The `temporalTrend` function returns the results of a given calculation (weighed by the
194   tracklet length or not) over time by averaging the value for a given time window over each
195   tracklet. Furthermore, computing a studentized 95% confidence interval by bootstrapping
196   over the tracklets is also possible with the `temporalBoot` function.
197   -   The `idStateSeq` function helps to identify and extract arbitrary patterns regarding
198   changes among behavioral states, spatial regions or areas of interest, patch crosses, or
199   any other motifs using a versatile regular-expression syntax.

200
201   MoveR offers extensive functionalities addressing various objectives; however, the upcoming
202   example will highlight only common procedures. For the installation procedure, more examples,
203   and tutorials on how to benefit from MoveR's potential, See the package documentation website
204   built with pkgdown v2.0.7. [52]: https://qpetitjean.github.io/MoveR/.
205
206   **3. Illustrative examples**
207
208   For this example, we download and import a sample dataset from the MoveR package using the
209   `DLsampleData` and `readTrex` functions (full code is reported in supplementary material).
210
211   Briefly, the dataset consists of video recording (1920x1080 pixels) of 24 parasitic micro-wasp
212   individuals (genus *Trichogramma*) placed in a circular arena (diameter: 2.5cm, see [53]) for 110
213   minutes at 25 fps (see the left panel of Figure 2). Over the exposure duration, the temperature

214 steadily increased from 18℃ to 45℃ and then decreased back to 18℃ (temperature changing
215 rate: 0.5℃ per minute). Individuals were then tracked using TRex (v1.1.3) [27]. To reduce space
216 allocation and computing time, we reduced the dataset by removing the movements recorded
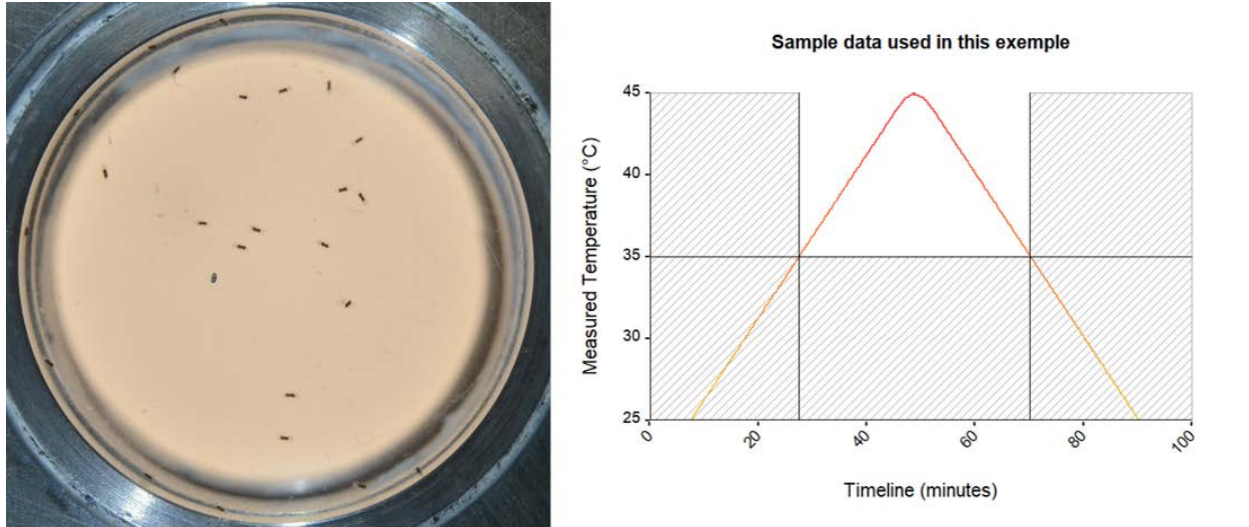217 below 35℃ (see the right panel of Figure 2).
218

