

Package ‘mbOmic’

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Type Package

Title Integrative analysis of the microbiome and metabolome

Version 1.0.0

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Description More about what it does (maybe more than one line)

Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Imports magrittr, psych, WGCNA, data.table, ggraph, tidygraph

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`b.extra`*b.extra*

Description

obtain the b slot from mbSet

Usage

```
b.extra(obj)
```

`check_mbSet`*check_mbSet*

Description

check function for mbSet

Usage

```
check_mbSet(object)
```

`cor.test`*cor.test*

Description

genetic methods to perform the correlation test

Usage

```
cor.test(object, parallel = FALSE, ncore = 4, ...)
```

```
## S4 method for signature 'mbSet'
```

```
cor.test(object, parallel = FALSE, ncore = 4, ...)
```

Arguments

`parallel`, logical

`ncore`, integer number of core

`cor2df`*cor2df*

Description`cor2df`**Usage**`cor2df(res)`

`m.extra`*m.extra*

Description`obtain the m slot from mbSet`**Usage**`m.extra(obj)`

`m.filter`*test the metabolite profile*

Description`test the metabolite profile`**Usage**`m.filter(m, minNSamples = 2)`

`mb.cor-class`*mb.cor*

Description`define the class of mb.cor`**Slots**`r`, matrix r value`p.adj`, matrix adjustment p value`p`, matrix p value

mbSet	<i>An S4 class to represent a bank account.</i>
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Description

obtain the m express matrix from mbSet create the mbSet class

Usage

```
mbSet(m, b, pData = NULL)
```

```
mbSet(m, b, pData = NULL)
```

Slots

b ExpressionSet contain the expression of OTU

m ExpressionSet metabolites abundance

pData AnnotationDataFrame phenodata

nb.extra	<i>nb</i>
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Description

nb

Usage

```
nb.extra(obj)
```

nm.extra	<i>nm</i>
----------	-----------

Description

nm

Usage

```
nm.extra(obj)
```

<code>pickST</code>	<i>Automatic network construction and module detection by one-step method</i>
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Description

Automatic network construction and module detection by one-step method

Usage

```
pickST(m, threshold.d = 0.05, threshold = 0.8, plot = TRUE, powers = NULL)
```

<code>plot_network</code>	<i>plot network</i>
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Description

plot network

Usage

```
plot_network(net, corr, centrality_degree_mode = "out")
```

<code>print.mb.module</code>	<i>print.mb.module</i>
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Description

mb.module print

Usage

```
## S3 method for class 'mb.module'
print(object)
```

<code>print.mbSet</code>	<i>print</i>
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Description

print

Usage

```
## S3 method for class 'mbSet'
print(obj)
```

<code>samples.extra</code>	<i>samples</i>
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Description

obtain the samples

Usage

```
samples.extra(obj)
```

<code>show, mbSet-method</code>	<i>show</i>
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Description

show

Usage

```
## S4 method for signature 'mbSet'
show(object)
```

<code>wgcna</code>	<i>wgcna</i>
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Description

wgcna

Usage

```
wgcna (
  object,
  group,
  minN,
  power = NULL,
  powers = 1:30,
  threshold.d = 0.05,
  threshold = 0.8,
  message = F,
  ...
)
```

wgcna,mbSet-method *wgcna*

Description*wgcna***Usage**

```
## S4 method for signature 'mbSet'
wgcna (
  object,
  group,
  minN,
  power = NULL,
  powers = 1:30,
  threshold.d = 0.05,
  threshold = 0.8,
  message = F,
  ...
)
```

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