

# Package ‘meconetcomp’

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**Type** Package

**Title** Compare Microbial Networks of 'trans\_network' Class of 'microeco' Package

**Version** 0.1.0

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**Description** Compare microbial co-occurrence networks created from 'trans\_network' class of 'microeco' package <<https://github.com/ChiLiubio/microeco>>. This package is the extension of 'trans\_network' class of 'microeco' package and especially useful when different networks are constructed and analyzed simultaneously.

**URL** <https://github.com/ChiLiubio/meconetcomp>

**Depends** R (>= 3.5.0)

**Imports** microeco, magrittr, dplyr, igraph, reshape2

**Suggests** rgexf, ape, file2meco

**License** GPL-3

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cal_module	<i>Assign modules to each network</i>
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## Description

Calculating modularity of networks and assign the modules to nodes for each network.

## Usage

```
cal_module(
  network_list,
  undirected_method = "cluster_fast_greedy",
  directed_method = "cluster_optimal",
  ...
)
```

## Arguments

**network\_list** a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

**undirected\_method** default "cluster\_fast\_greedy"; the modularity algorithm for undirected network; see `cal_module` function of `trans_network` class for more algorithms.

**directed\_method** default 'cluster\_optimal'; the modularity algorithm for directed network.

**...** other parameters (except for method) passed to `cal_module` function of `trans_network` class.

## Value

list, with module attribute in nodes of each network

**Examples**

```
data(soil_amp_network)
soil_amp_network <- cal_module(soil_amp_network)
```

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cal_network_attr	<i>Calculate network topological property for each network</i>
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**Description**

Calculate the topological properties of all the networks and merge the results into one table.

**Usage**

```
cal_network_attr(network_list)
```

**Arguments**

network\_list a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

**Value**

data.frame

**Examples**

```
data(soil_amp_network)
test <- cal_network_attr(soil_amp_network)
```

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edge_comp	<i>Generate a microtable object with paired nodes distributions of edges across networks</i>
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**Description**

Generate a microtable object with paired nodes distributions of edges across networks. Useful for the edge comparisons across different networks. The return `otu_table` in microtable object has the binary numbers in which 1 represents the presence of the edge in the corresponding network.

**Usage**

```
edge_comp(network_list)
```

**Arguments**

`network_list` a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

**Value**

microtable object

**Examples**

```
data(soil_amp_network)
test <- edge_comp(soil_amp_network)
# test is a microtable object
```

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<code>edge_tax_comp</code>	<i>Taxonomic sum of linked nodes in edges across networks</i>
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**Description**

Taxonomic sum of linked nodes in edges across networks.

**Usage**

```
edge_tax_comp(network_list, taxrank = "Phylum", label = "+", rel = TRUE)
```

**Arguments**

`network_list` a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

`taxrank` default "Phylum"; Which taxonomic level is used for the sum of nodes in edges.

`label` default "+"; "+" or "-" or c("+", "-"); the edge label used for the selection of edges for the sum.

`rel` default TRUE; TRUE represents using ratio, the denominator is the number of selected edges; FALSE represents the absolute number of the sum of edges.

**Value**

data.frame

**Examples**

```
data(soil_amp_network)
test <- edge_tax_comp(soil_amp_network)
# test is a microtable object
```

---

get_edge_table	<i>Get edge property table for each network</i>
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**Description**

Get edge property table for each network in the list with multiple networks.

**Usage**

```
get_edge_table(network_list)
```

**Arguments**

`network_list` a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

**Value**

list, with `res_edge_table` in each network

**Examples**

```
data(soil_amp_network)
soil_amp_network <- get_edge_table(soil_amp_network)
```

---

get_node_table	<i>Get node property table for each network</i>
----------------	---

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**Description**

Get node property table for each network in the list with multiple networks.

**Usage**

```
get_node_table(network_list, ...)
```

**Arguments**

`network_list` a list with multiple networks; all the networks should be `trans_network` object created from `trans_network` class of `microeco` package.

