Package 'ChemmineR'

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Type Package

Title Cheminformatics Toolkit for R

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Description ChemmineR is a cheminformatics package for analyzing drug-like small molecule data in R. Its latest version contains functions for efficient processing of large numbers of molecules, physicochemical/structural property predictions, structural similarity searching, classification and clustering of compound libraries with a wide spectrum of algorithms. In addition, it offers visualization functions for compound clustering results and chemical structures.

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Depends R (>= 2.10.0), methods

biocViews Cheminformatics, BiomedicalInformatics, Pharmacogenetics, Pharmacogenomics, MicrotitrePlateAssay, CellBasedAssays, Visualization, Infrastructure, DataImport, Clustering, Proteomics,Metabolomics

Imports rjson, graphics, stats, RCurl, DBI, digest, BiocGenerics, Rcpp (>= 0.11.0), ggplot2,grid,gridExtra, png,base64enc,DT,rsvg

Suggests RSQLite, scatterplot3d, gplots, fmcsR, snow, RPostgreSQL, BiocStyle, knitr, knitcitations, knitrBootstrap, ChemmineDrugs, png,rmarkdown, BiocManager

Enhances ChemmineOB

URL https://github.com/girke-lab/ChemmineR

VignetteBuilder knitr

LinkingTo Rcpp, BH

SystemRequirements GNU make

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R **topics documented:**

---

addDescriptorType   *Add Descriptor Type*

Description

Add a new descriptor type to the database. Normally descriptor types are added as needed, but if you are doing a parrallel data load you must pre-load the descriptor type to prevent duplicate defintion errors.

Usage

```
addDescriptorType(conn, descriptorType)
```

Arguments

conn   Any database connection object.

descriptorType The name of the descriptor.

Value

No return value.

Author(s)

Kevin Horan

Examples

```
## Not run:
conn =  initDb(...)
addDescriptor(conn,"fp")

## End(Not run)
```

---

addNewFeatures   *Add New Features*

Description

Adds new features to a database without adding any data. Note that if you are loading new data anyway, it is much more efficient to use the loadSdf function and include the new features then. This function will have to read all compounds out of the database first.

Usage

```
addNewFeatures(conn, featureGenerator)
```

Arguments

conn   A database connection object, such as is returned by `initDb`.

featureGenerator
                    A function which returns a data frame containing the new features. It may also
                    contain features which are already in the database, these will simply be ignored.
                    See the description of fct in `loadSdf` for details.

Value

No value is returned.

Author(s)

Kevin Horan

See Also

`loadSdf`

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample)
   addNewFeatures(conn, function(sdfset)
data.frame(MW = MW(sdfset),
               rings(sdfset,type="count",upper=6, arom=TRUE))
 )

unlink("test.db")
```

---

ap	*Return atom pair component of* AP/APset

Description

Returns atom pair component of objects of class AP or APset as list of vectors.

Usage

```
ap(x)
```

Arguments

x   Object of class AP and APset

Details

...

Value

List   with one to many of following components:

numeric   atom pairs

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Functions: SDF2apcmp, apset2descdb, cmp.search, cmp.similarity

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:50]
sdf <- sdfset[[1]]

## Compute atom pair library
ap <- sdf2ap(sdf)
(apset <- sdf2ap(sdfset))
view(apset[1:4])

## Return main components of APset object
cid(apset[1:4]) # compound IDs
ap(apset[1:4]) # atom pair descriptors

## Return atom pairs in human readable format
db.explain(apset[1])
```

AP-class   *Class "AP"*

Description

Container for storing the atom pair descriptors of a single compound as numeric vector. The atom pairs are used as structural similarity measures and for compound similarity searching.

Objects from the Class

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

Slots

AP: Object of class "numeric"

Methods

ap signature(x = "AP"): returns atom pairs as numeric vector

coerce signature(from = "APset",to = "AP"): as(apset,"AP")

show signature(object = "AP"): prints summary of AP

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Related classes: SDF, SDFset, SDFstr, APset.

Functions: SDF2apcmp, apset2descdb, cmp.search, cmp.similarity

Examples

```
showClass("AP")

## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:50]
sdf <- sdfsample[[1]]

## Compute atom pair library
ap <- sdf2ap(sdf)
(apset <- sdf2ap(sdfset))
view(apset[1:4])

## Return main components of APset object
cid(apset[1:4]) # compound IDs
ap(apset[1:4]) # atom pair descriptors

## Return atom pairs in human readable format
db.explain(apset[1])

## Coerce APset to other objects
apset2descdb(apset) # returns old list-style AP database
tmp <- as(apset, "list") # returns list
as(tmp, "APset") # converst list back to APset

## Compound similarity searching with APset
cmp.search(apset, apset[1], type=3, cutoff=0.2)
plot(sdfset[names(cmp.search(apset, apset[6], type=2, cutoff=0.4))])

## Identify compounds with identical AP sets
cmp.duplicated(apset, type=2)

## Structure similarity clustering
cmp.cluster(db=apset, cutoff = c(0.65, 0.5))[1:20,]
```

---

apfp   *Frequent Atom Pairs*

Description

Ranked set of 4096 most frequent atom pairs observed in the compound collection from DrugBank with a MW < 1000. Their atom pairs were generated with the sdf2ap function. The provided data frame is sorted row-wise by atom pair frequency and only the 4096 most frequent atom pairs are included. This data set can be used as predefined atom pair selection when computing atom pair fingerprints with the desc2fp function.

Usage

```
data(apfp)
```

Format

Object of class `data.frame`. First column contains atom pair (AP) IDs and the second column their frequency in DrugBank compounds.

Details

Object stores 4096 most frequent atom pairs generated from DrugBank compounds.

Source

DrugBank: http://www.drugbank.ca/

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

Examples

```
data(apfp)
apfp[1:4,]
```

---

apset   *Atom pairs stored in* `APset` *object*

Description

Atom pairs for 100 molecules stored in `sdfsample`.

Usage

```
data(apset)
```

Format

Object of class `apset`

Details

Object stores atom pairs of 100 molecules.

Source

```
apset <-sdf2ap(sdfsample)
```

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

Examples

```
data(apset)
apset[1:4]
view(apset[1:4])
```

APset-class   *Class "APset"*

Description

List-like container for storing the atom pair descriptors of a many compounds as objects of class AP. This container is used for structure similarity searching of compounds.

Objects from the Class

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

Slots

AP: Object of class "list"

ID: Object of class "character"

Methods

[signature(x = "APset"): subsetting of class with bracket operator

[[signature(x = "APset"): returns single component as AP object

[[<- signature(x = "APset"): replacement method for single AP component

[<- signature(x = "APset"): replacement method for several AP components

ap signature(x = "APset"): returns atom pair list from AP slot

c signature(x = "APset"): concatenates two APset containers

cid signature(x = "APset"): returns all compound identifiers from ID slot

cid<- signature(x = "APset"): replacement method for compound identifiers in ID slot

coerce signature(from = "APset",to = "AP"): as(apset,"AP")

coerce signature(from = "APset",to = "list"): as(apset,"list")

coerce signature(from = "list",to = "APset"): as(list,"APset")

length signature(x = "APset"): returns number of entries stored in object

show signature(object = "APset"): prints summary of APset

view signature(x = "APset"): prints extended summary of APset

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in J Chem Inf Comput Sci.

See Also

Related classes: SDF, SDFset, SDFstr, AP, FPset, FP.

Functions: SDF2apcmp, apset2descdb, cmp.search, cmp.similarity

Examples

```
showClass("APset")

## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:50]
sdf <- sdfsample[[1]]

## Compute atom pair library
ap <- sdf2ap(sdf)
(apset <- sdf2ap(sdfset))
view(apset[1:4])

## Return main components of APset object
cid(apset[1:4]) # compound IDs
ap(apset[1:4]) # atom pair descriptors

## Return atom pairs in human readable format
db.explain(apset[1])

## Coerce APset to other objects
apset2descdb(apset) # returns old list-style AP database
tmp <- as(apset, "list") # returns list
as(tmp, "APset") # converst list back to APset

## Compound similarity searching with APset
cmp.search(apset, apset[1], type=3, cutoff=0.2)
plot(sdfset[names(cmp.search(apset, apset[6], type=2, cutoff=0.4))])

## Identify compounds with identical AP sets
cmp.duplicated(apset, type=2)

## Structure similarity clustering
cmp.cluster(db=apset, cutoff = c(0.65, 0.5))[1:20,]
```

---

apset2descdb   APset *to list-style AP database*

Description

Coerces APset to old list-style descriptor database used by search/cluster functions.

Usage

```
apset2descdb(apset)
```

Arguments

apset   Object of class apset

Details

...

Value

list	with following components
descdb	list of atom pair sets
cids	compound IDs
sdfsegs	start/end coordinates for each molecule in SD file; only populated when cmp.parse is used for import
source	path/name of SD file
type	import method

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Functions: SDF2apcmp, sdf2ap, cmp.search, cmp.similarity

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:50]
sdf <- sdfsample[[1]]

## Compute atom pair library
ap <- sdf2ap(sdf)
(apset <- sdf2ap(sdfset))
view(apset[1:4])

## Return main components of APset object
cid(apset[1:4]) # compound IDs
ap(apset[1:4]) # atom pair descriptors

## Return atom pairs in human readable format
db.explain(apset[1])
```

```
## Coerce APset to other objects
apset2descdb(apset) # returns old list-style AP database
tmp <- as(apset, "list") # returns list
as(tmp, "APset") # converst list back to APset

## Compound similarity searching with APset
cmp.search(apset, apset[1], type=3, cutoff=0.2)
plot(sdfset[names(cmp.search(apset, apset[6], type=2, cutoff=0.4))])

## Identify compounds with identical AP sets
cmp.duplicated(apset, type=2)

## Structure similarity clustering
cmp.cluster(db=apset, cutoff = c(0.65, 0.5))[1:20,]
```

---

atomblock	*Return atom block*

Description

Returns atom block(s) from an object of class SDF or SDFset.

Usage

```
atomblock(x)
```

Arguments

x   object of class SDF or SDFset

Details

...

Value

matrix if SDF is provided or list of matrices if SDFset is provided

Author(s)

Thomas Girke

References

...

See Also

header, atomcount, bondblock, datablock, cid, sdfid

Examples

```
## SDF/SDFset instances
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

## Extract atome block
atomblock(sdf)
atomblock(sdfset[1:4])

## Replacement methods
sdfset[[1]][[2]][1,1] <- 999
sdfset[[1]]
atomblock(sdfset)[1:2] <- atomblock(sdfset)[3:4]
atomblock(sdfset[[1]]) == atomblock(sdfset[[3]])
view(sdfset[1:2])
```

---

atomcount   *Molecular property functions*

Description

Functions to compute molecular properties: weight, formula, atom frequencies, etc.

Usage

```
atomcount(x, addH = FALSE, ...)

atomcountMA(x, ...)

MW(x, mw=atomprop, ...)

MF(x, ...)
```

Arguments

x	object of class SDFset or SDF
mw	data.frame with atomic weights; imported by default with data(atomprop); supports custom data sets
addH	'addH = TRUE' should be passed on to any of these function to add hydrogens that are often not specified in SD files
...	Arguments to be passed to/from other methods.

Details

...

Value

named vector	MW and MF
list	atomcount
matrix	atomcountMA

Author(s)

Thomas Girke

References

Standard atomic weights (2005) from: http://iupac.org/publications/pac/78/11/2051/

See Also

Functions: `datablock`, `datablocktag`

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Compute properties; to consider missing hydrogens, set 'addH = TRUE'
MW(sdfset[1:4], addH = FALSE)
MF(sdfset[1:4], addH = FALSE)
atomcount(sdfset[1:4], addH = FALSE)
propma <- atomcountMA(sdfset[1:4], addH = FALSE)
boxplot(propma, main="Atom Frequency")

## Example for injecting a custom matrix/data frame into the data block of an
## SDFset and then writing it to an SD file
props <- data.frame(MF=MF(sdfset), MW=MW(sdfset), atomcountMA(sdfset))
datablock(sdfset) <- props
view(sdfset[1:4])
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE, cid=TRUE)
```

---

atomprop *Standard atomic weights*

Description

Data frame with atom names, symbols, standard atomic weights, group number and period number.

Usage

```
data(atomprop)
```

Format

The format is a data frame with 117 rows and 6 columns.

Source

Columns 1 to 4 from: http://iupac.org/publications/pac/78/11/2051/ Columns 5 to 6 from: http://en.wikipedia.org/wiki/Li

References

Pure Appl. Chem., 2006, Vol. 78, No. 11, pp. 2051-2066

Examples

```
data(atomprop)
atomprop[1:4,]
```

---

atomsubset   *Subset SDF/SDFset Objects by Atom Index to Obtain Substructure*

Description

Function to obtain a substructure from SDF/SDFset objects by providing a row index for the atom block in an SDF referencing the atoms of interest. The function subsets both the atom and bond block(s) accordingly.

Usage

```
atomsubset(x, atomrows, type="new", datablock = FALSE)
```

Arguments

x   object of class SDFset or SDF

atomrows   The argument atomrows can be assigned a numeric index referencing the atoms
                in the atom block of x. If x is of class SDF, the index needs to be provided as
                vector. If x is of class SDFset, the same number of index vectors as molecules
                stored in x need to be passed on in a list with component names identical to the
                component (molecule) names stored in x.

type   The argument type="new" assigns new atom numbers to a subsetted SDF, while
                type="old" maintains the numbering of the source SDF.

datablock   By default the data block(s) in SDF/SDFset objects are removed after atom sub-
                setting. The setting datablock=TRUE will maintain the data block information
                in the subsetted result.

Details

...

Value

object of class SDF or SDFset

Author(s)

Thomas Girke

References

...

See Also

...

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Subset one or more molecules with atom index(es) to obtain substructure(s)
atomsubset(sdfset[[1]], atomrows=1:18)
indexlist <- list(1:18, 1:12)
names(indexlist) <- cid(sdfset[1:2])
atomsubset(sdfset[1:2], atomrows=indexlist)
```

---

batchByIndex   *Batch by Index*

Description

When doing a select were the condition is a large number of ids it is not always possible to include them in a single SQL statement. This function will break the list of ids into chunks and allow the indexProcessor to deal with just a small number of ids.

Usage

```
batchByIndex(allIndices, indexProcessor, batchSize = 1e+05)
```

Arguments

allIndices   A vector of values that will be broken into batches and passed as an argument to the indexProcessor function.

indexProcessor   A function that takes one batch if indices. It is called once for each batch. The return value from this function is ignored. To accumulate results you can write to a global variable using the "«-" operator.

batchSize   The size of each batch. The last batch may be smaller than this value.

Value

No value is returned.

Author(s)

Kevin Horan

See Also

parBatchByIndex

Examples

```
## Not run:
result=NA
indices = 1:10000

#run a query on each batch of indexes, appending each result to
# "result" as we go.
batchByIndex(indices, function(indexBatch){
df = dbGetQuery(dbConnection, generateQuery(indexBatch))
result <<- if(is.na(result)) df else  rbind(result,df)
},1000)

## End(Not run)
```

---

bondblock   *Return bond block*

Description

Returns bond block(s) from an object of class SDF or SDFset.

Usage

```
bondblock(x)
```

Arguments

x   object of class SDF or SDFset

Details

...

Value

matrix if SDF is provided or list of matrices if SDFset is provided

Author(s)

Thomas Girke

References

...

See Also

header, atomcount, atomblock, datablock, cid, sdfid

Examples

```
## SDF/SDFset instances
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

## Extract bond block
bondblock(sdf)
bondblock(sdfset[1:4])

## Replacement methods
sdfset[[1]][[3]][1,1] <- 999
sdfset[[1]]
bondblock(sdfset)[1:2] <- bondblock(sdfset)[3:4]
bondblock(sdfset[[1]]) == bondblock(sdfset[[3]])
view(sdfset[1:2])
```

---

bonds   *Bonds, charges and missing hydrogens*

Description

Returns information about bonds, charges and missing hydrogens in SDF and SDFset objects.

Usage

```
bonds(x, type = "bonds")
```

Arguments

x	SDF or SDFset containers
type	If type="bonds" (default), a data.frame is returned with columns: atom (atom labels), Nbondcount (observed bond count), Nbondrule (bond count according to position in periodic table) and charge (charge of each atom).
	If type="charge", all charged atoms are returned and if type="addNH", the number of missing hydrogens are returned for each molecule.

Details

It is used by many other functions (e.g. MW, MF, atomcount, atomcuntMA and plot) to correct for missing hydrogens that are often not specified in SD files.

Value

If x is of class SDF, then a single data.frame or vector is returned. If x is of class SDFset, then a list of data.frames or vecotors is returned that has the same length and order as x.

Author(s)

Thomas Girke

References

...

See Also

Functions: conMA

Class: SDF and SDFset

Examples

```
## Instances of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Returns data frames with bonds and charges
bonds(sdfset[1:2], type="bonds")

## Returns charged atoms in each molecule
bonds(sdfset[1:2], type="charge")

## Returns the number of missing hydrogens in each molecule
bonds(sdfset[1:2], type="addNH")
```

---

browseJob	*Open ChemMine Tools Job in Web Browser*

Description

Launches a web browser to view the results of a ChemMine Tools web job with an interactive online viewer. Note that this reassigns the job to the current logged in user within the browser, so it becomes no longer accessible by the result and status functions. Any results should be saved within R before launching a browser.

Usage

```
browseJob(object)
```

Arguments

object   A jobToken job as returned by the function launchCMTool

Value

Returns an URL string which can be used to access the job results. The function also attempts to open the url with the browseURL function. As this URL can only be used once, the returned string is only useful if the browseURL function fails to open a browser.

Author(s)

Tyler William H Backman

References

See ChemMine Tools at <http://chemmine.ucr.edu>.

See Also

Functions: `toolDetails`, `listCMTools`, `launchCMTool`, `result`, `status`

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")

## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
status(job1)
result1 <- result(job1)

## open job in web browser
browseJob(job1)

## End(Not run)
```

---

bufferLines   *Buffer File Input*

Description

Buffer the input of files to increase efficiency

Usage

```
bufferLines(fh, batchSize, lineProcessor)
```

Arguments

fh	file handle
batchSize	How many lines to read in each batch
lineProcessor	Each batch of lines will be passed to this function for processing

Value

No return value

Author(s)

Kevin Horan

Examples

```
## Not run:
fh = file("filename")
bufferLines(fh,100,function(lines) {
message("found ",length(lines)," lines")
})

## End(Not run)
```

---

bufferResultSet   *Buffer Query Results*

Description

Allow query results to be processed in batches for efficiency.

