Package ‘segclust2d’

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Type Package

Title Bivariate Segmentation/Clustering Methods and Tools

Version 0.3.3

URL `https://github.com/rpatin/segclust2d`

BugReports `https://github.com/rpatin/segclust2d/issues`

Description Provides two methods for segmentation and joint segmentation/clustering of
bivariate time-series. Originally intended for ecological segmentation
(home-range and behavioural modes) but easily applied on other series,
the package also provides tools for analysing outputs from R packages 'moveHMM' and 'marcher'.
The segmentation method is a bivariate extension of Lavielle's method available in 'adehabitatLT'
(Lavielle, 1999 <doi:10.1016/S0304-4149(99)00023-X> and 2005 <doi:10.1016/j.sigpro.2005.01.012>).
This method rely on dynamic programming for efficient segmentation.
The segmentation/clustering method alternates steps of dynamic programming with an Expectation-Maximization algorithm.
This is an extension of Picard et al (2007) <doi:10.1111/j.1541-0420.2006.00729.x> method
(formerly available in 'cghseg' package) to the bivariate case.
The method is fully described in Patin et al (2018) <doi:10.1101/444794>.

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LazyData TRUE

RoxygenNote 7.3.1

Depends R (>= 3.3.0)

Imports RColorBrewer (>= 1.1-2), dplyr (>= 1.0.0), plyr (>= 1.8.4),
reshape2 (>= 1.4.1), ggplot2(>= 2.1.0), magrittr, Rcpp, zoo,
grDevices, graphics, stats, utils, scales, rlang, methods, cli

Suggests knitr, rmarkdown, testthat, dygraphs (>= 1.1.1-1), xts (>=
0.9-7), leaflet (>= 1.0.1), sp (>= 1.2-3), adehabitatLT,
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R topics documented:

add_covariates *Covariate Calculations*

Description

Add several covariates to movement observations `add_covariates` add several covariates to a data frame with movement information. It adds : distance between location, spatial angle, speed, smoothed speed, persistence and rotation velocity (calculated with spatial angle).

Usage

```
add_covariates(x, ...)

## S3 method for class 'Move'
add_covariates(x, coord.names = c("x", "y"), ...)

## S3 method for class 'ltraj'
add_covariates(x, coord.names = c("x", "y"), ...)

## S3 method for class 'data.frame'
add_covariates(
  x,
  coord.names = c("x", "y"),
  smoothed = FALSE,
  timecol = "dateTime",
  units = "hour",
  radius = NULL,
  ...
)
```

Arguments

`x`	movement data
`...`	additional arguments
`coord.names`	names of coordinates column in `x`
`smoothed`	whether speed are smoothed or not
`timecol`	names of POSIXct time column
`units`	units for time calculation. Default "hour"
`radius`	for spatial angle calculations

Value

data.frame with additional covariates

Examples

```
## Not run: add_covariates(move_object, coord.names = c("x","y"), smoothed = T)
## Not run:
data(simulmode)
simple_data <- simulmode[,c("dateTime","x","y")]
full_data   <- add_covariates(simple_data, coord.names = c("x","y"),
 timecol = "dateTime",smoothed = TRUE, units ="min")

## End(Not run)
```

`angular_speed` *Calculate angular speed along a path*

Description

`angular_speed` calculate turning angle between locations, taking a dataframe as input.

Usage

```
angular_speed(x, coord.names = c("x", "y"))
```

Arguments

`x`	data.frame with locations
`coord.names`	names of coordinates column in `x`

Value

vector of turning angle.

Author(s)

Remi Patin, Simon Benhamou.

`apply_rowSums` *apply_rowSums*

Description

Internal function for Expectation-Maximization (EM) algorithm.

Usage

```
apply_rowSums(rupt, x)
```

Arguments

`rupt`	current estimated breaks in signal
`x`	bivariate signal

`apply_subsampling` *Internal function for subsampling*

Description

if subsample = FALSE do nothing.

Usage

```
apply_subsampling(x, is_segclust, subsample, subsample_over, subsample_by)
```

Arguments

`x`	data.frame to be subsampled
`is_segclust`	TRUE or FALSE whether the function was called from ‘segclust()‘ or ‘segmentation()‘
`subsample`	if FALSE disable subsampling
`subsample_over`	maximum number of row accepted
`subsample_by`	subsampling parameters

Details

else if subsample_by is missing, subsample only if nrow(x) > subsample_over, then it subsample with the minimum needed to get a data.frame smaller than subsample_over

if subsample_by is provided, use it to subsample.

Value

a data.frame

`argcheck_diag.var` *Check for argument 'diag.var'*

Description

Check whether argument 'diag.var' was provided. If not, propose default value.

Usage

```
argcheck_diag.var(diag.var, seg.var)
```

Arguments

`diag.var`	names of the variables on which statistics are calculated.
`seg.var`	for behavioral segmentation: names of the variables used for segmentation (either one or two names).

Value

a vector of character string

`argcheck_Kmax` *Check for argument 'Kmax'*

Description

Check whether argument 'Kmax' was provided and is adequate before subsampling. Propose adequate value if Kmax is not provided.

Usage

```
argcheck_Kmax(Kmax, lmin, datalength)
```

Arguments

`Kmax`	maximum number of segments.
`lmin`	minimum length of segments.
`datalength`	length of data provided

Value

an integer

`argcheck_lmin` *Check for argument 'lmin'*

Description

Check whether argument 'lmin' was provided and is adequate before subsampling

Usage

```
argcheck_lmin(lmin, is_segclust)
```

Arguments

`lmin`	minimum length of segments.
`is_segclust`	TRUE if function is called from `segclust` ; FALSE otherwise, if function is called from `segmentation`.

Value

a NULL object

`argcheck_ncluster` *Check for argument 'ncluster'*

Description

Check whether argument 'ncluster' was provided and is adequate

Usage

```
argcheck_ncluster(ncluster, Kmax)
```

Arguments

`ncluster`	number of cluster into which segments should be grouped. Can be a vector if one want to test several number of clusters.
`Kmax`	maximum number of segments.

Value

a NULL object

`argcheck_order.var` *Check for argument 'order.var'*

Description

Check whether argument 'order.var' was provided. If not, propose default value.

Usage

```
argcheck_order.var(order.var, diag.var)
```

Arguments

`order.var`	names of the variable with which states are ordered.
`diag.var`	names of the variables on which statistics are calculated.

