Package ‘rcdk’

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Imports  fingerprint, rJava, methods, png, iterators, itertools
Suggests xtable, RUnit, knitr, rmarkdown
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License   LGPL
LazyLoad  yes
Description  Allows the user to access functionality in the 'CDK', a Java framework for chemoinformatics. This allows the user to load molecules, evaluate fingerprints, calculate molecular descriptors and so on. In addition, the 'CDK' API allows the user to view structures in 2D.
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Atoms

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<th>Operations on atoms</th>
</tr>
</thead>
<tbody>
<tr>
<td>get.symbol</td>
<td>returns the chemical symbol for an atom.</td>
</tr>
<tr>
<td>get.point3d</td>
<td>returns the 3D coordinates of the atom</td>
</tr>
<tr>
<td>get.point2d</td>
<td>returns the 2D coordinates of the atom</td>
</tr>
<tr>
<td>get.atomic.number</td>
<td>returns the atomic number of the atom</td>
</tr>
<tr>
<td>get.hydrogen.count</td>
<td>returns the number of implicit H's on the atom. Depending on where the molecule was read from this may be NULL or an integer greater than or equal to 0</td>
</tr>
<tr>
<td>get.charge</td>
<td>returns the partial charge on the atom. If charges have not been set the return value is NULL, otherwise the appropriate charge.</td>
</tr>
<tr>
<td>get.formal.charge</td>
<td>returns the formal charge on the atom. By default the formal charge will be 0 (i.e., NULL is never returned)</td>
</tr>
<tr>
<td>is.aromatic</td>
<td>returns TRUE if the atom is aromatic, FALSE otherwise</td>
</tr>
<tr>
<td>is.aliphatic</td>
<td>returns TRUE if the atom is part of an aliphatic chain, FALSE otherwise</td>
</tr>
<tr>
<td>is.in.ring</td>
<td>returns TRUE if the atom is in a ring, FALSE otherwise</td>
</tr>
<tr>
<td>get.atom.index</td>
<td>returns the index of the atom in the molecule (starting from 0)</td>
</tr>
<tr>
<td>get.connected.atoms</td>
<td>returns a list of atoms that are connected to the specified atom</td>
</tr>
</tbody>
</table>

Usage

```r
get.symbol(atom)
get.point3d(atom)
get.point2d(atom)
get.atomic.number(atom)
get.hydrogen.count(atom)
get.charge(atom)
get.formal.charge(atom)
ge.connected.atoms(atom, mol)
ge.atom.index(atom, mol)
is.aromatic(atom)
is.aliphatic(atom)
is.in.ring(atom)
```
bpdata

Arguments

atom
A \texttt{objRef} representing an \texttt{IAtom} object

mol
A \texttt{objRef} representing an \texttt{IAtomContainer} object

Value

In the case of \texttt{get.point3d} the return value is a 3-element vector containing the X, Y and Z coordinates of the atom. If the atom does not have 3D coordinates, it returns a vector of the form \texttt{c(NA,NA,NA)}. Similarly for \texttt{get.point2d}, in which case the return vector is of length 2.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

\texttt{get.atoms}

---

bpdata  \hspace{2cm} Boiling Point Data

Description

Structures and associated boiling points for 277 molecules, primarily alkanes and substituted alkanes.

Usage

\texttt{bpdata}

Format

A \texttt{data.frame} with two columns:

\begin{verbatim}
[.1]   SMILES character Structure in SMILES format
[.2]    BP   numeric Boiling point in Kelvin
\end{verbatim}

The names of the molecules are used as the row names

References

cdk.version

Get Current CDK Version

**Description**

Returns a string containing the version of the CDK used in this package.

**Usage**

```java
cdk.version()
```

**Value**

A string representing the CDK version.

**Author(s)**

Rajarshi Guha (<rajarshi.guha@gmail.com>)

---

**cdkFormula-class**

Class cdkFormula, a class for handling molecular formula.

**Description**

This class handles molecular formulae. It provides extra information such as the IMolecularFormula Java object, elements contained and number of them.

**Objects from the Class**

Objects can be created using `new` constructor and filled with a specific mass and window accuracy.

**Note**

No notes yet.

**Author(s)**

Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

**References**

A parallel effort to expand the Chemistry Development Kit: [http://cdk.sourceforge.net](http://cdk.sourceforge.net)

**See Also**

`get.formula`, `set.charge.formula`, `get.isotopes.pattern`, `isValid.formula`, `isvalid.formula`, `get.charge`, `set.isotopes.pattern`, `isValid.charge`, `isvalid.charge`, `get.charge`, `set.charge`
compare.isotope.pattern

Compare isotope patterns.

Description
Computes a similarity score between two different isotope abundance patterns.

Usage
compare.isotope.pattern(iso1, iso2, ips = NULL)

Arguments
iso1  The first isotope pattern, which should be a jobjRef corresponding to the IsotopePattern class
iso2  The second isotope pattern, which should be a jobjRef corresponding to the IsotopePattern class
ips   An instance of the IsotopePatternSimilarity class. If NULL one will be constructed automatically

Value
A numeric value between 0 and 1 indicating the similarity between the two patterns

Author(s)
Miguel Rojas Cherto

References
http://cdk.github.io/cdk/2.0/docs/api/org/openscience/cdk/formula/IsotopePatternSimilarity.html

See Also
get.isotope.pattern.similarity
do.aromaticity

**Perform Aromaticity Detection, atom typing or isotopic configuration**

**Description**
These methods can be used to perform aromaticity detection, atom typing or isotopic configuration on a molecule object. In general, when molecules are loaded via `load.molecules` these are performed by default. If molecules are obtained via `parse.smiles` these operations are not performed and so the user should call one or both of these methods to correctly configure a molecule.