219
220
221 ***Figure 2.*** *Frames extracted from a video recording of 24 parasitic micro-wasps (genus*
222 *Trichogramma) placed in a thermostated circular arena (left). Temperature ramp over which the*
223 *movements of parasitic micro-wasp were recorded. The shaded area corresponds to the part of*
224 *the data removed from the original dataset (i.e., moments where the temperature was below*
225 *35℃), while the white area corresponds to the remaining data used in the following example*
226 *(right).*
227
228 Here, we aim to clean the dataset, assign R.O.I. identities to particle locations, compute basic
229 descriptors, and identify activity states (active vs. inactive) on micro-wasps movements to display
230 temporal trends. In other words, we want to identify the moments where the general pattern of
231 micro-wasps movement changes.
232
233 After importing (`readTrex` function, for code, see supplementary material 2. Importing the data)
234 and cleaning the dataset by removing infinite values (i.e., undetected or lost particles), and
235 spurious detection performed outside the arena (for code, see supplementary material 3. Cleaning
236 the data), we are generating the coordinates of several circular R.O.I. with increasing distance to
237 the center of the arena (for code, see supplementary material 4. Identify the tracklets within an
238 ROI.). Then, using `assignROI`, we assign the R.O.I.'s identity to the particles' position and
239 visualize the tracklets using the `drawTracklets` function (see Figure 3). As the R.O.I.s are circular
240 and the larger ones include smaller ones, a particle detected within the center of the arena (ROI_1
241 in Figure 3) is also included within the larger R.O.I.s (e.g., particles in ROI_1 are also included in
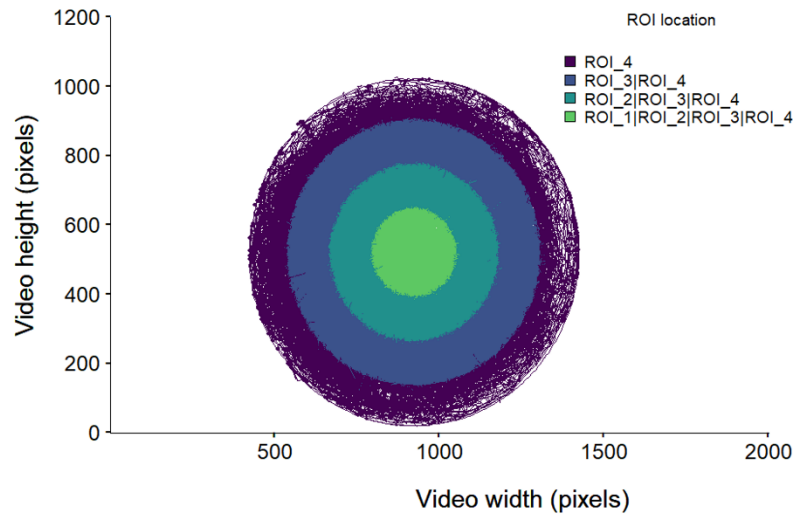242 ROI_2, 3 and 4, see Figure 3).
243

244

245

Figure 3. *Particle trajectories are colored according to their location among four circular R.O.I.s. Colors indicate the ROI where particles are detected. As larger R.O.I.s include smaller ones, particles located at the arena's center are considered within the R.O.I. 1, 2, 3, and 4.*

249

250 Next, we are computing some basic descriptors such as the speed, turning angle, turning angle
251 variance, and sinuosity (using `speed`, `turnAngle` and `sinuosity` functions, respectively; for
252 code, see supplementary material 5.1. Compute basic descriptors).