Value

a vector of character string

`argcheck_ordering` *Check for argument 'order'*

Description

Check whether argument 'order' was provided for plot.segmentation and segmap. If not, propose default value.

Usage

```
argcheck_ordering(order, seg.type, order.var)
```

Arguments

`order`	TRUE or FALSE depending on whether cluster be ordered
`seg.type`	types of the segmentation
`order.var`	name of the variable to order the cluster

Value

a boolean

`argcheck_scale.variable` *Check for argument 'scale.variable'*

Description

Check whether argument 'scale.variable' was provided. If not, propose default value.

Usage

```
argcheck_scale.variable(scale.variable, is_segclust)
```

Arguments

`scale.variable`	minimum length of segments.
`is_segclust`	TRUE if function is called from `segclust` ; FALSE otherwise, if function is called from `segmentation`.

Value

a boolean

`argcheck_seg.var` *Check for argument 'seg.var'*

Description

Check whether argument 'seg.var' was adequately provided. If provided, also check for its length (1 or 2) and for the existence of corresponding column names in x If unprovided, use default value (segmentation only) and tests if column names exists.

Usage

```
argcheck_seg.var(x, seg.var, is_segclust)
```

Arguments

`x`	data used for segmentation. Supported: data.frame, Move object, ltraj object
`seg.var`	for behavioral segmentation: names of the variables used for segmentation (either one or two names).
`is_segclust`	TRUE if function is called from `segclust` ; FALSE otherwise, if function is called from `segmentation`.

Value

a list with a data.frame and a vector with two character strings

`argcheck_segclust` *Check for argument 'ncluster' and 'nseg'*

Description

Check whether argument 'ncluster' and 'nseg' were provided. If not, propose default value based on BIC.

Usage

```
argcheck_segclust(ncluster, nseg, ncluster.BIC, Kopt.BIC)
```

Arguments

`ncluster`	number of cluster
`nseg`	number of segment
`ncluster.BIC`	optimal number of cluster selected by BIC
`Kopt.BIC`	optimal number of segment selected by BIC for each number of cluster

Value

a list with two integers

`argcheck_segmentation` *Check for argument 'nseg'*

Description

Check whether argument 'nseg' was provided. If not, propose default value based on Lavielle's criterium

Usage

```
argcheck_segmentation(nseg, Kopt.lavielle)
```

Arguments

`nseg`	number of segment
`Kopt.lavielle`	optimal number of segment selected with Lavielle's criterium

Value

an integer

argcheck_type_coord *Check for deprecated 'type' and 'coord.names' argument*

Description

Check whether argument 'type' and 'coord.names' were provided and communicate adequately if need be.

Usage

```
argcheck_type_coord(...)
```

Arguments

`...`	additional parameters transmitted from `segmentation` or `segclust`

Value

a NULL object

arma_repmat *arma_repmat*

Description

C++ Armadillo version for repmat function. Repeat a matrix in bloc.

Usage

```
arma_repmat(A, n, m)
```

Arguments

`A`	matrix
`n`	number of repetition in line
`m`	number of repetition in column

`augment` *Generic function for augment*

Description

see broom::augment for more informations

Usage

```
augment(x, ...)
```

Arguments

`x`	object to be augmented
`...`	additional arguments

`bisig_plot` *bisig_plot draws the plots of the bivariate signal on the same plot (scale free)*

Description

bisig_plot draws the plots of the bivariate signal on the same plot (scale free)

Usage

```
bisig_plot(x, rupt = NULL, mu = NULL, pop = NULL, merge.seg = FALSE)
```

Arguments

`x`	the signal to be plotted
`rupt`	optional, if given add vertical lines at change points (rupt should a vector)
`mu`	optional the mean of each class of segment,
`pop`	optional the cluster to whom each segment belongs to,
`merge.seg`	should segment be merged ?

Value

no value

`calc_BIC` *Calculate BIC*

Description

`BIC` calculates BIC given log-likelihood, number of segment and number of class

Usage

```
calc_BIC(likelihood, ncluster, nseg, n)
```

Arguments

`likelihood`	log-likelihood
`ncluster`	number of cluster
`nseg`	number of segment
`n`	number of observations

Value

a data.frame with BIC, number of cluster and number of segment

`calc_dist` *Calculate distance between locations*

Description

`calc_dist` calculate distance between locations, taking a dataframe as input. Distance can also be smoothed over the two steps before and after the each point.

Usage

```
calc_dist(x, coord.names = c("x", "y"), smoothed = FALSE)
```

Arguments

`x`	data.frame with locations
`coord.names`	names of coordinates column in `x`
`smoothed`	whether distance are smoothed or not

Value

vector of distance

Author(s)

Remi Patin

Examples

```
## Not run: calc_dist(df,coord.names = c("x","y"), smoothed = T)
```

calc_speed *Calculate speed along a path*

Description

`calc_dist` calculate speed between locations, taking a dataframe as input. Speed can also be smoothed over the two steps before and after the each point.

Usage

```
calc_speed(
  x,
  coord.names = c("x", "y"),
  timecol = "dateTime",
  smoothed = FALSE,
  units = "hour"
)
```

Arguments

`x`	data.frame with locations
`coord.names`	names of coordinates column in `x`
`timecol`	names of POSIXct time column
`smoothed`	whether speed are smoothed or not
`units`	units for time calculation. Default "hour"

Value

vector of distance

Author(s)

Remi Patin

Examples

```
## Not run: calc_speed(df,coord.names = c("x","y"), timecol = "dateTime",
smoothed = T)
## End(Not run)
```

`calc_stat_states` *Calculate state statistics*

Description

`calc_stat_states` calculates statistics of a given segmentation : mean and variance of the different states.

Usage

```
calc_stat_states(data, df.segm, diag.var, order.var = NULL)
```

Arguments

`data`	the data.frame with the different variable
`df.segm`	output of prep_segm function
`diag.var`	names of the variables on which statistics are calculated
`order.var`	names of the variable with which states are ordered

Value

a data.frame with mean and variance of the different states

Examples

```
## Not run: calc_stat_states(data, diag.var = c("dist","angle"),
order.var='dist', type='hmm',hmm.model=mod1.hmm)
## End(Not run)
```

`check_repetition` *Check for repetition in the series*

Description

`check_repetition` checks whether the series have identical or near-identical repetition larger than lmin. if that is the case, throw an error, the algorithm cannot yet handle these repetition, because variance on the segment would be null.

