

# Package ‘metapone’

January 27, 2022

**Type** Package

**Title** Conducts pathway test of metabolomics data using a weighted permutation test

**Version** 1.0.0

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**Description** The package conducts pathway testing from untargetted metabolomics data. It requires the user to supply feature-level test results, from case-control testing, regression, or other suitable feature-level tests for the study design. Weights are given to metabolic features based on how many metabolites they could potentially match to. The package can combine positive and negative mode results in pathway tests.

**Depends** R (>= 4.1.0), BiocParallel, fields, markdown

**Imports** methods

**biocViews** Technology, MassSpectrometry, Metabolomics, Pathways

**License** Artistic-2.0

**LazyLoad** yes

**NeedsCompilation** no

**Suggests** rmarkdown, knitr

**VignetteBuilder** knitr

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**R topics documented:**

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metapone-package	<i>Conducts pathway test of metabolomics data using a weighted permutation test</i>
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**Description**

The package conducts pathway testing from untargetted metabolomics data. It requires the user to supply feature-level test results, from case-control testing, regression, or other suitable feature-level tests for the study design. Weights are given to metabolic features based on how many metabolites they could potentially match to. The package can combine positive and negative mode results in pathway tests. The package conducts a permutation test that is based on the hypergeometric test for metabolic pathway analysis.

**Details**

The package conducts a weighted hypergeometric test using permutations on metabolomics data. The weights are assigned based on how many metabolites each data feature can match to. The user can tune a parameter to change the penalty for multiple-matched features.

**Author(s)**

Tianwei Yu<yutianwei@cuhk.edu.cn>

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fable	<i>Accessor functions for the feature mapping table in a metaponeResult object.</i>
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### Description

Returns a list containing the mapped features in each pathway.

### Usage

```
## S4 method for signature 'metaponeResult'  
fable(object)
```

### Arguments

object            A metaponeResult object.

### Details

Each pathway is represented by a `data.frame` as an item in the list object. The dataframe include information of `m.z`, `retention.time`, `p.value`, `statistic`, `HMDB_ID`, `theoretical.m.z`, `ion.type`, `fractional.counts`.

### Value

The method returns a list. Each item is for a pathway. Matched significant metabolites are included.

### Author(s)

Tianwei Yu <yutianwei@cuhk.edu.cn>

### See Also

`ptable`

### Examples

```
data(hmdbCompMZ.metapone)  
data(pa)  
data(pos)  
data(neg)  
r<-metapone(pos, neg, pa, hmdbCompMZ=hmdbCompMZ.metapone, p.threshold=0.05,  
  n.permu=100, fractional.count.power=0.5, max.match.count=10)  
fable(r)[1:6]
```

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`hmdbCompMZ`*the m/z values of common adduct ions of HMDB metabolites*

---

**Description**

Monoisotopic mass of common adduct ions.

**Usage**

```
data("hmdbCompMZ")
```

**Format**

A data frame with 5704350 observations on the following 3 variables.

`HMDB_ID` HMDB ID.

`ion.type` Adduct ion type.

`m.z` the m/z of the adduct ion.

**Source**

<https://hmdb.ca/>

**References**

<https://hmdb.ca/>

**Examples**

```
data(hmdbCompMZ)
```

---

`hmdbCompMZ.metapone`*the m/z values of common adduct ions of metapone metabolites*

---

**Description**

Monoisotopic mass of common adduct ions, limited to those included in the pathways in metapone.

**Usage**

```
data("hmdbCompMZ.metapone")
```

**Format**

A data frame with 79350 observations on the following 3 variables.

HMDB\_ID HMDB ID.

ion.type Adduct ion type.

m.z the m/z of the adduct ion.

**Details**

The main difference of using this dataset vs using hmdbCompMZ, is the metabolite universe in testing is limited to those metabolites matched to metapone pathways, not all HMDB metabolites.

**Source**

<https://hmdb.ca/>

**References**

<https://hmdb.ca/>

**Examples**

```
data(hmdbCompMZ)
```

---

metapone

*METAbolic pathway testing using both POSitive and NEgative mode data*

---

**Description**

Metapone conducts pathway tests for untargeted metabolomics data. It has three main characteristics: (1) expanded database combining SMPDB and Mummichog databases, with manual cleaning to remove redundancies; (2) A new weighted testing scheme to address the issue of metabolite-feature matching uncertainties; (3) Can consider positive mode and negative mode data in a single analysis.