Usage

```
bufferResultSet(rs, rsProcessor, batchSize = 1000,closeRS=FALSE)
```

Arguments

rs	A DBIResult object, usually from dbSendQuery.
rsProcessor	Each batch will be passed as a data frame to this function for processing.
batchSize	The number of rows to read in each batch
closeRS	Should the result set be closed by this function when it is done?

Value

No value.

Author(s)

Kevin Horan

Examples

```
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (rs, rsProcessor, batchSize = 1000)
{
    while (TRUE) {
        chunk = fetch(rs, n = batchSize)
        if (dim(chunk)[1] == 0)
            break
        rsProcessor(chunk)
    }
  }
```

---

byCluster *By Cluster*

Description

Re-organize a vector valued clustering into an list which groups cluster members together

Usage

```
byCluster(clustering, excludeSingletons = TRUE)
```

Arguments

clustering   A named vector in which the names are cluster members and the values are cluster labels. This is format output by jarvisPatrick.

excludeSingletons

If true only clusters with more than 1 member will be in the output, otherwise all clusters will be used.

Value

A list with a slot for each cluster. Each slot of the list is a vector containing the cluster members.

Author(s)

Kevin Horan

See Also

[jarvisPatrick](#)

Examples

```
data(apset)
cl = jarvisPatrick(nearestNeighbors(apset,cutoff=0.6),k=2)
print(byCluster(cl))
```

---

canonicalize *Canonicalize*

Description

Canonicalizes the atom numbering of a compound. The implimentation of this function is in Open Babel and requires the ChemmineOB package to function.

Usage

```
canonicalize(sdf)
```

Arguments

sdf   Any sdfset object.

Value

A new SDFset in which all compounds have been canonicalized

Author(s)

Kevin Horan

References

http://openbabel.org/api/2.3/canonical_code_algorithm.shtml

See Also

[canonicalNumbering](#)

Examples

```
## Not run:
data(sdfsample)
canonicalSdf = canonicalize(sdfsample[1])

## End(Not run)
```

---

canonicalNumbering   *Canonical Numbering*

Description

Computes a re-arrangement required to transform the atom numbering of the given compound into the canonical atom numbering. This function uses the OBGraphSym and CanonicalLabels classes of Open Babel to compute the re-arrangement.

Usage

```
canonicalNumbering(sdf)
```

Arguments

sdf   Any sdfset object.

Value

A list of vectors of index values. Each item in the list corresponds to one of the given compounds. The values of a list item are the re-arrangement of the atoms. For example, if the value in item 1, column 1 is 25, that means that atom number 1 in the original compound should become atom number 25 in the canonical version of that compound.

Author(s)

Kevin Horan

References

http://openbabel.org/api/2.3/canonical_code_algorithm.shtml

See Also

canonicalize

Examples

```
## Not run:
data(sdfsample)
labels = canonicalNumbering(sdfsample[1])

## End(Not run)
```

---

cid   *Return compound IDs*

Description

Returns the compound identifiers from the ID slot of an `SDFset` object.

Usage

```
cid(x)
```

Arguments

x   object of class `SDFset` or `APset`

Details

...

Value

character vector

Author(s)

Thomas Girke

References

...

See Also

atomblock, atomcount, bondblock, datablock, header, sdfid

Examples

```
## SDFset/APset instances
data(sdfsample)
sdfset <- sdfsample
apset <- sdf2ap(sdfset[1:4])

## Extract compound IDs from SDFset/APset
cid(sdfset[1:4])
cid(apset[1:4])

## Extract IDs defined in SD file
sdfid(sdfset[1:4])

## Assigning compound IDs and keeping them unique
unique_ids <- makeUnique(sdfid(sdfset))
cid(sdfset) <- unique_ids
cid(sdfset[1:4])

## Replacement Method
cid(sdfset) <- as.character(1:100)
```

---

cluster.sizestat   *generate statistics on sizes of clusters*

Description

'cluster.sizestat' is used to do simple statistics on sizes of clusters generated by 'cmp.cluster'. It will return a dataframe which maps a cluster size to the number of clusters with that size. It is often used along with 'cluster.visualize'.

Usage

```
cluster.sizestat(cls, cluster.result=1)
```

Arguments

cls   The clustering result returned by 'cmp.cluster'

cluster.result   If multiple cutoff values are used in clustering process, this argument tells which
                    cutoff value is to be considered here.

Details

'cluster.sizestat' depends on the format that is returned by 'cmp.cluster' - it will treat the first column as the indecies, and the second column as the cluster sizes of effective clustering. Because of this, when multiple cutoffs are used when 'cmp.cluster' is called, 'cluster.sizestat' will only consider the clustering result of the first cutoff. If you want to work on an alternative cutoff, you have to manually reorder/remove columns.

Value

Returns a data frame of two columns.

cluster size   This column lists cluster sizes

count   This column lists number of clusters of a cluster size

Author(s)

Y. Eddie Cao

See Also

cmp.cluster, cluster.visualize

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)

## Binning clustering using variable similarity cutoffs.
cluster <- cmp.cluster(db=apset, cutoff = c(0.65, 0.5))

## Statistics on sizes of clusters
cluster.sizestat(cluster[,c(1,2,3)])
cluster.sizestat(cluster[,c(1,4,5)])
```

---

cluster.visualize   *visualize clustering result using multi-dimensional scaling*

Description

'cluster.visualize' takes clustering result returned by 'cmp.cluster' and generate multi-dimensional scaling plot for visualization purpose.

Usage

```
cluster.visualize(db, cls, size.cutoff, distmat=NULL, color.vector=NULL, non.interactive="", clust
```

Arguments

db   The desciptor database, in the format returned by 'cmp.parse'.

cls   The clustering result returned by 'cmp.cluster'.

size.cutoff   The cutoff size for clusters considered in this visualization. Clusters of size smaller than the cutoff will not be considered.

distmat   A distance matrix that corresponds to the 'db'. If not provided, it will be computed on-the-fly in an efficient manner.

color.vector   Colors to be used in the plot. If the number of colors in the vector is not enough for the plot, colors will be reused. If not provided, color will be generated and randomly sampled from 'rainbow'.

non.interactive

If provided, will enable the non-interactive mode, and the plot will be in an eps file named after this value.

cluster.result Used to select the clustering result if multiple clustering results are present in 'cls'.

dimensions   Dimensionality to be used in visualization. See details.

quiet   Whether to supress the progress bar.

highlight.compounds

A vector of compound IDs, corresponding to compounds to be highlighted in the plot. A highlighted compound is represented as a filled circle.

highlight.color

Color used for highlighted compounds. If not set, a highlighted compounds will have the same color as that used for other compounds in the same cluster.

...   Further arguments will be passed to 'cmp.similarity' to calculate similarity matrix.

Details

'cluster.visualize' internally calls the 'cmdscale' function to generate a set of points in 2-D for the compounds in selected clusters. Note that for compounds in clusters smaller than the cutoff size, they will not be considered in this calculation - their entries in 'distmat' will be discarded if 'distmat' is provided, and distances involving them will not be computed if 'distmat' is not provided.

To determine the value for 'size.cutoff', you can use 'cluster.sizestat' to see the size distribution of clusters.

Because 'cmp.cluster' function allows you to perform multiple clustering processes simultaneously with different cutoff values, the 'cls' parameter may point to a data frame containing multiple clustering results. The user can use 'cluster.result' to specify which result to use. By default, this is set to 1, and the first clustering result will be used in visualization. Whatever the value is, in interactive mode (described below), all clustering result will be displayed when a compound is selected in the interactive plot.

If the colors provided in 'color.vector' are not enough to distinguish clusters by colors, the function will silently reuse the colors, resulting multiple clusters colored in the same color. We suggest you use 'cluster.sizestat' to see how many clusters will be selected using your 'size.cutoff', or simply provide no 'color.vector'.

If 'non.interative' is not set, the final plot is interactive. You will be able to select points by clicking them. When you click on any point, information about the compound represented by that point will be displayed. This includes the cluster ID, cluster size, compound index in the SDF and compound name if any. You can then perform another selection. To exit this process, right click on X11 device or press ESC in non-X11 device (Quartz and Windows).

By default, 'dimensions' is set to 2, and the built-in 'plot' function will be used for plotting. If you need to do 3-Dimensional plotting, set 'dimensions' to 3, and pass the returned value to 3D plot utilities, such as 'scatterplot3d' or 'rggobi'. This package does not perform 3D plot on its own.

Value

This function returns a data frame of MDS coordinates and clustering result. This value can be passed to 3D plot utilities such as 'scatterplot3d' and 'rggobi'.

The last column of the output gives whether the compounds have been clicked in the interactive mode.

Author(s)

Y. Eddie Cao

See Also

[cmp.parse](), [cmp.cluster](), [cluster.sizestat]()

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset

## cluster db with 2 cutoffs
clusters <- cmp.cluster(db, cutoff=c(0.5, 0.4))

## Return size stats
sizestat <- cluster.sizestat(clusters)

## Visualize results, using a cutoff of 3, write to file 'test.eps'
coord <- cluster.visualize(db, clusters, 2, non.interactive="test.eps")

## Not run:
## visualize it in interactive mode, using a cutoff of 3 and the 2nd clustering result
coord <- cluster.visualize(db, clusters, cluster.result=2, 3)

## 3D visualization with scatterplot3d
coord <- cluster.visualize(db, clusters, 3, dimensions=3)
library(scatterplot3d)
scatterplot3d(coord)


## End(Not run)
```

---

cmp.cluster *cluster compounds using a descriptor database*

Description

'cmp.cluster' uses structural compound descriptors and clusters the compounds based on their pairwise distances. cmp.cluster uses single linkage to measure distance between clusters when it merges clusters. It accepts both a single cutoff and a cutoff vector. By using a cutoff vector, it can generate results similar to hierarchical clustering after tree cutting.

Usage

```
cmp.cluster(db, cutoff, is.similarity = TRUE, save.distances = FALSE,
        use.distances = NULL, quiet = FALSE, ...)
```

Arguments

db	The desciptor database, in the format returned by 'cmp.parse'.
cutoff	The clustering cutoff. Can be a single value or a vector. The cutoff gives the maximum distance between two compounds in order to group them in the same cluster.
is.similarity	Set when the cutoff supplied is a similarity cutoff. This cutoff is the minimum similarity value between two compounds such that they will be grouped in the same cluster.
save.distances	whether to save distance for future clustering. See details below.
use.distances	Supply pre-computed distance matrix.
quiet	Whether to suppress the progress information.
...	Further arguments to be passed to `cmp.similarity`.

Details

`cmp.cluster` will compute distances on the fly if use.distances is not set. Furthermore, if save.distances is not set, the distance values computed will never be stored and any distance between two compounds is guaranteed not to be computed twice. Using this method, `cmp.cluster` can deal with large databases when a distance matrix in memory is not feasible. The speed of the clustering function should be slowed when using a transient distance calculation.

When save.distances is set, `cmp.cluster` will be forced to compute the distance matrix and save it in memory before the clustering. This is useful when additional clusterings are required in the future without re-computed the distance matrix. Set save.distances to TRUE if you only want to force the clustering to use this 2-step approach; otherwise, set it to the filename under which you want the distance matrix to be saved. After you save it, when you need to reuse the distance matrix, you can 'load' it, and supply it to `cmp.cluster` via the use.distances argument.

`cmp.cluster` supports a vector of several cutoffs. When you have multiple cutoffs, `cmp.cluster` still guarantees that pairwise distances will never be recomputed, and no copy of distances is kept in memory. It is guaranteed to be as fast as calling `cmp.cluster` with a single cutoff that results in the longest processing time, plus some small overhead linear in processing time.

Value

Returns a `data.frame`. Besides a variable giving compound ID, each of the other variables in the data frame will either give the cluster IDs of compounds under some clustering cutoff, or the size of clusters that the compounds belong to. When N cutoffs are given, in total 2*N+1 variables will be generated, with N of them giving the cluster ID of each compound under each of the N cutoffs, and the other N of them giving the cluster size under each of the N cutoffs. The rows are sorted by cluster sizes.

Author(s)

Y. Eddie Cao, Li-Chang Cheng

See Also

[cmp.parse1](), [cmp.parse](), [cmp.search](), [cmp.similarity]()

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads atom pair and atom pair fingerprint samples provided by library
data(apset)
db <- apset
fpset <- desc2fp(apset)

## Clustering of 'APset' object with multiple cutoffs
clusters <- cmp.cluster(db=apset, cutoff=c(0.5, 0.85))

## Clustering of 'FPset' object with multiple cutoffs. This method allows to call
## various similarity methods provided by the fpSim function.
clusters2 <- cmp.cluster(fpset, cutoff=c(0.5, 0.7), method="Tversky")

## Saves the distance matrix before clustering:
clusters <- cmp.cluster(db, cutoff=0.65, save.distances="distmat.rda")
# Later one reload the matrix and pass it the clustering function.
load("distmat.rda")
clusters <- cmp.cluster(db, cutoff=0.60, use.distances=distmat)
```

---

cmp.duplicated *quickly detect compound duplication in a descriptor database*

Description

'cmp.duplicated' detects duplicated compounds from a descriptor database generated by 'cmp.parse'.
Two compounds are said to duplicate each other when their descriptors are the same.

Usage

```
cmp.duplicated(db, sort = FALSE, type=1)
```

Arguments

db	The desciptor database, in the format returned by 'cmp.parse'.
sort	Whether to sort the descriptors for a compound. See details.
type	Returns results as vector (type=1) or data frame (type=2).

Details

'cmp.duplicated' will take the descriptors in the descriptor database, concatenate all descriptors for the same compound into a string, and use this string as the identification of a compound. If two compounds share the same identification string, they are said to duplicate each other.

'cmp.duplicated' assume the the database passed in as argument to follow the format generated by 'cmp.parse'. That is, 'db' is a list, 'db$descdb' is a list, and each entry of 'db$descdb' is an array of numeric values that give descriptors for one compound.

By default, 'cmp.duplicated' will assume the descriptors for a compound is already sorted. That is each entry in 'db\$descdb' is a sorted array. This is true for database generated by 'cmp.parse'. If you generate the database using some other tools, you might want to enable sorting.

Value

Returns a logic array, telling whether a compound in the database is a duplication of a compound appearing before this one. For example, if the i-th element of the array is TRUE, it means that the i-th compound in the database is a duplication of a compound listed before this compound in the database.

The returned array can be used to remove duplication. Simply use it to index the descriptor database.

If you are interested in what compound is duplicated, you can do a search in the database with cutoff set to 1.

Author(s)

Y. Eddie Cao

See Also

cmp.parse, cmp.search

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset

## Manually create a duplication (here compound 1 and 10)
db[10] <- db[1]

## Find duplication
dup <- cmp.duplicated(db)
dup
cid(db[dup])

## Remove all duplications
db <- db[!dup]
```

---

cmp.parse *Parse an SDF file and compute descriptors for all compounds*

Description

'cmp.parse' will take a SDF file, parse all the compounds encoded, compute their atom-pair descriptors, and return the descriptors as a list. The list contains two names, 'descdb' and 'cids'. 'descdb' is a vector of descriptors, and 'cids' is a list of names of compounds found in the SDF file. The returned list is usually used to a database, against which similarity search can be performed using the 'search' function. These two functions will parse all compounds in the SDF file. To parse a single compound, use 'cmp.parse1' instead.