Usage

```
check_repetition(x, lmin, rounding = FALSE, magnitude = 3)
```

Arguments

`x`	the bivariate series to be tested
`lmin`	minimum length of segment
`rounding`	whether or not series are rounded
`magnitude`	number of magnitude of standard deviation below which values are rounded. i.e if magnitude = 3, difference smaller than one thousandth of the standard deviation are rounded to the same value.

Value

a boolean, TRUE if there is any repetition larger or equal to lmin.

Examples

```
set.seed(42)
dat <- rbind(base::sample(seq(1,10),  size= 100, replace = TRUE),
             base::sample(seq(1,10),  size= 100, replace = TRUE))
check_repetition(dat, lmin = 3)
check_repetition(dat, lmin = 5)
```

`chooseseg_lavielle` *Internal Function for choosing optimal number of segment*

Description

Choosing optimal number of segment using Marc Lavielle's method. From Emilie Lebarbier. Method based on identifying breaks in the slope of the contrast.

Usage

```
chooseseg_lavielle(J, S = 0.75, ...)
```

Arguments

`J`	likelihood for each number of segment
`S`	threshold for choosing the number of segment. See adehabitatLT::chooseseg
`...`	additional arguments

Value

a list with optimal number of segment and full data.frame of the calculus

choose_kmax *Finding best segmentation with a different threshold S*

Description

Choosing optimal number of segment using Marc Lavielle's method. From Emilie Lebarbier. Method based on identifying breaks in the slope of the contrast.

Usage

```
choose_kmax(x, S = 0.75)
```

Arguments

`x`	`segmentation-class` object
`S`	threshold for choosing the number of segment. See adehabitatLT::chooseseg

Value

the optimal number of segment given threshold S.

Examples

```
## Not run:
res.seg <- segmentation(df, coord.names = c("x","y"), Kmax = 30, lmin = 10)
# find the optimal number of segment according to Lavielle's criterium with a
# different threshold.
choose_kmax(res.seg, S = 0.60)

## End(Not run)
```

colsums_sapply *colsums_sapply*

Description

Internal function for Expectation-Maximization (EM) algorithm.

Usage

```
colsums_sapply(i, rupt, x, mu, tau)
```

Arguments

`i`	number of signal
`rupt`	current estimated breaks in signal
`x`	bivariate signal
`mu`	mean parameter for each signal
`tau`	tau

`cumsum_cpp` *cumsum_cpp*

Description

C++ function for cumulative sum (replacing R cumsum)

Usage

```
cumsum_cpp(x)
```

Arguments

`x`	Numerical Vector

`DynProg` *DynProg computes the change points given a cost matrix matD and a maximum number of segments Kmax*

Description

DynProg computes the change points given a cost matrix matD and a maximum number of segments Kmax

Usage

```
DynProg(matD, Kmax)
```

Arguments

`matD`	the cost Matrix os size n x n
`Kmax`	the maximal number of segments

Value

a list with J.est a vector with Kmax value, the Kth is the minimum contrast for a model with K segments (-J.est is the log-likelihood) and with t.test a matrix, line K are the coordinates of the change points for a model with K segments

`DynProg_algo_cpp` *DynProg_algo_cpp*

Description

This function finds the best segmentation given a Cost Matrix using a dynamic programming algorithm. C++ implementation of DynProg

Usage

```
DynProg_algo_cpp(matD, Kmax)
```

Arguments

`matD`	Cost Matrix
`Kmax`	number of segments

`EM.algo_simultanee` *EM.algo_simultanee calculates the MLE of phi for given change-point instants*

Description

EM.algo_simultanee calculates the MLE of phi for given change-point instants

Usage

```
EM.algo_simultanee(x, rupt, P, phi, eps = 1e-06, sameSigma = FALSE)
```

Arguments

`x`	bivariate signal
`rupt`	the sequence of change points
`P`	number of clusters
`phi`	starting value for the parameter
`eps`	eps
`sameSigma`	TRUE if segments have the same variance

Value

a list with phi, the MLE, tau =(taukj) the probability for segment k to belong to class,lvinc = lvinc,empty = empty,dv = dv

`EM.algo_simultanee_Cpp` *EM.algo_simultanee calculates the MLE of phi for given change-point instants and for a fixed number of clusters*

Description

EM.algo_simultanee calculates the MLE of phi for given change-point instants and for a fixed number of clusters

Usage

```
EM.algo_simultanee_Cpp(x, rupt, P, phi, eps = 1e-06, sameSigma = FALSE)
```

Arguments

`x`	bivariate signal
`rupt`	the sequence of change points
`P`	number of clusters
`phi`	starting value for the parameter
`eps`	eps
`sameSigma`	TRUE if segments have the same variance

Value

a list with phi, the MLE, tau =(taukj) the probability for segment k to belong to class,lvinc = lvinc,empty = empty,dv = dv

`EM.init_simultanee` *EM.init_simultanee proposes an initial value for the EM algorithm based on a hierarchical clustering algorithm (ascending)*

Description

EM.init_simultanee proposes an initial value for the EM algorithm based on a hierarchical clustering algorithm (ascending)

Usage

```
EM.init_simultanee(x, rupt, K, P)
```

Arguments

`x`	the bivariate signal
`rupt`	the change point instants, data.frame
`K`	number of segments
`P`	number of clusters

Value

phi0 : candidate for the EMalgorithm

`Estep_simultanee` *Estep_simultanee computes posterior probabilities and incomplete-data log-likelihood for mixture models*

Description

Estep_simultanee computes posterior probabilities and incomplete-data log-likelihood for mixture models

Usage

```
Estep_simultanee(logdensity, phi, eps = 1e-09)
```

Arguments

`logdensity`	is a K*P matrix containing the conditional log-densities for each segment
`phi`	a list containing the parameters of the mixture
`eps`	eps

Value

a list with tau a K*P matrix, tau kj is the posterior probability for segment k to belong to class j and lvinc, the incomplete log likelihood P(X=x)

`find_mu_sd` *Find mean and standard deviation of segments*

Description

`find_mu_sd` calculates statistics of a given segmentation : mean and variance of the different states.

