Package 'MetaboList'

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Type Package

Title Annotation of Metabolites from Liquid Chromatography-Mass Spectrometry Data

Version 2.0

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Imports enviPick, ggplot2, scales, utils, stats, graphics,grDevices, dplyr

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Description Automatic metabolite annotation from Liquid Chromatography-Mass Spectrometry (LC-MS and LC-MS/MS DIA) analysis.

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LazyData TRUE

NeedsCompilation no

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R topics documented:

AIF *Automatic Metabolite Annotation from LC-MS DIA experiments.*

Description

Analysis and annotation of LC-MS/MS DIA data with the use of in-house mass spectral libraries.

Usage

```
AIF(fileMS1,fileMS2,CE=0, database,rtw=7,
ppm_tol=10,dmzgap=50,drtdens =20,drtgap=25,
drtsmallMS1=100,drtsmallMS2=30,dmzdensMS1=15,
dmzdensMS2=30,drtfill=5,drttotal=100,minpeakMS1=5,
minpeakMS2=3,recurs=2,weight=2,SB=3, SN=2,
minintMS1=1000,minintMS2=100,maxint=9e+09,
ion_mode="positive",ppm=TRUE,ended=6)
```

Arguments

fileMS1	A .mzXML file extension with the MS/MS experiment obtained at particular collision energy (CE).
fileMS2	A .mzXML file extension with the MS/MS experiment obtained at particular collision energy (CE).
CE	Collision energy employed for the MS/MS experiment.
database	A csv file with data arranged in columns including the names in the first row: Metabolite; Monoisotopic mass for the precursor; Mass Fragment 1; Mass Fragment 2; Mass Fragment 3... There is no need to used retention times as a constraint.
rtw	numeric. The difference between the theoretical retention time value and the experimental. Default value=3
ppm_tol	numeric. Mass error in ppm between the theoretical m/z value and the experimental. Default value=10
dmzgap	Arguments to be passed from enviPickwrap
dmzdensMS1	Arguments to be passed from enviPickwrapfor MS1 mode
dmzdensMS2	Arguments to be passed from enviPickwrapfor MS2 mode
drtgap	Arguments to be passed from enviPickwrap
drtsmallMS1	Arguments to be passed from enviPickwrap for MS1 mode
drtsmallMS2	Arguments to be passed from enviPickwrap for MS2 mode
drtdens	Arguments to be passed from enviPickwrap
drtfill	Arguments to be passed from enviPickwrap
drttotal	Arguments to be passed from enviPickwrap
minpeakMS1	Mininum number of scans that comprise a peak for MS1 mode.

minpeakMS2	Mininum number of scans that comprise a peak for MS2 mode.
recurs	Arguments to be passed from enviPickwrap
weight	Arguments to be passed from enviPickwrap
SB	Arguments to be passed from enviPickwrap
SN	Arguments to be passed from enviPickwrap
minintMS1	Arguments to be passed from enviPickwrap. Value for the MS1 mode.
minintMS2	Arguments to be passed from enviPickwrap. Value for the MS2 mode
maxint	Arguments to be passed from enviPickwrap
ion_mode	Arguments to be passed from enviPickwrap
ppm	Arguments to be passed from enviPickwrap
ended	Arguments to be passed from enviPickwrap

Value

ms1	Peak picking for MS1 level
ms2	Peak picking for MS2 level
annotationfull	Matrix with the metabolites annotated.
RawData1	Raw scans from raw data.
RawData2	Raw scans from raw data.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)

CE.isolation("AIFpos1000-AIF.mzXML","fileposB")

#Reading the database.csv file:
# database<- read.csv("C:/database.csv")

#Processing peak-picking and annotation with default parameters

#aif5<-AIF(fileMS,fileMS2CE5,database,CE=5, ion_mode = "positive")
```

`CE.isolation` *Separation of MS/MS files with regards collision energy*

Description

Isolation of MS/MS events acquired at different collision energies into single files at particular collision energy

Usage

```
CE.isolation(file, output)
```

Arguments

`file`	A mzXML file from the LC-MS/MS experiment in positive or negative ionization mode.
`output`	Multiple mzXML files separated by collision energies.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)
#Reading the file.mzXML
#CE.isolation("AIFpos1000-AIF.mzXML","fileposB")
```

`elemental.formula` *List from elemental formula*

Description

Obtain a list from elemental formula given in the database. Use internally by the Isotopic.R function. Adaptation from R-package OrgMassSpecR.

