Package 'AGcurve'

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Type Package

Title Functions for calculating AG-curve from x,y coordinate data

Version 0.1.0

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Depends R (>= 2.10), stats

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Description AGcurve is a small package of functions used for performing
spatial point pattern analysis using the AG-curve (agglomerative)
technique. The AG-curve is, basically, a graphical representation of
a cluster dendrogram that illustrates the rate of cluster merging.
The original work on the AG-curve was done by
Takai, Tamura and Motoyama, 2017 (A New Graphical Approach to
Classify Spatial Point Patterns Based on Hierarchical Cluster
Analysis, J Japanese Society of Computational Statistics 30(1): 1-14.
https://dx.doi.org/10.5183/jjscs.1611001_229).

License GPL (>=3)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

R topics documented:

AGcurve   *Wrapper for producing an AG-curve.*

Description

Convenient wrapper for producing an AG-curve from spatial coordinates.

Usage

```
AGcurve(xy, method = "ward.D", dS = NULL)
```

Arguments

xy   A numeric array of spatial coordinates.

method   A character string passed to hclustDist() that specifies the hierarchical clustering
              method to be passed to stats::hclust.

dS   An optional numeric value passed to hclustDist() that specifies the denominator
              used in down-scaling each value of input xy.

Details

hclustDist returns a data frame consisting of the numbers of clusters as a function of height in the
dendrogram.

Value

Returns a data frame of height and k values describing the AG-curve suitable for plotting.

Author(s)

Bjorn J. Brooks

Examples

```
xy <- data.frame(x=sample(1:100, size=20,   # Some example coordinates
                          replace=TRUE,      # weighted toward 1
                          prob=2^(100:1)),
                 y=sample(1:100, size=20,
                          replace=TRUE,
                          prob=2^(100:1)))
rownames(xy) <- LETTERS[1:20]               # Set names of coord points
fit <- hclustDist(xy, method="single")      # Dendrogram
AG <- AGcurve(xy, method="single")          # AG-curve

# Plot
par(mfrow=c(1,2))                           # Set multiplot panels
layout(matrix(c(1,2,2), nrow=1, ncol=3))    # Customize size of plot panels
plot(fit, xlab='Cluster Group')             # Plot dendrogram
plot(AG$k, AG$h, type='b',
     xlab='Numnber of Clusters (k)',        # Plot AG-curve
     ylab='Height, h[k]',
     main='AG-curve (corresponds to rate of branching in dendrogram)')
```

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cumGain *Calculates the cumulative gain between sequential values.*

Description

Calculate the sum of every gain in a series, i.e., for the series x = 4, 3, 2, 5, 6 the cumulative gain is 3 + 1 = 4.

Usage

```
cumGain(x)
```

Arguments

x   A numeric vector of values.

Details

cumGain returns the cumulative gain between consecutive values in a series.

Value

Returns a single value sum of all gains.

Author(s)

Bjorn J. Brooks

Examples

```
x <- c(400, 500, 500, 450, 550)  # Some example elevation values
cumGain(x)                       # Calc. cum gain (AKA tot. ascent)
```

---

cumLoss *Calculates the cumulative loss between sequential values.*

Description

Calculate the sum of every loss in a series, i.e., for the series x = 4, 3, 2, 5, 6 the cumulative loss is 1 + 1 = 2.

Usage

```
cumLoss(x)
```

Arguments

x   A numeric vector of values.

Details

cumLoss returns the cumulative loss between consecutive values in a series.

Value

Returns a single value sum of all losses.

Author(s)

Bjorn J. Brooks

Examples

```
x <- c(400, 500, 500, 450, 550)  # Some example elevation values
cumLoss(x)                       # Calc. cum loss (AKA tot. descent)
```

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hclustDist   *Wrapper for hierarchical clustering of spatial coordinates.*

Description

Convenient wrapper for hierarchical clustering spatial coordinates.

Usage

```
hclustDist(xy, method = "ward.D", dS = NULL)
```

Arguments

xy	A numeric array of spatial coordinates.
method	A character string specifying the hierarchical clustering method to be passed to stats::hclust.
dS	An optional numeric value specifying the denominator to be used in down-scaling each value of input xy.

Details

hclustDist returns results from hierarchical clustering using the stats::hclust() function.

Value

Returns an object of class *hclust*, see stats::hclust.

Author(s)

Bjorn J. Brooks

Examples

```
xy <- data.frame(x=c(0, 0, 2, 3),          # Some example coordinates
                 y=c(0, 1, 4, 5))
rownames(xy) <- LETTERS[1:4]               # Set names of coord points
fit <- hclustDist(xy)

# Plot
par(mfrow=c(1,2))
plot(xy, pch='')
text(xy, labels=rownames(xy))

plot(fit)
```

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