Usage

```
find_mu_sd(df.states, diag.var)
```

Arguments

`df.states`	a list of data.frame
`diag.var`	names of the variables on which statistics are calculated

Value

a data.frame with mean and variance of the different states

`Gmean_simultanee` *Gmean_simultanee calculates the cost matrix for a segmentation model with changes in the mean and variance for all signals*

Description

Gmean_simultanee calculates the cost matrix for a segmentation model with changes in the mean and variance for all signals

Usage

```
Gmean_simultanee(Don, lmin, sameVar = FALSE)
```

Arguments

`Don`	the bivariate signal
`lmin`	minimum size for a segment, default value is 2
`sameVar`	whether variance is the same for each segment.

Value

the cost matrix G(i,j) which contains the variance of the data between point (i+1) to point j

`Gmixt_algo_cpp` *Gmixt_algo_cpp*

Description

Internal C++ algorithm for computing the cost matrix.

Usage

```
Gmixt_algo_cpp(zi, lgi, P, mvec, wk, svec, prop)
```

Arguments

`zi`	vector of observations
`lgi`	vector of indices
`P`	number of class
`mvec`	vector of means for each class
`wk`	temporary vector for calculations
`svec`	vector of standard deviations for each class
`prop`	mixture vector

`Gmixt_simultanee` *Gmixt_simultanee calculates the cost matrix for a segmentation/clustering model*

Description

Return matrix G(i,j), the mixture density for segment between points (i+1) to j :

$$G(i,j) = \sum_{p=1}^{P} \log(\pi_p f(y^{ij};\theta_p))$$

Rq: this density if factorized in order to avoid numerical zeros in the log

Usage

```
Gmixt_simultanee(Don, lmin, phi)
```

Arguments

`Don`	the bivariate signal
`lmin`	the minimum size for a segment
`phi`	the parameters of the mixture

Value

a matrix

`Gmixt_simultanee_fullcpp` *Gmixt_simultanee_fullcpp*

Description

C++ function replacing Gmixt_simultanee

Usage

```
Gmixt_simultanee_fullcpp(Don, lmin, prop, mu, s)
```

Arguments

`Don`	Bivariate Signal
`lmin`	minimum length of segments
`prop`	mixture parameters
`mu`	mean parameters
`s`	standard deviation parameters

`hybrid_simultanee` `hybrid_simultanee` *performs a simultaneous seg - clustering for bivariate signals.*

Description

It is an algorithm which combines dynamic programming and the EM algorithm to calculate the MLE of phi and T, which are the mixture parameters and the change point instants. this algorithm is run for a given number of clusters, and estimates the parameters for a segmentation/clustering model with P clusters and 1:Kmax segments

Usage

```
hybrid_simultanee(
  x,
  P,
  Kmax,
  lmin = 3,
  sameSigma = TRUE,
  sameVar.init = FALSE,
  eps = 1e-06,
  lissage = TRUE,
  pureR = FALSE,
  ...
)
```

Arguments

`x`	the two-dimensional signal, one line per dimension
`P`	the number of classes
`Kmax`	the maximal number of segments
`lmin`	minimum length of segment
`sameSigma`	should segment have the same variance
`sameVar.init`	sameVar.init
`eps`	eps
`lissage`	should likelihood be smoothed
`pureR`	should algorithm run in full R or use Rcpp speed improvements
`...`	additional parameters

Value

a list with Linc, the incomplete loglikelihood =Linc,param=paramtau posterior probability

---

`initialisePhi` *initialisePhi is the constructor for a set of parameters for a segclust model*

Description

initialisePhi is the constructor for a set of parameters for a segclust model

Usage

```
initialisePhi(P, val = -Inf)
```

Arguments

`P`	number of classes
`val`	the value used for initialisation default is -Inf

Value

a set of parameter phi

`likelihood` *Generic function for likelihood*

Description

Generic function for likelihood

Usage

```
likelihood(x, ...)
```

Arguments

`x`	object from which likelihood can be extracted
`...`	additional parameters

`logdens_simultanee_cpp` *logdens_simultanee_cpp*

Description

Calculate logdensity of a bivariate signal

Usage

```
logdens_simultanee_cpp(xk, mu, sigma, prop)

logdens_simultanee(xk, phi)
```

Arguments

`xk`	the bivariate signal
`mu`	mean parameter for each signal
`sigma`	standard deviation parameter for each signal
`prop`	mixture parameter
`phi`	parameters of the mixture, P components

Value

the value of the log density

map_segm — `plot_segm` *plot segmented movement data on a map.*

Description

`plot_segm` plot segmented movement data on a map.

Usage

```
map_segm(
  data,
  output,
  interactive = FALSE,
  html = FALSE,
  scale = 1,
  UTMstring = "+proj=longlat +datum=WGS84 +no_defs",
  width = 400,
  height = 400,
  order = NULL,
  pointsize = 1,
  linesize = 0.5,
  coord.names = c("x", "y"),
  ...
)
```

Arguments

`data`	the data.frame with the different variable
`output`	outputs of the segmentation or segclust algorithm for one number of segment
`interactive`	should graph be interactive with leaflet ?
`html`	should the graph be incorporated in a markdown file through htmltools::tagList()
`scale`	for dividing coordinates to have compatibility with leaflet
`UTMstring`	projection of the coordinates
`width`	width
`height`	height
`order`	should cluster be ordered
`pointsize`	size of points
`linesize`	size of lines
`coord.names`	names of coordinates
`...`	additional arguments

Value

a ggplot object

Examples

```
## Not run:
#res.seg is a result of the segmentation-only algorithm :
nseg = 10
outputs = res.seg$outputs[[paste(nseg, "segments")]]
map <- map_segm(data=res.seg$data,output=outputs)
#res.segclust is a result of the segmentation-clusturing algorithm :
nseg = 10; ncluster = 3
outputs = res.segclust$outputs[[paste(ncluster,"class -",nseg, "segments")]]
map <- map_segm(data=res.seg$data,output=outputs)

## End(Not run)
```

`matrixRupt` *matrixRupt transforms a vector of change point into a data.frame with start and end of every segment*

Description

matrixRupt transforms a vector of change point into a data.frame with start and end of every segment

Usage

```
matrixRupt(x, vectorRupt)
```

Arguments

`x`	the
`vectorRupt`	the vector containing the change point

Value

the matrix of change point

`Mstep_simultanee` *Mstep_simultanee computes the MLE within the EM framework*

Description

Mstep_simultanee computes the MLE within the EM framework

Usage

```
Mstep_simultanee(x, rupt, tau, phi, sameSigma = TRUE)
```

Arguments

`x`	the bivariate signal
`rupt`	the rupture dataframe
`tau`	the K*P matrix containing posterior probabilities of membership to clusters
`phi`	the parameters of the mixture
`sameSigma`	TRUE if all segment have the same variance