Usage

```
cmp.parse(filename)
```

Arguments

filename   The file name of the SDF file

Details

The 'filename' can be a local file or an URL. It is interactive, and will display the parsing progress. Since the parsing will also compute of atom-pair descriptors, it is time consuming. You will be reminded to save the parsing result for future use at the end of parsing.

'type' is either set to the default value 'normal' or 'file-backed'. When set to 'file-backed', the parsing work will be delegated to a separate package called 'ChemmineRpp', and the database will be stored in a file instead of in the primary memory. Therefore, 'file-backed' mode can handle larger compound libraries. In 'file-backed' mode, 'dbname' will be used to name the database file. A suffix '.cdb' will be appended to the given name.

The type of the database is transparent to other part of the package. For example, calling 'cmp.search' against a database in 'file-backed' mode will cause the package to load the descriptors from the database file progressively.

Value

Return a list that can be used as the database against which similarity search can be performed. The 'search' and 'cmp.cluster' functions both expect a database returned by 'cmp.parse'.

descdb   A vector containing the descriptors for all the compounds.

cids   Compound ID information found in the SDF file. It is the first line of SDF of a compound.

Author(s)

Y. Eddie Cao, Li-Chang Cheng

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in *J Chem Inf Comput Sci*.

See Also

cmp.parse1, cmp.search, cmp.cluster, cmp.similarity

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset
# (optinally) save the db for future use
save(db, file="db.rda", compress=TRUE)
# ...
# later, in a separate session, you can load it back:
load("db.rda")
```

---

cmp.parse1   *Parsing an SDF file and calculate the descriptor for one compound*

Description

Read SDF information from an SDF file or connection, parse the first compound, and calculate the descriptor for that compound. The returned descriptor can be added to database returned by 'cmp.parse' or be used as the query structure when calling 'search'. This function will only parse one compound and return only the descriptor. To parse all compounds in an SDF file, use 'cmp.parse'.

Usage

```
cmp.parse1(filename)
```

Arguments

filename   The file name of the SDF file or a URL or a connection.

Details

'cmp.parse1' can take a file name or a URL or a connection. When a connection is used, the current line must be the first line of SDF of the compound to be parsed. 'cmp.parse1' will skip the header and parse from the 4th line. Therefore, the compound ID information will be skipped. After the parsing is done, if 'filename' is a connection, it will then point to the line after the connection table of SDF. You can use some other procedure to parse the annotation block.

Value

Return the descriptor, which is encoded as a vector.

Author(s)

Y. Eddie Cao, Li-Chang Cheng

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in *J Chem Inf Comput Sci*.

See Also

[cmp.parse](#), [cmp.search](#), [cmp.cluster](#), [cmp.similarity](#)

Examples

```
# load an SDF file from web and parse it
## Not run: structure <- cmp.parse1("http://bioweb.ucr.edu/ChemMineV2/compound/Aurora/b32:NNQS2MBRHAZTI===/s
```

---

cmp.search	*Search a descriptor database for compounds similar to query compound*

Description

Given descriptor of a query compound and a database of compound descriptors, search for compounds that are similar to the query compound. User can limit the output by supplying a cutoff similarity score or a cutoff that limits the number of returned compounds. The function can also return the scores together with the compounds.

Usage

```
cmp.search(db, query, type=1, cutoff = 0.5, return.score = FALSE, quiet = FALSE,
 mode = 1,visualize = FALSE, visualize.browse = TRUE, visualize.query = NULL)
```

Arguments

db	The compound descriptor database returned by 'cmp.parse'.
query	The query descriptor, which is usually returned by 'cmp.parse1'.
type	Returns results in form of position indices (type=1), named vector with compound IDs (type=2) or data frame (type=3).
cutoff	The cutoff similarity (when cutoff <= 1) or the number of maximum compounds to be returned (when cutoff > 1).
return.score	Whether to return similarity scores. If set to TRUE, a data frame will be returned; otherwise, only the compounds' indices in the database will be returned in the order of decreasing scores.
quiet	Whether to disable progress information.

mode	Mode used when computing similarity scores. This value is passed to 'cmp.similarity'.
visualize	
visualize.browse	
visualize.query	

Details

'cmp.search' will go through all the compound descriptors in the database and calculate the similarity between the query compound and compounds in the database. When cutoff similarity score is set, compounds having a similarity score higher than the cutoff will be returned. When maximum number of compounds to return is set to N via 'cutoff', the compounds having the highest N similarity scores will be returned.

Value

When 'return.score' is set to FALSE, a vector of matching compounds' indices in the database will be returned. Otherwise, a data frame will be returned:

| ids | The indices of matching compounds in the database. |
| scores | The similarity scores between the matching compounds and the query compound |

Author(s)

Y. Eddie Cao, Li-Chang Cheng

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in *J Chem Inf Comput Sci*.

See Also

cmp.parse1, cmp.parse, cmp.search, cmp.cluster, cmp.similarity, sdf.visualize

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset
query <- db[1]

## Ooptinally, save the db for future use
save(db, file="db.rda", compress=TRUE)

## Search for similar compounds using similarity cutoff
```

```
cmp.search(db, query, cutoff=0.2, type=1) # returns index
cmp.search(db, query, cutoff=0.2, type=2) # returns named vector
cmp.search(db, query, cutoff=0.2, type=3) # returns data frame

## in the next session, you may use load a saved db and do the search:
load("db.rda")
cmp.search(db, query, cutoff=3)
## you may also use the loaded db to do clustering:
cmp.cluster(db, cutoff=0.35)
```

---

cmp.similarity   *Compute similarity between two compounds using their descriptors*

Description

Given descriptors for two compounds, 'cmp.similarity' returns the similarity measure between the two compounds.

Usage

```
cmp.similarity(a, b, mode = 1, worst = 0)
```

Arguments

a	Descriptor of the first compound.
b	Descriptor of the second compound.
mode	Mode used when computing the distance. See details below.
worst	The worst value you are expecting. If 'cmp.similarity' finds the upper bound of similarity is worse than it, it will return a 0 and potentially save some computation.

Details

'cmp.similarity' uses descriptor information generated by 'cmp.parse' and 'cmp.parse1'. Basically, a descriptor is a vector of numbers. The vector actually reprsents the set of descriptors of structural fragment. Similarity measurement uses Tanimoto coefficient.

'cmp.similarity' supports 3 different modes. In mode 1, normal Tanimoto coefficient is used. In mode 2, it uses the size of descriptor intersection over the size of the smaller descriptor, mainly to deal with compounds that vary a lot in size. In mode 3, it is similar to mode 2, except that it raises the similarity to the power 3 to penalize small values. When mode is 0, 'cmp.similarity' will select mode 1 or mode 3, based on the size differences between the two descriptors.

When 'cmp.similarity' is used in searching compounds with a threshold similarity value, or in clustering with a cutoff distance, the threshold similarity and cutoff distance can be used to decide a 'worse' value. 'cmp.similarity' can compute an upper bound of similarity easier, and by comparing this upper bound to the 'worst' value, it can potentially skip the real computation if it finds the similarity will be below the 'worst' value and will be useless to the caller.

Value

Return a numeric value between 0 and 1 which gives the similarity between the two compounds.

Author(s)

Y. Eddie Cao, Li-Chang Cheng

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in *J Chem Inf Comput Sci*.

Peter Willett (1998). "Chemical Similarity Searching", in *J. Chem. Inf. Comput. Sci*.

See Also

cmp.parse1, cmp.parse, cmp.search, cmp.cluster

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)

## Compute similarities among two compounds
cmp.similarity(apset[1], apset[2])

## Search apset database with a query compound
cmp.search(apset, apset[1], type=3, cutoff = 0.3)
```

---

conMA   *Bond Matrices*

Description

Creates a bond matrix from SDF and SDFset objects. The matrix contains the atom labels in the row and column titles and the bond types are given in the data part as follows: 0 is no connection, 1 is a single bond, 2 is a double bond and 3 is a triple bond.

Usage

```
conMA(x, exclude = "none")
```

Arguments

x	SDF or SDFset containers
exclude	if exclude="none", then all atoms will be considered in the resulting connection table; if exclude=c("H"), then the H atoms will be excluded. Any number of atom labels to be excluded can be passed on to this argument in form of a character vector.

Details

...

Value

If `x` is of class SDF, then a single bond `matrix` is returned. If `x` is of class `SDFset`, then a `list` of matrices is returned that has the same length as `x`.

Author(s)

Thomas Girke

References

...

See Also

Functions: `bonds`

Class: `SDF` and `SDFset`

Examples

```
## Instances of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Create bond matrix for first two molecules in sdfset
conMA(sdfset[1:2], exclude=c("H"))

## Return bond matrix for first molecule and plot its structure with atom numbering
conMA(sdfset[[1]], exclude=c("H"))
plot(sdfset[1], atomnum = TRUE, noHbonds=FALSE , no_print_atoms = "", atomcex=0.8)

## Return number of non-H bonds for each atom
rowSums(conMA(sdfset[[1]], exclude=c("H")))
```

---

connections	*Database Connections*

Description

Get a connection to one of the pre-build compound databases. The DrugBank database is distributed in the ChemmineDrugs package.

The DUD database will be downloaded the first time it is called. It will download a 1.8GB zipped file which will expand to abut 9GB. A directory to store the database in can be passed to the `DUD()` function.

Usage

```
DUD(destinationDir=".")

DrugBank()
```

Arguments

destinationDir   The directory to store the downloaded DUD database in.

Value

A connection object to the ether the DUD or DrugBank database. This object must be passed to
other functions which make use of the connection.

Author(s)

Kevin Horan

Examples

```
dbConn = DrugBank()
```

---

datablock   *Return data block*

Description

Returns data block(s) from an object of class SDF or SDFset.

Usage

```
datablock(x)

datablocktag(x, tag)
```

Arguments

x   object of class SDF or SDFset
tag   numeric position (index) or character name of entry in data block vector

Details

...

Value

named character vector if SDF is provided or list of named character vectors if SDFset is
provided

Author(s)

Thomas Girke

References

...

See Also

atomblock, atomcount, bondblock, header, cid, sdfid

Examples

```
## SDF/SDFset instances
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

## Extract data block
datablock(sdf)
datablock(sdfset[1:4])
datablocktag(sdfset, tag="PUBCHEM_OPENEYE_CAN_SMILES")

## Replacement methods
sdfset[[1]][[1]][1] <- "test"
sdfset[[1]]
datablock(sdfset)[1] <- datablock(sdfset[2])
view(sdfset[1:2])

## Example for injecting a custom matrix/data frame into the data block of an
## SDFset and then writing it to an SD file
props <- data.frame(MF=MF(sdfset), MW=MW(sdfset), atomcountMA(sdfset))
datablock(sdfset) <- props
view(sdfset[1:4])
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE, cid=TRUE)
```

---

datablock2ma   *SDF data blocks to matrix*

Description

Convert data blocks in SDFset to character matrix with datablock2ma, then store its numeric columns as numeric matrix and its character columns as character matrix.

Usage

```
datablock2ma(datablocklist, cleanup = " \\(.*", ...)

splitNumChar(blockmatrix)
```

Arguments

datablocklist	list of data block vectors; can be created with datablock(sdfset)
blockmatrix	matrix returned by datablock2ma
cleanup	character pattern to be used to clean up the name fields of the data block vectors; the exact pattern matches are replaced by nothing (deleted).
...	option to pass on additional arguments

Details

...

Value

`datablock2ma`	`character matrix`
`splitNumChar`	`list with two components, a numeric matrix and a character matrix`

Author(s)

Thomas Girke

References

...

See Also

Classes: `SDFset`

Examples

```
## SDFset instance
data(sdfsample)
sdfset <- sdfsample

# Convert data block to matrix
blockmatrix <- datablock2ma(datablocklist=datablock(sdfset))
blockmatrix[1:4, 1:4]

# Split matrix to numeric matrix and character matrix
numchar <- splitNumChar(blockmatrix=blockmatrix)
names(numchar)
numchar[[1]][1:4,]
numchar[[2]][1:4,]
```

---

db.explain   *Explain an atom-pair descriptor or an array of atom-pair descriptors*

Description

'db.explain' will take an atom-pair descriptor in numeric or a set of such descriptors, and interpret what they represent in a more human readable way.

Usage

```
db.explain(desc)
```

Arguments

`desc`	The descriptor or the array/vector of descriptors

Details

'desc' can be a single numeric giving a single descriptor or can be any container data type, such as vector or array, such that 'length(desc)' returns 2 or larger.

Value

Return a character vector describing the descriptors.

See Also

cmp.parse

Examples

```
## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset

## Return atom pairs of first compound in human readable format
db.explain(db[1])
```

---

db.subset   *Subset a descriptor database and return a sub-database for the se-
                         lected compounds*

Description

'db.subset' will take a descriptor database generated by 'cmp.parse' and an array of indecies, and return a new database for compounds corresponding to these indecies. The returned value is a descriptor database as returned by the cmp.parse function.

Usage

```
db.subset(db, cmps)
```

Arguments

db   The database generated by 'cmp.parse'

cmps   An array of indecies that correspond to a set of selected compounds from the
                database

Details

'db.subset' creates a sub-database from 'db' by only including infomration that is relevant to compounds indexed by 'cmps'.

Value

Return a descriptor database for the selected compounds. The format of the database is compatible with the one returned by `cmp.parse`.

See Also

`cmp.parse`, `sdf.subset`

Examples

```
## Note: this functionality has become obsolete since the introduction of the
## 'apset' S4 class.

## Load sample SD file
# data(sdfsample); sdfset <- sdfsample

## Generate atom pair descriptor database for searching
# apset <- sdf2ap(sdfset)

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset
olddb <- apset2descdb(db)

## Create a sub-database for the 1st and 2nd compound in that SDF
db_sub <- db.subset(olddb, c(1, 2))
```

---

dbTransaction   *DB Transaction*

Description

Run any db statements inside a transaction. If any error is raised the transaction will be rolled back, otherwise it will be committed at the end.

Usage

```
dbTransaction(conn, expr)
```

Arguments

conn	A database connection object, such as is returned by `initDb`.
expr	Any block of code.

Value

The value of the given block of code will be returned upon successfully commiting the transaction. Otherwise an error will be raised.

Author(s)

Kevin Horan

Examples

```
    conn = initDb("test15.db")
dbTransaction(conn,{
# any db code here
})
```

---

desc2fp   *Fingerprints from descriptor vectors*

Description

Generates fingerprints from descriptor vectors such as atom pairs stored in `APset` or `list` containers. The obtained fingerprints can be used for structure similarity comparisons, searching and clustering. Due to their compact size, computations on fingerprints are often more time and memory efficient than on their much more complex atom pair counterparts.

Usage

```
desc2fp(x, descnames=1024, type = "FPset")
```

Arguments

x	Object of classe `APset` or `list` of vectors
descnames	Descriptor set to consider for fingerprint encoding. If a single value from 1-4096 is provided then the function uses the corresponding number of the most frequent atom pairs stored in the `apfp` data set provided by the package. Alternatively, one can provide here any custom atom pair selection in form of a `character` vector.
type	return fingerprint set as `FPset`, `matrix` or `character` vector

Details

...

Value

`matrix` or `character` vectors

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Functions: sdf2ap, SDF2apcmp, apset2descdb, cmp.search, cmp.similarity

Related classes: SDF, SDFset, SDFstr, APset.

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:10]

## Compute atom pair library
apset <- sdf2ap(sdfset)

## Compute atom pair fingerprint matrix using internal atom pair
## selection containing 4096 most common atom pairs in DrugBank.
## For details see ?apfp. The following example uses from this
## set the 1024 most frequent atom pairs:
fpset <- desc2fp(x=apset, descnames=1024, type="FPset")

## Alternatively, one can provide any custom atom pair selection. Here
## 1024 most common ones in apset object.
fpset1024 <- names(rev(sort(table(unlist(as(apset, "list"))))))[1:1024])
fpset2 <- desc2fp(x=apset, descnames=fpset1024, type="FPset")

## A more compact way of storing fingerprints is as character values
fpchar <- desc2fp(x=apset, descnames=1024, type="character")

## Convert character fingerprints back to FPset or matrix
fpset <- as(fpchar, "FPset")
fpma <- as.matrix(fpset)

## Similarity searching returning Tanimoto similarity coefficients
fpSim(x=fpset[1], y=fpset)

## Clustering example
simMAap <- sapply(cid(fpset), function(x) fpSim(x=fpset[x], fpset, sorted=FALSE))
hc <- hclust(as.dist(1-simMAap), method="single")
plot(as.dendrogram(hc), edgePar=list(col=4, lwd=2), horiz=TRUE)
```

---

draw_sdf *draw_sdf*

Description

Draws an sdf object in the 2D plane using ggplot2 library. Permits customization of bond colors and atom colors.

