

# Package ‘iontree’

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**Type** Package

**Title** Data management and analysis of ion trees from ion-trap mass spectrometry

**Version** 1.10.0

**Depends** methods, rJava, RSQLite, XML

**Suggests** iontreeData

**Author** Mingshu Cao

**Maintainer** Mingshu Cao <mingshu.cao@agresearch.co.nz>

**Description** Ion fragmentation provides structural information for metabolite identification. This package provides utility functions to manage and analyse MS2/MS3 fragmentation data from ion trap mass spectrometry. It was designed for high throughput metabolomics data with many biological samples and a large number of ion trees collected. Tests have been done with data from low-resolution mass spectrometry but could be readily extended to precursor ion based fragmentation data from high resolution mass spectrometry.

**License** GPL-2

**biocViews** Metabolomics, MassSpectrometry

**LazyLoad** yes

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iontree-package	<i>MSn-iontree: Ion tree management and analysis</i>
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## Description

management and analysis of ion fragmentation data

## Details

Package: iontree  
 Type: Package  
 LazyLoad: yes

This package provides functions to retrieve MSn fragmentation data, build MS2/MS3 ion trees from ion-trap low resolution mass spectrometry and to create a relational database (SQLite-based) for routine management of ion tree data. Other functions include metrics for MS2 spectral simialrity measurement, iontree plotting and DB operations.

## Author(s)

Mingshu Cao  
 Maintainer: Mingshu Cao <mingshu.cao@agresearch.co.nz>

## References

JRAP – a Java library was used for parsing mzXML and mzML  
<http://sashimi.svn.sourceforge.net/viewvc/sashimi/trunk/jrap/stax/software/>

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buildIonTree	<i>Build ion tree</i>
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**Description**

build an ion tree derived from the specified m/z and RT ranges in one sample based on ms2 and ms3 raw data, see saveMSnRaw and hasMS2.

**Usage**

```
buildIonTree(mzRange = c(340.5, 341.5), rtRange = c(270, 282), ms2, ms3)
```

**Arguments**

mzRange	mz range
rtRange	rt range
ms2	ms2 data as list
ms3	ms3 data as list

**Note**

the full time range is used for direct infusion mass spectrometry. For instance, rtRange=c(0, 300) is used for 5-min total elution time.

**Author(s)**

Mingshu Cao

**Examples**

```
#mz=867
#mzDelta=0.5
#mzRange=c(mz-mzDelta, mz+mzDelta)
#rtRange=c(1, 600)
#hasMS2(MS2RAW, mzRange=c(mz-mzDelta, mz+mzDelta), rtRange=c(0, 600))

#idx.ms2=1
#ms2=MS2RAW[[idx.ms2]]
#ms3=MS3RAW[[idx.ms2]]

#tree1=buildIonTree(mzRange, rtRange=c(0, 600), ms2, ms3)
#plot(tree1)
```

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createDB

*Create a SQLite database*

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**Description**

create a relational database based on a schema defined in this package if argument sql is not specified. There are two tables (experiment and mz) defined to capture necessary information to annotate ions or peaks.

**Usage**

```
createDB(dbname = "mzDB.db", sql = "mzDBSchema.sql")
```

**Arguments**

dbname	database name
sql	predefined schema, or a modified definition

**Value**

A database file saved in the current folder

**Author(s)**

Mingshu Cao

**Examples**

```
## Not run:  
createDB(dbname="my.db")  
  
## End(Not run)
```

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distMS2

*Distance metric for MS2 spectral similarity measurement*

---

**Description**

distance metric for MS2 spectral comparison. MS2 spectrum is provided as 2-col matrix.

