

Package ‘UseScape’

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Title Clustering of movement metrics to create a spatial representation of the type of use an animal makes on the landscape

Version 0.0.0.1

Description Extraction of properties related to intensity of use such as the number of visits, the average and variation in time spent, and the average and variation in interval between visits. UseScape then combines and synthesizes these properties into a single spatial representation of the type of use an animal makes on the landscape. Spatial representation of use takes previously extracted movement data and clusters them using mixture-modeling. This visual representation informs users on the functional role a location plays for their species of interest.

Depends adehabitatLT, mclust, moveHMM

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clust_stack	<i>Back-association of population-level clustering to individual clusters</i>
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Description

Generate individual-level rasters of population-level clustering. For each individual, the function generates a raster stack containing a raster of the most likely cluster, and several rasters giving the probability of observing each cluster.

Usage

```
clust_stack(ls1, pop, ind, table, min_fix = 3)
```

Arguments

table	The output of table_cluster
grid	The output of the loop function
pop_clust	The output of the pop_clust function
ind_clust	The output of the ind_clust function

Value

A list of raster stack object.

Examples

```
data(puehcirc)
traj<-na.omit(puehcirc)
ls1<-loop_id(traj, res=300)
table<-table_cluster(traj, ls1)
ind<-ind_clust(table)
pop<-pop_clust(traj, ind)
stack<-clust_stack(ls1, pop, ind, table, min_fix = 3)
plot(stack[[1]][[1]]) #Plot first individuals
plot(stack[[2]][[1]]) #Plot second individuals
```

clust_use	<i>Function for clustering intensity of use metrics</i>
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Description

Apply mixture-model clustering to intensity of use metrics("Number visits", "Total duration", "Mean duration", "CV duration", "SD duration", "Mean interval", "CV interval", "SD interval")

Usage

```
clust_use(stck, col = c(1, 2, 3, 4, 6, 7), nb_clust = 1:5, min_fix = 3)
```

Arguments

stack	stack that is produced from timing2stack
col	specific parameters to be used ("Number visits", "Total duration", "Mean duration", "CV duration", "SD duration", "Mean interval", "CV interval", "SD interval"). By default, the function exclude SD Duration and SD interval.
nb_clust	select the range of possible clusters that may be identified
min_fix	set the minimum number of fixes within a cell for it to be included in the clustering (3 is the minimum when considering cv_duration and cv_interval)

Details

The function applies mixture-model clustering using the mclust package to a stack of intensity of use metrics.

Value

return a list with the clustering outputs, a raster of the classification ,and a raster of associated uncertainty.

Examples

```
traj1<-sim_mov(type="OU", npatches=3, grph=T)
timing_ls<-traj2timing(traj1, res=50, grid=NULL)
stack<-timing2stack(timing_ls, col=1,2,3,4,6,7)
test<-clust_use(stack)
plot(test[[2]], col=c("grey", "blue", "green", "red", "purple", "orange"))
plot(test[[3]]) #Uncertainty
mask<-mask_uncertain(test, p=0.01)
plot(mask, col=c("grey", "blue", "green", "red", "purple", "orange"))
```

ind_clust

*Individual-level clustering of intensity of use metrics***Description**

Perform individual-level clustering (first step) of intensity of use metrics. This function uses the output of table_cluster and perform a mixture-model. Users can select which variables will be used and the maximum number of clusters. See also mclust

Usage

```
ind_clust(
  table,
  nb_clust = 1:5,
  min_fix = 3,
  vars = c("Number.visits", "Total.duration", "Mean.duration", "CV.duration",
    "Mean.interval", "SD.interval")
)
```

Arguments

table	An output from the table_cluster function
nb_clust	The number of clusters to be tested, see the documentation for mclust for more information. Default = 1:5.
min_fix	The minimum of locations in a pixel needed to be included in the analysis. Default=3.
vars	The variable to be included. Default = c("Number.visits", "Total.duration", "Mean.duration", "CV.duration", "Mean.interval", "SD.interval")

Value

A list object with each element representing an individual.