253

254 The previous basic descriptors then enable to identify the activity states based in a two-
255 dimensional space (i.e., the speed and the variance of the turning angle; for code, see
256 supplementary material 5.2 Activity states: 2D non-hierarchical clustering) using the `activity2`
257 function. This method uses the density-based clustering algorithm from [23] and implemented by
258 [41] to detect two clusters, assuming inactive states fit a Gaussian distribution. States within the
259 95% confidence ellipsis or below its major and minor radii are labeled inactive (0), and others as
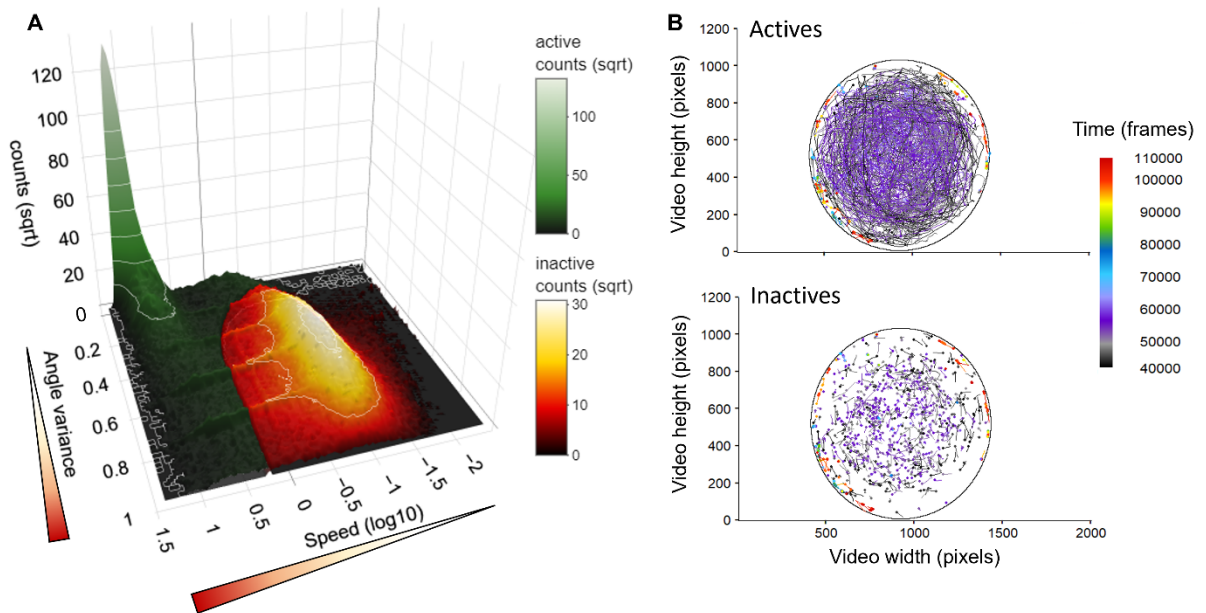260 active (1) (See Figure 4).

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262
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Figure 4. *3d density map of the active and inactive states according to the non-hierarchical classification (density-based clustering) performed on smoothed particles speed (log-transformed) and turning angle variance (A) and representation of a sample of active (B, upper panel) and inactive (B lower panel) parts of particles trajectories (i.e., 2000 tracklets). In the 3D density map (A), the active and inactive state distributions are respectively represented as a gradient of dark green to white and dark red to white according to the increasing number of counts. Also, for the representation of the active and inactive parts of a sample of the particles' trajectories (B), we can observe that the active tracklets are generally longer than the inactive parts.*

We then analyze the changes of previous descriptors over time using `temporalTrend` and `temporalBoot` functions, yielding a trend and a studentized 95% confidence interval. (For code, see supplementary material 5.3 Compute and draw temporal trends).

Finally, we can graphically (in this example) retrieve the moment at which movements start to decrease or even stop, as shown by both the evolution of the sinuosity (Figure 5A), the speed (Figure 5B), and the activity rate (Figure 5C) of the individuals over time.
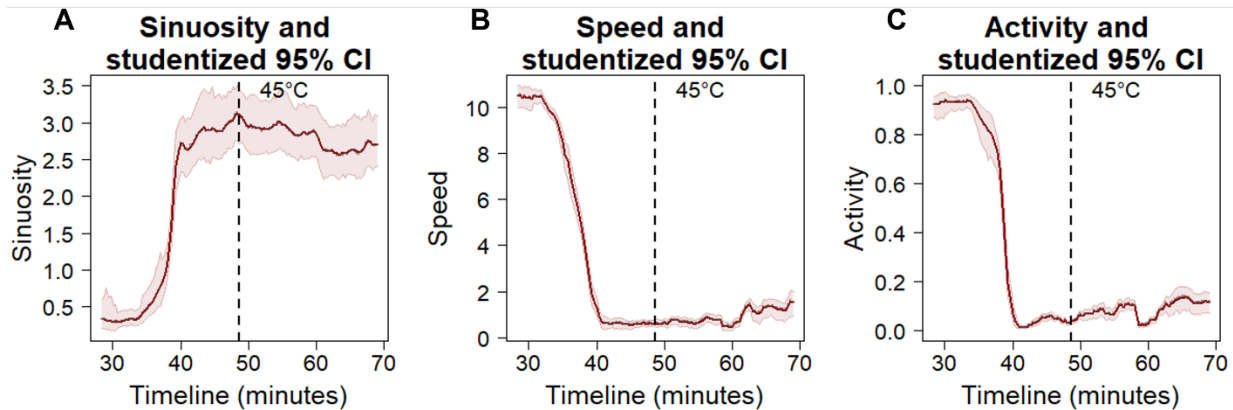
Figure 5. *Evolution of the sinuosity (A) speed (B) and activity (C) of Trichogramma individuals (dark red line) and studentized 95% confidence interval (light red envelope) over time (expressed in frame). The dashed line indicates when the maximum temperature has been reached over the ramp: 45°C.*