Usage

```
draw_sdf(sdf, filename = "test.jpg", alpha_edge = 0.5, alpha_node = 1, numbered = FALSE, font_size =
```

Arguments

sdf	An instance of a SDF or list of SDFs
filename	Filename to save image to. Defaults to 'test.jpg'. If set to NULL, does not save image.
alpha_edge	alpha of bonds in your image. Defaults to 0.5. 0 is fully transparent, 1 is fully opaque.
alpha_node	alpha of atoms in your image. Defaults to 1.0.
numbered	If 1 or TRUE, displays numbering of atoms at their location. If 2, displays a second numbering style.
font_size	Controls size of text to be displayed at atom locations. Beware when plotting multiple SDFs in one image. Ggplot will still scale fonts as if text is being plotted in one image.
node_vertical_offset	
	Upward shift of atom text. Upward shit is in SDF units, not ggplot units.
bgcolor	An rgb(r,g,b,alpha) or similar object. produces a background of the specified color.
node_background_color	
	A common color as a text string (e.g. 'white', 'pink') or an rgb(r,g,b,alpha). Draws a filled circle of the color specified before drawing text over each node.
bgraster	A readPNG object or a path to an object that can be understood using readPNG. Will be used as background.
node_policy	Mapping that defines how atom strings should be displayed. Simplest would be c('default'='black')
edge_policy	Mapping that defines how bonds should be displayed. Simplest is c('default'='black'), though this will display all Hydrogen bonds as well.
bond_dist_offset	
	Defines space between double or triple bonds, in SDF units.
fmcsR_sdf	A second SDF object to run fmcsR on.

Details

Requires ggplot2. Additional features require grid, gridExtra, fmcsR, or png. Most matrix operations vectorized.

Value

Returns a ggplot2 object. Calling draw_sdf(...) rather than assigning it will result in R trying to print a ggplot2 object.

Author(s)

John A. Sharifi

Examples

```
library(ChemmineR)  # if not already imported
data(sdfsample)
draw_sdf(sdfsample[[1]])
```

---

exactMassOB *Exact Mass (Monoisotopic Mass)*

Description

Computes the exact mass of each compound given.

Usage

```
exactMassOB(sdfset)
```

Arguments

sdfset   Any SDFset object.

Value

A vector of mass values.

Author(s)

Kevin Horan

Examples

```
## Not run:
library(ChemmineR)
data(sdfsample)
mass = exactMassOB(sdfsample)

## End(Not run)
```

ExtSDF-class *Class "ExtSDF"*

Description

This is a subclass of SDF and thus inherits all the slots and methods from that class. It adds a list of extended attributes for atoms and bonds. These attributes can curretnly only be populated from a V3000 formatted SDF file.

Objects from the Class

Objects can be created by calls of the form new("ExtSDF",...). The function read.SDFset will also return objects of this class if the argument extendedAttributes is set to "TRUE".

Slots

extendedAtomAttributes: Object of class "list"

extendedBondAttributes: Object of class "list"

Methods

getAtomAttr signature(x = ″ExtSDF″): returns atom attributes as a named list of values

getBondAttr signature(x = ″ExtSDF″): returns bond attributes as a named list of values

show signature(object = ″ExtSDF″): prints summary of SDF as well as any defined extended attributes for the atoms or bonds

Author(s)

Kevin Horan

References

SDF V3000 format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Related classes: SDF, SDFset, SDFstr, AP, APset

Examples

```
showClass("ExtSDF")
```

---

findCompounds   *Find Compounds in Database*

Description

Searches the SQL database using features computed at load time. Each feature used should be specified in the featureNames parameter. Then a set of filters can be given to search for specific compounds.

Usage

```
findCompounds(conn, featureNames, tests)
```

Arguments

conn	A database connection object, such as is returned by [initDb](#).
featureNames	A list of all feature names used in any test.
tests	A vector of filters that must all be true for a compound to be returned. For example: c("MW <= 400","RINGS > 3") would return all compounds with a molecular weight of 400 or less and a more than 3 rings, assuming these features exist in the database. The syntax for each test is "<feature name> <SQL operator> <value>". These tests will simply be concatenated together with " AND " in-between them and tacked on the end of a WHERE clause of an SQL statement. So any SQL that will work in that context is fine.

Value

Returns a list of compound ids. The actual compounds can be fetched with [getCompounds](#).

Author(s)

Kevin Horan

See Also

[getCompounds](#)

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test1.db")

data(sdfsample)

#load data and compute 3 features: molecular weight, with the MW function,
# and counts for RINGS and AROMATIC, as computed by rings, which returns a data frame itself.
ids=loadSdf(conn,sdfsample,
  function(sdfset)
data.frame(MW = MW(sdfset),  rings(sdfset,type="count",upper=6, arom=TRUE))
 )
    #search for compounds with molecular weight less than 200
    lightIds = findCompounds(conn,"MW",c("MW < 200"))
    MW(getCompounds(conn,lightIds)) # should find one compound with weight 140
unlink("test1.db")
```

---

findCompoundsByName   *Find compound by name*

Description

Find the ids of compounds given the names.

Usage

```
findCompoundsByName(conn, names, keepOrder = FALSE, allowMissing = FALSE)
```

Arguments

conn   A database connection object, such as is returned by [initDb](#).

names   A list of names of compounds to search for. The names are those that would be
                returned by [sdfid](#). An error will be raised if any names are not found.

keepOrder   If true, the order of the output compound ids will be the same as the input names.
                This imposes a performance hit that can be significant for large datasets, thus it
                should be left FALSE unless needed.

allowMissing   When this is false an error will be raised when names queried were not found in
                the database. If true, just those that are found will be returned with no error or
                warning.

Value

Returns the compound ids for compounds with the given name. The output order is not guaranteed
unless keepOrder is set to TRUE. An error will be raised if any name cannot be found.

Author(s)

Kevin Horan

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test4.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample)

    # find id of compound 650003
    findCompoundsByName(conn,c("650003"))
unlink("test4.db")
```

---

fingerprintOB   *Fingerprints from OpenBabel*

Description

Generates fingerprints from SDFsets using OpenBabel. The name of the fingerprint can also be set and can be anything available through OpenBabel. You can see what this list is by executing "obabel -L fingerprints". Results are returned as an FPset.

Usage

```
fingerprintOB(sdfSet, fingerprintName)
```

Arguments

sdfSet   Input compounds to generate fingerprints for.

fingerprintName

> The name of the fingerprint in Open Babel. A list of available names can be found by executing "obabel -L fingerprints". Currently that list is: "FP2", "FP3", "FP4", and "MACCS".

Value

An FPset with an element for each given compound.

Author(s)

Kevin Horan

Examples

```
## Not run:
data(sdfsample)
fpset = fingerprintOB(sdfsample)

## End(Not run)
```

---

fold   *Fold*

Description

Fold a fingerprint. This takes the second half of the fingerprints and combines with the first half with a logical 'OR' operation. The result is a fingerprint with half as many bits.

Usage

```
fold(x, count = 1, bits = NULL)
```

Arguments

x   The fingerprint(s) to fold. This can be either an FP or an FPset object.

count   The number of times to fold this fingerprint. Folding will stop early if the fingerprint is reduced down to 1 bit before reaching the requested fold count.

bits   Fold this fingerprint until it is bits bits long. An exception will be thrown if bits is not reachable.

Value

The new, folded, fingerprint.

Author(s)

Kevin Horan

Examples

```
fp = new("FP",fp=c(1,0,1,1, 0,0,1,0))
foldedFp = fold(fp,bits=4)
```

---

foldCount   *foldCount*

Description

Returns the number of times this fingerprint has been folded.

Usage

```
foldCount(x)
```

Arguments

x   Either an FP or an FPset object.

Value

Returns the number of times this fingerprint has been folded.

Author(s)

Kevin Horan

Examples

```
fp = new("FP",fp=c(1,0,1,1, 0,0,1,0))
foldedFp=fold(fp)
fc = foldCount(foldedFp) # == 1
```

FP-class   *Class* "FP"

Description

Container for storing the fingerprint of a single compound. The FPset class is used for storing the fingerprints of many compounds.

Objects from the Class

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

Slots

fp: Object of class "numeric"

foldCount: Object of class "numeric"

type: Object of class "character"

Methods

as.character signature(x = "FP"): returns fingerprint as character string

as.numeric signature(x = "FP"): returns fingerprint as numeric vector

as.vector signature(x = "FP"): returns fingerprint as numeric vector

coerce signature(from = "FPset",to = "FP"): coerce FPset component to list with many FP objects

coerce signature(from = "numeric",to = "FP"): construct FP object from numeric vector

show signature(object = "FP"): prints summary of FP

c signature(x = "FP"): concatenates any number of FP objects

fold signature(x = "FP"): fold fingerprint in half

foldCount signature(x = "FP"): number of times this object has been folded

fptype signature(x = "FP"): the type of this fingerprint

numBits signature(x = "FP"): the number of bits in this fingerprint

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in J Chem Inf Comput Sci.

See Also

Related classes: SDF, SDFset, SDFstr, AP, APset, FPset.

Examples

```
showClass("FP")

## Instance of FP class
data(apset)
fpset <- desc2fp(apset)
(fp <- fpset[[1]])

## Class usage
fpc <- as.character(fp)
fpn <- as.numeric(fp)
as(fpn, "FP")
as(fpset[1:4], "FP")
```

---

fp2bit   *Convert base 64 fingerprints to binary*

Description

The function converts the base 64 encoded PubChem fingerprints to a binary `matrix` or a `character` vector. If applied to a `SDFset` object, then its data block needs to contain the PubChem fingerprint information.

Usage

```
fp2bit(x, type = 3, fptag = "PUBCHEM_CACTVS_SUBSKEYS")
```

Arguments

x	Object of class `SDFset`, `matrix` or `character`
type	If set to 1, the results are returned as binary `matrix`. If set to 2, the results are returned as `character` strings in a named *vector*. If set to 3 (default), the results are returned as `FPset` object.
fptag	Name tag in SDF data block where the PubChem fingerprints are stored. Default is set to "PUBCHEM_CACTVS_SUBSKEYS".

Details

...

Value

`matrix`, `character` or `FPset`

Author(s)

Thomas Girke

References

See PubChem fingerprint specification at: ftp://ftp.ncbi.nih.gov/pubchem/specifications/pubchem_fingerprints.txt

See Also

Functions: `fpSim`

Examples

```
## Load PubChem SDFset sample
data(sdfsample); sdfset <- sdfsample
cid(sdfset) <- sdfid(sdfset)

## Convert base 64 encoded fingerprints to FPset object
fpset <- fp2bit(sdfset)

## Pairwise compound structure comparisons
fpSim(fpset[1], fpset[2])

## Structure similarity searching: x is query and y is fingerprint database
fpSim(x=fpset[1], y=fpset, method="Tanimoto", cutoff=0, top="all")

## Compute fingerprint based Tanimoto similarity matrix
simMA <- sapply(cid(fpset), function(x) fpSim(x=fpset[x], fpset, sorted=FALSE))

## Hierarchical clustering with simMA as input
hc <- hclust(as.dist(1-simMA), method="single")

## Plot hierarchical clustering tree
plot(as.dendrogram(hc), edgePar=list(col=4, lwd=2), horiz=TRUE)
```

FPset-class   *Class* "FPset"

Description

Container for storing fingerprints of many compounds. This container is used for structure similarity searching of compounds.

Objects from the Class

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

Slots

    `fpma`: Object of class `"matrix"` with compound identifiers stored in row names

    `foldCount`: Object of class `"numeric"`

    `type`: Object of class `"character"`

Methods

    [`signature(x = "FPset")`: subsetting of class with bracket operator

    [[`signature(x = "FPset")`: returns single component as FP object

    [<- `signature(x = "FPset")`: replacement method for several components

    as.character `signature(x = "FPset")`: returns content as named character vector

    as.matrix `signature(x = "FPset")`: returns content as numeric matrix

    c `signature(x = "FPset")`: concatenates any number of `FPset` containers

    cid `signature(x = "FPset")`: returns all compound identifiers from row names

    cid<- `signature(x = "FPset")`: replacement method for compound identifiers

    coerce `signature(from = "FPset",to = "FP")`: `as(fpset,"FP")`

    coerce `signature(from = "matrix",to = "FPset")`: `as(fpma,"FPset")`

    coerce `signature(from = "character",to = "FPset")`: `as(fpchar,"FPset")`

    length `signature(x = "FPset")`: returns number of entries stored in object

    show `signature(object = "FPset")`: prints summary of `FPset`

    view `signature(x = "FPset")`: prints extended summary of `FPset`

    fold `signature(x = "FPset")`: fold fingerprint in half

    foldCount `signature(x = "FPset")`: number of times this object has been folded

    fptype `signature(x = "FPset")`: the type of these fingerprints

    numBits `signature(x = "FPset")`: the number of bits in these fingerprints

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", in J Chem Inf Comput Sci.

See Also

Related classes: SDF, SDFset, SDFstr, AP, APset, FP.

Examples

```
showClass("FPset")

## Instance of FPset class
data(apset)
(fpset <- desc2fp(apset))
view(fpset)

## Class usage
fpset[1:4] # behaves like a list
fpset[[1]] # returns FP object
length(fpset) # number of compounds
cid(fpset) # returns compound ids
fpset[1] <- 0 # replacement
cid(fpset) <- 1:length(fpset) # replaces compound ids
c(fpset[1:4], fpset[11:14]) # concatenation

## Coerce FPset from/to other objects
fpma <- as.matrix(fpset) # coerces to matrix
fpchar <- as.character(fpset) # coerces to character strings
as(fpma, "FPset")
as(fpchar, "FPset")

## Compound similarity searching with FPset
fpSim(x=fpset[1], y=fpset, method="Tanimoto", cutoff=0.4, top=4)
```

---

fpSim *Fingerprint Search*

Description

Search function for fingerprints, such as PubChem or atom pair fingerprints. Enables structure similarity comparisons, searching and clustering.

Usage

```
fpSim(x, y, sorted=TRUE, method="Tanimoto",
addone=1, cutoff=0, top="all", alpha=1, beta=1,
parameters=NULL,scoreType="similarity")
```

Arguments

x	Query molecule of class numeric, FP or FPset (of length one) containing binary fingerprint data. Both x and y need to have the same number of bits and should contain the same type of fingerprints.
y	Subject molecule(s) of class numeric, matrix, FP or FPset containing binary fingerprint data.
sorted	return results sorted or unsorted
method	Similarity coefficient to return. One can choose here from several predefined similarity measures: "Tanimoto" (default), "Euclidean", "Tversky" or "Dice". Alternatively, one can pass on any custom similarity function containing the arguments a, b, c and d. For instance, one can define "myfct <- function(a, b, c,

d) c/(alpha*a + beta*b + c)" and then pass on `method=myfct`. The variable 'c' is the number of "on-bits" common in both compounds, 'd' is the number of "off-bits" common in both compounds, and 'a' and 'b' are the number of "on-bits" that are unique in one or the other compound, respectively.

The predefined methods will run a C++ version of this function which is about twice as fast as the R version. When a custom similarity function is given however, it will fall back to using the R version.

addone   Value to add to numerator and denominator of similarity coefficient to avoid devision by zero when fingerprint(s) contain only "off-bits" (zeros). Note: if `addone > 0` then fingerprints with no "on-bits" will receive the highest similarity score. Typically, this occurs only with extremely small molecules.

cutoff   allows to restrict results to hits above a similarity cutoff value; default `cutoff=0` returns results for all compounds in y.

top   allows to restrict number of subject molecules to return; default `top="all"` returns results for all compounds in y above `cutoff` value.

alpha   Only used when method="Tversky". Allows to specify the weighting variable 'alpha' of the Tversky index: c/(alpha*a + beta*b + c)

beta   Only used when method="Tversky". Allows to specify the weighting variable 'beta' of the Tversky index.

parameters   Parameters for computing Z-scores, E-values, and p-values. Pass this data if you want these scores returned. This data can be generated with the [genParameters](#) function.

scoreType   If using the `parameters` argument, this argument specified which type of score the `cutoff` and `sorted` arguments should be applied to. It should be one of "similarity" (default), "zscore", "evalue", or "pvalue".

Value

Returns `numeric vector` with similarity coefficients as values and compound identifiers as names.

Author(s)

Thomas Girke, Kevin Horan

References

Tanimoto similarity coefficient: Tanimoto TT (1957) IBM Internal Report 17th Nov see also Jaccard P (1901) Bulletin del la Societe Vaudoisedes Sciences Naturelles 37, 241-272.

