

Package ‘HCV’

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Title Hierarchical Clustering from Vertex-Links

Description Hierarchical clustering for spatial data, which requires clustering results not only homogeneous in non-geographical features among samples but also geographically close to each other within a cluster. It modified typically used hierarchical agglomerative clustering algorithms for introducing the spatial homogeneity, by considering geographical locations as vertices and converting spatial adjacency into whether a shared edge exists between a pair of vertices (Tzeng & Hsu, 2022) <[arXiv:2201.08302](#)>. The constraints of the vertex links automatically enforce the spatial contiguity property at each step of iterations. In addition, methods to find an appropriate number of clusters and to report cluster members are also provided.

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Suggests alphahull, knitr, fields (>= 11.4)

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getCluster	<i>Determining Appropriate Clusters for HCV Objects</i>
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Description

The function provides two methods to determine an appropriate number of clusters for an HCV object, and reports individual cluster members. One of the methods is a novel internal index named Spatial Mixture Index (SMI), considering both the within-cluster sum of squared difference of geographical attributes and non-geographical attributes. The other is an M3C-based method taking account of the stability of clusters.

Usage

```
getCluster(
  HCObj,
  method = c("SMI", "M3C"),
  Kmax = 10,
  niter = 25,
  criterion = "PAC"
)
```

Arguments

HCObj	an object resulting from calling the HCV function.
method	character indicating the method to determine an appropriate number of clusters. Default 'SMI' is faster, while 'M3C' is more precise but slower.
Kmax	integer for the upper bound of the potential number of clusters to be considered.
niter	integer for the number of resampling, only used in method='M3C'.
criterion	character indicating whether to use 'PAC' or 'entropy' as the objective function. Default is 'PAC'. Only used in method='M3C'. See the reference for details.

Value

A vector giving the cluster ID assigned for each sample.

Author(s)

ShengLi Tzeng and Hao-Yun Hsu.

References

John, Christopher R., et al. (2020). M3C: Monte Carlo reference-based consensus clustering. Scientific reports, 10(1), 1-14.

See Also

[M3C](#)

Examples

```
set.seed(0)
pcase <- synthetic_data(3,30,0.02,100,2,2)
HCVobj <- HCV(pcase$geo, pcase$feat)
smi <- getCluster(HCVobj,method="SMI")
oldpar <- par(no.readonly = TRUE)
par(mfrow=c(2,2))
labcolor <- (pcase$labels+1)%%3+1
plot(pcase$feat, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Feature domain')
plot(pcase$geo, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Geometry domain')
plot(pcase$feat, col=factor(smi),pch=19, xlab = 'First attribute',
     ylab = 'Second attribute',main = 'Feature domain')
plot(pcase$geo, col=factor(smi),pch=19, xlab = 'First attribute',
     ylab = 'Second attribute',main = 'Geometry domain')
par(oldpar)
```

Description

This function implements the hierarchical clustering for spatial data. It modified typically used hierarchical agglomerative clustering algorithms for introducing the spatial homogeneity, by considering geographical locations as vertices and converting spatial adjacency into whether a shared edge exists between a pair of vertices.

Usage

```
HCV(  
  geometry_domain,  
  feature_domain,  
  linkage = "ward",  
  diss = "none",  
  adjacency = FALSE,  
  dist_method = "euclidean"  
)
```

Arguments

<code>geometry_domain</code>	one of the three formats: (i) n by d matrix (NA not allowed), (ii) a <code>SpatialPolygonsDataFrame</code> object defining polygons, (iii) a matrix with 0-1 value adjacency (with <code>adjacency=TRUE</code>)
<code>feature_domain</code>	either (i) n by p matrix (NA allowed) for n samples with p attributes, or (ii) n by n matrix (NA not allowed) with dissimilarity between n samples (with <code>diss = 'precomputed'</code>)
<code>linkage</code>	the agglomeration method to be used, one of "ward", "single", "complete", "average" (= UPGMA), "weight" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC). Default is 'ward'.
<code>diss</code>	character indicating if <code>feature_domain</code> is a dissimilarity matrix: 'none' for not dissimilarity, and 'precomputed' for dissimilarity. Default is 'none'.
<code>adjacency</code>	logical indicating if <code>geometry_domain</code> is a adjacency matrix. Default is FALSE.
<code>dist_method</code>	the distance measure to be used when <code>feature_domain</code> is not a dissimilarity matrix (<code>diss = 'none'</code>), one of "euclidean", "correlation", "abscor", "maximum", "manhattan", "canberra", "binary" or "minkowski". Default is 'euclidean'.

Details

`geometry_domain` can be a user-specified adjacency matrix, an n by d matrix with geographical coordinates for point-level data, or a `SpatialPolygonsDataFrame` object defining polygons for areal data. If an adjacency matrix is given, the user should use `adjacency=TRUE`.

Value

An object of class `hclust` which describes the tree produced by the clustering process. See the documentation in `hclust`.

Author(s)

ShengLi Tzeng and Hao-Yun Hsu.

