

Package ‘NetFrac’

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Type Package

Title Netfrac - Community distance calculation within sequence similarity networks

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Description The NetFrac package allows the users to calculate the eight following network measures: NetUniFrac, Motifs, Spp, Spép, Spelp, Spinp distances and the Transfer index (two variants), between species communities present in a given sequence similarity network. The shortest path in a phylogenetic tree is traditionally used to estimate evolutionary distances between species. However, the shortest path concept can be extended to sequence similarity networks. The five following distances (NetUniFrac, Spp, Spép, Spelp, and Spinp) can be seen as network analogues of the traditional UniFrac distance used to assess distances between species communities in a phylogenetic tree, whereas the Transfer index is designed for estimating the rate and direction of horizontal gene transfers, or species dispersal, between different phylogenetic, or ecological, species communities.

Depends igraph,
plyr,
MLmetrics,
doParallel,
SDDE,
ape,
netresponse,
Rcpp

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Suggests knitr,
rmarkdown

VignetteBuilder knitr

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dist_paths	<i>Shortest path distances</i>
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Description

Takes as input the network as well as the species communities to be compared and gives as output the pairwise distance matrix between species communities. The use of the NetFrac function is recommended if the global distances (between all pair of communities) are needed.

Usage

```
dist_paths(x, col1, col2, distance = "paths", paths = "single", info = NULL, type = "graph", maxcores
```

Arguments

x	The igraph object to be analyzed
col1	Community one
col2	Community two
distance	Distances that are implemented in NetFrac. See also the NetFrac function
paths	Take into account all possible shortest paths or only one
info	Information about the tree if the input is a tree
type	Tree or network
maxcores	Number of parallel cores to be used for calculation (one by default)

See Also

[NetFrac](#)

multicore	<i>multicore</i>
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Description

Uses parallel cores for bigger networks.

Usage

```
multicore(nc = 1)
```

Arguments

nc	number of cores
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NetFrac	<i>Title</i>
Description	
Title	
Usage	
<pre>NetFrac(x, distances = "UniFrac", paths = "single", mats = "", maxcores = 1, share_weight = 0)</pre>	
Arguments	
x	The network(or tree) that will be analyzed. The network must be in the igraph format, the edges being accessible with E(x) and vertices with V(x). The communities are under V(x)\$tax and the branch weights under E(x)\$weight. These functions are applicable with igraph objects only
distances	Distances or indices to calculate: Transfer, Transfer2, Spaths, UniFrac and Motifs. The transfer, paths and Unifrac distances can also be calculated for trees
paths	this parameter is used to decide whether all the shortest paths between network nodes should be calculated ("all"), or only one of them ("single"). The last option can significantly reduce the time of computation. For Motifs distance, decide the size of the motifs (i.e. 2 or 3)
mats	the similarity matrix used to reconnect the network. See also reconnect
maxcores	uses the multicore function to set up the number of cores to be used
share_weight	weight if there are mixed communities. For now, only 0 is implemented
Value	
<pre>\$'Spp' A B A 0.0000000 0.5555556 B 0.5555556 0.0000000 \$Spep A B A 0.0000000 0.6296296 B 0.6296296 0.0000000 \$Spelp A B A 0.0000000 0.6296296 B 0.6296296 0.0000000 \$Spinp A B A 0.0000000 0.9907407 B 0.9907407 0.0000000</pre>	

```
$Transfer
A B
A 0.0000000 0.6666667
B 0.3333333 0.0000000
```

Examples

```
NetFrac(net_a)
NetFrac(net_a,"Spaths","all")
```

NetUnifrac	<i>NetUnifrac</i>
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Description

Calculates the network version of the UniFrac distance.

Usage

```
NetUnifrac(igraph, tax1 = "", tax2 = "", weight = TRUE)
```

Arguments

igraph	The igraph object
tax1	The first community
tax2	The second community
weight	Use weights of the edges if existing

Examples

```
NetUnifrac(net_a,"A","B")
```

reconnect	<i>Connect the network using a similarity matrix</i>
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Description

Creates a fully connected network using a similarity matrix between nodes.

Usage

```
reconnect(graph, matrice = "")
```

Arguments

graph	The disconnected igraph object
matrice	The similarity matrix containing pairwise distances between the nodes

See Also

```
reconnect\_btw
```

reconnect_btw

Connect the network a graph using betweenness centrality

Description

Creates a fully connected network using the betweenness centrality principle.

Usage

```
reconnect_btw(graph)
```

Arguments

graph The disconnected igraph object

See Also

[reconnect](#)

set_color

Set colors for the communities in the network

Description

Visualizes the network by adding different colors to different species communities, when plotting either with R own color list or a provided color list.

Usage

```
set_color(graph, colors_list = "")
```

Arguments

graph The igraph object used to define colors. The nodes accessed with V() should have a \$tax attribute which links them to a community, so a different color can be assigned to each community.

colors_list Optional; the colors can be defined in a list with the community names defined with names(). Otherwise, the function will return the numbers already associated to R colors.

Examples

```
foo_CAT_env <- c("red","green","blue","grey")
names(foo_CAT_env) = c("host","ubiquitous","water","unknown")
CAT_env <- set_color(CAT_env, foo_CAT_env)
plot(CAT_env)
```

subgroup_graph	<i>Create a subgraph based on chosen species communities</i>
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Description

Creates another igraph object containing only the nodes from some chosen species communities (two or more), and the edges connecting them.

Usage

```
subgroup_graph(graph, groups)
```

Arguments

graph	The igraph object
groups	The communities that should be isolated, indicated as a list of two items

Examples

```
CAT_env1 <- set_color(subgroup_graph(CAT_env, c("host", "ubiquitous")))
plot(CAT_env1)
```

Transfer	<i>Algorithm for a fast calculation of the Transfer index</i>
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Description

The Transfer index can be used to calculate the proportion of species/sequences of community X that have been affected by horizontal gene transfers from species/sequences of community Y. The Transfer index is assymetric. If the threshold alpha ($0 < \alpha < 1$) is satisfied, the distance is incremented. The operation is repeated for every node of the network. The result is a pairwise matrix reporting the Transfer index for each pair of species communities.

Usage

```
Transfer(graph)
```

Arguments

graph	The igraph object
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Examples

```
Transfer(net_a)
```

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