PubChem fingerprint specification: ftp://ftp.ncbi.nih.gov/pubchem/specifications/pubchem_fingerprints.txt

See Also

Functions: fp2bit

Examples

```
## Load PubChem SDFset sample
data(sdfsample); sdfset <- sdfsample
cid(sdfset) <- sdfid(sdfset)

## Convert base 64 encoded fingerprints to character vector or binary matrix
```

```
fpset <- fp2bit(sdfset)

## Alternatively, one can use atom pair fingerprints
## Not run:
fpset <- desc2fp(sdf2ap(sdfset))

## End(Not run)

## Pairwise compound structure comparisons
fpSim(x=fpset[1], y=fpset[2], method="Tanimoto")

## Structure similarity searching: x is query and y is fingerprint database
fpSim(x=fpset[1], y=fpset)

## Controlling the output
fpSim(x=fpset[1], y=fpset, method="Tversky", cutoff=0.4, top=4, alpha=0.5, beta=1)

## Use custom distance function
myfct <- function(a, b, c, d) c/(a+b+c+d)
fpSim(x=fpset[1], y=fpset, method=myfct)

## Compute fingerprint-based Tanimoto similarity matrix
simMA <- sapply(cid(fpset), function(x) fpSim(x=fpset[x], fpset, sorted=FALSE))

## Hierarchical clustering with simMA as input
hc <- hclust(as.dist(1-simMA), method="single")

## Plot hierarchical clustering tree
plot(as.dendrogram(hc), edgePar=list(col=4, lwd=2), horiz=TRUE)
```

---

fptype	*fptype*

Description

Returns the type label of this fingerprint

Usage

```
fptype(x)
```

Arguments

x   Either an `FP` or an `FPset` object.

Value

The type label of this fingerprint.

Author(s)

Kevin Horan

Examples

```
fp = new("FP",fp=c(1,0,1,1, 0,0,1,0),type="testFP")
type = fptype(fp) # == "testFP"
```

---

fromNNMatrix   *From Nearest Neighbor Matrix*

Description

Converts a nearest neighbor matrix into a list that can be used with the jarvisPatrick function.

Usage

```
fromNNMatrix(data, names = rownames(data))
```

Arguments

data   A matrix containing integer valued indexes which represent items to be clus-
              tered. The index values contained in the matrix must be smaller than the num-
              ber of rows in the matrix. Each row in the matrix represents one item and the
              columns are the nearest neighbors of that item.

names   The names for each row. The rownames of data will be used if not given.

Value

A list containing the slots "indexes" and "names".

Author(s)

Kevin Horan

See Also

[jarvisPatrick](#)

Examples

```
data(apset)

nn = nearestNeighbors(apset,cutoff=0.6)
nnMatrix = nn$indexes

cl = jarvisPatrick(fromNNMatrix(nnMatrix),k=2)
```

---

genAPDescriptors   *Generate AP Descriptors*

Description

Generates Atom Pair descriptors using a fast C function.

Usage

```
genAPDescriptors(sdf,uniquePairs=TRUE)
```

Arguments

sdf	A single SDF object.
uniquePairs	When the same atom pair occurs more than once in a single compound, should the names be unique or not? Setting this to true will take slightly longer to compute.

Value

A vector of descriptors for the compound given. An AP object can be generated as shown in the example below.

Author(s)

Kevin Horan

Examples

```
library(ChemmineR)
data(sdfsample)
sdf = sdfsample[[2]]
ap = new("AP", AP=genAPDescriptors(sdf))
```

---

generate3DCoords   *Generate 3D Coords*

Description

Uses Open Babel to compute 3D coordinates given an SDFset with only 2D coordinates.

Usage

```
generate3DCoords(sdf)
```

Arguments

sdf	Any sdfset object.

Value

A new SDFset in which all compounds have 3D coordinates.

Author(s)

Kevin Horan

Examples

```
## Not run:
data(sdfsample)
sdf3D = generate3DCoords(sdfsample[1])

## End(Not run)
```

---

genParameters   *Generate Parameters*

Description

Generate statistics from a fingerprint database for use in caluclating z-scores, E-values, and p-values later.

Usage

```
genParameters(fpset, similarity = fpSim, sampleFraction = 1, ...)
```

Arguments

fpset	The database of fingerprints. Needs to be in the format expected by the similarity function. For the default similarity function, this would be an FPset.
similarity	A function to compute the similarity between two fingerprints. The first argument should be a single query and the second argument should be a set of fingerprints.
sampleFraction	The fraction of all pairs to use for estimating parameters. See Details section.
...	Extra parameters will be passed on to the similarity function.

Details

A beta function will be fit to the distribution of similarity scores produced by the given similarity function. By default, all pairwise similarities will be computed. Since this can be expensive for large databases, one can also sample pairs to use. This can be done by setting sampleFraction to the fraction of all pairwise similarities to use. For example, for a database of 100 fingerprints, there are 10,000 pairs. Setting sampleFraction to 0.5 will result in only 5,000 pairs being used to estimate the parameters.

Parameters are conditioned on the number of set bits. This function therefore groups fingerprints by the number of set bits they have and then estimates parameters for each group. A set of global parameters is also estimated and returned for use in cases where there was not enough data to estimate the parameters for a particular number of set bits.

Value

A data frame with the following columns:

count	The number of similarities used to estimate these parameters
avg	the mean
variance	the variance
alpha	The alpha paramber of the Beta function
beta	The beta parameter of the Beta function

There will be a row for each possible count of 1 bits. So for a database of 1024 bit fingerprints, there will be 1025 rows for the possible values of 0-1024 bits. There will also be one additional row at the end with the global parameters. This can be used for cases where there are no parameters estimated for the current query 1-bit count.

Author(s)

Kevin Horan

References

Pierre Baldi and Ramzi Nasr, "When is Chemical Similarity Significant? The Statistical Distribution of Chemical Similarity Scores and Its Extreme Values" Journal of Chemical Information and Modeling 2010 50 (7), 1205-1222

See Also

[fpSim](#)

Examples

```
library(ChemmineR)
data(apset)
fpset=desc2fp(apset) #get a fingerprint database

params = genParameters(fpset)
scores = fpSim(fpset[[1]],fpset,parameters=params,top=10)
```

---

getAllCompoundIds *Get ALl Compound Ids*

Description

Return a vector of every compound id in the given database.

Usage

```
getAllCompoundIds(conn)
```

Arguments

conn	A database connection object, such as is returned by [initDb](#).

Value

A vector of compound_id numbers

Author(s)

Kevin Horan

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test1.db")

data(sdfsample)

#load data
ids=loadSdf(conn,sdfsample)
ids2=getAllCompoundIds(conn)
#ids == ids2

unlink("test1.db")
```

getCompoundFeatures   *Get Compound Features*

Description

Get feature values for specific compounds.

Usage

```
getCompoundFeatures(conn, compoundIds, featureNames, filename = NA, keepOrder = FALSE, allowMissing
```

Arguments

conn	A database connection object, such as is returned by [initDb](#).
compoundIds	A vector of compound_id numbers from this database. These are not compound names. Features will be fetched for each compound given here.
featureNames	A vector of features to fetch the value for, for each given compound.
filename	If given, dump the results into a comma seperated values (CSV) file instead of returning a data frame. This can avoid some potential memory limits when fetching large sets of data.
keepOrder	Ensure that the output order of values matches the order in which the compound ids where given. This will make things a little slower, so should only be used where required.
allowMissing	If false, raise an exception if a compound cannot be found, otherwise just silently ignore it and return data for whatever compound were found.
batchSize	The number of compounds to fetch in a single query. If you find your running out of memory you can try reducing this values, as well as try writing the result to a file using the filename parameter.

Value

If `filename` is not given, returns a data frame with the compound_id and any given feature names. Each row represents one compound. If `filename` is given a filename then no value is returned, but the given file is created.

Author(s)

Kevin Horan

Examples

```
#create and initialize a new SQLite database
   conn = initDb("test1.db")

data(sdfsample)

#load data
ids=loadSdf(conn,sdfsample,
  function(sdfset)
data.frame(MW = MW(sdfset),  rings(sdfset,type="count",upper=6, arom=TRUE))
 )

f = getCompoundFeatures(conn,ids,c("mw","rings"))

unlink("test1.db")
```

---

getCompoundNames   *Get Compound Names*

Description

Fetch the names of the given compound ids, if they exist

Usage

```
getCompoundNames(conn, compoundIds, keepOrder = FALSE, allowMissing = FALSE)
```

Arguments

conn	A database connection object, such as is returned by [initDb](#).
compoundIds	A vector of compound ids.
keepOrder	If true, the order of the output compound ids will be the same as the input names. This imposes a performance hit that can be significant for large datasets, thus it should be left FALSE unless needed.
allowMissing	When this is false an error will be raised when compound ids queried were not found in the database. If true, just those that are found will be returned with no error or warning.

Value

Returns a vector of compound names.The rownames will be the compound ids. Compound ids not found, or for which a name is not defined, will be represented as NA.

Author(s)

Kevin Horan

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test2.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample)

    getCompoundNames(conn,ids[1:3])
unlink("test3.db")
```

---

getCompounds   *Get Compounds From Database*

Description

Create SDF objects from the given set of compound ids. Id numbers can be found using the findCompounds function.

Usage

```
    getCompounds(conn,compoundIds,filename=NA, keepOrder = FALSE, allowMissing = FALSE)
```

Arguments

conn	A database connection object, such as is returned by initDb.
compoundIds	A vector of compound ids, as returned by loadSdf or findCompounds.
filename	If given, writes the compounds directly to the file named.
keepOrder	If true, the order of the output compound ids will be the same as the input names. This imposes a performance hit that can be significant for large datasets, thus it should be left FALSE unless needed.
allowMissing	When this is false an error will be raised when compound ids queried were not found in the database. If true, just those that are found will be returned with no error or warning.

Value

An SDFset with the requested compounds or nothing if filename was specified. A warning will be raised if not all compounds could be found.

Author(s)

Kevin Horan

See Also

[loadSdf](#) [findCompounds](#).

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test3.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample)

    #returns a SDFset with 3 compounds
    getCompounds(conn, ids[1:3])

unlink("test3.db")
```

---

getIds-deprecated   *Import Compounds from PubChem*

Description

Accepts one or more PubChem compound ids and downloads the corresponding compounds from PubChem Power User Gateway (PUG) returning results in an SDFset container. The ChemMine Tools web service is used as an intermediate, to translate queries from plain HTTP POST to a PUG SOAP query.

Usage

```
    getIds(cids)
```

Arguments

cids   A numeric object which contains one or more PubChem cids

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Tyler Backman

References

PubChem PUG SOAP: http://pubchem.ncbi.nlm.nih.gov/pug_soap/pug_soap_help.html

Chemmine web service: http://chemmine.ucr.edu

PubChem help: http://pubchem.ncbi.nlm.nih.gov/search/help_search.html

Examples

```
## Not run:
## fetch 2 compounds from PubChem
compounds <- getIds(c(111,123))
## End(Not run)
```

---

grepSDFset *String search in* SDFset

Description

Convenience grep function for string searching in SDFset containers.

Usage

```
grepSDFset(pattern, x, field = "datablock", mode = "subset", ignore.case = TRUE, ...)
```

Arguments

pattern	search pattern
x	SDFset
field	delimits search to specific section in SDF; can be header, atomblock, bondblock or datablock
mode	if mode = "index", then the match positions are returned as vector; if mode = "subset", a list with SDF components is returned where every entry has at least one query match
ignore.case	TRUE turns off case sensitivity
...	option to pass on additional arguments

Details

...

Value

numeric	index vector where the name field contains the component positions in the SDFset and the values the row positions in each sub-component.
list	if mode = "subset"

Author(s)

Thomas Girke

References

...

See Also

Class: `SDFset`

Examples

```
## Instances of SDFset class
data(sdfsample)
sdfset <- sdfsample

## String Searching in SDFset
q <- grepSDFset("65000", sdfset, field="datablock", mode="subset")
as(q, "SDFset")
grepSDFset("65000", sdfset, field="datablock", mode="index")
```

---

groups	*Enumeration of Functional Groups and Atom Neighbors*

Description

Returns frequency information of functional groups in molecules provided as SDF or `SDFset` objects. Alternatively, the function can return for each atom its atom/bond neighbor information.

Usage

```
groups(x, groups = "fctgroup", type = "countMA")
```

Arguments

x	SDF or `SDFset` containers
groups	if `groups="fctgroup"`, frequencies of functional groups are returned; if `groups="neighbors"`, atom/bond neighbor information is returned.
type	if `type="all"`, then the complete neighbor information is generated for each atom in a molecule; if `type="count"`, the neighbors are enumerated in a list and if `type="countMA"`, then the counts of atom neighbors or functional groups are returned in a frequency matrix.

Details

At this point this function is in an experimental stage.

Value

...

Author(s)

Thomas Girke

References

...

See Also

...

Examples

```
## Instances of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Enumerate functional groups
groups(sdfset[1:20], groups="fctgroup", type="countMA")

## Report atom/bond neighbors
groups(sdfset[1:4], groups="neighbors", type="countMA")
groups(sdfset[1:4], groups="neighbors", type="count")
groups(sdfset[1:4], groups="neighbors", type="all")
```

---

header *Return header block*

Description

Returns header block(s) from an object of class SDF or SDFset.

Usage

```
header(x)
```

Arguments

x   object of class `SDF` or `SDFset`

Details

...

Value

named `character` vector if SDF is provided or `list` of named `character` vectors if SDFset is provided

Author(s)

Thomas Girke

References

...

See Also

atomblock, atomcount, bondblock, datablock, cid, sdfid

Examples

```
## SDF/SDFset instances
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

## Extract header block
header(sdf)
header(sdfset[1:4])

## Replacement methods
sdfset[[1]][[1]][1] <- "test"
sdfset[[1]]
header(sdfset)[1] <- header(sdfset[2])
view(sdfset[1:2])
```

---

initDb   *Iinitialize SQL Database*

Description

This will ensure that the database connection given is ready for use. If it does not find the tables it needs, it will try to create them.

Usage

```
initDb(handle)
```

Arguments

handle   This can be either a filename, in which case we assume it is the name of an SQLite database and use RSQLite to connect to it, or else any DBI Connection.

Value

Returns a connection object that can be used with other database oriented functions.

Author(s)

Kevin Horan

See Also

RSQLite

Examples

```
#create and initialize a new SQLite database
conn = initDb("test.db")
```

---

jarvisPatrick   *Jarvis-Patrick Clustering*

Description

Function to perform Jarvis-Patrick clustering. The algorithm requires a nearest neighbor table, which consists of neighbors for each item in the dataset. This information is then used to join items into clusters with the following requirements: (a) they are contained in each other's neighbor list (b) they share at least 'k' nearest neighbors The nearest neighbor table can be computed with nearestNeighbors. For standard Jarvis-Patrick clustering, this function takes the number of neighbors to keep for each item. It also has the option of passing a cutoff similarity value instead of the number of neighbors. In this mode, all neighbors which meet the cutoff criteria will be included in the table. This is a setting that is not part of the original Jarvis-Patrick algorithm. It allows to generate tighter clusters and to minimize some limitations of this method, such as joining completely unrelated items when clustering small data sets. Other extensions, such as the linkage parameter, can also help improve the clustering quality.

Usage

```
jarvisPatrick(nnm,  k, mode="a1a2b", linkage="single")
```

Arguments

nnm   A nearest neighbor table, as produced by nearestNeighbors.

k   Minimum number of nearest neighbors two rows (items) in the nearest neighbor
                 table need to have in common to join them into the same cluster.

mode   If mode = "a1a2b" (default), the clustering is run with both requirements (a) and
                 (b); if mode = "a1b" then (a) is relaxed to a unidirectional requirement; and if
                 mode = "b" then only requirement (b) is used. The size of the clusters generated
                 by the different methods increases in this order: "a1a2b" < "a1b" < "b". The run
                 time of method "a1a2b" follows a close to linear relationship, while it is nearly
                 quadratic for the much more exhaustive method "b". Only methods "a1a2b" and
                 "a1b" are suitable for clustering very large data sets (e.g. >50,000 items) in a
                 reasonable amount of time.

linkage   Can be one of "single", "average", or "complete", for single linkage, average
                 linkage and complete linkage merge requirements, respectively. In the context
                 of Jarvis-Patrick, average linkage means that at least half of the pairs between
                 the clusters under consideration must pass the merge requirement. Similarly, for
                 complete linkage, all pairs must pass the merge requirement. Single linkage is
                 the normal case for Jarvis-Patrick and just means that at least one pair must meet
                 the requirement.

Details

...

Value

Depending on the setting under the type argument, the function returns the clustering result in a named vector or a nearest neighbor table as matrix.

Note

...

Author(s)

Thomas Girke

References

Jarvis RA, Patrick EA (1973) Clustering Using a Similarity Measure Based on Shared Near Neighbors. IEEE Transactions on Computers, C22, 1025-1034. URLs: http://davide.eynard.it/teaching/2012_PAMI/JP.pdf, http://www.btluke.com/jpclust.html, http://www.daylight.com/dayhtml/doc/cluster/index.pdf

See Also

Functions: cmp.cluster `trimNeighbors nearestNeighbors`

Examples

```
## Load/create sample APset and FPset
data(apset)
fpset <- desc2fp(apset)

## Standard Jarvis-Patrick clustering on APset/FPset objects
jarvisPatrick(nearestNeighbors(apset,numNbrs=6), k=5, mode="a1a2b")
jarvisPatrick(nearestNeighbors(fpset,numNbrs=6), k=5, mode="a1a2b")