**Usage**

```
distMS2(a, b, topIon = 20)
```

**Arguments**

a	MS2 spectrum
b	MS2 spectrum
topIon	the number of the most intense ions used for comparison

**Author(s)**

Mingshu Cao

**References**

Cao M, Koulman A, Johnson LJ, Lane GA and Rasmussen S. 2008. Plant Physiology. Vol.146 No.4

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formatSpec	<i>Format mass spec matrix data into a string format, or vice versa</i>
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**Description**

argument `x` is a 2-column matrix of `mz` and intensity, or a string format of `mz-intensity` pairs. Character pair of `mz` and intensity is separated by semicolon, for example, `150 2345.6; 151 4325.67; ...` which is often used to represent a mass spectrum as seen in NIST and MassBank.

**Usage**

```
formatSpec(x, fromTo = c("mat2str", "str2mat"))
```

**Arguments**

<code>x</code>	2-col matrix or type of character depends on "fromTo"
<code>fromTo</code>	type of conversion

**Author(s)**

Mingshu Cao

**Examples**

```
x="150 2345.6; 151 4325.67;"  
formatSpec(x, fromTo="str2mat")
```

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getMetaInfo	<i>Get metadata information from data file in mzXML</i>
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**Description**

print out some useful header information, such as instrumentation, ionization, range of `mz` and `RT`, and the number of `MSn` scans etc.

**Usage**

```
getMetaInfo(filename)
```

**Arguments**

<code>filename</code>
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**Author(s)**

Mingshu Cao

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getMSnRaw	<i>Get MSn raw data</i>
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### Description

query MSn data by the attribute of 'msLevel' and get MSn raw data into a R list. Users may just use function "saveMSnRaw" to retrieve ion tree from a data file and avoid a direct Java function call.

### Usage

```
getMSnRaw(msdata, msLevel = 2)
```

### Arguments

msdata	msdata is a reference to a Java ArrayList. Obtained by calling getMSData Java function. msdata=jcall("XCMS", "Ljava/util/ArrayList;", "getMSData", filename);
msLevel	msLevel in integer

### Value

preMZ	ancestral precursor ions
rt	retention time
msn.sp	a list of spectrum (m/z, intensity)

### Note

MS1 data could be queried by msLevel=1. The return type is still a list but different components (rt, tic, sp).

### Author(s)

Mingshu Cao

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hasMS2	<i>Check which samples have MS2 spectra generated</i>
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### Description

check whether MS2 data are available for the ion/peak specified by mzRange and rtRange among samples.

### Usage

```
hasMS2(MS2RAW, mzRange = c(1854, 1854.5), rtRange = c(280, 400))
```

**Arguments**

MS2RAW	MS2 raw data in R binary file, see saveMSnRaw
mzRange	m/z range
rtRange	rt range

**Value**

return sample index

**Author(s)**

Mingshu Cao

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iontree-class                      *Class "iontree"*

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**Description**

iontree representation in S4 class

**Objects from the Class**

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

**Slots**

**mz:** Object of class "numeric" peak or ion m/z  
**rt:** Object of class "numeric" peak or ion RT  
**MS2:** Object of class "matrix" ms2 spectrum  
**MS3:** Object of class "list" ms3 spectrum/spectra

**Methods**

**plot** signature(x = "iontree"): ...  
**show** signature(object = "iontree"): ...

**Note**

To be extended to MSn where n>3

**Author(s)**

Mingshu Cao

**Examples**

```
showClass("iontree")
```

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metaDataImport	<i>Data entry of meta information</i>
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### Description

data entry of table "experiment". Such meta information may include brief description of sample origin, biological treatment, extraction method, chromatography, ionization, polarity, collision energy and those might affect comparative analysis of iontrees. R default data editor was used to help provide necessary information. SQLite database browsers are also freely available for different platforms.

### Usage

```
metaDataImport(dbname = "mzDB.db")
```

### Arguments

dbname	database name
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### Note

A known issue: a call to use data editor (fix) might cause access violation, that was occasionally observed.