Usage

```
elemental.formula(elemental.formula)
```

Arguments

`elemental.formula`
: Elemental formula

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
#library(MetaboList)
#Reading the library and indicating type of adduct
#Isotopic(library,name=c("M+H"))
```

`Filter_AIF` *Automatic Metabolite Annotation from LC-MS DIA experiments.*

Description

Analysis and annotation of LC-MS/MS DIA data with the use of in-house mass spectral libraries.

Usage

```
Filter_AIF(aif5,a=1,database,rttol=0.2)
```

Arguments

aif5	DIA file processed
a	Rule to restrict number of product ions.
database	database employed for targeted annotation.
rttol	numeric. Retention time tolerance for aligning fragments and precursors.Default value=0.2min

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)

CE.isolation("AIFpos1000-AIF.mzXML","fileposB")

#Reading the database.csv file:
# database<- read.csv("C:/database.csv")

#Processing peak-picking and annotation with default parameters

#aif5<-AIF(fileMS,fileMS2CE5,database,CE=5, ion_mode = "positive")

#Filter_AIF(aif5,full=TRUE,a=0,database)
```

FullMS *Processing and Annotation of LC-MS Full-Scan data*

Description

Peak picking of MS data is performed by the enviPick algorithm embedded. Second, it is performed a targeted extraction with a mass tolerance and m/z interval windows constraints for general peak grouping and library interrogation. Retention time might be considered as optional constraints. Library listing needs to follow the format following the exampled attached.

Usage

```
FullMS(file, database, rtw = 10, mzw = 0.0004,ppm_tol=10,Peak_Assy=5,
dmzgap = 50,dmzdens = 20, drtgap = 25, drtsmall = 50,
drtdens = 20, drtfill = 5,drttotal = 100, minpeak = 5,
recurs = 3, weight = 1,SB = 2, SN = 1.5, minint = 1000,
maxint = 9e+09, ion_mode = "positive",
ppm = TRUE,ended=6)
```

Arguments

file	A mzXML file from the LC-MS/MS experiment in positive or negative ionization mode.
database	A file with data arranged in columns as follows: Molecular Formula; Retention time (optional); Neutral mass; Compound name
rtw	numeric. The difference between the theoretical retention time value and the experimental. Default value=3
ppm_tol	numeric. Mass error in ppm between the theoretical mass value and the experimental. Default value=10
Peak_Assy	numeric. Maximum peak assymetry threshold. Default value=5
mzw	numeric. The difference between the theoretical m/z value and the experimental (Da). Default value=0.004
dmzgap	Arguments to be passed from enviPickwrap
dmzdens	Arguments to be passed from enviPickwrap
drtgap	Arguments to be passed from enviPickwrap
drtsmall	Arguments to be passed from enviPickwrap
drtdens	Arguments to be passed from enviPickwrap
drtfill	Arguments to be passed from enviPickwrap
drttotal	Arguments to be passed from enviPickwrap
minpeak	Arguments to be passed from enviPickwrap
recurs	Arguments to be passed from enviPickwrap
weight	Arguments to be passed from enviPickwrap
SB	Arguments to be passed from enviPickwrap
SN	Arguments to be passed from enviPickwrap
minint	Arguments to be passed from enviPickwrap
maxint	Arguments to be passed from enviPickwrap
ion_mode	Arguments to be passed from enviPickwrap
ppm	Arguments to be passed from enviPickwrap
ended	Arguments to be passed from enviPickwrap