`...` parameter passed to `get_node_table` function of `trans_network` class.

**Value**

list, with `res_node_table` in each network

## Examples

```
data(soil_amp_network)
soil_amp_network <- get_node_table(soil_amp_network, node_roles = FALSE)
```

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node\_comp

*Generate a microtable object with node distributions across networks*

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## Description

Generate a microtable object with node distributions across networks. Useful for the node information comparisons across different networks.

## Usage

```
node_comp(network_list, property = "name")
```

## Arguments

network_list	a list with multiple networks; all the networks should be <code>trans_network</code> object created from <code>trans_network</code> class of <code>microeco</code> package.
property	default "name"; a colname of <code>res_node_table</code> in each network; the default "name" represents using node presence/absence information in the <code>otu_table</code> of final output, in which 1 represents presence of the node in the corresponding network; For other options (such as degree), the results in the output <code>otu_table</code> are the actual values of <code>res_node_table</code> .

## Value

microtable object

## Examples

```
data(soil_amp_network)
test <- node_comp(soil_amp_network)
# test is a microtable object
```

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soil_amp	<i>The soil_amp data</i>
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**Description**

The soil\_amp data is the 16S rRNA gene amplicon sequencing dataset of Chinese wetland soils.  
Reference: An et al. 2019 <doi:10.1016/j.geoderma.2018.09.035>; Liu et al. 2022 <10.1016/j.geoderma.2022.115866>

**Usage**

```
data(soil_amp)
```

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soil_amp_network	<i>The soil_amp_network data</i>
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**Description**

The soil\_amp\_network data is a list storing three trans\_network objects created based on soil\_amp data. Three networks are created for IW, CW and TW groups, respectively.

**Usage**

```
data(soil_amp_network)
```

---

soil_measure_diversity	<i>The soil_measure_diversity data</i>
------------------------	--

---

**Description**

The soil\_measure\_diversity data is a table storing all the abiotic factors and functional diversity based on the metagenomic sequencing and MetaCyc pathway analysis.

**Usage**

```
data(soil_measure_diversity)
```

---

stool_met	<i>The stool_met data</i>
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**Description**

The stool\_met data is the metagenomic species abundance dataset of stool samples selected from R ExperimentHub package. It has 198 samples, collected from the people with alcohol drinking habit, and 92 species.

**Usage**

```
data(stool_met)
```

---

subnet_property	<i>Calculate properties of sub-networks selected according to features in samples</i>
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**Description**

Extracting sub-network according to the presence of features in each sample across networks and calculate the sub-network properties.

**Usage**

```
subnet_property(network_list)
```

**Arguments**

`network_list` a list with multiple networks; all the networks should be `trans_network` object created from [trans\\_network](#) class of `microeco` package.

**Value**

```
data.frame
```

**Examples**

```
data(soil_amp_network)
test <- subnet_property(soil_amp_network)
```



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subset_network	<i>Extract subset of network according to the edge intersection of networks</i>
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**Description**

Extracting a network according to the edge intersection of networks.

**Usage**

```
subset_network(network_list, venn = NULL, name = NULL)
```

**Arguments**

network_list	a list with multiple networks; all the networks should be trans_network object created from <a href="#">trans_network</a> class of microeco package.
venn	default NULL; a microtable object which must be converted by trans_comm function of trans_venn class.
name	default NULL; integer or character; must be a number or one of colnames of the otu_table in venn.

**Value**

a trans\_network object, with only the extracted edges in the network

**Examples**

```
data(soil_amp_network)
# first obtain edge distribution
tmp <- edge_comp(soil_amp_network)
# obtain edge intersection using trans_venn class
tmp1 <- microeco::trans_venn$new(tmp)
# convert intersection result to microtable object
tmp2 <- tmp1$trans_comm()
# extract the intersection of all the three networks ("IW", "TW" and "CW")
test <- subset_network(soil_amp_network, venn = tmp2, name = "IW&TW&CW")
# test is a trans_network object
```

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