**Usage**
```r
do.aromaticity(molecule)
do.typing(molecule)
do.isotopes(molecule)
```

**Arguments**
- `molecule`: The molecule on which the operation is to be performed. Should of class `objRef` with a `jclass` attribute of `IAtomContainer`

**Value**
No return value. If the operations fail an exception is thrown and an error message is printed

**Author(s)**
Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**
`load.molecules`, `parse.smiles`

eval.atomic.desc

**Evaluate an Atomic Descriptor**

**Description**
The CDK implements a number of descriptors divided into three main groups - atomic, molecular and bond. This method evaluates the specified atomic descriptor(s) for a molecule

**Usage**
```r
eval.atomic.desc(molecule, which.desc, verbose=FALSE)
```
eval.desc

Arguments

molecule A reference to a CDK IAtomContainer object
which.desc The fully qualified class name of the descriptor to evaluate or a vector such names
verbose If TRUE, progress will be written to the screen, otherwise the function performs silently

Value

A data.frame is returned.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

get.atomic.desc.names get.desc.names eval.desc

eval.desc Evaluate a Molecular Descriptor

Description

The CDK implements a number of descriptors divided into three main groups - atomic, molecular and bond. This method evaluates the specified molecular descriptor(s) for a molecule

Usage

eval.desc(molecules, which.desc, verbose=FALSE)

Arguments

molecules A single IAtomContainer object or a list of references to CDK IAtomContainer objects
which.desc The fully qualified class name of the descriptor to evaluate or a vector such names
verbose If TRUE, progress will be written to the screen, otherwise the function performs silently

Value

A data.frame is returned. For a single molecule it will have one row, for multiple molecules it will have the number of rows equal to the number of molecules
generate.2d.coordinates

**Author(s)**
Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**
get.desc.names get.desc.categories

**Examples**
```r
smiles <- c('CCC', 'c1ccccc1', 'CC(=O)C')
mols <- sapply(smiles, parse.smiles)
dnames <- get.desc.names('constitutional')
descs <- eval.desc(mols, dnames, verbose=TRUE)
```

---

**Description**
This function will generate reasonable 2D coordinates based purely on connectivity information.

**Usage**
generate.2d.coordinates(molecule)

**Arguments**
molecule An IAtomContainer object that can be obtained by loading them from disk or drawing them in the editor.

**Value**
Returns the input molecule with 2D coordinates added.

**Author(s)**
Rajarshi Guha (<rajarshi.guha@gmail.com>)
**generate.formula**

Generate molecular formulae given a target mass and a set of elements and counts.

**Description**

These functions generate a list of cdkFormula objects or strings given a mass and a set of elements and their possible counts (specified as a range). `generate.formula.iter` employs recently updated code making it much faster than `generate.formula`.

In addition, `generate.formula.iter` returns an iterator, using which very large sets of formulae can be generated without excessive memory consumption. By default this method returns molecular formulae as strings, rather than cdkFormula objects. By default this method does not perform any validation, and even if `validation = TRUE` no validation is performed. `generate.formula` can perform validation, but this results in significantly slower run times.

**Usage**

```r
generate.formula(mass, window=0.01, elements=list(c("C",0,50),c("H",0,50),
         c("N",0,50),c("O",0,50),
         c("S",0,50)),
         validation=FALSE, charge=0.0)
generate.formula.iter(mass, window = 0.01,
         elements = list(
            C=c(0,50),
            H=c(0,50),
            N=c(0,50),
            O=c(0,50),
            S=c(0,50)),
         validation = FALSE,
         charge = 0.0,
         as.string=TRUE)
```

**Arguments**

- **mass**  The mass value from which to be generate the formulas.
- **window**  The window accuracy in the same units as mass.
- **elements**  Elements to take into account.
- **validation**  TRUE, if the method should only generate valid formulas. If FALSE, nonsensical formulae my be generated which must be filtered out by the user.
- **charge**  The charge value of the formula.
- **as.string**  If TRUE the formula is returned as a string, otherwise as a IMolecularFormula object
get.adjacency.matrix

Value
List of IMolecularFormula objects or strings, representing molecular formulae

Author(s)
Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

See Also
get.formula, set.charge.formula, get.isotopes.pattern, isValid.formula

Examples

mfSet <- generate.formula(18.03383, charge=1,
    elements=list(c("C",0,50),c("H",0,50),c("N",0,50)))
for (i in mfSet) {
    print(i)
}

mit <- generate.formula.iter(18.03383, charge=1,
    elements=list(C=c(0,50), H=c(0,50), N=c(0,50)))
hit <- itertools::iHasNext(mit)
while (itertools::hasNext(hit))
    print(iterators::nextElem(hit))

get.adjacency.matrix

Get adjacency matrix for a molecule.

Description
The adjacency matrix for a molecule with $N$ non-hydrogen atoms is an $N \times N$ matrix where the element $[i,j]$ is set to 1 if atoms $i$ and $j$ are connected by a bond, otherwise set to 0.

Usage
get.adjacency.matrix(mol)

Arguments
mol A jobjRef object with Java class IAtomContainer

Value
A $N \times N$ numeric matrix

Author(s)
Rajarshi Guha <rajarshi.guha@gmail.com>
get.atomic.desc.names

See Also

get.connection.matrix

Examples

```r
m <- parse.smiles("CC=C")[[1]]
get.adjacency.matrix(m)
```

get.atomic.desc.names  *Get the names of the available atomic descriptors*

Description

The CDK implements a number of descriptors divided into three main groups - atomic, molecular and bond. This method returns the names of the available atomic descriptors.

Usage

```
get.atomic.desc.names(type = "all")
```

Arguments

type  
A string which can be one of "all", "topological", "geometrical" "hybrid", "constitutional", "electronic", allowing you to choose atomic descriptors of specific categories. The keyword "all" will return all available descriptors

Value

A vector of fully qualified descriptor names.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

eval.atomic.desc get.desc.names eval.desc
get.atoms

Get the atoms from a molecule or bond

Description
This function returns a list containing IAtom objects from a molecule or a bond.

Usage
get.atoms(object)
get.atom.count(molecule)

Arguments
- object: A jObjRef representing an IAtomContainer, IMolecule or IBond object
- molecule: A jobjRef representing an IAtomContainer

Value
A list containing jobjRef’s to a CDK IAtom object or else the number of atoms in the molecule

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also
get.bonds, get.point3d, get.symbol

get.bonds

Get the bonds from a molecule

Description
This function returns a list containing IABond objects from a molecule

Usage
get.bonds(molecule)

Arguments
- molecule: A jObjRef representing an IAtomContainer, IMolecule

Value
A list containing jobjRef’s to a CDK IBond object
get.connected.atom

**Author(s)**
Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**
get.atoms, get.connected.atom

---

get.connected.atom  Get the atom connected to an atom in a bond

**Description**
This function returns the atom that is connected to a specified in a specified bond. Note that this function assumes 2-atom bonds, mainly because the CDK does not currently support other types of bonds.