Value

phi the updated value of the parameters

`Mstep_simultanee_cpp` *Mstep_simultanee computes the MLE within the EM framework*

Description

Mstep_simultanee computes the MLE within the EM framework

Usage

```
Mstep_simultanee_cpp(x, rupt, tau, phi, sameSigma = TRUE)
```

Arguments

`x`	the bivariate signal
`rupt`	the rupture dataframe
`tau`	the K*P matrix containing posterior probabilities of membership to clusters
`phi`	the parameters of the mixture
`sameSigma`	whether segments have the same variance

Value

phi the updated value of the parameters

`neighborsbis` *neighbors tests whether neighbors of point k,P can be used to re-initialize the EM algorithm and to improve the log-likelihood.*

Description

neighbors tests whether neighbors of point k,P can be used to re-initialize the EM algorithm and to improve the log-likelihood.

Usage

```
neighborsbis(
  kv.hull,
  x,
  L,
  k,
  param,
  P,
  lmin,
  eps,
  sameSigma = TRUE,
  pureR = FALSE
)
```

Arguments

`kv.hull`	convex hull of likelihood
`x`	the initial dataset
`L`	the likelihood
`k`	the points of interest
`param`	param outputs of segmentation
`P`	the number of class
`lmin`	minimal size of the segment to be implemented
`eps`	eps
`sameSigma`	should segments have same variance ?
`pureR`	should algorithm use only R functions or benefit from Rcpp faster algorithm

Value

smoothing likelihood

`plot_segm` *Plot segmentation on time-serie*

Description

`plot_segm` plot segmented time serie.

Usage

```
plot_segm(
  data,
  output,
  interactive = FALSE,
  diag.var,
  x_col = "expectTime",
  html = FALSE,
  order = FALSE,
  stationarity = FALSE
)
```

Arguments

`data`	the data.frame with the different variable
`output`	outputs of the segmentation or segclust algorithm for one number of segment
`interactive`	should graph be interactive through leaflet ?
`diag.var`	names of the variables on which statistics are calculated
`x_col`	column name for time
`html`	should the graph be incorporated in a markdown file through htmltools::tagList()
`order`	should cluster be ordered
`stationarity`	if TRUE, cut each segment in three and plot each part with its own mean to assess stationarity of each segment

Value

a graph

Examples

```
## Not run:
#res.segclust is the results of the segmentation-clustering algorithm
ncluster = 3
nseg = 10
 g <- plot_segm(data = res.segclust$data, output =
  res.segclust$outputs[[paste(ncluster,"class -",nseg, "segments")]],
   diag.var = x$`Diagnostic variables`,x_col = 'dateTime)
#res.seg is the results of the segmentation-only algorithm
```

```
nseg = 10
 g <- plot_segm(data = res.segclust$data,
 output = res.segclust$outputs[[paste(nseg, "segments")]],
  diag.var = x$`Diagnostic variables`,x_col = 'dateTime)


## End(Not run)
```

`plot_states` *Plot states statistics*

Description

`plot_states` plot states statistics

Usage

```
plot_states(outputs, diag.var, position_width = 0.3, order = FALSE)
```

Arguments

`outputs`	outputs of the segmentation or segclust algorithm for one number of segment
`diag.var`	names of the variables on which statistics are calculated
`position_width`	width between different model if several models are compared
`order`	should cluster be ordered

Value

a graph

Examples

```
## Not run:
#res.segclust is the results of the segmentation-clustering algorithm
ncluster = 3
nseg = 10
g <- plot_states(output = res.segclust$outputs[[
  paste(ncluster,"class -",nseg, "segments")
]],
diag.var = c("dist","angle2")
#res.seg is the results of the segmentation-only algorithm
nseg = 10
g <- plot_states(output = res.segclust$outputs[[paste(nseg, "segments")]],
diag.var = c("dist","angle2"))

## End(Not run)
```

prepare_HMM *Prepare HMM output for proper comparison plots*

Description

prepare_HMM

Usage

```
prepare_HMM(data, hmm.model = NULL, diag.var, order.var = diag.var[1])
```

Arguments

data	data
hmm.model	hmm.model
diag.var	diag.var
order.var	order.var

Examples

```
## Not run:
# Example taken from moveHMM package.
# 1. simulate data
# define all the arguments of simData
nbAnimals <- 1
nbStates <- 2
nbCovs <- 2
mu<-c(15,50)
sigma<-c(10,20)
angleMean <- c(pi,0)
kappa <- c(0.7,1.5)
stepPar <- c(mu,sigma)
anglePar <- c(angleMean,kappa)
stepDist <- "gamma"
angleDist <- "vm"
zeroInflation <- FALSE
obsPerAnimal <- c(50,100)

data <- moveHMM::simData(nbAnimals=nbAnimals,nbStates=nbStates,
                stepDist=stepDist,angleDist=angleDist,
                stepPar=stepPar,anglePar=anglePar,nbCovs=nbCovs,
                zeroInflation=zeroInflation,
                obsPerAnimal=obsPerAnimal)

### 2. fit the model to the simulated data
# define initial values for the parameters
mu0 <- c(20,70)
sigma0 <- c(10,30)
kappa0 <- c(1,1)
```

```
stepPar0 <- c(mu0,sigma0) # no zero-inflation, so no zero-mass included
anglePar0 <- kappa0 # the angle mean is not estimated,
# so only the concentration parameter is needed
formula <- ~cov1+cos(cov2)
m <- moveHMM::fitHMM(data=data,nbStates=nbStates,stepPar0=stepPar0,
         anglePar0=anglePar0,formula=formula,
         stepDist=stepDist,angleDist=angleDist,angleMean=angleMean)

### 3. Transform into a segmentation-class object
res.hmm <- prepare_HMM(data=data,
hmm.model = m, diag.var = c("step","angle"))
### 4. you can now apply the same function than for segclust2d outputs
plot(res.hmm)
segmap(res.hmm)

## End(Not run)
```

`prepare_shiftfit` *Prepare shiftfit output for proper comparison plots*

Description

`prepare_shiftfit`

Usage

```
prepare_shiftfit(
  data,
  shiftfit.model = NULL,
  diag.var,
  order.var = diag.var[1]
)
```

Arguments

`data`	data
`shiftfit.model`	shiftfit.model
`diag.var`	diag.var
`order.var`	order.var