**Usage**

```
metapone(pos = NULL, neg = NULL, pa, hmdbCompMZ, pos.adductlist =  
c("M+H", "M+NH4", "M+Na", "M+ACN+H", "M+ACN+Na", "M+2ACN+H", "2M+H",  
"2M+Na", "2M+ACN+H"), neg.adductlist = c("M-H", "M-2H", "M-2H+Na",  
"M-2H+K", "M-2H+NH4", "M-H2O-H", "M-H+Cl", "M+Cl", "M+2Cl"),  
use.fractional.count = TRUE, match.tol.ppm = 5, p.threshold = 0.05,  
n.permu = 200, fractional.count.power = 0.5, max.match.count = 10)
```

**Arguments**

<code>pos</code>	The positive ion mode test results. A matrix with four columns: m/z, retention time, p-value, test statistic. The package doesn't require both <code>pos</code> and <code>neg</code> to be present. One ion mode result is sufficient.
<code>neg</code>	The negative ion mode test results. A matrix with four columns: m/z, retention time, p-value, test statistic. The package doesn't require both <code>pos</code> and <code>neg</code> to be present. One ion mode result is sufficient.
<code>pa</code>	Pathway information. A data frame with five columns: database pathway ID, pathway name, HMDB ID, KEGG ID, category of pathway.
<code>hmdbCompMZ</code>	the m/z values of common adduct ions of HMDB metabolites. See the help file of <code>hmdbCompMZ</code> for details.
<code>pos.adductlist</code>	The vector of positive adduct ions to be considered.
<code>neg.adductlist</code>	The vector of negative adduct ions to be considered.
<code>use.fractional.count</code>	A lot of features match to multiple metabolites by m/z. Whether to discount such matches by using fractional counts.
<code>match.tol.ppm</code>	The ppm level when conducting m/z match.
<code>p.threshold</code>	The threshold of p-values of metabolic features to be considered significant.
<code>n.permu</code>	The number of permutations in permutation test.
<code>fractional.count.power</code>	The fractional counts are taken to this power to transform the weights.
<code>max.match.count</code>	When calculating fractional counts, some features might be matched to too many. In that case the number of matches is capped by the value of <code>max.match.count</code> .

**Value**

The method returns a generic S4 object of class "metapone.result":

<code>@test.results</code>	A matrix with 6 columns: "p_value", "n_significant metabolites", "n_mapped_metabolites", "n_metabolites", "significant metabolites", "mapped_metabolites". Each row is for a pathway.
<code>@mapped.features</code>	A list. Each item is for a pathway. The item lists matched significant metabolites.

**Author(s)**

Tianwei Yu<yutianwei@cuhk.edu.cn>

**References**

<https://smpdb.ca/> <https://shuzhao-li.github.io/mummichog.org/software.html>

**See Also**

`hmdbCompMZ`, `pa`

## Examples

```
data(hmdbCompMZ.metapone)
data(pa)
data(pos)
data(neg)
r<-metapone(pos, neg, pa, hmdbCompMZ=hmdbCompMZ.metapone, p.threshold=0.05,
  n.permu=100, fractional.count.power=0.5, max.match.count=10)
hist(ptable(r)[,1])
```

---

metaponeResult-class    *Class "metaponeResult"*

---

## Description

This class represents the results of pathway testing. The testing result contain two major components: the significant level of each pathway, and the features matched to each pathway.

## Objects from the Class

Objects can be created by calls of the form `new("metaponeResult", ...)`.

## Slots

**test.result:** a dataframe containing `p_value`, `n_significant` metabolites, `n_mapped_metabolites`, `n_metabolites`, significant metabolites, mapped\_metabolite IDs and pathway name.

**mapped.features:** A list containing `n` entries, where `n` is the number of pathways. Each entry is a data frame, containing the features mapped to this pathway. The information include `m.z`, `retention.time`, `p.value`, `statistic`, `HMDB_ID`, `theoretical m.z`, `ion.type`, fractional counts.