## Jarvis-Patrick clustering only with requirement (b)
jarvisPatrick(nearestNeighbors(fpset,numNbrs=6), k=5, mode="b")

## Modified Jarvis-Patrick clustering with minimum similarity 'cutoff'
## value (here Tanimoto coefficient)
jarvisPatrick(nearestNeighbors(fpset,cutoff=0.6, method="Tanimoto"), k=2 )

## Output nearest neighbor table (matrix)
nnm <- nearestNeighbors(fpset,numNbrs=6)

## Perform clustering on precomputed nearest neighbor table
jarvisPatrick(nnm, k=5)
```

---

jarvisPatrick_c   *Jarvis Patrick Clustering in C code*

Description

This not meant to be used directly, use `jarvisPatrick` instead. It is exposed so other libraries can make use of it.

Usage

```
jarvisPatrick_c(neighbors,minNbrs,fast=TRUE,bothDirections=FALSE,linkage = "single")
```

Arguments

neighbors   A matrix of integers. Non integer matricies will be coerced. Each row represensts one element, indexed 1 to N. The values in row i should be the index value of the neighbors of i. Thus, each value should itself be a valid row index.

minNbrs   The minimum number of common neibhbors needed for two elements to be merged.

fast   If true, only the neibhors given in each row are checked to see if they share minNbrs neighbors in common. If false, all pairs of elements are compared. For a matrix of size NxM, the first method yeilds a running time of O(NM), while the second yeilds a running time of O(N^2).

bothDirections If true, two elements must contain each other in their neighbor list in order to be merged. If false and fast is true, then only one element must contain the other as a neighbor. If false and fast is false, than neither element must contain the other as a neighbor, though in all cases there must still be at least minNbrs neibhros in common.

linkage   See jarvisPatrick for details.

Value

A cluster array with no names.

Author(s)

Kevin Horan

---

jobToken-class   *Class* "jobToken"

Description

Container for storing a reference to a remote job ran on the ChemMine Tools web server.

Objects from the Class

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

Slots

tool_name: Object of class "character"

jobId: Object of class "character"

Methods

show signature(object = "jobToken"): check the status of a launched job

Author(s)

Tyler William H Backman

References

See ChemMine Tools at <http://chemmine.ucr.edu>.

See Also

Functions: launchCMTool, toolDetails, listCMTools, result, browseJob, status

Examples

```
showClass("jobToken")
## Not run:
## launch a job on the server and obtain jobToken back
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check status of the job
status(job1)

## obtain results
result1 <- result(job1)
result1

## End(Not run)
```

---

largestComponent   *Largest Component*

Description

If a single compound in an SDF file contains more than one disconnected component, this function will return an SDF with only the largest component, removing all other components. This will be applied to each SDF in the given SDFset.

Usage

```
largestComponent(sdfSet)
```

Arguments

sdfSet   any SDFset object.

Value

a new SDFset containing only single component compounds.

Author(s)

Kevin Horan

Examples

```
## Not run:
sdf = smiles2sdf(c("Cl.CCC1C2CC3C4C5(CC(C2C5O)N3C1O)C6=CC=CC=C6N4C TEST"))
lg = largestComponent(sdf)

## End(Not run)
```

---

launchCMTool   *Launch a Tool on ChemMine Tools*

Description

Accepts a tool name (string), input options, and input data to launch a remote web tool on the ChemMine Tools website.

Usage

```
launchCMTool(tool_name, input = "", ...)
```

Arguments

tool_name	A tool name matching verbatim an existing tool name as listed by listCMTools.
input	Input data in the format required for this tool as listed by listCMTools.
...	Additional options as mentioned by running toolDetails on the tool specified.

Details

By running the function toolDetails on a tool of choice, you can see a pre-generated example function call for this tool.

Value

jobToken	for details see ?"jobToken-class"

Author(s)

Tyler William H Backman

References

See ChemMine Tools at <http://chemmine.ucr.edu>.

See Also

Functions: toolDetails, listCMTools, result, browseJob, status

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")

## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
status(job1)
result1 <- result(job1)

## End(Not run)
```

---

listCMTools   *List all available ChemMine Tools*

Description

Connects to the ChemMine Tools web service and obtains a list of all available tools, and their input and output formats.

Usage

```
listCMTools()
```

Value

data.frame   A four column data.frame which describes a tool on each row

Author(s)

Tyler William H Backman

References

See ChemMine Tools at <http://chemmine.ucr.edu>.

See Also

Functions: toolDetails, launchCMTool, result, browseJob, status

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")
```

```
## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
status(job1)
result1 <- result(job1)

## End(Not run)
```

---

listFeatures   *List Features*

Description

List the available features in the given database. These features can be used in the [findCompounds](#)
function.

Usage

```
listFeatures(conn)
```

Arguments

conn   Database connection

Value

A vector of character feature names.

Author(s)

Kevin Horan

See Also

[findCompounds](#)

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test7.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample,fct=function(sdfset) cbind(mw=MW(sdfset)))
listFeatures(conn) # produces c("mw")
unlink("test7.db")
```

loadSdf	*Load SDF and SMILES Data*

Description

Load an SDF or SMILES formatted file or SDFSet objects into the database. This will also load arbitrary features from the data as well as descriptor data. The `fct` parameter can be used to specify a function which will compute features which will then be indexed and stored in the database. These features can later be used to quickly search for compounds. Descriptors can also be computed and stored in another table.

Usage

```
loadSdf(conn, sdfFile, fct = function(x) data.frame(), descriptors=function(x) data.frame(descript
Nlines = 50000, startline = 1, restartNlines = 1e+05,updateByName=FALSE)
loadSmiles(conn, smileFile, ...)
```

Arguments

conn	A database connection object, such as is returned by [initDb]().
sdfFile	Either the filename of an SDF formated file, or and SDFSet object.
smileFile	The filename of an SMILES formated file.
...	When calling loadSmiles, any of the arguments for loadSdf can be used and will be passed to loadSdf internally.
fct	A function to extract features from the data. It will be handed an SDFSet generated from the data being loaded. This may be done in batches, so there is no guarantee that the given SDFSset will contain the whole dataset. This function should return a data frame with a column for each feature and a row for each compound given, and in the same order. Each of these features will become a new, indexed, table in the database which can be used later to search for compounds. The column name will become the feature name. If not given, no features are computed.
descriptors	This function will also be given an SDFSet object, which may be done in batches. It should return a data frame with the following two columns: "descriptor" and "descriptor_type". The "descriptor" column should contain a string representation of the descriptor, and "descriptor_type" is the type of the descriptor. Our convention for atom pair is "ap" and "fp" for finger print. The order should be maintained. If not given no descriptors are computed.
Nlines	When reading data from a file, the number of lines to read at a time. See also [sdfStream]().
startline	When reading data from a file, the line number to start reading from.See also [sdfStream]()
restartNlines	When reading data from a file and startline > 1, the number of lines to look forward to find the start of the next compound. See also [sdfStream]()
updateByName	If true we make the assumption that all compounds, both in the existing database and the given dataset, have unique names. This function will then avoid re-adding existing, identical compounds, and will update existing compounds with a new definition if a new compound definition with an existing name is given.

If false, we allow duplicate compound names to exist in the database, though not
duplicate definitions. So identical compounds will not be re-added, but if a new
version of an existing compound is added it will not update the existing one, it
will add the modified one as a completely new compound with a new compound
id.

Details

Arguments to loadSmiles are the same as those to loadSdf. LoadSmiles will convert its input into
an SDFSet and then call loadSdf.

New features can also be added using this function. However, all compounds must have all features
so if new features are added to a new set of compounds, all existing features must be computable
by the `fct` function given. If new features are detected, all existing compounds will be run through
`fct` in order to compute the new features for them as well.

For example, if dataset X is loaded with features F1 and F2, and then at a later time we load dataset
Y with new feature F3, the `fct` function used to load dataset Y must compute and return features
F1, F2, and F3. `loadSdf` will call `fct` with both datasets X and Y so that all features are available
for all compounds. If any features are missing an error will be raised.

If just new features are being added, but no new compounds, use the [addNewFeatures](#) function.

Value

Returns the compound id numbers of each compound loaded. These can be used to retrieve com-
pounds later. These are id numbers computed by the database and are not extracted from the com-
pound data itself.

Author(s)

Kevin Horan

See Also

[sdfStream](#)

Examples

```
    #create and initialize a new SQLite database
    conn = initDb("test6.db")

data(sdfsample)

#just load the data with no features or descriptors
ids=loadSdf(conn,sdfsample)
unlink("test6.db")

    conn = initDb("test5.db")
#load data and compute 3 features: molecular weight, with the MW function,
# and counts for RINGS and AROMATIC, as computed by rings, which returns a data frame itself.
ids=loadSdf(conn,sdfsample,
  function(sdfset)
data.frame(MW = MW(sdfset),  rings(sdfset,type="count",upper=6, arom=TRUE))
 )
unlink("test5.db")
```

makeUnique	*Uniquify CMP names*

Description

Creates unique CMP names by appending a counter to each duplicatation set. The function can be used for any character vector.

Usage

```
makeUnique(x, silent = FALSE)
```

Arguments

x	character vector
silent	`silent = TRUE` suppresses message about duplicate count

Details

The function is important to maintain unique compound names in the ID slot of `SDFset` containers.

Value

character	of same length as x but without duplications

Author(s)

Thomas Girke

References

...

See Also

Functions: `cid`, `sdfid`

Examples

```
## SDFset instance
data(sdfsample)
sdfset <- sdfsample

## Create unique compound IDs
unique_ids <- makeUnique(sdfid(sdfset))
cid(sdfset) <- unique_ids
cid(sdfset[1:4])
```

maximallyDissimilar   *Maximally Dissimilar*

Description

Find a set of compounds that are far away from each other.

Usage

```
maximallyDissimilar(compounds, n, similarity = cmp.similarity)
```

Arguments

compounds   The set of items from which to pick n dissimlar items. This can be a list of anything that the similarity function will accept. By default this will be an APset.

n   The number of dissimilar items to return.

similarity   The similarity function to use. By default Tanimoto will be used on APset objects. Internally, this will be converted to a distance function using `1-similarity(a,b)`, so whatever similarity function you use should return a value between 0 and 1.

Details

This will run in O(length(compounds)n) time. Based on the algorithm described in (Higgs,1997).

Value

A vector of indexes of the dissimilar items.

Author(s)

Kevin Horan

References

Higgs, R.E., Bemis, K.G., Watson, I.A., and Wikel, J.H. 1997. Experimental designs for selecting molecules from large chemical databases. J. Chem. Inf. Comput. Sci. 37, 861-870

Examples

```
data(apset)
maximallyDissimilar(apset,10)
```

nearestNeighbors   *Nearest Neighbors*

Description

Computes the nearest neighbors of descriptors in an FPset or APset object for use with the `jarvisPatrick` clustering function. Only one of numNbrs or cutoff should be given, `cutoff` will take precedence if both are given. If numNbrs is given, then that many neighbors will be returned for each item in the set. If `cutoff` is given, then, for each item X, every neighbor that has a similarity value greater than or equal to the cutoff will be returned in the neighbor list for X.

Usage

```
nearestNeighbors(x, numNbrs = NULL, cutoff = NULL, ...)
```

Arguments

x	Either an FPset or an APset.
numNbrs	Number of neighbors to find for each item. If not enough neighbors can be found the matrix will be padded with NA.
cutoff	The minimum similarity value an item must have to another item in order to be included in that items neighbor list. This parameter takes precedence over numNbrs. This parameter allows to obtain tighter clustering results.
...	These parameters will be passed into the distance function used, either `cmp.similarity` or `fpSim`, for APset and FPset, respectively.

Value

The return value is a list with the following components:

indexes	index values of nearest neighbors, for each item. If `cutoff` is used, this will be a list of lists, otherwise it will be a matrix
names	The names of each item in the set, as returned by cid
similarities	The similarity values of each neighbor to the item for that row. This will also be either a list of lists or a matrix, depending on whether or not `cutoff` was used. Each similarity values corresponds to the id number in the same position in the indexes entry

Author(s)

Kevin Horan

See Also

jarvisPatrick trimNeighbors

Examples

```
data(sdfsample)
ap = sdf2ap(sdfsample)
nnm = nearestNeighbors(ap,cutoff=0.5)
clustering = jarvisPatrick(nnm,k=2,mode="a1b")
```

---

numBits   *numBits*

Description

Returns the number of bits in a fingerprint.

Usage

```
numBits(x)
```

Arguments

x   Either an `FP` or an `FPset` object.

Value

The number of bits in this fingerprint object.

Author(s)

Kevin Horan

Examples

```
fp = new("FP",fp=c(1,0,1,1, 0,0,1,0))
n = numBits(fp) # == 8
```

---

obmol   *obmol*

Description

Return reference to an OBMol from OpenBabel, if available. Operates on SDF or SDFset objects.

Usage

```
obmol(x)
```

Arguments

x   object of class `SDF` or `SDFset`

Value

A pointer to an OBMol object, or a vector of pointers for an `SDFset`.

Author(s)

Kevin Horan

See Also

header, atomcount, bondblock, datablock, cid, sdfid

Examples

```
## SDF/SDFset instances
if(require(ChemmineOB)){
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

obmolRef = obmol(sdf)
}
```

---

openBabelPlot   *Plot compound structures*

Description

Plots compound structure(s) for molecules stored in SDF and SDFset containers.

Usage

```
openBabelPlot(sdfset, height=600, noHbonds = TRUE, regenCoords=FALSE)
```

Arguments

sdfset	Object of class SDFset
height	The height of the image in pixels. The generated image is always square, so this will also be the width.
noHbonds	If TRUE, then the C-hydrogens and their bonds - explicitly defined in an SDF - are excluded from the plot.
regenCoords	If ChemmineOB is installed and this option is TRUE, then Open Babel will be used to re-generate the 2D coords for each compound before plotting it. This often results in a nicer layout. If you want to save the results of the coord regeneration, call the regenerateCoords function first yourself and save the result.

Details

The function openBablePlot depicts a 2D compound structure based on the XY-coordinates specified in the atom block of an SDF. If more than one compound is given in the SDFset, they will be arranged in a grid layout.

Author(s)

Kevin Horan

See Also

sdf.visualize

Examples

```
## Not run:
## Import SDFset sample set
data(sdfsample)
(sdfset <- sdfsample)

## Plot single compound structure
openBabelPlot(sdfset[1])

## Plot several compounds structures
openBabelPlot(sdfset[1:4])

## End(Not run)
```

---

parBatchByIndex   *Parallel Batch By Index*

Description

Takes an index set, breaks it into batches and runs the given function on each batch in parallel using the given cluster. See batchByIndex for the non-parallel version.

When doing a select were the condition is a large number of ids it is not always possible to include them in a single SQL statement. This function will break the list of ids into chunks and allow the indexProcessor to deal with just a small number of ids.

Usage

```
parBatchByIndex(allIndices, indexProcessor, reduce, cl, batchSize = 1e+05)
```

Arguments

allIndices   A vector of values that will be broken into batches and passed as an argument to the indexProcessor function.

indexProcessor A function that takes one batch if indices. It is called once for each batch, possibly in parallel. The return value of this function is collected into a list and passed to the reduce function after all jobs have finished.

reduce   This function is run after all jobs have finished. It is called with a list of return values from the indexProcessor function runs. The order of batchs is maintained. The return value of the reduce function is then returned.

                The idea is that this function merges all the results together into one result.

cl   A SNOW cluster to run jobs on.

batchSize   The size of each batch. The last batch may be smaller than this value.

Value

The return value of the reduce function is returned.

Author(s)

Kevin Horan

See Also

[batchByIndex](#)

Examples

```
## Not run:

cl = makeCluster(2) # create a SNOW cluster

#function to run a query for each batch of indexes
job = function(indexBatch)
dbGetQuery(dbConnection, paste("SELECT weight FROM table WHERE id IN (",paste(indexBatch,collapse=","),")"))

# function to combine all the results, in this case by summing them up
reduce = function(results) sum(unlist(results))

indices = 1:10000

#run queries in parallel and then sum the results
totalWeight = parBatchByIndex(indices,job,reduce,cl, 1000)


## End(Not run)
```

---

plotStruc   *Plot compound structures*

Description

Plots compound structure(s) for molecules stored in SDF and SDFset containers.