Examples

```
## Not run:
data(simulshift)
# 1. subsample to a reasonable size
subdata <- simulshift[seq(1,30000,by = 100),]
# 2. use algorithm from marcher package
MWN.fit <- with(subdata,
marcher::estimate_shift(T=indice, X=x, Y=y,n.clust = 3))
# 3. convert output
MWN.segm <- prepare_shiftfit(subdata,MWN.fit,diag.var = c("x","y"))
# 4. use segclust2d functions
plot(MWN.segm)
plot(MWN.segm,stationarity = TRUE)
segmap(MWN.segm)

## End(Not run)
```

`prep_segm` *Find segment and states for a Picard model*

Description

`prep_segm` find the different segment and states of a given HMM model

Usage

```
prep_segm(data, param, seg.type = NULL, nseg = NULL)
```

Arguments

`data`	the data.frame with the different variable
`param`	the param output of the segmentation
`seg.type`	either 'hybrid' or 'dynprog'
`nseg`	number of segment chosen

Value

a data.frame with states of the different segments

`prep_segm_HMM` *Internal function for HMM*

Description

`prep_segm_HMM`

Usage

```
prep_segm_HMM(data, hmm.model)
```

Arguments

`data`	data
`hmm.model`	hmm.model

`prep_segm_shiftfit` *Internal function for HMM*

Description

`prep_segm_shiftfit`

Usage

```
prep_segm_shiftfit(data, shiftfit.model)
```

Arguments

`data`	data
`shiftfit.model`	shiftfit.model

`relabel_states` *Relabel states of a segmentation/clustering output*

Description

`relabel_states` relabel the states of a segmentation/clustering output. This allows merging different states into the same if for instance several of the model states represent the same behavioural states.

Usage

```
relabel_states(mode.segclust, newlabel, ncluster, nseg, order = TRUE)
```

Arguments

`mode.segclust`	segclust output
`newlabel`	a vector with the new names ordered, corresponding to state_ordered
`ncluster`	the number of cluster for which you want relabeling
`nseg`	the number of segment for which you want relabeling
`order`	boolean, whether this changes the ordered states or not. FALSE value obsolete for now

Value

a segmentation object with state names changed for the segmentation specified by ncluster and nseg

repmat *repmat repeats a matrix*

Description

repmat repeats a matrix

Usage

```
repmat(a, n, m)
```

Arguments

a	the base matrix
n	number of repetition in lines
m	number of repetition in columns

Value

a matrix with n repeats of a in lines et m in columns

ruptAsMat *ruptAsMat is an internal function to transform a vector giving the change point to matrix 2 columns matrix in which each line gives the beginning and the end of a segment*

Description

ruptAsMat is an internal function to transform a vector giving the change point to matrix 2 columns matrix in which each line gives the beginning and the end of a segment

Usage

```
ruptAsMat(vectRupt)
```

Arguments

vectRupt	the vector of change point

Value

the matrix containing the segments

`segclust` *Segmentation/Clustering of movement data - Generic function*

Description

Joint Segmentation/Clustering of movement data. Method available for data.frame, move and ltraj objects. The algorithm finds the optimal segmentation for a given number of cluster and segments using an iterated alternation of a Dynamic Programming algorithm and an Expectation-Maximization algorithm. Among the different segmentation found, the best one can be chosen using the maximum of a BIC penalized likelihood.

Usage

```
segclust(x, ...)

## S3 method for class 'data.frame'
segclust(x, ...)

## S3 method for class 'Move'
segclust(x, ...)

## S3 method for class 'ltraj'
segclust(x, ...)
```

Arguments

`x`	data.frame with observations
`...`	additional parameters given to `segclust_internal`.

Value

a `segmentation-class` object

Examples

```
#' @examples
df <-  test_data()$data
#' # data is a data.frame with column 'x' and 'y'
# Simple segmentation with automatic subsampling
# if data has more than 1000 rows:
res <- segclust(df,
 Kmax = 15, lmin = 10, ncluster = 2:4,
 seg.var = c("x","y"))
 # Plot results
 plot(res)
 segmap(res, coord.names = c("x","y"))
 # check penalized likelihood of
 # alternative number of segment possible.
 # There should be a clear break if the segmentation is good
 plot_BIC(res)
## Not run:
# Advanced options:
# Run with automatic subsampling if df has more than 500 rows:
res <- segclust(df, Kmax = 30, lmin = 10, ncluster = 2:4,
                seg.var = c("x","y"), subsample_over = 500)
# Run with subsampling by 2:
res <- segclust(df, Kmax = 30, lmin = 10, ncluster = 2:4,
                seg.var = c("x","y"), subsample_by = 2)
# Disable subsampling:
res <- segclust(df, Kmax = 30, lmin = 10,
                ncluster = 2:4, seg.var = c("x","y"), subsample = FALSE)
# Disabling automatic scaling of variables for segmentation (standardazing
# the variables) :
 res <- segclust(df, Kmax = 30, lmin = 10,
                 seg.var = c("dist","angle"), scale.variable = FALSE)

## End(Not run)
```

segclust2d — *segclust2d: tools for segmentation of animal GPS movement data*

Description

Provides two methods for segmentation and joint segmentation/clustering of bivariate time-series. Originally intended for ecological segmentation (home-range and behavioural modes) but easily applied on other series, the package also provides tools for analysing outputs from R packages moveHMM and marcher.

Details

The segmentation method is a bivariate extension of Lavielle's method available in adehabitatLT (Lavielle 1999; and 2005). This method rely on dynamic programming for efficient segmentation.

The segmentation/clustering method alternates steps of dynamic programming with an Expectation-Maximization algorithm. This is an extension of Picard et al (2007) method (formerly available in cghseg package) to the bivariate case.

The full description of the method is published in Patin et al. (2020).

References:

Lavielle, M. (1999) Detection of multiple changes in a sequence of dependent variables. *Stochastic Processes and their Applications*, **83**: 79–102.

Lavielle, M. (2005) Using penalized contrasts for the change-point problem. Report number 5339, Institut national de recherche en informatique et en automatique.

Patin, R., Etienne, M. P., Lebarbier, E., Chamaille-Jammes, S., & Benhamou, S. (2020). Identifying stationary phases in multivariate time series for highlighting behavioural modes and home range settlements. *Journal of Animal Ecology*, 89(1), 44-56.