**Usage**
get.connected.atom(bond, atom)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bond</td>
<td>A jObjRef representing an IBond object</td>
</tr>
<tr>
<td>atom</td>
<td>A jObjRef representing an IAtom object</td>
</tr>
</tbody>
</table>

**Value**
A jObjRef representing an IAtom object

**Author(s)**
Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**
get.atoms
get.connection.matrix

Description

The connection matrix for a molecule with \( N \) non-hydrogen atoms is an \( N \times N \) matrix where the element \([i,j]\) is set to the bond order if atoms \( i \) and \( j \) are connected by a bond, otherwise set to 0.

Usage

get.connection.matrix(mol)

Arguments

- mol: A jobjRef object with Java class IAtomContainer

Value

A \( N \times N \) numeric matrix

Author(s)

Rajarshi Guha <rajarshi.guha@gmail.com>

See Also

get.adjacency.matrix

Examples

```r
m <- parse.smiles("CC=C")[[1]]
get.connection.matrix(m)
```

get.desc.categories

Description

This function returns the broad descriptor categories that are available. Examples include topological, geometrical and so on. You can use a specific category to avoid calculating all descriptors for a set of molecules and saves you having to select individual descriptors by hand.

Usage

get.desc.categories()
get.desc.names

Description
The CDK implements a number of descriptors divided into three main groups - atomic, molecular and bond. Currently the package will only evaluate molecular descriptors. This function returns the class names of the available descriptors, which can then be used to calculate descriptors for a specific molecule.

By default all available descriptor class names are returned. However it is possible to specify that a subset of the descriptors should be considered. The subset is specified by keyword and can be one of: topological, geometrical, hybrid, constitutional, protein, electronic.

Usage
get.desc.names(type = "all")

Arguments

type Indicates which subset of molecular descriptors should be considered

Value
A character vector of descriptor class names

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also
eval.desc, get.desc.categories
get.element.types  Obtain the type of stereo element support for atom.

Description

Supported elements types are

**Bicoordinate** an central atom involved in a cumulated system (not yet supported)

**Tricoordinate** an atom at one end of a geometric (double-bond) stereo bond or cumulated system

**Tetracoordinate** a tetrahedral atom (could also be square planar in future)

**None** the atom is not a (supported) stereo element type

Usage

get.element.types(mol)

Arguments

mol A jObjRef representing an IAtomContainer

Value

A factor of length equal in length to the number of atoms, indicating the element type

Author(s)

Rajarshi Guha <rajarshi.guha@gmail.com>

See Also

get.stereocenters, get.stereo.types

get.fingerprint  Evaluate Fingerprints

Description

This function evaluates fingerprints of a specified type for a set of molecules or a single molecule. Depending on the nature of the fingerprint, parameters can be specified. Currently five different fingerprints can be specified:

- **standard** - Considers paths of a given length. The default is but can be changed. These are hashed fingerprints, with a default length of 1024
- **extended** - Similar to the standard type, but takes rings and atomic properties into account into account
• graph - Similar to the standard type by simply considers connectivity
• hybridization - Similar to the standard type, but only consider hybridization state
• maccs - The popular 166 bit MACCS keys described by MDL
• estate - 79 bit fingerprints corresponding to the E-State atom types described by Hall and Kier
• pubchem - 881 bit fingerprints defined by PubChem
• kr - 4860 bit fingerprint defined by Klekota and Roth
• shortestpath - A fingerprint based on the shortest paths between pairs of atoms and takes into account ring systems, charges etc.
• signature - A feature,count type of fingerprint, similar in nature to circular fingerprints, but based on the signature descriptor
• circular - An implementation of the ECFP6 fingerprint

Depending on whether the input is a single IAtomContainer object, a list or single vector is returned. Each element of the list is an S4 object of class fingerprint-class or featvec-class, which can be manipulated with the fingerprint package.

Usage

get.fingerprint(molecule, type = 'standard',
         fp.mode = 'bit', depth=6, size=1024, verbose=FALSE)

Arguments

molecule An IAtomContainer object that can be obtained by loading them from disk or drawing them in the editor.
type The type of fingerprint. See description for possible values. The default is the standard binary fingerprint.
fp.mode The type of fingerprint to return. Possible values are 'bit', 'raw', and 'count'. The 'raw' mode will return a featvec-class type of fingerprint, representing fragments and their count of occurence in the molecule. The 'count' mode is similar, except that it returns hash values of fragments and their count of occurrence. While any of these values can be specified, a given fingerprint implementation may not implement all of them, and in those cases the return value is NULL.
depth The search depth. This argument is ignored for the 'pubchem', 'maccs', 'kr' and 'estate' fingerprints
size The length of the fingerprint bit string. This argument is ignored for the 'pubchem', 'maccs', 'kr', 'signature', 'circular' and 'estate' fingerprints
verbose If TRUE, exceptions, if they occur, will be printed

Value

Objects of class fingerprint-class or featvec-class, from the fingerprint package. If there is a problem during fingerprint calculation, NULL is returned.
get.formula

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

References

See Also
load.molecules

Examples

```r
## get some molecules
sp <- get.smiles.parser()
smiles <- c("CCC", "CCN", "CCN(C)(C)", "c1ccccccc1ccccc1c1ccccccc1", "C1CCC1CC(CN(C)(C))CC(=O)CC")
mols <- parse.smiles(smiles)

## get a single fingerprint using the standard
## (hashed, path based) fingerprinter
fp <- get.fingerprint(mols[[1]])

## get MACCS keys for all the molecules
fps <- lapply(mols, get.fingerprint, type="maccs")

## get Signature fingerprint
## feature, count fingerprinter
fps <- lapply(mols, get.fingerprint, type="signature", fp.mode="raw")
```

get.formula
Get the formula object from a formula character.

Description
This function returns a formula object containing mass, string character and isotopes when is given a character/string formula.

