

# Rdisop

October 5, 2010

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RcppVersion      *Rcpp Version and License Information*

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## Description

RcppVersion displays the version of Rcpp/RcppTemplate that was used to build this package.

## Usage

```
RcppVersion()
```

## Author(s)

Dominick Samperi

## Examples

```
RcppVersion()
```

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addMolecules      *Add/subtract sum formulae*

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## Description

Simple arithmetic modifications of sum formulae.

## Usage

```
addMolecules(formula1, formula2, elements = NULL)
subMolecules(formula1, formula2, elements = NULL)
```

## Arguments

formula1	Sum formula
formula2	Sum formula
elements	list of allowed chemical elements, defaults to full periodic system of elements

**Details**

addMolecules() adds the second argument to the first. subMolecules() subtracts the second argument from the first.

This can be useful to revert e.g. adduct/fragment formation found in ESI mass spectrometry, or to mimick simple chemical reactions. No chemical checks are performed.

**Value**

A list with the elements

formula	repeated sum formula
mass	exact mass of molecule
score	dummy value, always 1.0
isotopes	a list of isotopes

**Author(s)**

Steffen Neumann <sneumann@IPB-Halle.DE>

**Examples**

```
# For proton-Adduct of Ethanol:
subMolecules("C2H7O", "H")
```

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decomposeIsotopes *Mass Decomposition of Isotope Patterns*

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**Description**

Calculate the elementary compositions from an exact Mass or Isotope Pattern, obtained e.g.\ by FTICR or TOF mass spectrometers

**Usage**

```
decomposeMass(mass, ppm=2.0, mzabs=0.0001, elements=NULL, filter=NULL, z=0, maxi
decomposeIsotopes(masses, intensities, ppm=2.0, mzabs=0.0001,
elements=NULL, filter=NULL, z=0, maxisotopes = 10)
isotopeScore(molecule, masses, intensities, elements = NULL, filter = NULL, z =
```

**Arguments**

mass	A single exact mass (or m/z value)
masses	A vector of masses (or m/z values) of an isotope cluster
intensities	Abolute or relative intensities of the masses peaks
ppm	allowed deviation of hypotheses from given mass
mzabs	absolute deviation in dalton (mzabs and ppm will be added)
z	charge z of m/z peaks for calculation of real mass. 0 is for auto-detection
maxisotopes	maximum number of isotopes shown in the resulting molecules

elements	list of allowed chemical elements, defaults to CHNOPS
filter	NYI, will be a selection of DU, DBE and Nitrogen rules
molecule	a molecule as obtained from getMolecule() or decomposeMass / decomposeIsotopes

### Details

Sum formulas are calculated which explain the given mass or isotope pattern.

### Value

A list of molecules, which contain the sub-lists

formula	potential formulae
mass	exact mass of hypothesis
score	calculated score
isotopes	a list of isotopes

### Author(s)

Steffen Neumann <sneumann@IPB-Halle.DE>

### References

For a description of the underlying IMS see: WABI Paper

### See Also

[decomposeMass](#)

### Examples

```
# For Glutamate:  
decomposeIsotopes(c(147.0529,148.0563), c(100.0,5.561173))
```

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getMolecule	<i>Calculate mass and isotope information for a molecule given as sum formula</i>
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### Description

Parse the sum formula and calculate the theoretical exact mass and the isotope distribution.

### Usage

```
getMolecule(formula, elements = NULL, z = 0, maxisotopes = 10)  
getMass(molecule)  
getFormula(molecule)  
getIsotope(molecule, index)  
getScore(molecule)  
getValid(molecule)
```

**Arguments**

formula	Sum formula
elements	list of allowed chemical elements, defaults to full periodic system of elements
z	charge z of molecule for exact mass calculation
maxisotopes	maximum number of isotopes shown in the resulting molecules
molecule	an initialized molecule as returned by getMolecule() or the decomposeMass() and decomposeIsotope() functions
index	return the n-th isotope mass/abundance pair of the molecule

**Details**

getMolecule() Parse the sum formula and calculate the theoretical exact mass and the isotope distribution. For a given element, return the different mass values.

**Value**

getMolecule: A list with the elements

formula	repeated sum formula
mass	exact mass of molecule
score	probability, for given molecules a dummy value which is always 1.0
valid	result of neutrogen rule check
isotopes	a list of isotopes

getMass, getFormula and getScore: return the mass of the molecule as string or real value

**Author(s)**

Steffen Neumann <sneumann@IPB-Halle.DE>

**References**

For a description of the underlying IMS see: WABI Paper

**Examples**

```
# For Ethanol:  
getMolecule("C2H6O")
```

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initializeCHNOPS     *Initialize (a subset of) elements of the periodic system of elements (PSE)*

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### Description

Initialize the information about name, mass and isotopes. To reduce the number of decomposition hypotheses, subsets of elements can be created.

### Usage

```
initializeCHNOPS ()  
initializeCHNOPSMgKCaFe ()  
initializePSE ()  
initializeElements (names)
```

### Arguments

names                vector of element names within PSE

### Details

These functions return full, pre-defined or user-defined (sub-) lists of elements.

### Value

A list with the elements

formula	repeated sum formula
mass	exact mass of molecule
isotopes	a list of isotopes

The initializeCharges() is special, since it allows to parse charges such as `getMolecule ("H3O+", elements=c(initializeCHNOPS(), initializeCharges()))`

### Author(s)

Steffen Neumann <sneumann@IPB-Halle.DE>

### References

For a description of the underlying IMS see: WABI Paper  
Isotope patterns obtained through wikipedia.org

### See Also

[getMolecule](#)

### Examples

```
# For Ethanol:  
elements <- initializeCHNOPS()
```

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