Picard, F., Robin, S., Lebarbier, E. and Daudin, J.-J. (2007), A Segmentation/Clustering Model for the Analysis of Array CGH Data. *Biometrics*, 63: 758-766. doi:10.1111/j.1541-0420.2006.00729.x

Author(s)

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Authors:

- Marie-Pierre Etienne
- Emilie Lebarbier
- Simon Benhamou

See Also

Useful links:

- https://github.com/rpatin/segclust2d
- Report bugs at https://github.com/rpatin/segclust2d/issues

---

segclust_internal *Internal segmentation/clustering function*

Description

Internal segmentation/clustering function

Usage

```
segclust_internal(
  x,
  seg.var,
  diag.var,
  order.var,
  Kmax,
  ncluster,
  lmin,
  scale.variable,
  sameSigma = FALSE,
  ...
)
```

Arguments

`x`	data.frame with observations
`seg.var`	names of the variables used for segmentation (either one or two names).
`diag.var`	names of the variables on which statistics are calculated.
`order.var`	names of the variable with which states are ordered.
`Kmax`	maximum number of segments.

`ncluster`	number of cluster into which segments should be grouped. Can be a vector if one want to test several number of clusters.
`lmin`	minimum length of segments.
`scale.variable`	TRUE or FALSE for automatic scaling of variables (reduction and centering)
`sameSigma`	does segments have same variance ?
`...`	additional arguments given to `chooseseg_lavielle`

`segmap_list` — `segmap_list` *create maps with a list of object of* `segmentation` *class*

Description

`segmap_list` create maps with a list of object of `segmentation` class

Usage

```
segmap_list(
  x_list,
  ncluster_list = NULL,
  nseg_list = NULL,
  pointsize = 1,
  linesize = 0.5,
  coord.names = c("x", "y")
)
```

Arguments

`x_list`	list of segmentation objects for different individuals or path
`ncluster_list`	list of number of cluster to be selected for each individual. If empty, the function takes the default one
`nseg_list`	list of number of segment to be selected for each individual. If empty, the function takes the default one
`pointsize`	size of points
`linesize`	size of lines
`coord.names`	names of coordinates

Value

a ggplot2 graph

`segmentation` *Segmentation of movement data - Generic function*

Description

Segmentation of movement data. No clustering. Method available for data.frame, move and ltraj object. The algorithm finds for each number of segment the optimal segmentation using a Dynamic Programming approach. The number of segment is then chosen using Lavielle's (2005) procedure based on locating rupture in the penalized likelihood.

Usage

```
segmentation(x, ...)

## S3 method for class 'data.frame'
segmentation(x, ...)

## S3 method for class 'Move'
segmentation(x, ...)

## S3 method for class 'ltraj'
segmentation(x, ...)

segmentation_internal(
  x,
  seg.var,
  diag.var,
  order.var,
  lmin,
  Kmax,
  scale.variable,
  sameSigma = FALSE,
  ...
)
```

Arguments

`x`	data.frame with observations
`...`	additional parameters given to chooseseg_lavielle
`seg.var`	names of the variables used for segmentation (either one or two names).
`diag.var`	names of the variables on which statistics are calculated.
`order.var`	names of the variable with which states are ordered.
`lmin`	minimum length of segments.
`Kmax`	maximum number of segments.
`scale.variable`	TRUE or FALSE for automatic scaling of variables (reduction and centering)
`sameSigma`	does segments have same variance ?

Value

a segmentation-class object

Examples

```
df <-  test_data()$data
#' # data is a data.frame with column 'x' and 'y'
# Simple segmentation with automatic subsampling
# if data has more than 1000 rows:
res <- segmentation(df, Kmax = 30, lmin = 10, seg.var = c("x","y"))
 # Plot results
 plot(res)
 segmap(res)
 # check likelihood of alternative number of segment possible. There should
 # be a clear break if the segmentation is good
 plot_likelihood(res)
## Not run:
# Advanced options:
# Run with automatic subsampling if df has more than 500 rows:
res <- segmentation(df, Kmax = 30, lmin = 10,
 seg.var = c("x","y"),  subsample_over = 500)

# Run with subsampling by 2:
res <- segmentation(df, Kmax = 30, lmin = 10,
seg.var = c("x","y"), subsample_by = 2)

# Disable subsampling:
res <- segmentation(df, Kmax = 30, lmin = 10,
 seg.var = c("x","y"), subsample = FALSE)

# Run on other kind of variables :
 res <- segmentation(df, Kmax = 30, lmin = 10, seg.var = c("dist","angle"))

# Automatic scaling of variables for segmentation
(set a mean of 0 and a standard deviation of 1 for both variables)

 res <- segmentation(df, Kmax = 30, lmin = 10,
 seg.var = c("dist","angle"), scale.variable = TRUE)


## End(Not run)
```

---

segmentation-class *segmentation class description*

Description

segmentation class description

print.segmentation prints object of segmentation class plot.segmentation plot object of segmentation class - wrapper for plot_segm

likelihood.segmentation deprecated function for plotting likelihood estimates of segmentation object. Now use plot_likelihood.

plot_likelihood plot likelihood estimates of a segmentation object - works only for picard segmentation.

get_likelihood returns likelihood estimates of a segmentation object. Deprecated, now use logLik.segmentation.

logLik.segmentation returns log-likelihood estimates of a segmentation object

plot_BIC plot BIC estimates of a segmentation object - works only for segclust algorithm.

BIC returns BIC-based penalized log-likelihood estimates of a segmentation object when segmentation/clustering has been run.

stateplot plot state distribution of a segmentation object

states return data.frame with states statistics a segmentation object

segment return data.frame with segment information of a segmentation object

augment.segmentation return data.frame with original data and state information of a segmentation object

segmap create maps with object of segmentation class (interpreting latitude/longitude)

Usage

```
## S3 method for class 'segmentation'
print(x, max.level = 1, ...)

## S3 method for class 'segmentation'
plot(x, nseg, ncluster, interactive = FALSE, xcol = "indice", order, ...)

## S3 method for class 'segmentation'
likelihood(x, ...)

plot_likelihood(x)

get_likelihood(x)

## S3 method for class 'segmentation'
logLik(object, ...)

plot_BIC(x)

## S3 method for class 'segmentation'
BIC(object, ...)

stateplot(x, nseg, ncluster, order)

states(x, nseg, ncluster)
```

```
segment(x, nseg, ncluster)

## S3 method for class 'segmentation'
augment(x, nseg, ncluster, colname_state = "state", ...)

segmap(
  x,
  interactive = FALSE,
  nseg,
  ncluster,
  html = FALSE,
  scale = 1,
  width = 400,
  height = 400,
  order,
  pointsize = 1,
  linesize = 0.5,
  ...
)
```