Value

ms	Annotated metabolites.
RawData1	Raw scans from raw data.
PP	Results obtained throughout enviPick algorithm performed on MS level 1.
Peaklist	Matrix with the peak picked obtained throughout enviPick algorithm.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)
#Reading the file.mzXML
# file<-fullMS.mzXML

#Reading the database.csv file:
# database<- read.csv("C:/FullMS1.csv")

#Processing peak-picking and annotation with default parameters
# FullMS_results<-FullMS(file,database, ion_mode = "positive",)

#Output:
#FullMS_results$ms
```

Isotopic *Preparation library Full-MS.*

Description

Generates a given a library of MS1 metabolites, a list of adducts and isotopes. Adapted from R package OrgMassSpecR.

Usage

```
Isotopic(library, name=c("M+H"),adducts)
```

Arguments

library	Library of MS1 metabolites.
name	Name of the adduct to generate.
adducts	List of adducts.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
#library(MetaboList)
#Reading the library and indicating type of adduct
#Isotopic(library,name=c("M+H"))
```

PeakGroup *Peak Grouping for multiple DIA files*

Description

Annotated metabolites from single DIA files acquired at different collision energies are subjected to peak grouping. The function groups metabolites that are presented along the DIA files.

Usage

```
PeakGroup(aif1,aif2,aif3)
```

Arguments

aif1	Result obtained from AIF
aif2	Result obtained from AIF
aif3	Result obtained from AIF

Value

csv	A Peakgroup.csv files for each metabolite

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)
#Reading the file.mzXML for Full-MS scan and MS/MS.
#The files were previously separated with the SEPC.R function.

#fileMS<-"fullMS.mzXML"
#fileMS2CE5<-"fileMS2CE5.mzXML"

# Separation by collision energy
#CE.isolation("AIFpos1000-AIF.mzXML","fileposB")

#Reading the database.csv file:
# database<- read.csv("C:/database.csv")

#Processing peak-picking and annotation with default parameters

#aif5<-AIF(fileMS,fileMS2CE5,databasepos,CE=5,
#ion_mode = "positive",mzw = 0.005,rtw = 7
#,minintMS2=1,minintMS1=1)
#aif10<-AIF(fileMS,fileMS2CE10,databasepos,CE=10,
#ion_mode = "positive",rtw = 7, mzw = 0.005
#,minintMS2=1,minintMS1=1)
#aif20<-AIF(fileMS,fileMS2CE20,databasepos, CE=20,
#ion_mode = "positive",rtw = 7, mzw = 0.005,
#minintMS2=1,minintMS1=1)

# Peak grouping

#Peakgroup<-PeakGroup(aif5,aif10,aif20)
```

PeakGroupMS1 *Peak Grouping for MS1 file*

Description

Annotated metabolites from single MS1 files are subjected to peak grouping.

Usage

```
PeakGroupMS1(annotation_pos)
```

Arguments

annotation_pos	Result obtained from FullMS

Value

csv	A Peakgroup.csv files for each metabolite

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)

#fullmsposH<-FullMS(file, databaseH,mzw = 0.0015,rtw=NULL)



#PeakGroupMS1_Qtof<-PeakGroupMS1(fullmsposH)
```

---

plot_EIC *Plot an Extracted Ion Chromatogram (EIC)*

Description

Plot an Extracted Ion Chromatogram (EIC) either from processed MS1 or MS/MS file with FullMS or AIF.

