nomads

Exploring the pattern and drivers of nomadism in large solitary carnivores

Function explanation

step1 Fix time window length

- **Description**

This function is to find the fixed time window length for a resident movement track.

- **Usage**

time_lag_var <- step1(mvtrk, window = 1:30, method = "smooth")

- **Arguments**

mvtrk: A dataframe for one animal individual, containing columns named "x", "y", and "Time". "x" and "y" should be numeric vectors, representing the coordinates of tracking locations. "Time" should be a lubricate format datetime object containg year, month, day, hour, minute, second.

window: Numeric vector, the time window lengths to be calculated.

method: Character, specifying the method used to find the fixed time window. (This function is still under construction)

- **Value**

Returned dataframe will contain two columns, "time_lag" and "var". (This will be further improved, will return a fixed time window length only)

- **Authors**

J. W. wrote the function; H. B. and J. W. conceptualized the idea.

step2 Calculate oscillation values based on fixed time window length

- **Description**

This function serves for the plotting the oscillation of used area size for one movement track. Better used with further plotting.

- **Usage**

disp_outl <- step2(mvtrk, STBL_PRED = 7)

ggplot(disp_outl, aes(x = time, y = Var, color = as.factor(clusterID))) + geom_point(alpha = 0.5, size = 0.5) + theme_bw() + xlab("Time") + ylab("Variance")

- **Arguments**

mvtrk: A dataframe for one animal individual, containing columns named "x", "y", and "Time". "x" and "y" should be numeric vectors, representing the coordinates of tracking locations. "Time" should be a lubricate format datetime object containg year, month, day, hour, minute, second.

STBL_PRED: A number indicating fixed time window. Default set as 7 (days).

- **Value**

Returned dataframe will classify all movement points to residence or non-residence phase, excluding points within the last 7 (or other values set for PRED STBL) days. Columnes include "time" and "clusterID". Points representing residence phase will be assigned 0 for cluster ID, while other non-residence phases will each have a distinct ID.

- **Authors**

J. W. wrote the function; H. B. and J. W. conceptulized the idea.

***step3* Calculate movement features for each phase**

- **Description**

This function is to calculate the intended movement features of each phase. Residence phase will have resident patch size and resident period. Non-resident phase will have displacement, distance (accumulated steps), and period.

- **Usage**

features <- (mvtrk, disp_outl, STBL_PRED = 7)

#see residence phase features features[[1]]

#see non-residence phase features features[[2]]

- **Arguments**

mvtrk: A dataframe for one animal individual, containing columns named "x", "y", and "Time". "x" and "y" should be numeric vectors, representing the coordinates of tracking locations. "Time" should be a lubricate format datetime object containg year, month, day, hour, minute, second.

disp_outl: the returned dataframe of function *step2*, should be in accordance with **mvtrk**, belonging to the same track.

STBL_PRED: A number indicating fixed time window. Default set as 7 (days).

- **Values**

The returned list will have 2 elements. The first one stands for the residence phases, while the second for the non-residence phases.

- **Authors**

J. W. wrote the function; H. B. and J. W. conceptulized the idea.