Usage

```
## Convenience plot method
# plot(x, griddim, print_cid=cid(x), print=TRUE, ...)

## Less important for user
plotStruc(sdf, atomcex = 1.2, atomnum = FALSE, no_print_atoms = c("C"),
          noHbonds = TRUE, bondspacer = 0.12, colbonds=NULL, bondcol="red",
 regenCoords=FALSE, ...)
```

Arguments

sdf	Object of class SDF
atomcex	Font size for atom labels
atomnum	If TRUE, then the atom numbers are included in the plot. They are the position numbers of each atom in the atom block of an SDF.
no_print_atoms	Excludes specified atoms from being plotted.
noHbonds	If TRUE, then the C-hydrogens and their bonds - explicitly defined in an SDF - are excluded from the plot.
bondspacer	Numeric value specifying the plotting distance for double/triple bonds.

colbonds   Highlighting of subgraphs in main structure by providing a numeric vector of
                  atom numbers, here position index in atom block. The bonds of connected atoms
                  will be plotted in the color provided under bondcol.

bondcol   A character or numeric vector of length one to specify the color to use for sub-
                  structure highlighting under colbonds.

regenCoords   If ChemmineOB is installed and this option is TRUE, then Open Babel will be
                  used to re-generate the 2D coords for each compound before plotting it. This
                  often results in a nicer layout. If you want to save the results of the coord re-
                  generation, call the regenerateCoords function first yourself and save the re-
                  sult.

...   Arguments to be passed to/from other methods.

Details

The function plotStruc depicts a single 2D compound structure based on the XY-coordinates
specified in the atom block of an SDF. The generic method plot can be used as a convenient
shorthand to plot one or many structures at once. Both functions depend on the availability of the
XY-coordinates in the source SD file and only 2D (not 3D) representations are plotted correctly.

Additional arguments that can only be passed on to the plot function when supplied with an SDFset
object:

griddim: numeric vector of length two to define the dimensions for arranging several structures in
one plot.

print_cid: character vector for printing custom compound labels. Default is print_cid=cid(sdfset).

print: if print=TRUE, then a summary of the SDF content for each supplied compound is printed
to the screen. This behavior is turned off with print=TRUE.

Value

Prints summary of SDF/SDFset to screen and plots their structures to graphics device.

Note

The compound depictions created by this function are not as pretty as the structure representations
generated with the sdf.visualize function. This will be improved in the future.

Author(s)

Thomas Girke

References

...

See Also

sdf.visualize

Examples

```
## Import SDFset sample set
data(sdfsample)
(sdfset <- sdfsample)

## Plot single compound structure
plotStruc(sdfset[[1]])

## Plot several compounds structures
plot(sdfset[1:4])

## Highlighting substructures (here all rings)
myrings <- as.numeric(gsub(".*_", "", unique(unlist(rings(sdfset[1])))))
plot(sdfset[1], colbonds=myrings)

## Customize plot
plot(sdfset[1:4], griddim=c(2,2), print_cid=letters[1:4], print=FALSE, noHbonds=FALSE)
```

---

propOB   *Properties from OpenBabel*

Description

Generates the following descriptors: "cansmi", "cansmiNS", "formula", "HBA1", "HBA2", "HBD", "InChI", "InChIKey", "logP", "MR", "MW", "nF","title", "TPSA".

Usage

```
propOB(sdfSet)
```

Arguments

sdfSet   An SDFset object.

Value

A data frame with a row for each compound in the given data frame and a named column for each property.

Author(s)

Kevin Horan

Examples

```
## Not run:
library(ChemmineR)
data(sdfsample)
propOB(sdfsample)

## End(Not run)
```

---

pubchemCidToSDF   *Import Compounds from PubChem*

Description

Accepts one or more PubChem compound ids and downloads the corresponding compounds from PubChem Power User Gateway (PUG) returning results in an `SDFset` container.

Usage

```
pubchemCidToSDF(cids)
```

Arguments

cids   A `numeric` object which contains one or more PubChem cids

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Kevin Horan

References

PubChem PUG REST: https://pubchem.ncbi.nlm.nih.gov/pug_rest/PUG_REST_Tutorial.html

Examples

```
## Not run:
## fetch 2 compounds from PubChem
compounds <- pubchemCidToSDF(c(111,123))
## End(Not run)
```

---

pubchemFPencoding   *Enncoding of PubChem Fingerprints*

Description

Data frame with bit positions and substructure specifications.

Usage

```
data(pubchemFPencoding)
```

Format

The format is a data frame with 881 rows and 2 columns.

Source

From: ftp://ftp.ncbi.nih.gov/pubchem/specifications/pubchem_fingerprints.txt

References

See: ftp://ftp.ncbi.nih.gov/pubchem/specifications/pubchem_fingerprints.txt

Examples

```
data(pubchemFPencoding)
pubchemFPencoding[1:4,]
```

---

pubchemName2CID   *Translate compound name to pubchem compound id*

Description

Takes any compound name and queries pubchem to find its pubchem id (CID).

Usage

```
pubchemName2CID(name)
```

Arguments

name   Any compound name, used to query pubchem to find the compound.

Value

The result is the pubchem compound id. If the name is not found, NA will be returned.

Author(s)

Kevin Horan

References

PubChem PUG REST: https://pubchem.ncbi.nlm.nih.gov/pug_rest/PUG_REST_Tutorial.html

Examples

```
## Not run:
## fetch 2 compounds from PubChem
cid <- pubchemName2CID("CHEMBL460363")

## End(Not run)
```

---

pubchemSDFSearch   *PubChem Similarity (Fingerprint) Search*

Description

Accepts one `SDFset` container and performs a similarity PubChem fingerprint search, returning hits in an `SDFset` container. If the input object contains multiple items, only the first is used as a query.

Usage

```
pubchemSDFSearch(sdf)
```

Arguments

sdf   A `SDFset` object which contains one compound

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Kevin Horan

References

PubChem PUG REST: https://pubchem.ncbi.nlm.nih.gov/pug_rest/PUG_REST_Tutorial.html

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## get a sample compound
data(sdfsample); sdfset <- sdfsample[2]
## search a compound on PubChem
compounds <- pubchemSDFSearch(sdfset)
## End(Not run)
```

---

pubchemSmilesSearch   *PubChem Similarity (Fingerprint) SMILES Search*

Description

Accepts one SMILE string or `SMIset` container and performs a PubChem fingerprint search, returning hits in an `SDFset` container. If the input object contains multiple items, only the first is used as a query.

Usage

```
pubchemSmilesSearch(smiles)
```

Arguments

smiles	A SMIset object which contains one compound, or a SMILES string

Value

SDFset	for details see ?"SDFset-class"

Author(s)

Kevin Horan

References

PubChem PUG REST: https://pubchem.ncbi.nlm.nih.gov/pug_rest/PUG_REST_Tutorial.html

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## get a sample compound
data(sdfsample); sdfset <- sdfsample[2]
## search a compound on PubChem
compounds <- pubchemSmilesSearch(sdfset)
## End(Not run)
```

---

read.AP   *Read Atom Pair/Fingerprint Strings*

Description

Function to convert atom pairs (AP) or fingerprints (e.g. AP fingerprints) stored as character strings to APset or FPset objects (e.g. generated by sdfStream). Alternatively, one can provide the AP or fingerprint strings in a named character vector.

Usage

```
read.AP(x, type, colid, isFile = class(x) == "character" & length(x) == 1)
```

Arguments

x	name of file from where to read the AP/APFP character strings; or named character vector containing the AP/APFP strings
type	type="ap" for AP character string input, and type="fp" for fingerprint character string input
colid	column containing AP/FP character strings if x is a file
isFile	Is x a file name or not?

Details

...

Value

object of class APset or FPset

Author(s)

Thomas Girke

References

...

See Also

sdf2ap, sdfStream

Examples

```
## Load sample data
library(ChemmineR)
data(sdfsample); sdfset <- sdfsample
## Not run: write.SDF(sdfset, "test.sdf")

## Define descriptor set in a simple function
desc <- function(sdfset) {
        cbind(SDFID=sdfid(sdfset),
              # datablock2ma(datablocklist=datablock(sdfset)),
              MW=MW(sdfset),
              groups(sdfset),
              APFP=desc2fp(x=sdf2ap(sdfset), descnames=1024, type="character"),
              AP=sdf2ap(sdfset, type="character"),
              rings(sdfset, type="count", upper=6, arom=TRUE)
        )
}

## Run sdfStream with desc function and write results to a file called 'matrix.xls'
sdfStream(input="test.sdf", output="matrix.xls", fct=desc, Nlines=1000)

## Select molecules from SD File using line index from sdfStream
indexDF <- read.delim("matrix.xls", row.names=1)[,1:4]
indexDFsub <- indexDF[indexDF$MW < 400, ] # Selects molecules with MW < 400
sdfset <- read.SDFindex(file="test.sdf", index=indexDFsub, type="SDFset")

## Write result directly to SD file without storing larger numbers of molecules in memory
read.SDFindex(file="test.sdf", index=indexDFsub, type="file", outfile="sub.sdf")

## Read AP/APFP strings from file into APset or FP object
apset <- read.AP(x="matrix.xls", type="ap", colid="AP")
apfp <- read.AP(x="matrix.xls", type="apfp", colid="APFP")

## Alternatively, one can provide the AP/APFP strings in a named character vector
apset <- read.AP(x=sdf2ap(sdfset[1:20], type="character"), type="ap")
apfp <- read.AP(x=desc2fp(x=sdf2ap(sdfset[1:20]), descnames=1024, type="character"), type="apfp")

## End(Not run)
```

read.SDFindex   *Extract Molecules from SD File by Line Index*

Description

Extracts specific molecules from SD File based on a line position index computed by the `sdfStream` function.

Usage

```
read.SDFindex(file, index, type = "SDFset", outfile)
```

Arguments

file	file name of source SD file used to generate `index`
index	data frame containing in the first two columns the start and end positions (index) of molecules in an SD File, respectively. Typically, this index would be imported with `read.table/read.delim` from a tabular descriptor file generated by the `sdfStream` function.
type	if `type="file"`, the SDF output will be written to a file named as specified under `outfile`; if `type="SDFset"`, the SDF data is collected will be a `SDFset` container.
outfile	name of output file when `type="file"`

Details

...

Value

Writes molecules in SDF format to file or collects them in `SDFset` container.

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Import/export functions: `read.SDFset`, `read.SDFstr`, `read.SDFstr`, `read.SDFset`, `write.SDFsplit`

Examples

```
## Load sample data
library(ChemmineR)
data(sdfsample); sdfset <- sdfsample
## Not run: write.SDF(sdfset, "test.sdf")

## Define descriptor set in a simple function
desc <- function(sdfset) {
        cbind(SDFID=sdfid(sdfset),
              # datablock2ma(datablocklist=datablock(sdfset)),
              MW=MW(sdfset),
              groups(sdfset),
              # AP=sdf2ap(sdfset, type="character"),
              rings(sdfset, type="count", upper=6, arom=TRUE)
        )
}

## Run sdfStream with desc function and write results to a file called 'matrix.xls'
sdfStream(input="test.sdf", output="matrix.xls", fct=desc, Nlines=1000)

## Select molecules from SD File using line index from sdfStream
indexDF <- read.delim("matrix.xls", row.names=1)[,1:4]
indexDFsub <- indexDF[indexDF$MW < 400, ] # Selects molecules with MW < 400
sdfset <- read.SDFindex(file="test.sdf", index=indexDFsub, type="SDFset")

## Write result directly to SD file without storing larger numbers of molecules in memory
read.SDFindex(file="test.sdf", index=indexDFsub, type="file", outfile="sub.sdf")

## End(Not run)
```

---

read.SDFset	*SD file to* SDFset

Description

Imports one or many molecules from an SD/MOL file and stores it in an SDFset container. Supports both the V2000 and V3000 formats.

Usage

```
read.SDFset(sdfstr = sdfstr,skipErrors=FALSE, ...)
```

Arguments

sdfstr	path/name to an SD file; alternatively an SDFstr object can be provided
skipErrors	If true, molecules which fail to parse will be removed from the output. Otherwise and error will be thrown and processing of the input will stop.
...	option to pass on additional arguments. Possible arguments are:
	datablock: true or false, whether to include the data fields or not. Defaults to TRUE.
	tail2vec: true or false, whether to return data feilds as a vector or not. Defaults to TRUE.
	extendedAttributes: true or false, whether to parse the extended attributes available on the V3000 format. Defaults to FALSE.

Details

...

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Thomas Girke

References

SDF format defintion: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: `read.SDFstr`

Examples

```
## Write instance of SDFset class to SD file
data(sdfsample); sdfset <- sdfsample
# write.SDF(sdfset[1:4], file="sub.sdf")

## Import SD file
# read.SDFset("sub.sdf")

## Pass on SDFstr object
sdfstr <- as(sdfset, "SDFstr")
read.SDFset(sdfstr)
```

---

read.SDFstr   *SD file to* SDFstr

Description

Imports one or many molecules from an SD/MOL file and stores it in an `SDFstr` container.

Usage

```
read.SDFstr(sdfstr)
```

Arguments

sdfstr   path/name to an SD file; alternatively one can pass on a `character` vector containing lines of an SD file

Details

...

Value

SDFstr   for details see ?"SDFstr-class"

Author(s)

Thomas Girke

References

SDF format defintion: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: `read.SDFset`

Examples

```
## Write instance of SDFstr class to SD file
data(sdfsample); sdfset <- sdfsample
sdfstr <- as(sdfset, "SDFstr")
# write.SDF(sdfset[1:4], file="sub.sdf")

## Import SD file
# read.SDFstr("sub.sdf")

## Pass on SDFstr object
sdfstr <- as(sdfset, "SDFstr")
read.SDFset(sdfstr)
```

---

read.SMIset   *SMILES file to* SMIset

Description

Imports one or many molecules from a SMILES file and stores content in a `SMIset` container. The input file is expected to contain one SMILES string per row with tab-separated compound identifiers at the end of each line. The compound identifiers are optional.

Usage

```
read.SMIset(file, removespaces = TRUE, ...)
```

Arguments

file   path/name to a SMILES file

removespaces if set to TRUE spaces will be removed

...   option to pass on additional arguments

Details

...

Value

SMIset   for details see ?"SMIset-class"

Author(s)

Thomas Girke

References

SMILES (Simplified molecular-input line-entry system) format definition: http://en.wikipedia.org/wiki/Simplified_mole
input_line-entry_system

See Also

Functions: read.SDFset

Examples

```
## Write instance of SMIset class to SMILES file
data(smisample); smiset <- smisample
# write.SMI(smiset[1:4], file="sub.smi")

## Import SMILES file
# read.SMIset("sub.smi")
```

---

regenerateCoords   *Re-generate 2D Coordinates*

Description

This uses Open Babel (requires ChemmineOB package) to re-generate the 2D coordinates of compounds. This often results in a nicer layout of the compound when plotting.

Usage

```
regenerateCoords(sdf)
```

Arguments

sdf   A SDF or SDFset object whose coordinates will be re-generated.

Value

Either an SDF object if given an SDF, or else and SDFset.

Author(s)

Kevin Horan

See Also

[plotStruc](#)

Examples

```
## Not run:
data(sdfsample)
prettySdfset = regenerateCoords(sdfsample[1:4])

## End(Not run)
```

---

result   *Obtain the resulting output data from a ChemMine Tools Job*

Description

Accepts a jobToken job as returned by the function launchCMTool and returns the final result. If the job is still running, the function will loop until the job is ready.

Usage

```
result(object)
```

Arguments

object   A jobToken job as returned by the function launchCMTool

Value

Output will be in the format specified for this tool, as listed with the listCMTools function.

Author(s)

Tyler William H Backman

References

See ChemMine Tools at http://chemmine.ucr.edu.