Usage

```
plot_EIC(fullms,peakID=333,ms=1,CE=0)
```

Arguments

fullms	A fullms or DIA file processed by FullMS or AIF.
peakID	Identity of the EIC desired to plot. The peakID is indicated in the ouput obtained with FullMS or AIF.
ms	numeric. MS level of EIC desired to plot.
CE	numeric. Collision energy for the file processed.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)
#Reading the file.mzXML
# file<-fullMS.mzXML

#Reading the database.csv file:
# database<- read.csv("C:/FullMS1.csv")

#Processing peak-picking and annotation with default parameters
# FullMS_results<-FullMS(file,database, ion_mode = "positive",)

#Output:
#FullMS_results$ms

#plot_EIC(fullmsposH,peakID=413)
```

ScoresDIA *Statistical analysis for a pair of peak grouped metabolites from LC-MS/MS DIA analysis.*

Description

Peak-to-peak Pearson correlation coefficient, peak-to-peak shape ratio and product/precursor ion intensity ratios are calculated for a product and precursor metabolites from LC-MS/MS DIA experiment.

Usage

```
ScoresDIA(input,file,ID1,ID2,CE)
```

Arguments

input	Peak grouped for a particular metabolite obtained with the PeakGroup.
file	LC-MS/MS DIA file processed by the AIF.
ID1	PeakID of the precursor ion metabolite.
ID2	PeakID of the product ion metabolite.
CE	numeric. Collision energy for the file processed.

Value

Score	Peak-to-peak Pearson correlation coefficient for a pair of EIC peaks.
IntensityRatio	Peak intensity ratio between product and precursor ion metabolite.
AssymetriRatio	Score for the chromatogram peak shape based on assymmetry factor.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)

#CE.isolation("AIFpos1000-AIF.mzXML","fileposB")

#Reading the database.csv file:
# database<- read.csv("C:/database.csv")

#Processing peak-picking and annotation with default parameters

#aif5<-AIF(fileMS,fileMS2CE5,database,CE=5, ion_mode = "positive")
#aif10<-AIF(fileMS,fileMS2CE10,database,CE=10, ion_mode = "positive")

#Peakgroup<-PeakGroup(aif5,aif10)

#Scores5<-ScoresDIA(Peakgroup$Glutamine,aif5,ID1=90, ID2 = 95,CE=5)
```

ScoresMS1 *Statistical Analysis for a pair of peaks annotated for a particular metabolite.*

Description

Isotopic distribution or multiple adducts of a particular compound can be evaluated by the ScoresMS1.R function that searches the output generated by the FullMS.R function for compounds annotated with multiple adducts or isotopes, calculating the isotope peak intensity ratio between monoisotopic or first isotopologue and the next one. Function calculates PPC based on intensity for both peaks at each scan forming EICs.

Usage

```
ScoresMS1(fullmspos,fullmsposb,ID1,ID2)
```

Arguments

fullmspos	Results achieved by FullMS.R function for a particular adduct.
fullmsposb	Results achieved by FullMS.R function for a particular adduct
ID1	PeakID of the peak corresponding to fileA.
ID2	PeakID of the peak corresponding to fileB.

Value

Score	Peak-to-peak Pearson correlation coefficient for a pair of EIC peaks.
IntensityRatio	Isotope peak intensity ratio between monoisotopic or first isotopologue and the next one.
AssymetriRatio	Score for the chromatogram peak shape based on assymmetry factor.
name	Metabolite name.

Author(s)

Manuel D Peris Diaz

References

1. R-MetaboList: a flexible tool for metabolite extraction from high-resolution data-independent acquisition mass spectrometry analysis. Metabolites. Soon

2. A Survey of Orbitrap All Ion Fragmentation Analysis Assessed by an R MetaboList Package to Study Small-Molecule Metabolites. Chromatographia. 2018, 81, 981-994.

Examples

```
library(MetaboList)
#Reading the file.mzXML
# file<-fullMS.mzXML

#Reading the database.csv file:
# database<- read.csv("C:/FullMS1.csv")

#Processing peak-picking and annotation with default parameters
# FullMS_results<-FullMS(file,database, ion_mode = "negative",)


#ScoresMS1<-ScoresMS1(FullMS_results,FullMS_results,ID2=149,ID1=148)
```

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