## Methods

**ptable** signature(object = "metaponeResult"): return the `data.frame` of test statistics for each pathway, including `p_value`, `n_significant` metabolites, `n_mapped_metabolites`, `n_metabolites`, significant metabolites, mapped\_metabolite IDs and pathway name.

**ftable** signature(object = "metaponeResult"): Returns a list containing the mapped features in each pathway. Each pathway is represented by a `data.frame` as an item in the list object. The dataframe include information of `m.z`, `retention.time`, `p.value`, `statistic`, `HMDB_ID`, `theoretical m.z`, `ion.type`, fractional counts.

## Author(s)

Tianwei Yu

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neg	<i>Example negative mode data from the Dorm Room Inhalation to Vehicle Emission (DRIVE) study</i>
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---

**Description**

Data matrix from negative mode results. It is the test results from the data generated using C18 hydrophobic reversed-phase chromatography with negative ESI.

**Usage**

```
data("neg")
```

**Format**

A data frame with 3337 observations on the following 4 variables.

`m.z` a numeric vector. The mass-to-charge ratio of the features.

`retention.time` a numeric vector. The retention time of the features.

`p.value` a numeric vector. The p-values of the features.

`statistic` a numeric vector. The test statistics of the features.

**References**

Liang D, Moutinho JL, Golan R, Yu T, Ladva CN, Niedzwiecki M, Walker DI, Sarnat SE, Chang HH, Greenwald R, Jones DP, Russell AG, Sarnat JA (2018) Use of high-resolution metabolomics for the identification of metabolic T signals associated with traffic-related air pollution. *Environment International*. 120:145-154.

**Examples**

```
data(neg)
```

---

pa	<i>Pathway-metabolite match file.</i>
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---

**Description**

mapps pathways with metabolites.

**Usage**

```
data("pa")
```



**Format**

A data frame with 5395 observations on the following 5 variables.

database a character vector  
pathway.name a character vector  
HMDB.ID a character vector  
KEGG.ID a character vector  
category a character vector

**Source**

<https://smpdb.ca/> <https://shuzhao-li.github.io/mummichog.org/software.html>

**Examples**

```
data(pa)
```

---

pos	<i>Example positive mode data from the Dorm Room Inhalation to Vehicle Emission (DRIVE) study</i>
-----	---

---

**Description**

The data is from the DRIVE study. It is the test results from the data generated using hydrophilic interaction liquid chromatography (HILIC) with positive electrospray ionization (ESI).

**Usage**

```
data("pos")
```

**Format**

A data frame with 2252 observations on the following 4 variables.

m.z a numeric vector. The mass-to-charge ratio of the features.  
retention.time a numeric vector. The retention time of the features.  
p.value a numeric vector. The p-values of the features.  
statistic a numeric vector. The test statistics of the features.

**References**

Liang D, Moutinho JL, Golan R, Yu T, Ladva CN, Niedzwiecki M, Walker DI, Sarnat SE, Chang HH, Greenwald R, Jones DP, Russell AG, Sarnat JA (2018) Use of high-resolution metabolomics for the identification of metabolic T signals associated with traffic-related air pollution. *Environment International*. 120:145-154.

**Examples**

```
data(pos)
```

---

ptable	<i>Accessor functions for the test result table in a metaponeResult object.</i>
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---

**Description**

return the data.frame of test statistics for each pathway.

**Usage**

```
## S4 method for signature 'metaponeResult'  
ptable(object)
```

**Arguments**

object            A metaponeResult object.

**Details**

Includes p\_value, n\_significant metabolites, n\_mapped\_metabolites, n\_metabolites, significant metabolites, mapped\_metabolite IDs and pathway name.

**Value**

The method returns a data frame with 6 columns: "p\_value", "n\_significant metabolites", "n\_mapped\_metabolites", "n\_metabolites", "significant metabolites", "mapped\_metabolites".

**Author(s)**

Tianwei Yu <yutianwei@cuhk.edu.cn>

**See Also**

fable

**Examples**

```
data(hmdbCompMZ.metapone)  
data(pa)  
data(pos)  
data(neg)  
r<-metapone(pos, neg, pa, hmdbCompMZ=hmdbCompMZ.metapone,  
  p.threshold=0.05,n.permu=100,fractional.count.power=0.5, max.match.count=10)  
head(ptable(r))
```

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