Usage
get.formula(mf, charge=0)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mf</td>
<td>A string containing the formula of the molecular formula of chemical object.</td>
</tr>
<tr>
<td>charge</td>
<td>The charge of the molecular formula.</td>
</tr>
</tbody>
</table>
Value

Objects of class cdkFormula, from the IMolecularFormula package

Author(s)

Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

References

A parallel effort to expand the Chemistry Development Kit: http://cdk.sourceforge.net

See Also

set.charge.formula, get.isotopes.pattern, isValid.formula, generate.formula

Examples

```r
formula <- get.formula('NH4', charge = 1)
formula
```

get.isotope.pattern.generator

Construct an isotope pattern generator.

Description

Constructs an instance of the CDK IsotopePatternGenerator, with an optional minimum abundance specified. This object can be used to generate all combinatorial chemical isotopes given a structure.

Usage

```r
get.isotope.pattern.generator(minAbundance = NULL)
```

Arguments

- `minAbundance`: The minimum abundance

Value

A jobjRef corresponding to an instance of IsotopePatternGenerator

Author(s)

Miguel Rojas Cherto

References

http://cdk.github.io/cdk/1.5/docs/api/org/openscience/cdk/formula/IsotopePatternGenerator.html
get.isotope.pattern.similarity

Construct an isotope pattern similarity calculator.

Description

A method that returns an instance of the CDK IsotopePatternSimilarity class which can be used to compute similarity scores between pairs of isotope abundance patterns.

Usage

get.isotope.pattern.similarity(tol = NULL)

Arguments

tol

The tolerance

Value

A jobRef corresponding to an instance of IsotopePatternSimilarity

Author(s)

Miguel Rojas Cherto

References

http://cdk.github.io/cdk/1.5/docs/api/org/openscience/cdk/formula/IsotopePatternSimilarity.html

See Also

compare.isotope.pattern

get.isotopes.pattern

Generate the isotope pattern.

Description

This function get the isotope pattern given a cdkFormula object. It modifies as the IMolecularFormula Java object as the its mass.

Usage

generate.isotopes.pattern(formula, minAbund=0.1)
get.mol2formula

Parser a molecule to formula object.

Description
This function convert a molecule object to a formula object.

Usage
get.mol2formula(molecule, charge=0)

Arguments
molecule   The molecule to be parsed.,
charge   The charge characterizing the molecule.,

Value
Objects of class MolecularFormulaManipulator, from the IMolecularFormulaManipulator package

Author(s)
Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

See Also
set.charge.formula, get.isotopes.pattern, isValid.formula
get.murcko.fragments

Examples

```r
molecule <- parse.smiles("N")[[1]]
convert.implicit.to.explicit(molecule)
formula <- get.mol2formula(molecule, charge=0)
```

get.murcko.fragments  Molecule Fragmentation Methods

Description

A variety of methods for fragmenting molecules are available ranging from exhaustive, rings to more specific methods such as Murcko frameworks. Fragmenting a collection of molecules can be a useful for a variety of analyses. In addition fragment based analysis can be a useful and faster alternative to traditional clustering of the whole collection, especially when it is large.

Note that exhaustive fragmentation of large molecules (with many single bonds) can become time consuming.

Usage

```r
get.murcko.fragments(mols, min.frag.size = 6, as.smiles = TRUE, single.framework = FALSE)
get.exhaustive.fragments(mols, min.frag.size = 6, as.smiles = TRUE)
```

Arguments

- `mols`: A molecule object or list of molecule objects. Each object should have a `jclass` of `IAtomContainer`
- `min.frag.size`: The size of the smallest fragments to be considered
- `as.smiles`: If TRUE, the fragments are returned as SMILES strings, otherwise as `IAtomContainer` objects
- `single.framework`: If TRUE, then a single framework (i.e., the framework consisting of the union of all ring systems and linkers) is returned for each molecule. Otherwise, all combinations of ring systems and linkers are returned

Value

- `get.murcko.fragments` returns a list with each element being a list with two elements: `rings` and `frameworks`. Each of these elements is either a character vector of SMILES strings or a list of `IAtomContainer` objects.
- `get.exhaustive.fragments` returns a list of length equal to the number of input molecules. Each element is a character vector of SMILES strings or a list of `IAtomContainer` objects.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)
See Also

load.molecules, parse.smiles.

Examples

```r
mol <- parse.smiles('c1cccc(c)CN(c2ccc(ccc2[N+](=O)[O-])c3c(nc(nc3CC)N)N)C')[[1]]
mf1 <- get.murcko.fragments(mol, as.smiles=TRUE, single.framework=TRUE)
mf1 <- get.murcko.fragments(mol, as.smiles=TRUE, single.framework=FALSE)
```

---

### Description

Returns a list of all the properties of a molecule. The names of the list are set to the property names.

### Usage

```r
get.properties(molecule)
```

### Arguments

- `molecule` A Java object of class IAtomContainer or IMolecule

### Value

A list of the property values, with names equal to the property names. NULL property values are returned as NA.

### Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

### See Also

get.property, set.property, remove.property

### Examples

```r
smiles <- 'c1cccc1'
mol <- parse.smiles(smiles)[[1]]
set.property(mol, 'prop1', 23.45)
set.property(mol, 'prop2', 'inactive')
get.properties(mol)
```
**get.property**

Get the Value of a Molecule Property

### Description

This function retrieves the value of a keyed property that has previously been set on the molecule. The `get.title` function is simply a wrapper around `get.property` that directly provides access to the molecule title.

### Usage

```
get.property(molecule, key)
ge.title(molecule)
```

### Arguments

- **molecule**: A Java object of class `IAtomContainer`
- **key**: A string naming the property

### Value

The value of the property is the key is found else NA. For `get.title`, the title of the molecule if available otherwise NA

### Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

### See Also

`get.properties, set.property, remove.property`

### Examples

```r
smiles <- 'c1ccccc1'
mol <- parse.smiles(smiles)[1]
set.property(mol, 'prop1', 23.45)
set.property(mol, 'prop2', 'inactive')
ge.property(mol, 'prop1')
```
get.smiles  

*Get the SMILES for a Molecule*

**Description**

The function will generate a SMILES representation of an IAtomContainer object. The default parameters of the CDK SMILES generator are used. This can mean that for large ring systems the method may fail. See CDK Javadocs for more information.

