Package: matrixcut (via r-universe)

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Version 0.0.1

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Title Determines Clustering Threshold Based on Similarity Values

Maintainer Matthew Cserhati <csmatyi@protonmail.com>

Description The user must supply a matrix filled with similarity values. The software will search for significant differences between similarity values at different hierarchical levels. The algorithm will return a Loess-smoothed plot of the similarity values along with the inflection point, if there are any. There is the option to search for an inflection point within a specified range. The package also has a function that will return the matrix components at a specified cutoff. References: Mullner. <ArXiv:1109.2378>; Cserhati, Carter. (2020, Journal of Creation 34(3):41-50), <https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Imports igraph, stats, inflection

NeedsCompilation no

Author Matthew Cserhati [aut, cre] (<https://orcid.org/0000-0002-3673-9152>)

Depends R (>= 3.5.0)

Config/pak/sysreqs libglpk-dev libxml2-dev

Repository https://csmatyi.r-universe.dev

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`componentplot` *Draws a Plot Showing the Number of Components as a Function of the Cutoff Value.*

Description

The function takes a square sequence similarity matrix and calculates the number of independent components in which the sequence similarity between the members is greater than a specified value (between 0 and 1). It creates a plots showing the number of components corresponding to a given cutoff value. The function also depicts the inflection point with a vertical line. Upper and lower bounds can be provided between which the inflection point will be found (if it exists).

Version 0.0.1. Author: Dr. Matthew Cserhati Email: csmatyi@protonmail.com March 19, 2023

Arguments

`mx`	a square sequence similarity matrix
`lower_bound`	lower bounds for calculating the inflection point in, default = 0
`upper_bound`	upper bounds for calculating the inflection point in, default = 1

Value

A plot showing the number of components as a function of the cutoff threshold.

References

Mullner. <ArXiv:1109.2378>

Cserhati, Carter. (2020, Journal of Creation 34(3):41-50), <https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf>

Examples

```
componentplot(xenarthra,0.75,0.9)
componentplot(xenarthra)
```

cutoffplot — *Draws a Plot Showing the Number of Similarity Values as a Function of the Cutoff Value.*

Description

The function takes a square sequence similarity matrix and creates a plot showing the number of similarity values above a given cutoff value, drawn on the x-axis, ranging from 0 to 1. The function also depicts the inflection point with a vertical line. Upper and lower bounds can be provided between which the inflection point will be found (if it exists).

Version 0.0.1. Author: Dr. Matthew Cserhati Email: csmatyi@protonmail.com March 19, 2023

Arguments

mx	a square sequence similarity matrix
lower_bound	lower bounds for calculating the inflection point in, default = 0
upper_bound	upper bounds for calculating the inflection point in, default = 1

Value

A plot showing the number of similarity values as a function of the cutoff threshold.

References

Mullner. <ArXiv:1109.2378>

Cserhati, Carter. (2020, Journal of Creation 34(3):41-50), <https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf>

Examples

```
cutoffplot(liliales,0.7,0.85)
cutoffplot(liliales)
```

liliales — *Chloroplast genome sequence similarity matrix for 163 Liliales species*

Description

Chloroplast genome sequence similarity matrix for 163 Liliales species

Usage

```
liliales
```

Format

'liliales' Chloroplast genome sequence similarity matrix for 163 Liliales species

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`matrixcut` *Calculates The Component Membership in a Sequence Similarity Matrix at a given Cutoff Value*

Description

The function takes a square sequence similarity matrix and calculates those independent components in which the sequence similarity between the members is greater than a specified value (between 0 and 1). The result provied by the function is a list of species with their component membership.

Version 0.0.1. Author: Dr. Matthew Cserhati Email: csmatyi@protonmail.com March 19, 2023

Arguments

`mx`	a square sequence similarity matrix
`cut`	a given cutoff value to calculate components for, default value = -1

Value

The inflection point: cutoff value for the optimal number of clusters

A list of the species together with their cluster membership.

References

Mullner. <ArXiv:1109.2378>

Cserhati, Carter. (2020, Journal of Creation 34(3):41-50), <https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf>

Examples

```
matrixcut(primates,0.8)
matrixcut(primates)
```

`primates` *Mitochondrial genome sequence similarity matrix for 31 primate species*

Description

Mitochondrial genome sequence similarity matrix for 31 primate species

Usage

```
primates
```

Format

‘primates‘ Mitochondrial genome sequence similarity matrix for 31 primate species

`xenarthra` *Mitochondrial genome sequence similarity matrix for 37 Xenarthra species*

Description

Mitochondrial genome sequence similarity matrix for 37 Xenarthra species

Usage

```
xenarthra
```

Format

‘xenarthra‘ Mitochondrial genome sequence similarity matrix for 37 Xenarthra species

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