Examples

```
data(puechcirc)
traj<-na.omit(puechcirc)
ls1<-loop_id(traj, res=300)
table<-table_cluster(traj, ls1)
ind<-ind_clust(table)
pop<-pop_clust(traj, ind)
stack<-clust_stack(ls1, pop, ind, table, min_fix = 3)
plot(stack[[1]][[1]]) #Plot first individuals
plot(stack[[2]][[1]]) #Plot second individuals
```

loop_id	<i>Looping over all individuals</i>
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Description

Extract the timing history and intensity of use metrics for all individuals in a traj object

Usage

```
loop_id(traj, res = 100)
```

Arguments

traj	An object produce by the function adehabitatLT with multiple individuals
res	Grid size, will be apply to all individuals

Value

A list object containing a raster stack object for each individual

Examples

```

data(puechcirc)
traj<-na.omit(puechcirc)
ls1<-loop_id(traj, res=300)
table<-table_cluster(traj, ls1)
ind<-ind_clust(table)
pop<-pop_clust(traj, ind)
stack<-clust_stack(ls1, pop, ind, table, min_fix = 3)
plot(stack[[1]][[1]]) #Plot first individuals
plot(stack[[2]][[1]]) #Plot second individuals

```

mask_uncertain	<i>Mask uncertain pixel from classification</i>
----------------	---

Description

Remove pixel with uncertainty higher than a specific value from a plot

Usage

```
mask_uncertain(out, p = 0.05)
```

Arguments

out	output of clust_use
p	uncertainty threshold (values with uncertainty higher than p will be masked). Default = 0.05

Details

Remove pixel with uncertainty higher than a specific value from a plot

Value

return a raster object

Examples

```

traj1<-sim_mov(type="OU", npatches=3, grph=T)
timing_ls<-traj2timing(traj1, res=50, grid=NULL)
stck<-timing2stack(timing_ls, col=1,2,3,4,6,7)
test<-clust_use(stck)
plot(test[[2]], col=c("grey", "blue", "green", "red", "purple", "orange"))
plot(test[[3]]) #Uncertainty
mask<-mask_uncertain(test, p=0.01)
plot(mask, col=c("grey", "blue", "green", "red", "purple", "orange"))

```

pop_clust	<i>Population-level clustering of intensity of use metrics</i>
-----------	--

Description

Combine individual-level clustering of movement metrics into a population-level clustering (second step). Users can define the number of clusters. See also mclust

Usage

```
pop_clust(traj, ls, n_clust = 1:5)
```

Arguments

traj	The trajectory object
ls	Individual-level clustering object, the output of ind_clust.
n_clust	The number of clusters to be tested, see the documentation for mclust for more information. Default = 1:5.

Value

A list object with each element representing an individual.

Examples

```
data(puechcirc)
traj<-na.omit(puechcirc)
ls1<-loop_id(traj, res=300)
table<-table_cluster(traj, ls1)
ind<-ind_clust(table)
pop<-pop_clust(traj, ind)
stack<-clust_stack(ls1, pop, ind, table, min_fix = 3)
plot(stack[[1]][[1]]) #Plot first individuals
plot(stack[[2]][[1]]) #Plot second individuals
```

res_test	<i>Test several pixel sizes (resolution) and estimate the coefficient of variation in residency time</i>
----------	--

Description

Test several pixel sizes (resolution) and estimate the coefficient of variation in residency time

Usage

```
res_test(mov, res_seq = c(50, 100, 150), unit_time = "secs")
```

Arguments

mov	simulated movement, replace with trajectory object of interest
res_seq	a vector of pixel size.
unit_time	time unit for parameters

Details

The function estimates the coefficient of variation in residency time calculated over grid of varying pixel size and produce a graph showing their values

Value

a graph showing the coefficient of variation in residency time as a function of pixel size.

Examples

```
code examples using function - these are vital #####
traj1<-sim_mov(type="OU", npatches=3, grph=T)
res_test(traj1, res_seq=c(50,100,150))
```

sim_mov

Simulation of patch-based movement trajectory

Description

Simulate a movement trajectory with a user defined number of patches and interpatch movement.