**Usage**

```r
get.smiles(molecule, flavor = smiles.flavors(c('Generic')), smigen = NULL)
```

**Arguments**

- `molecule`: A Java object of class IAtomContainer.
- `flavor`: Customizations for SMILES generation. See `smiles.flavors`.
- `smigen`: An instance of SmilesGenerator, which can be useful if you are generating SMILES for a large number of molecules.

**Value**

An R character object containing the SMILES.

**Author(s)**

Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**

`smiles.flavors`, `parse.smiles`

**Examples**

```r
m <- parse.smiles('C\C=C\N(C)c1ccccc1')[[1]]
get.smiles(m)
gget.smiles(m, smiles.flavors(c('Generic','UseAromaticSymbols')))```
**get.smiles.parser**  

Get a SMILES Parser

---

**Description**

This function returns a reference to a SMILES parser object. If you are parsing multiple SMILES strings, it is preferable to create your own parser and supply it to `parse.smiles` rather than forcing that function to instantiate a new parser for each call.

**Usage**

```python
get.smiles.parser()
```

**Value**

A `jobjRef` to a CDK SmilesParser object

**Author(s)**

Rajarshi Guha (<rajarshi.guha@gmail.com>)

**See Also**

- `get.smiles`
- `get.smiles.parser`
- `view.molecule.2d`

---

**get.stereo.types**  

Obtain the stereocenter type for atom.

---

**Description**

Supported stereo center types are

- **True**  the atom has constitutionally different neighbors
- **Para**  the atom resembles a stereo centre but has constitutionally equivalent neighbors (e.g. inositol, decalin). The stereocenter depends on the configuration of one or more stereocenters.
- **Potential**  the atom can supported stereo chemistry but has not be shown ot be a true or para center
- **Non**  the atom is not a stereocenter (e.g. methane)

**Usage**

```python
get.stereo.types(mol)
```

**Arguments**

- `mol`  A `jobjRef` representing an IAtomContainer
Value

A factor of length equal in length to the number of atoms indicating the stereocenter type.

Author(s)

Rajarshi Guha <rajarshi.guha@gmail.com>

See Also

get.stereocenters, get.element.types

description

This method identifies stereocenters based on connectivity.

Usage

get.stereocenters(mol)

Arguments

mol A jObjRef representing an IAtomContainer

Value

A logical vector of length equal in length to the number of atoms. The i’th element is TRUE if the i’th element is identified as a stereocenter.

Author(s)

Rajarshi Guha <rajarshi.guha@gmail.com>

See Also

get.element.types, get.stereo.types
get.total.charge | Get the Total Charges for the Molecule

**Description**

get.total.charge returns the summed partial charges for a molecule and get.total.formal.charge returns the summed formal charges. Currently, if one or more partial charges are unset, the function simply returns the sum of formal charges (via get.total.formal.charge). This is slightly different from how the CDK evaluates the total charge of a molecule (via AtomContainerManipulator.getTotalCharge()), but is in line with how OEChem determines net charge on a molecule.

In general, you will want to use the get.total.charge function.

**Usage**

get.total.charge(molecule)
get.total.formal.charge(molecule)

**Arguments**

molecule | A Java object of class IAtomContainer

**Value**

A double value indicating the total partial charge or total formal charge

**Author(s)**

Rajarshi Guha (<rajarshi.guha@gmail.com>)

get.total.hydrogen.count | Get the Total Hydrogen Count for a Molecule

**Description**

The function will return the summed implicit hydrogens of all atoms in the specified AtomContainer

**Usage**

get.total.hydrogen.count(molecule)

**Arguments**

molecule | A Java object of class IAtomContainer
Value
An integer value indicating the number of implicit hydrogens

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

get.tpsa

Commonly Used Molecular Descriptors

Description
These methods will return the value for the corresponding descriptors. While they can always be evaluated using eval.desc, they are common enough that separate functions are provided.

Usage
get.tpsa(molecule)
get.alogp(molecule)
get.xlogp(molecule)
get.volume(molecule)

Arguments
molecule A JobjRef representing an IAtomContainer object

Details
It's important to note that ALogP and XLogP assumes that the molecule has explicit hydrogens. If the molecule is read from an SD file, explicit H's are usually present. On the other hand, if the molecule is obtained from a SMILES, explicit hydrogens must be added.

The molecular volume is calculated using a group contribution method rather than the an analytical method. This allows to avoid the use of 3D structures.

Value
Single numeric value representing TPSA, ALogP, XLogP or molecular volume.

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also
eval.desc
hasNext

Does This Iterator Have A Next Element

Description

hasNext is a generic function that indicates if the iterator has another element.

Usage

hasNext(obj, ...)

## S3 method for class 'iload.molecules'
hasNext(obj, ...)

Arguments

obj an iterator object.

... additional arguments that are ignored.

Value

Logical value indicating whether the iterator has a next element. In the context of reading a structure file, this indicates whether there are more molecules to read

See Also

iload.molecules

is.connected

Get the Largest Component in aDisconnected Molecule

Description

These methods allow one to check whether a molecule is fully connected or else retrieve the largest disconnected component

Usage

generate

...is connected(mol)

Arguments

mol A jObjRef representing an IAtomContainer object
Value

For `get.largest.component`, if the input molecule has more than one disconnected component, the largest is returned. Otherwise, the molecule itself is returned.

For `is.connected`, TRUE if the molecule is fully connected, FALSE otherwise.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

Examples

```r
m <- parse.smiles("CC.CCCCCC.CCCC")[[1]]
largest <- get.largest.component(m)
length(get.atoms(largest)) == 6
```

isvalid.formula

Validate a cdkFormula object.

Description

This function validates a cdkFormula object. At the moment is using the nitrogen Rule and RDBE Rule.

Usage

```r
isvalid.formula(formula, rule = c("nitrogen","RDBE"))
```

Arguments

- `formula`: A cdkFormula object.
- `rule`: The rules to be applied: nitrogen and RDBE.

Value

Objects of class MolecularFormulaChecker, from the IMolecularFormula package

Author(s)

Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

References

A parallel effort to expand the Chemistry Development Kit: [http://cdk.sourceforge.net](http://cdk.sourceforge.net)

See Also

- `get.formula`
- `set.charge.formula`
- `get.isotopes.pattern`
- `generate.formula`
Examples

```r
formula <- get.formula('NH4', charge = 0)
isvalid.formula(formula, rule = c("nitrogen","RDBE"))
```

Description

The CDK can read a variety of molecular structure formats. This function encapsulates the calls to the CDK API to load a structure given its filename.

Usage

