

# Package: matrixcut (via r-universe)

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**Version** 0.0.1

**Date** 2023-03-19

**Title** Determines Clustering Threshold Based on Similarity Values

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**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](https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**Imports** igraph, stats, inflection

**NeedsCompilation** no

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**Depends** R (>= 3.5.0)

**Repository** CRAN

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componentplot	<i>Draws a Plot Showing the Number of Components as a Function of the Cutoff Value.</i>
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## 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: csmaty@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](https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf)>

## Examples

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

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cutoffplot	<i>Draws a Plot Showing the Number of Similarity Values as a Function of the Cutoff Value.</i>
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### 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: csmaty@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](https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf)>

### Examples

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

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liliales	<i>Chloroplast genome sequence similarity matrix for 163 Liliales species</i>
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### 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	<i>Calculates The Component Membership in a Sequence Similarity Matrix at a given Cutoff Value</i>
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**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 provided by the function is a list of species with their component membership.

Version 0.0.1. Author: Dr. Matthew Cserhati Email: csmaty@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](https://dl0.creation.com/articles/p137/c13759/j34-3_64-73.pdf)>

**Examples**

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

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primates	<i>Mitochondrial genome sequence similarity matrix for 31 primate species</i>
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**Description**

Mitochondrial genome sequence similarity matrix for 31 primate species

**Usage**

primates

**Format**

## 'primates' Mitochondrial genome sequence similarity matrix for 31 primate species

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xenarthra	<i>Mitochondrial genome sequence similarity matrix for 37 Xenarthra species</i>
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**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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