Usage

```
sim_mov(
  type = c("2states", "OU"),
  npatches = 5,
  ratio = 5,
  nswitch = 150,
  ncore = 200,
  spacecore = 200,
  seq_visit = sample(1:npatches, nswitch, replace = T),
  stepDist = "gamma",
  angleDist = "vm",
  stepPar = c(0.5, 3, 1, 5),
  anglePar = c(pi, 0, 0.5, 2),
  s = diag(40, 2),
  grph = F
)
```

Arguments

type	whether movement within patches should be based on a 2states process (from package moveHMM) or a Bivariate Ornstein-Uhlenbeck process (OU) (from package adehabitatLT)
npatches	Number of patches, default=5
ratio	Ratio (in percent) of locations associated to interpatch movement, default=5
nswitch	Number of switch/depart from patches, default=150
ncore	Number of locations within a patch per visit, default=200
spacecore	Minimum distance between center of patches, default=200
seq_visit	Specify the sequence of visit among patches, default is random sequence
stepDist	Distribution for step length if 2states specified in type, see simData of moveHMM package
angleDist	Distribution for turn angle if 2states specified in type, see simData of moveHMM package
stepPar	Parameters for step length distribution if 2states specified in type, see simData of moveHMM package
anglePar	Parameters for turn angle distribution if 2states specified in type, see simData of moveHMM package
s	Parameters for the OU process, see simm.mou of adehabitatLT package
grph	Whether a graph of the trajectory should be produced, default=F

Details

See moveNT package

Value

A lttraj (adehabitatLT) object

Examples

```
traj1<-sim_mov(type="OU", npatches=3, grph=T)
traj2<-sim_mov(type="2states", npatches=2, grph=T)
```

table_cluster

Convert a list of timing2stack object to a data.frame for clustering

Description

Convert output of loop_id function to a data.frame.

Usage

```
table_cluster(traj, ls)
```


Arguments

traj	The trajectory used in loop (a traj object)
ls	The output of the loop_id function

Value

A data.frame object.

Examples

```
data(puechcirc)
traj<-na.omit(puechcirc)
ls1<-loop_id(traj, res=300)
table<-table_cluster(traj, ls1)
ind<-ind_clust(table)
pop<-pop_clust(traj, ind)
stack<-clust_stack(ls1, pop, ind, table, min_fix = 3)
plot(stack[[1]][[1]]) #Plot first individuals
plot(stack[[2]][[1]]) #Plot second individuals
```

timing2stack	<i>Timing history to raster stack conversion</i>
--------------	--

Description

Extract use metrics from timing history

Usage

```
timing2stack(timing_ls, unit_time = "secs")
```

Arguments

timing_ls	timing history for each pixel
unit_time	time unit for timing_ls parameter

Details

This function extract the intensity of use metrics from the timing history and return a stack object of a raster layer for each metric.

Value

a raster stack object

Examples

```
traj1<-sim_mov(type="OU", npatches=3, grph=T)
timing_ls<-traj2timing(traj1, res=50, grid=NULL)
stck<-timing2stack(timing_ls)
plot(stck)
```

traj2timing

*Calculation of timing history from movement data***Description**

Transform an ltraj object to a timing history (entry and exit time in each pixel) using a user-specified grid size.

Usage

```
traj2timing(mov, res = 100, grid = NULL)
```

Arguments

mov	Movement trajectory, need to be a ltraj object
res	Grid size (based on coordinate system of movement trajectory)
grid	User specified grid (a raster), needs to have a larger extent than the movement trajectory

Details

Using a specific grid cell size, this function return the timing history (entry and exit time in each pixels) based on an individual trajectory.

Value

A list of objects containing the timing history and the grid use.

Examples

```
traj1<-sim_mov(type="OU", npatches=3, grph=T)
timing_ls<-traj2timing(traj1, res=50, grid=NULL)
```

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