```r
load.molecules(molfiles=NA, aromaticity = TRUE, typing = TRUE, isotopes = TRUE, verbose=FALSE)
iload.molecules(molfile, type="smi", aromaticity = TRUE, typing = TRUE, isotopes = TRUE, skip=TRUE)
```

Arguments

- **molfiles**: A character vector of filenames. Note that the full path to the files should be provided. URL's can also be used as paths. In such a case, the URL should start with "http://".
- **molfile**: A string containing the filename to load. Must be a local file.
- **type**: Indicates whether the input file is SMILES or SDF. Valid values are "smi" or "sdf".
- **aromaticity**: If TRUE then aromaticity detection is performed on all loaded molecules. If this fails for a given molecule, then the molecule is set to NA in the return list.
- **typing**: If TRUE then atom typing is performed on all loaded molecules. The assigned types will be CDK internal types. If this fails for a given molecule, then the molecule is set to NA in the return list.
- **isotopes**: If TRUE then atoms are configured with isotopic masses.
- **verbose**: If TRUE, output (such as file download progress) will be bountiful.
- **skip**: If TRUE, then the reader will continue reading even when faced with an invalid molecule. If FALSE, the reader will stop at the first invalid molecule.

Details

Note that if molecules are read in from formats that do not have rules for handling implicit hydrogens (such as MDL MOL), the molecule will not have implicit or explicit hydrogens. To add explicit hydrogens, make sure that the molecule has been typed (this is TRUE by default for this function) and then call `convert.implicit.to.explicit`. On the other hand for a format such as SMILES, implicit or explicit hydrogens will be present.
Value

load.molecules returns a list of CDK Molecule objects, which can be used in other rcdk functions.

iload.molecules is an iterating version of the loader and is applicable for large SMILES or SDF files. In contrast to load.molecules this does not load all the molecules into memory at one go, and as a result lets you process arbitrarily large structure files.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

view.molecule.2d, convert.implicit.to.explicit

Examples

## Not run:

## load a single file
amol <- load.molecules('foo.sdf')

## load multiple files
mols <- load.molecules(c('mol1.sdf', 'mol2.smi',

## iterate over a large file
moliter <- iload.molecules("big.sdf", type="sdf")
while(hasNext(moliter)) {
  mol <- nextElem(moliter)
  print(get.property(mol, "cdk:Title"))
}

## End(Not run)

matches Perform Substructure Searching & MCS Detection

Description

These functions perform substructure searches of a query, specified in SMILES or SMARTS forms, over one or more target molecules and maximum common substructure searches for pairs of molecules.

Usage

matches(query, target, return.matches=FALSE)
is.subgraph(query, target)
get.mcs(mol1, mol2, as.molecule = TRUE)
matches

Arguments

query A SMILES or SMARTS string
target A single IAtomContainer object or a list of IAtomContainer objects
mol1 An IAtomContainer
mol2 An IAtomContainer
return.matches If TRUE the lists of atom indices that correspond to the matching substructure are returned
as.molecule If TRUE the MCS is returned as a new IAtomContainer object. Otherwise a atom index mapping between the two molecules is returned as a 2D array of integers

Details

For the case of is.subgraph, the query molecule must be a single IAtomContainer or a valid SMILES string. Note that this method can be significantly faster than matches, but is limited by the fact that SMARTS patterns cannot be specified. This uses the "TurboSubStructure" SMSD method and so only searches for the first substructure match.

For MCS detection, the default SMSD algorithm is employed and the best scoring MCS is returned by default. Furthermore, one can obtain the resultant MCS either as an IAtomContainer in which the atoms and bonds are clones of the corresponding matching atoms and bonds in one of the molecule. Or else as a 2D array of dimensions Nx2 of atom index mappings. Here N is the size of the MCS and the first column represents the atom index from the first molecule and the second column the atom index from the second molecule.

Note that since the CDK SMARTS matcher internally will perform aromaticity perception and atom typing, the target molecules need not have these operations done on them beforehand for matches method. However, if is.subgraph or get.mcs is being used, the molecules should have aromaticity detected and atom typing performed explicitly.

If the atom indices of the matching substructures (in the target molecule) are desired, use the matches function directly.

Value

For matches with return.matches = FALSE, a boolean vector where each element is TRUE or FALSE depending on whether the corresponding element in targets contains the query or not. If return.matches = TRUE, the return value is a list of lists. The number of elements of the top level list equals the number of matches. Each element is a list of two elements, named "match" and "mapping". The first element is TRUE if the query matched the target. If so, the second element is a list of numeric vectors, giving the atom indices (0-indexed) of the target atoms that matched the query. If there was no match for this target molecule, this element will be NULL

For is.subgraph, a boolean vector, where each element is TRUE or FALSE depending on whether the corresponding element in targets contains the query or not.

For get.mcs an IAtomContainer object or a 2D array of atom index mappings between the two molecules.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)
See Also

load.molecules, get.smiles, do.aromaticity, do.typing, do.isotopes

Examples

smiles <- c('CCC', 'c1cccccl', 'C(C)(C=O)C(CCNC)C1CC1C(=O)')
mols <- sapply(smiles, parse.smiles)
query <- '[#6]=O'
doesMatch <- matches(query, mols)

## get mappings
mappings <- matches("CCC", mols, TRUE)

Molecule Operations on molecules

Description

Various functions to perform operations on molecules.

get.exact.mass returns the exact mass of a molecule

get.natural.mass returns the natural exact mass of a molecule

convert.implicit.to.explicit converts implicit hydrogens to explicit hydrogens. This function does not return any value but rather modifies the molecule object passed to it

is.neutral returns TRUE if all atoms in the molecule have a formal charge of 0, otherwise FALSE

Usage

get.exact.mass(molecule)
get.natural.mass(molecule)
convert.implicit.to.explicit(molecule)
is.neutral(molecule)

Arguments

molecule A jObjRef representing an IAtomContainer or IMolecule object

Details

In some cases, a molecule may not have any hydrogens (such as when read in from an MDL MOL file that did not have hydrogens). In such cases, convert.implicit.to.explicit will add implicit hydrogens and then convert them to explicit ones. In addition, for such cases, make sure that the molecule has been typed beforehand.
Value

- exact.mass returns a numeric
- get.natural.mass returns a numeric
- convert.implicit.to.explicit has no return value
- is.neutral returns a boolean.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

- get.atoms
- do.typing

Examples