### Author(s)

Mingshu Cao

### Examples

```
#to check information just loaded
#db=dbConnect(dbDriver("SQLite"), dbname="mzDB.db")
#dbListTables(db)
#q1=dbSendQuery(db, "SELECT * FROM experiment")
#fetch(q1, n=-1)
#dbClearResult(q1)
#dbDisconnect(db)
```



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mzImport	<i>Data entry of iontree into mz table</i>
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**Description**

import iontree object into table "mz" in the database

**Usage**

```
mzImport(iontree, dbname = "mzDB.db", exp.id)
```

**Arguments**

iontree	iontree as defined in this package
dbname	database name
exp.id	id in table of experiment

**Note**

see vignette for an example of batch loading

**Author(s)**

Mingshu Cao

**Examples**

```
#to check information just loaded
#db=dbConnect(dbDriver("SQLite"), dbname="mzDB.db")
#dbListTables(db)
#q1=dbSendQuery(db, "SELECT mz, rt, ms2 FROM mz")
#fetch(q1, n=-1)
#dbClearResult(q1)
#dbDisconnect(db)
```

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plot-methods	<i>Plot iontree</i>
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**Description**

plot iontree

**Methods**

```
signature(x = "iontree") plot spectral tree
```

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plotSpectrum	<i>Plot a spectrum</i>
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**Description**

plot a mass spectrum

**Usage**

```
plotSpectrum(x, y=NULL, top = 20, type = "h", scale100 = FALSE,  
            digit.label = 1, col = "black", pos = 0, main = "",  
            clickAddLabels = FALSE, ...)
```

**Arguments**

x	m/z
y	intensity
top	top intense m/z to be labelled
type	plot type
scale100	in scale of 0-100 if true
digit.label	m/z precision to be maintained
col	m/z label color
pos	m/z label position
main	title
clickAddLabels	click to add labels
...	as in plot

**Author(s)**

Mingshu Cao

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rs2iontree	<i>Convert a data frame into iontree</i>
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**Description**

Convert resultset, a data frame retrieved from database into a list of iontree objects.

**Usage**

```
rs2iontree(rs)
```

**Arguments**

rs                    resultset as a data frame

**Value**

a list of iontrees

**Author(s)**

Mingshu Cao

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saveMSnRaw                    *Retrieve MS2 and MS3 data and save as R binary in the current folder*

---

**Description**

save MS2 and MS3 data for later processing such as ion tree construction. R binary files "MS2RAW.Rdata" and "MS3RAW.Rdata" may be found in the current folder, which can be reloaded.

**Usage**

```
saveMSnRaw(dataFolder = "D:/Data/Raw")
```

**Arguments**

dataFolder            current data folder

**Author(s)**

Mingshu Cao

**Examples**

```
#saveMSnRaw("D:/Data/Raw")  
#load("D:/Data/Raw/MS2RAW.Rdata")  
#ls()
```

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searchMS2	<i>Search MS2 spectrum from sqlite database</i>
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**Description**

search MS2 spectra from the database. Ranking is based on the distance metric that defined by Cao et al. 2008, cosine and Tanimoto similarity.

**Usage**

```
searchMS2(querySpec, premz, dbname = "mzDB.db", scoreFun = "distMS2", output.record = 5, plot.top = TRUE)
```

**Arguments**

querySpec	query spectrum in 2-col matrix
preMZ	precursor m/z that query spectrum derived from
dbname	database name
scoreFun	score function, 'distMS2', 'cos' or 'tanimoto'
output.record	the number of records shown in console
plot.top	plot query spectrum and the top-ranked spectrum

**Value**

return top records

**Author(s)**

Mingshu Cao

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show-methods	<i>Show methods for class iontree</i>
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**Description**

show methods for class iontree

**Methods**

```
signature(object = "iontree") show iontree object
```

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topIons	<i>Retain spectrum with the most intense ions</i>
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**Description**

Retain the most intense ions in a spectrum and return sorted spectrum in 2-col matrix

**Usage**

```
topIons(mz, intensity, top)
```

**Arguments**

mz	m/z
intensity	intensity
top	the number of most intense m/z to be maintained

**Value**

return a 2-col matrix

**Author(s)**

Mingshu Cao

**Examples**

```
#Just sort:  
#topIons(mz, intensity, top=length(mz))
```

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