References

Carvalho, A. X. Y., Albuquerque, P. H. M., de Almeida Junior, G. R., and Guimaraes, R. D. (2009). Spatial hierarchical clustering. *Revista Brasileira de Biometria*, 27(3), 411-442.

See Also

[hclust](#)

Examples

```
set.seed(0)
pcase <- synthetic_data(3,30,0.02,100,2,2)
HCVobj <- HCV(pcase$geo, pcase$feat)
smi <- getCluster(HCVobj,method="SMI")
oldpar <- par(no.readonly = TRUE)
```

```

par(mfrow=c(2,2))
labcolor <- (pcase$labels+1)%3+1
plot(pcase$feat, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Feature domain')
plot(pcase$geo, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Geometry domain')
plot(pcase$feat, col=factor(smi),pch=19, xlab = 'First attribute',
     ylab = 'Second attribute',main = 'Feature domain')
plot(pcase$geo, col=factor(smi),pch=19, xlab = 'First attribute',
     ylab = 'Second attribute',main = 'Geometry domain')
par(oldpar)

```

plotMap

Drawing a Thematic Map with a Quantitative Feature

Description

Plot the polygons in a `SpatialPolygonsDataFrame` object, and turn the values of a quantitative feature into colors over individual polygons.

Usage

```

plotMap(
  map,
  feat,
  color = topo.colors(10),
  main = "",
  bar_title = "rank",
  zlim = NULL
)

```

Arguments

map	SpatialPolygonsDataFrame object consisting of data and polygons.
feat	numeric vector having the same elements as the number of polygons in the input map.
color	vector of distinct colors for converting values of feat.
main	character specifying the main title.
bar_title	character specifying the text over the color bar.
zlim	length-2 numeric vector specifying the range of values to be converted.

Value

A colored map.

See Also

[SpatialPolygonsDataFrame](#)

Examples

```
require(sp)
grd <- GridTopology(c(1,1), c(1,1), c(5,5))
polys <- as(grd, "SpatialPolygons")
centroids <- coordinates(polys)
gdomain <- SpatialPolygonsDataFrame(polys, data=data.frame(x=centroids[,1],
  y=centroids[,2], row.names=row.names(polys)))
feat <- gdomain$x*5+gdomain$y^2
plotMap(gdomain,feat)
```

synthetic_data

Generating Point-level Data Having Several Groups

Description

Generation of synthetic point-level data based on a method proposed by Lin et al. (2005).

Usage

```
synthetic_data(k, f, r, n, feature, geometry, homogeneity = TRUE)
```

Arguments

k	integer specifying the number of groups.
f	positive number controlling the concentration of generated samples toward large groups.
r	positive number controlling the variance of individual attributes on the feature domain.
n	integer specifying the total number of sampled points.
feature	integer specifying the number of attributes for the feature domain.
geometry	integer specifying the number of attributes for the geometry domain.
homogeneity	logical indicating whether to force the centers of the feature domain to be the same as those of the geometry domain. Default is TRUE.

Value

A list with two matrices and a vector of labels. One matrix is for the feature domain and the other is for the geometry domain, both of which have n sampled points. The vector of labels indicates which cluster each sample belongs to.

Author(s)

ShengLi Tzeng and Hao-Yun Hsu.

References

Lin, C. R., Liu, K. H., and Chen, M. S. (2005). Dual clustering: integrating data clustering over optimization and constraint domains. *IEEE Transactions on Knowledge and Data Engineering*, 17(5), 628-637.

Examples

```
set.seed(0)
pcase <- synthetic_data(3,30,0.02,100,2,2)
oldpar <- par(no.readonly = TRUE)
par(mfrow=c(1,2))
labcolor <- (pcase$labels+1)%%3+1
plot(pcase$feat, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Feature domain')
plot(pcase$geo, col = labcolor, pch=19, xlab = 'First attribute',
     ylab = 'Second attribute', main = 'Geometry domain')
par(oldpar)
```

tessellation_adjacency_matrix

Adjacency Matrix from Tessellation

Description

This function deals with spatial data having a point-level geometry domain. It converts the spatial proximity into an adjacency matrix based on Voronoi tessellation or Delaunay triangulation.

Usage

```
tessellation_adjacency_matrix(geometry_domain)
```

Arguments

`geometry_domain`

n by d matrix (NA not allowed) of geographical coordinates for n points in d -dimensional space.

Value

A matrix with 0-1 values indicating the adjacency between the n input points.

Author(s)

ShengLi Tzeng and Hao-Yun Hsu.

References

Gallier, J. (2011). Dirichlet–Voronoi Diagrams and Delaunay Triangulations. In Geometric Methods and Applications (pp. 301-319). Springer, New York, NY.

Examples

```
if( require(fields) & require(alphahull) ) {  
  pts <- Chicago03$x  
  rownames(pts) <- LETTERS[1:20]  
  Vcells <- delvor(pts)  
  plot(Vcells,wlines='vor',pch='.')  
  text(pts,rownames(pts))  
  Amat <- tessellation_adjacency_matrix(pts)  
}
```


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