```r
m <- parse.smiles('c1ccccc1')[[1]]

## Need to configure the molecule
do.aromaticity(m)
do.typing(m)
do.isotopes(m)

get.exact.mass(m)
get.natural.mass(m)

convert.implicit.to.explicit(m)
get.natural.mass(m)
do.isotopes(m) # Configure isotopes of newly added hydrogens
get.exact.mass(m)

is.neutral(m)
```

---

**parse.smiles**

### Parse a Vector of SMILES Strings

#### Description

This function parses a vector of SMILES strings to generate a list of `IAtomContainer` objects. Note that the resultant molecule will not have any 2D or 3D coordinates.

Note that the molecules obtained from this method will not have any aromaticity perception, atom typing or isotopic configuration done on them. This is in contrast to the `load.molecules` method. Thus, you should perform these steps manually on the molecules.

#### Usage

```r
parse.smiles(smiles, kekulise=TRUE)
```
remove.hydrogens

Arguments

smiles A SMILES string
kekulise If set to FALSE disables electron checking and allows for parsing of incorrect SMILES. If a SMILES does not parse by default, try setting this to FALSE - though the resultant molecule may not have consistent bonding. As an example, c4ccc2c(cc1=Nc3ncccc3(Cn12))c4 will not be parsed by default because it is missing a nitrogen. With this argument set to FALSE it will parse successfully, but this is a hack to handle an incorrect SMILES

Value

A list of jobRef to their corresponding CDK IAtomContainer objects. If a SMILES string could not be parsed, NA is returned instead.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

load.molecules, get.smiles, get.smiles.parser, view.molecule.2d, do.aromaticity, do.typing, do.isotopes

Examples

smiles <- c("CCC", "c1ccccc1", "C(C)(C=O)C(CCNC)C1CC1C(=O)"")
mol <- parse.smiles(smiles[1])
mols <- parse.smiles(smiles)

---

remove.hydrogens Remove Hydrogens from a Molecule

Description

This function generate a new IAtomContainer object in which the hydrogens have been removed. This can be useful for descriptor calculations.

Usage

remove.hydrogens(molecule)

Arguments

molecule A Java object of class IAtomContainer

Value

A jobRef that refers to a IAtomContainer object
Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

remove.property Remove A Property From a Molecule

Description
This function removes a keyed property from a molecule object. This deletes the key and its value from the molecule.

Usage
remove.property(molecule, key)

Arguments
molecule: A Java object of class IAtomContainer
key: A string naming the property

Value
None

Author(s)
Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also
get.property, set.property

set.charge.formula Set the charge to a cdkFormula object.

Description
This function sets the charge to a cdkFormula object. It modifies the IMolecularFormula Java object as its mass.

Usage
set.charge.formula(formula, charge=-1)
set.property

Arguments

- **formula**: A cdkFormula object.
- **charge**: The value of the charge to set.

Value

Returns the formula object with the specified charge

Author(s)

- Miguel Rojas-Cherto (<miguelrojasch@yahoo.es>)

References

A parallel effort to expand the Chemistry Development Kit: [http://cdk.sourceforge.net](http://cdk.sourceforge.net)

See Also

- `get.formula`, `get.isotopes.pattern`, `isvalid.formula`, `generate.formula`

---

**set.property** | **Set A Property On A Molecule**

Description

This function allows one to add a keyed property to a molecule. The key must be a string, but the value can be string, numeric or even an arbitrary Java object (of class `jobjRef`)

Usage

```java
set.property(molecule, key, value)
```

Arguments

- **molecule**: A Java object of class `IAtomContainer`
- **key**: A string naming the property
- **value**: The value of the property. This can be character, integer, double or of class `jobjRef`

Value

None

Author(s)

- Rajarshi Guha (<rajarshi.guha@gmail.com>)
See Also
get.property, get.properties, remove.property

Examples

```r
smiles <- 'c1ccccc1'
mol <- parse.smiles(smiles)[[1]]
set.property(mol, 'prop1', 23.45)
set.property(mol, 'prop2', 'inactive')
get.properties(mol)
```

Description

The CDK supports a variety of customizations for SMILES generation including the use of lower case symbols for aromatic compounds to the use of the ChemAxon CxSmiles format. Each ‘flavor’ is represented by an integer and multiple customizations are bitwise OR’ed. This method accepts the names of one or more customizations and returns the bitwise OR of them. See CDK documentation for the list of flavors and what they mean.

Usage

```
smiles.flavors(flavors = c("Generic"))
```

Arguments

- **flavors**
  A character vector of flavors. The default is Generic (Output non-canonical SMILES without stereochemistry, atomic masses). Possible values are
  - Absolute
  - AtomAtomMap
  - AtomicMass
  - AtomicMassStrict
  - Canonical
  - Cx2dCoordinates
  - Cx3dCoordinates
  - CxAtomLabel
  - CxAtomValue
  - CxCoordinates
  - CxFragmentGroup
  - CxMulticenter
  - CxPolymer
  - CxRadical
  - CxSmiles
• CxSmilesWithCoords
• Default
• Generic
• InChILabelling
• Isomeric
• Stereo
• StereoCisTrans
• StereoExTetrahedral
• StereoTetrahedral
• Unique
• UniversalSmiles
• UseAromaticSymbols

Value

A numeric representing the bitwise OR of the specified flavors

Author(s)

Rajarshi Guha <rajarshi.guha@gmail.com>

References

CDK documentation

See Also

gt.smiles

Examples

m <- parse.smiles('C1C=CCC1(N(C)c1cccccc1)')[[1]]
gt.smiles(m)
gt.smiles(m, smiles.flavors(c('Generic','UseAromaticSymbols')))

m <- parse.smiles("OS(=O)(=O)c1ccc(cc1)C(CC)CC |Sg:n:13:m:ht,Sg:n:11:n:ht|")[[1]]
gt.smiles(m,flavor = smiles.flavors(c("CxSmiles")))
gt.smiles(m,flavor = smiles.flavors(c("CxSmiles","UseAromaticSymbols")))
The CDK is capable of generating 2D structure diagrams. These methods allow one to view 2D structure diagrams. Depending on the method called a Swing JFrame is displayed which allows resizing of the image or a raster image (derived from a PNG byte stream) is is returned, which can be viewed using `rasterImage`. It is also possible to copy a 2D depiction to the system clipboard, which can then be pasted into various external applications.

### Usage