4. Impact

The tools developed in the MoveR R package workflow are designed to ease the management and analysis of video-tracking data for beginners and advanced users. By providing an efficient analysis pipeline, MoveR should pave the way for the increasing use of movement and behavioral data to tackle emergent questions encompassing the fields of ecology, evolution, and conservation biology. Here, we provide some examples of applications, but MoveR usages are not limited to these examples and may expand to a broader extent.

More precisely, MoveR can be used to investigate a large array of questions related to, for instance, the variability of responses among species, populations, or individuals by providing the necessary tools for animal video phenotyping. Indeed, while inter-specific variability of responses has been studied extensively, understanding the ecological drivers and effects of intra-specific variability on population dynamics and ecosystem functioning is still an emerging research field that needs further investigations [8,54]. While advances in machine learning algorithms conserving the identity of individuals within a group are growing, MoveR can efficiently allow specifying a reproducible and customized workflow for running computation among several individuals (i.e., tracklets) to, for instance, investigate further questions related to animal personality and syndromes [55–57] under laboratory or mesocosms settings.

In addition, under the context of global changes, the increasing use of synthetic compounds (especially in agricultural fields [58,59]) and the release of micropollutants such as pharmaceuticals [60], endocrine disruptors [61] or nanoparticles [62], and microplastics [63] MoveR represent an efficient tool to assess movements and behavioral alterations caused by such compounds on terrestrial and aquatic fauna. Indeed, the effects of contaminants and, more generally, multiple stressors and their interactive effects on animals' movement and behavior

314   have largely been overlooked until recently, despite a clear relationship between behavioral
315   alteration and cascading effects on individual and population fitness [4,5,64]. MoveR can hence
316   help ecophysiologists and ecotoxicologists assess the effects of various stress (e.g., xenobiotics,
317   parasitism, temperature changes) in animals by finding relevant and sensitive endpoints related
318   to animal movement and behavior.
319

320   Finally, MoveR can be useful for conservation purposes by, for instance, helping to better
321   understand how environmental or social factors affect movements and predict the dispersion of
322   invasive populations (i.e., progression front) [24] or biocontrol agents (i.e., pest-suppression
323   performance) [65] through video-phenotyping methods.
324

325   **5. Conclusions**
326

327   Collection, analyses, and resulting interpretations of movement and behavioral data overlap the
328   boundaries of several disciplines. Yet, the difficulties encountered in easily and efficiently
329   managing such a large amount of data still prevent us from tackling emerging questions linked to
330   fundamental ecology and evolution and their application to conservation biology. For this reason,
331   giving access to a flexible, reliable, and open framework to the scientific and conservation
332   manager communities is critical. MoveR includes a suite of flexible tools for importing, cleaning,
333   and filtering raw data from several video-tracking softwares and allows to compute basic and
334   more advanced metrics to quantify animal movement and behavior easily within a reproducible
335   environment.
336

347   **Data availability**
348   The data used to illustrate the use of the MoveR package in this article is hosted in the following
349   GitHub repository: https://github.com/qpetitjean/MoveR_SampleData, and can be directly
350   imported into the R environment using the `DLsampleData` function of the MoveR package. The
351   code used to illustrate the use of the MoveR package in this article is included in the
352   supplementary material. However, a more extensive version of this example/tutorial can be
353   found in the "*How to*" section of the package documentation website built with pkgdown v2.0.7.
354   [52]: https://qpetitjean.github.io/MoveR/

355

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