Arguments

`x`	a `segmentation` object generated by `segmentation`
`max.level`	argument to be passed to utils::str()
`...`	additional arguments
`nseg`	number of segment chosen
`ncluster`	number of classes chosen
`interactive`	whether plot are interactive (dygraphs/leaflet) or not (ggplot2)
`xcol`	column for x axis. can be POSIXct
`order`	should cluster be ordered
`object`	a segmentation-class object, created by segclust.
`colname_state`	column name for the added state column
`html`	whether htmltools::tagList should be applied on the returned object object for integrating in html pages
`scale`	for dividing coordinates to have compatibility with leaflet
`width`	width
`height`	height
`pointsize`	size of points
`linesize`	size of lines

Examples

```
## Not run:
plot(res.segclust)
plot(res.segclust, nseg = 10, ncluster = 3)

## End(Not run)

## Not run:
plot_likelihood(res.seg)

## End(Not run)

## Not run:
logLik(res.seg)

## End(Not run)

## Not run:
plot_BIC(res.segclust)

## End(Not run)

## Not run:
plot_BIC(res.segclust)

## End(Not run)

## Not run:
stateplot(res.segclust)
stateplot(res.seg)

## End(Not run)
## Not run:
states(res.segclust)
states(res.seg)

## End(Not run)

## Not run:
segment(res.segclust)
segment(res.segclust, ncluster = 3, nseg = 30)
segment(res.seg)
segment(res.seg, nseg = 4)

## End(Not run)
## Not run:
augment(res.segclust)
augment(res.segclust, ncluster = 3, nseg = 30)
augment(res.seg)
augment(res.seg, nseg = 4)

## End(Not run)
## Not run:
segmap(res.segclust, coord.names = c("x", "y"))
segmap(res.segclust, ncluster = 3, nseg = 30)
segmap(res.seg)
segmap(res.seg, nseg = 4)

## End(Not run)
```

`simulmode` *Simulations of behavioural mode*

Description

A dataset containing a simulation of 3 different behavioural mode

Usage

```
simulmode
```

Format

A data frame with 302 rows and 10 variables:

indice index of position

x x coordinates

y y coordinates

speed smoothed speed

spatial_angle angle at constant step length

dist raw speed

angle angular speed

vit_p persistence speed

vit_r rotation speed

vit_p_spa persistence speed calculated with spatial angles

vit_r_spa rotation speed calculated with spatial angles

dateTime arbitrary date in POSIXct format

`simulshift` *Simulations of home-range shift*

Description

A dataset containing a simulation of home-range shift

Usage

```
simulshift
```

Format

A data frame with 53940 rows and 10 variables:

indice index of position

x x coordinates

y y coordinates

dateTime arbitrary date in POSIXct format

`spatial_angle` *Calculate spatial angle along a path*

Description

`spatial_angle` calculate spatial angle between locations, taking a dataframe as input. Spatial angle is considered as the angle between the focus point, the first location entering a given circle and the last location inside.

Usage

```
spatial_angle(x, coord.names = c("x", "y"), radius = NULL)
```

Arguments

`x`	data.frame with locations
`coord.names`	names of coordinates column in `x`
`radius`	for angle calculation. Default is median of step length.

Value

vector of spatial angle.

Author(s)

Remi Patin, Simon Benhamou.

Examples

```
## Not run:
data(simulmode)
spatial_angle(simulmode)

## End(Not run)
```

`stat_segm` *Calculate statistics on a given segmentation*

Description

`stat_segm` calculates statistics of a given segmentation : mean and variance of the different states. it also creates standard objects for plot.

Usage

```
stat_segm(
  data,
  diag.var,
  order.var = NULL,
  param = NULL,
  seg.type = NULL,
  nseg
)
```

Arguments

`data`	the data.frame with the different variable
`diag.var`	names of the variables on which statistics are calculated
`order.var`	names of the variable with which states are ordered
`param`	parameters of output segmentation
`seg.type`	either 'hybrid' or 'dynprog'
`nseg`	number of segment chosen

Value

a list which first element is a data.frame with states of the different segments and which second element is a data.frame with mean and variance of the different states

Examples

```
## Not run:
#res.segclust is a result of a segmentation-clustering algorithm
param <- res.segclust$param[["3 class"]]
nseg = 10
out <- stat_segm(data, diag.var = c("dist","angle"),
 order.var = "dist", param = param, nseg=nseg, seg.type = "segclust")


## End(Not run)
```

`stat_segm_HMM` *Get segment statistic for HMM model*

Description

`stat_segm_HMM`

Usage

```
stat_segm_HMM(data, hmm.model = NULL, diag.var, order.var = NULL)
```

Arguments

`data`	data
`hmm.model`	hmm.model
`diag.var`	diag.var
`order.var`	order.var

`stat_segm_shiftfit` *Get segment statistic for shiftfit model*

Description

`stat_segm_shiftfit`

Usage

```
stat_segm_shiftfit(data, shiftfit.model = NULL, diag.var, order.var = NULL)
```

Arguments

`data`	data
`shiftfit.model`	shiftfit.model
`diag.var`	diag.var
`order.var`	order.var

`subsample_rename` *Internal function for subsampling*

Description

merge subsampled data.frame df with fulldata to add segmentation information on the full data.frame

Usage

```
subsample_rename(df, fulldata, colname)
```

Arguments

`df`	subsampled data.frame with additional information on segmentation
`fulldata`	full data.frame
`colname`	column name

`test_data` *Test function generating fake data*

Description

Test function generating fake data

Usage

```
test_data()
```

`wrap_dynprog_cpp` *DynProg Rcpp DynProg computes the change points given a cost matrix matD and a maximum number of segments Kmax*

Description

DynProg Rcpp DynProg computes the change points given a cost matrix matD and a maximum number of segments Kmax

Usage

```
wrap_dynprog_cpp(G, K)
```

Arguments

`G`	the cost Matrix os size n x n
`K`	the number of segments considered

Value

a list with J.est a vector with Kmax value, the Kth is the minimum contrast for a model with K segments (-J.est is the log-likelihood) and with t.test a matrix, line K are the coordinates of the change points for a model with K segments

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