```r
get.depictor(width = 200, height = 200, zoom = 1.3, style = "cow", 
annotate = "off", abbr = "on", suppressh = TRUE, 
showTitle = FALSE, smaLimit = 100, sma = NULL)

view.molecule.2d(molecule, ncol = 4, width = 200, height = 200, depictor = NULL)

view.image.2d(molecule, depictor = NULL)

copy.image.to.clipboard(molecule, depictor = NULL)
```

### Arguments

- **molecule**: If a single molecule is to be viewed this should be a reference to a `IAtomContainer` object. If multiple molecules are to be viewed this should be a list of such objects. If a character is specified then it is taken as the name of a file and the molecules are loaded from the file.

- **depictor**: A depiction object. If `NULL` then one with default settings is created.

- **ncol**: The number of columns if a grid is desired.

- **width**: The width of the image.

- **height**: The height of the image.

- **zoom**: Zoom factor.

- **style**: Depiction style. Possible values are 'cow', 'bow', 'wob', 'cob', 'nob'.

- **annotate**: Annotation style. By default no annotations are added. Possible values include 'number', 'mapidx', 'atomvalue', 'colmap'.

- **abbr**: Abbreviation style for functional groups. Possible values are 'groups', 'reagents', 'on'.

- **suppressh**: When TRUE show H's otherwise hide them.

- **showTitle**: When TRUE display title.

- **smaLimit**: How many SMARTS patterns should be highlighted?

- **sma**: A string containing the SMARTS pattern to match.
Details

For the case of `view.molecule.2d`, if a `jobjRef` is passed it should be a reference to an `IAtomContainer` object. In case the first argument is of class character it is assumed to be a file and is loaded by the function.

This function can be used to view a single molecule or multiple molecules. If a list of molecule objects is supplied the molecules are displayed as a grid of 2D viewers. In case a file is specified, it will display a single molecule or multiple molecules depending on how many molecules are loaded.

For `view.image.2d`, the image can be viewed via `rasterImage`.

`copy.image.to.clipboard` copies the 2D depiction to the system clipboard in PNG format. You can then paste into other applications.

Due to event handling issues, the depiction will show on OS X, but the window will be unresponsive. Also copying images to the clipboard will not work. As a result, on OS X we make use of a standalone helper that is run via the `system` command. Currently, this is supported for the `view.molecule.2d` method (for a single molecule) and the `copy.image.to.clipboard` method. In the future, other view methods will also be accessible via this mechanism. While this allows OS X users to view molecules, it is slow due to invoking a new process.

The depictions will work fine (i.e., no need to shell out) on Linux and Windows.

Value

`get.depictor` returns a depiction object that can be supplied to other methods. `view.molecule.2d` and `copy.image.to.clipboard` do not return anything. `view.image.2d` returns an array of the dimensions height x width x channels, from the original PNG version of the 2D depiction.

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

`view.table, rasterImage, readPNG`

Examples

```r
m <- parse.smiles("\c1cccc1C(=O)NC\")[[1]]

## Not run:
dep <- get.depictor(width=200, height=200)
img <- view.image.2d(m, dep)
plot(1:10, 1:10, pch=19)
rasterImage(img, 0,8, 2,10)

dep$setHeight(as.integer(400))
 dep$setWidth(as.integer(400))
 copy.image.to.clipboard(m,d) ## Paste into Word

## End(Not run)
```
Description

The CDK is capable of generating 2D structure diagrams. This function can be used to view a set of molecules along with some associated data. The format of the output is a table, where the first column are the 2D images of the molecules, followed by the data columns.

Usage

view.table(molecules, dat, cellx = 200, celly = 200)

Arguments

- molecules: A list of jobRef objects that represent IAtomContainer
- dat: A data.frame containing numeric or character columns. If columns are named they will be used in the data table. If not, names are autogenerated. The number of rows of the data.frame should be equal to the number of molecules
- cellx: Initial width of the table cells
- celly: Initial height of the table cells

Details

Due to event handling issues, the depiction will show on OS X, but the window will be unresponsive. The depictions will work fine on Linux and Windows.

Value

Nothing

Author(s)

Rajarshi Guha (<rajarshi.guha@gmail.com>)

See Also

view.molecule.2d

Examples

```r
smiles <- c('CCC', 'CCN', 'CCN(C)(C)',
            'c1ccccc1Cc1cccccc1',
            'CCCCCcCCCC(CN(C)(C)CC(=O)CC')
mols <- parse.smiles(smiles)
dframe <- data.frame(x = runif(4),
                      toxicity = factor(c('Toxic', 'Toxic', 'Nontoxic', 'Nontoxic')),
                      solubility = c('yes', 'yes', 'no', 'yes'))
## Not run: view.table(mols[1:4], dframe)
```
**write.molecules**  

**Write Molecules To Disk**

**Description**

This function writes one or more molecules to an SD file on disk, which can be of the single- or multi-molecule variety. In addition, if the molecule has keyed properties, they can also be written out as SD tags.

**Usage**

```r
write.molecules(mols, filename, together=TRUE, write.props=FALSE)
```

**Arguments**

- **mols**: A list of Java objects of class `IAtomContainer`
- **filename**: The name of the SD file to write. Note that if `together` is `FALSE` then this argument is taken as a prefix for the name of the individual files
- **together**: If `TRUE` then all the molecules are written to a single SD file. If `FALSE` each molecule is written to an individual file
- **write.props**: Should keyed properties be included in the SD file output

**Details**

This function can be used to write a single SD file containing multiple molecules. In case individual SD files are desired the `together` argument can be set to `FALSE`. In this case, the value of `filename` is used as a prefix, to which a numeric identifier and the suffix of `.sdf` is appended. In case, a single molecule is to be written to disk, simply specify the `filename` and use the default value of `together`

**Value**

The value of the property

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**See Also**

`load.molecules`, `set.property`, `get.property`, `remove.property`
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