

# Package ‘phyC’

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**Type** Package

**Title** Clustering cancer evolutionary trees

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**Description** This package includes the tree registration, clustering, visualizing trees' configurations, and calculating diversity.

**License** GPL (>= 2)

**RoxygenNote** 5.0.1

**Depends** igraph, ape, ggplot2, grDevices

**NeedsCompilation** no

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<code>create.meta</code>	<i>Internal function</i>
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**Description**

Internal function

**Usage**

```
create.metaTree(depth)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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<code>depth.max</code>	<i>Internal function</i>
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**Description**

Internal function

**Usage**

```
depth.max(trees)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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<code>diversity</code>	<i>Evaluating diversity and plot</i>
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**Description**

Evaluating diversity and plot

**Usage**

```
diversity(obj, color = NULL, plotit = T)
```

**Arguments**

<code>obj</code>	Object resulted from phyC.
<code>color</code>	If plotit=TRUE, color parameter of each cluster in the plot.
<code>plotit</code>	Whether plot the diversity or not (logical).

**Value**

ind.div Diversity of each tree.

div Diversity of each cluster.

**Author(s)**

Yusuke Matsui & Teppei Shimamura

**Examples**

```
library(phyC)
##generate edgeList and edgeLenList##
trees <- c(rmtree(5,3),rmtree(5,4))
edgeList <- lapply(trees,function(x)x$edge)
edgeLenList <- lapply(trees,function(x)x$edge.length)
##adopting phyC##
res <- phyC(edgeList,edgeLenList,cluster=2,type='nh')
div <- diversity(res)
```

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get.index

*Internal function*

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**Description**

Internal function

**Usage**

```
get.index(edge)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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get.maxdepth

*Internal function*

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**Description**

Internal function

**Usage**

```
get.maxdepth(trees)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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lichee2edge	<i>Constructing trees from variant allele frequency using LICHeE.</i>
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**Description**

Constructing trees from variant allele frequency using LICHeE.

**Usage**

```
lichee2edge(licheeDir = NULL, vaf, licheeParamIO = NULL,
  licheeParamFilter = NULL, licheeParamPhy = NULL)
```

**Arguments**

licheeDir	Directory of lichee.jar file.
vaf	Matrix of variant allele frequency. For more detail of data format, see <a href="http://viq854.github.io/lichee/">http://viq854.github.io/lichee/</a>
licheeparamIO	List of input/output and display options. For detail see <a href="http://viq854.github.io/lichee/">http://viq854.github.io/lichee/</a> . You can set the parameters of (normal,save,showNetwork,showTree).
licheeparamFilter	List of SSNV filtering and calling parameters. For detail see <a href="http://viq854.github.io/lichee/">http://viq854.github.io/lichee/</a> . You can set the parameters of (absent,present,maxVAFValid,minProfileSupport).
licheeparamParamPhy	List of phylogenetic network construction and tree search paramters. For detail see <a href="http://viq854.github.io/lichee/">http://viq854.github.io/lichee/</a> . You can set the parameters of (minClusterSize,minPrivateClusterSize,minRobustNodeSupport,maxClusterDist,completeNetwork,e,nTreeQPCluster).

**Value**

edgeList Rooted-constraint network of cancer lineage.

edgeLenList Edge length vector corresponding to the edgeList. The edge legnth means #addition SSNVs from parental clone.

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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meta.regis.tree	<i>Internal function</i>
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**Description**

Internal function

**Usage**

```
meta.regis.tree(meta, target)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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phyC

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*Clustering cancer evolutionary trees*


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**Description**

Clustering cancer evolutionary trees

**Usage**

```
phyC(edgeList, edgeLenlist, cluster, type = "nh", method = NULL)
```

**Arguments**

edgeList	List of edge matrix of input.
cluster	The number of clusters.
type	Clustering type. Select 'nh' (non hierarchical) or 'h' (hierarchical with ward's method).
edgeLenList	List of edge length vector. Index of vector should be corresponding to row index of edge matrix.
edgeLenList	List of edge length vector of input.

**Details**

This function perform the registration and the clustering. In the registration, we resolve the mono- and multi-furcation trees and we complete the number of leaves among the trees. In the resigration, identical tree topologies are regarded identical even if the label are different. In the clustering, we classify the trees into predefined number of subsets. When choose type='nh', we perform the Ward's clustering.

**Value**

trees Input trees.  
 regis.tree Registered trees.  
 cluster Index of the clusters.  
 dist Distance between trees.

**Author(s)**

Yusuke Matsui & Teppei Shimamura

**Examples**

```
library(phyC)
##generate edgeList and edgeLenList##
trees <- c(rmtree(5,3),rmtree(5,4))
edgeList <- lapply(trees,function(x)x$edge)
edgeLenList <- lapply(trees,function(x)x$edge.length)
##adopting phyC##
res <- phyC(edgeList,edgeLenList,cluster=2,type='nh')
```

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phyCMD

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*Constructing configuration of trees in clusters and plot*


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## Description

Constructing configuration of trees in clusters and plot

## Usage

```
phyCMD(obj, color = NULL, label = NULL, img.width = 250,
        img.height = 250, size = 0.2)
```

## Arguments

obj	Object resulted from phyC.
color	Vector of color parameter of each cluster in the plot.
label	Vector of labels of trees. Default is "Tree i"(i=1,2,...).
size	Size parameter of trees to be plotted in the Euclidean space. Usually, $0 < \text{size} < 1$ . Default is 0.2.
img.width(/img.height)	Image width (/ height) of the trees to be overlayed on the Euclidean space. The unit is "px". Default is 250.

## Details

This function performs classical multidimensional scaling with tree distance. The resulting plot includes the trees overlayed on the Euclidean coordinates.

## Value

dist Distance used for configuration

coord Coordinate of trees in the Euclidean space.

## Author(s)

Yusuke Matsui & Teppei Shimamura

## Examples

```
library(phyC)
##generate edgeList and edgeLenList##
trees <- c(rmtree(5,3),rmtree(5,4))
edgeList <- lapply(trees,function(x)x$edge)
edgeLenList <- lapply(trees,function(x)x$edge.length)
##adopting phyC##
res <- phyC(edgeList,edgeLenList,cluster=2,type='nh')
phyCMD(res)
```

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plot.phyC	<i>Plot trees in clusters</i>
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**Description**

Plot trees in clusters

**Usage**

```
## S3 method for class 'phyC'  
plot(obj, color = NULL, label = NULL)
```

**Arguments**

obj	Object resulted from phyC.
color	Vector of color parameter of each cluster in the plot.
label	Vector of labels of trees. Default is "Tree i"(i=1,2,...).

**Author(s)**

Yusuke Matsui & Teppei Shimamura

**Examples**

```
library(phyC)  
##generate edgeList and edgeLenList##  
trees <- c(rmtree(5,3),rmtree(5,4))  
edgeList <- lapply(trees,function(x)x$edge)  
edgeLenList <- lapply(trees,function(x)x$edge.length)  
##adopting phyC##  
res <- phyC(edgeList,edgeLenList,cluster=2,type='nh')  
plot.phyC(res)
```

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regis	<i>Internal function</i>
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**Description**

Internal function

**Usage**

```
regis(edgeList, edgeLenList)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

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resolve.monomulti	<i>Internal function</i>
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**Description**

Internal function

Internal function

**Usage**

```
resolve.monomulti(edgelist, edgeLenList)
```

```
rootFind(edge)
```

**Author(s)**

Yusuke Matsui & Teppei Shimamura

Yusuke Matsui & Teppei Shimamura



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