See Also

Functions: toolDetails, listCMTools, launchCMTool, browseJob, status

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")

## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
```

```
status(job1)
result1 <- result(job1)

## End(Not run)
```

---

rings   *Ring and Aromaticity Perception*

Description

Identifies all possible rings in molecules using the exhaustive ring perception algorithm from Hanser et al (1996). In addition, the function can return all smallest possible rings as well as aromaticity information for each ring.

Note that large molecules can cause this function to run for an extremely long amount of time. Use the upper parameter to limit the ring size if run time is a problem.

Usage

```
rings(x, upper = Inf, type = "all", arom = FALSE, inner = FALSE)
```

Arguments

x	SDF or SDFset containers
upper	allows to specify an upper length limit for ring predictions. The default setting upper=Inf will return all possible rings. Smaller length limits will reduce the search space resulting in shortened compute times.
type	if type="all", the function returns each ring of a compound as character vector of atom symbols that are numbered by their position in the atom block of an SDF/SDFset object. Note: the example below shows how to plot structures with the same numbering information for visual inspection. If type="arom", only aromatic rings are returned, while type="count" returns the ring and/or aromaticity counts for each compound in a matrix.
arom	if arom="TRUE", ring aromaticity information will be computed. If type="all", the output is a logical vector where 'TRUE' values indicate aromatic rings in the associated ring list. If type="arom", then the function returns only aromatic rings. A ring is considered aromatic if it meets the following requirements: (i) all atoms in the ring need to be sp2 hybridized. This means each atom has to have a double bond or at least one lone electron pair and it needs to be attached to an sp2 hybridized atom. (ii) In addition, Hueckel's rule '4n + 2' needs to be true, where 'n' is either zero or any positive integer. Note that setting arom="TRUE" will also set uppper=Inf.
inner	if inner="TRUE", only inner (smallest possible) rings will be returned. They are identified by first computing all possible rings and then selecting only the inner rings. Note: this requires the setting upper=Inf. If only rings below a certain size limit (e.g. 6) are of interest, then it will be more time efficient to set this limmit under the upper argument than identifying all smallest rings.

Details

...

Value

The settings `type="all"` and `type="arom"` return `lists`, and `type="count"` returns a `matrix`.

Author(s)

Thomas Girke

References

Hanser, Jauffret and Kaufmann (1996) A New Algorithm for Exhaustive Ring Perception in a Molecular Graph. Journal of Chemical Information and Computer Sciences, 36: 1146-1152. URL: http://pubs.acs.org/doi/abs/10.1021/ci960322f

See Also

...

Examples

```
## Instances of SDFset class
data(sdfsample)
sdfset <- sdfsample

## Return all possible rings for a single compound
rings(sdfset[1], upper=Inf, type="all", arom=FALSE, inner=FALSE)
plot(sdfset[1], print=FALSE, atomnum=TRUE, no_print_atoms="H")

## Return all possible rings for several compounds plus their
## aromaticity information
rings(sdfset[1:4], upper=Inf, type="all", arom=TRUE, inner=FALSE)

## Return rings with no more than 6 atoms
rings(sdfset[1:4], upper=6, type="all", arom=TRUE, inner=FALSE)

## Return rings with no more than 6 atoms that are also armomatic
rings(sdfset[1:4], upper=6, type="arom", arom=TRUE, inner=FALSE)

## Return shortest possible rings (no complex rings)
rings(sdfset[1:4], upper=Inf, type="all", arom=TRUE, inner=TRUE)

## Count shortest possible rings
rings(sdfset[1:4], upper=Inf, type="count", arom=TRUE, inner=TRUE)
```

SDF-class　　　　　　　　　　*Class "SDF"*

Description

Container for storing every element of a single molecule defined in an SD/MOL file without information loss in a list-like container. The import occurs via the `SDFstr` container class. The header block is stored as named character vector, the atom/bond blocks as matrices and the data block as named character vector.

Objects from the Class

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

Slots

header: Object of class "character"

atomblock: Object of class "matrix"

bondblock: Object of class "matrix"

datablock: Object of class "character"

obmolRef: Object of class "ExternalReferenceOrNULL"

version: Object of class "character"

Methods

[signature(x = "SDF"): subsetting of class with bracket operator

[[signature(x = "SDF"): returns one of the four object components

[[<- signature(x = "SDF"): replacement method for the four sub-components

[<- signature(x = "SDF"): replacement method for the four sub-components

atomblock signature(x = "SDF"): returns atom block as matrix

atomcount signature(x = "SDF"): returns atom frequency

bondblock signature(x = "SDF"): returns bond block as matrix

obmol signature(x = "SDF"): returns an OBMol pointer

coerce signature(from = "character",to = "SDF"): as(character,"SDF")

coerce signature(from = "list",to = "SDF"): as(list,"SDF")

coerce signature(from = "SDF",to = "character"): as(sdf,"character")

coerce signature(from = "SDF",to = "list"): as(sdf,"list")

coerce signature(from = "SDF",to = "SDFset"): as(sdf,"SDFset")

coerce signature(from = "SDF",to = "SDFstr"): as(SDF,"SDFstr")

coerce signature(from = "SDFset",to = "SDF"): as(sdfset,"SDF")

datablock signature(x = "SDF"): returns data block as named character vector

datablocktag signature(x = "SDF"): returns data block as named character vector with subsetting support

header signature(x = "SDF"): returns header block as named character vector

plot signature(x = "SDF"): plots molecule structure for SDF object

sdf2list signature(x = "SDF"): returns SDF object as list

sdf2str signature(sdf = "SDF"): returns SDF object as character vector

sdfid signature(x = "SDF"): returns molecule ID field from header block

show signature(object = "SDF"): prints summary of SDF

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Related classes: SDFset, SDFstr, AP, APset

Examples

```
showClass("SDF")

## Instances of SDF class
data(sdfsample); sdfset <- sdfsample
(sdf <- sdfset[[1]]) # returns first molecule in sdfset as SDF object

## Accessing SDF components
header(sdf); atomblock(sdf); bondblock(sdf); datablock(sdf)
sdfid(sdf)

## Plot molecule structure of SDF
plot(sdf) # plots to R graphics device
# sdf.visualize(sdf) # viewing in browser
```

---

sdf.subset   *Subset a SDF and return SDF segements for selected compounds*

Description

'sdf.subset' will take a descriptor database generated by 'cmp.parse' and an array of indices, and return an SDF string consisting of SDFs for compounds corresponding to that list of indices. The returned value is a character string.

Usage

```
sdf.subset(db, cmps)
```

Arguments

db	The database generated by 'cmp.parse'
cmps	An array of indecies that correspond to a set of selected compounds from the database

Details

'sdf.subset' depends on information embedded in the descriptor database returned by 'cmp.parse'. It also relies on the availability of the original SDF where the database has been generated from. Basically, when 'cmp.parse' parses the original SDF file, it will store the path of that SDF file as well as offset information for SDF segment in that file. Therefore, if the SDF file has been changed or deleted, 'sdf.subset' cannot function properly.

The result SDF will also have names added to compounds if they are not present in the original SDF.

Value

Return a character string whose content is the concatenation of SDFs for the selected compounds.

See Also

cmp.parse, sdf.visualize

Examples

```
## Note: this functionality has become obsolete since the introduction of the
## 'SDFset' and 'apset' S4 classes.

# load sample database from web
# db <- cmp.parse("http://bioweb.ucr.edu/ChemMineV2/static/example_db.sdf")
# select SDF for 1st and 2nd compound in that SDF
# sdf_segments <- sdf.subset(db, c(1, 2))
# now sdf_segments containt the 2 SDFs for those 2 compounds
```

---

sdf.visualize *Visualize an SDFset online using ChemMine Tools*

Description

'sdf.visualize' will take an SDFset object and send the compounds to the ChemMine Tools website, for visualization and futher analysis. The results are launched in the users web browser.

Usage

```
sdf.visualize(sdf)
```

Arguments

sdf   A SDFset object which containing the given compounds

Value

Returns the URL of the webpage containing all the SDFs and 2D images corresponding to the selected compounds.

Author(s)

Tyler Backman

References

ChemMine Tools web service: http://chemmine.ucr.edu

See Also

cmp.parse, sdf.subset, plotStruc

Examples

```
## Load sample SD file
data(sdfsample)
sdfset <- sdfsample

## Not run:
## Plot structures using web service ChemMine Tools
sdf.visualize(sdfset[1:4])

## End(Not run)
```

---

sdf2ap   *Atom pair library*

Description

Creates from a `SDFset` a searchable atom pair library that is stored in a container of class `APset`.

Usage

```
sdf2ap(sdfset, type = "AP",uniquePairs=TRUE)
```

Arguments

sdfset	Objects of classes SDFset or SDF
type	if type="AP", the function returns APset/AP objects; if type="character", it returns the result as a character vector of length one. The latter is useful for storing AP data in tabular files.
uniquePairs	When the same atom pair occurs more than once in a single compound, should the names be unique or not? Setting this to true will take slightly longer to compute.

Details

...

Value

APset	if input is SDFset
AP	if input is SDF

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Functions: desc2fp, SDF2apcmp, apset2descdb, cmp.search, cmp.similarity

Related classes: SDF, SDFset, SDFstr, APset.

Examples

```
## Instance of SDFset class
data(sdfsample)
sdfset <- sdfsample[1:50]
sdf <- sdfsample[[1]]

## Compute atom pair library
ap <- sdf2ap(sdf)
(apset <- sdf2ap(sdfset))
view(apset[1:4])

## Return main components of APset object
cid(apset[1:4]) # compound IDs
ap(apset[1:4]) # atom pair descriptors

## Return atom pairs in human readable format
db.explain(apset[1])

## Coerce APset to other objects
apset2descdb(apset) # returns old list-style AP database
tmp <- as(apset, "list") # returns list
as(tmp, "APset") # converst list back to APset

## Compound similarity searching with APset
cmp.search(apset, apset[1], type=3, cutoff=0.2)
plot(sdfset[names(cmp.search(apset, apset[6], type=2, cutoff=0.4))])

## Identify compounds with identical AP sets
cmp.duplicated(apset, type=2)

## Structure similarity clustering
cmp.cluster(db=apset, cutoff = c(0.65, 0.5))[1:20,]
```

SDF2apcmp   SDF *to* list *for AP generation*

Description

Returns SDF class as list containing the components for generating atom pair descriptors.

Usage

```
SDF2apcmp(SDF)
```

Arguments

SDF   SDF

Details

...

Value

list   with atom and bond components

Author(s)

Thomas Girke

References

Chen X and Reynolds CH (2002). "Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients", J Chem Inf Comput Sci.

See Also

Functions: `sdf2ap, apset2descdb, cmp.search, cmp.similarity`

Examples

```
## Instances of SDFset class
data(sdfsample)
sdf <- sdfsample[[1]]

## Return list
cmp <- SDF2apcmp(sdf)
```

---

sdf2list   SDF *to* list

Description

Returns objects of class SDF as `list`.

Usage

```
sdf2list(x)
```

Arguments

x   object of class SDF

Details

...

Value

`list`	with following components:
`character`	SDF header block
`matrix`	SDF bond block
`matrix`	SDF atom block
`character`	SDF data block

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: `sdfstr2list`, `sdf2str`, `SDFset2list`, `SDFset2SDF`

Examples

```
## Instance of SDF class
data(sdfsample); sdfset <- sdfsample
sdf <- sdfset[[1]]

## Return as list
sdf2list(sdf)
as(sdf, "list") # similar result
```

---

sdf2smiles	SDFset *to* character *Convert* SDFset *to SMILES (*character*)*

Description

Accepts compounds in an `SDFset` container and returns the corresponding SMILES (Simplified Molecular Input Line Entry Specification) strings as `SMIset` object. If ChemineOB is available then OpenBabel for the format conversion. Otherwise the compound is submitted to the ChemMine Tools web service for conversion with the Open Babel Open Source Chemistry Toolbox. If the input object contains multiple items, only the first is converted.

Usage

```
sdf2smiles(sdf)
```

Arguments

`sdf`	A `SDFset` object which containing the given compounds

Value

`character`	for details see ?"character"

Author(s)

Tyler Backman, Kevin Horan

References

Chemmine web service: http://chemmine.ucr.edu

Open Babel: http://openbabel.org

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## get a sample compound
data(sdfsample); sdfset <- sdfsample[1]
## convert to smiles
(smiles <- sdf2smiles(sdfset))
as.character(smiles)

## End(Not run)
```

---

sdf2str   SDF *to* SDFstr

Description

Converts SDF to SDFstr. Its main use is to facilitate the export to SD files. It contains optional arguments to generate custom SDF output.

Usage

```
sdf2str(sdf, head, ab, bb, db, cid = NULL, sig = FALSE, ...)
```

Arguments

sdf	object of class SDF
head	optional character vector to supply custom header block
ab	optional matrix to supply custom atom block
bb	optional matrix to supply custom bond block
db	optional character vector to supply custom data block
cid	character can be provided to inject custom compound ID into header block
sig	if = TRUE then the ChemmineR signature will be injected into the header block for tracking purposes
...	option to pass on additional arguments

Details

If the export function write.SDF is supplied with an SDFset object, then sdf2str is used internally to customize the export of many molecules to a single SD file using the same optional arguments.

Value

sdfstr   SDF data of one molecule collapsed to character vector

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Coerce functions: `sdfstr2list`, `sdf2str`, `SDFset2list`, `SDFset2SDF`

Export function: `write.SDF`

Examples

```
## Instance of SDF class
data(sdfsample); sdfset <- sdfsample
sdf <- sdfset[[1]]

## Customize SDF blocks for export to SD file
sdf2str(sdf=sdf, sig=TRUE, cid=TRUE) # uses default SDF components
sdf2str(sdf=sdf, head=letters[1:4], db=NULL) # uses custom components for header and datablock

## The same arguments can be supplied to the write.SDF function for
## batch export of custom SDFs
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE, cid=TRUE, db=NULL)
```

SDFDataTable   *SDF Data Table*

Description

Creates and HTML DataTable showing the compound image along with the fields in the compound data block. Using a browser, this table can be filtered and paged, among other things.

This uses the DT library to create the DataTable.

Usage

```
SDFDataTable(sdfset)
```

Arguments

sdfset   An SDFSet object

Value

Returns the result of the `datatable` function from the `DT` library. An HTML file can be created from this value by calling the `saveWidget` function on it.

Author(s)

Kevin Horan

References

DT library: https://rstudio.github.io/DT/ DataTables javascript library: https://datatables.net/

Examples

```
## Not run:  #depends on ChemmineOB
library(ChemmineR)
library(DT)
data(sdfsample)

# this will open a browser to display the result
x=SDFDataTable(sdfsample[1:3])

# if no GUI is available or you want to save the HTML result:
saveWidget(x,"output.html")

## End(Not run)
```

---

sdfid	*Return SDF compound IDs*

Description

Returns the compound identifiers from the header block of SDF or SDFset objects.

Usage

```
sdfid(x, tag = 1)
```

Arguments

x	object of class SDFset or SDF
tag	values from 1-4 to extract different header block fields; SDF ID is in first one (default)

Details

...

Value

character vector

Author(s)

Thomas Girke

References

...

See Also

`atomblock`, `atomcount`, `bondblock`, `datablock`, `header`, `cid`

Examples

```
## SDF/SDFset instances
data(sdfsample)
sdfset <- sdfsample
sdf <- sdfset[[1]]

## Extract IDs from header block
sdfid(sdf, tag=1)
sdfid(sdfset[1:4])

## Extract compound IDs from ID slot in SDFset container
cid(sdfset[1:4])

## Assigning compound IDs and keeping them unique
unique_ids <- makeUnique(sdfid(sdfset))
cid(sdfset) <- unique_ids
cid(sdfset[1:4])
```

---

sdfsample   *SD file in* SDFset *object*

Description

First 100 compounds from PubChem SD file: Compound_00650001_00675000.sdf.gz

Usage

```
data(sdfsample)
```

Format

Object of class `sdfset`

Details

Object stores 100 molecules from a sample SD file.

Source

ftp://ftp.ncbi.nih.gov/pubchem/Compound/CURRENT-Full/SDF/Compound_00650001_00675000.sdf.gz

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

Examples

```
data(sdfsample)
sdfset <- sdfsample
view(sdfset[1:4])
```

SDFset-class   *Class "SDFset"*

Description

List-like container for storing one or many objects of class SDF each containing the structure definition information of molecules provided by an SD/MOL file. The SDFset is the most important class in the ChemmmineR package for accessing and manipulating information stored in SD files.

Objects from the Class

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

Slots

SDF: Object of class "list" storing SDF components

ID: Object of class "character" storing compound identifiers

Methods

[signature(x = "SDFset"): subsetting of class with bracket operator

[[signature(x = "SDFset"): returns single component as SDF object

[[<- signature(x = "SDFset"): replacement method for single SDF component

[<- signature(x = "SDFset"): replacement method for several SDF components

atomblock signature(x = "SDFset"): returns all atom blocks as list

atomcount signature(x = "SDFset"): returns all atom frequencies as list

bondblock signature(x = "SDFset"): returns all bond blocks as list

obmol signature(x = "SDFset"): returns pointers to OBMol objects as a vector

c signature(x = "SDFset"): concatenates two SDFset containers

cid signature(x = "SDFset"): returns all compound identifiers from ID slot

header<- signature(x = "SDFset"): replacement method for header block

atomblock<- signature(x = "SDFset"): replacement method for atom block

bondblock<- signature(x = "SDFset"): replacement method for bond block

datablock<- signature(x = "SDFset"): replacement method for data block

coerce signature(from = "list", to = "SDFset"): as(list,"SDFset")

coerce signature(from = "SDF", to = "SDFset"): as(sdf,"SDFset")

coerce signature(from = "SDFset", to = "list"): as(sdfset,"list")

coerce signature(from = "SDFset", to = "SDF"): as(sdfset,"SDF")

coerce signature(from = "SDFset", to = "SDFstr"): as(sdfset,"SDFstr")

coerce signature(from = "SDFstr", to = "SDFset"): as(sdfstr,"SDFset")

datablock signature(x = "SDFset"): returns all data blocks as list

datablocktag signature(x = "SDFset"): returns all data blocks as named as list with subsetting support

header signature(x = "SDFset"): returns all header blocks as list

length signature(x = "SDFset"): returns number of entries stored in object

plot signature(x = "SDFset"): plots one or many molecule structures from SDFset object

sdfid signature(x = "SDFset"): returns molecule ID field from header block

SDFset2list signature(x = "SDFset"): returns SDFset object as list

SDFset2SDF signature(x = "SDFset"): returns SDFset object as list with SDF components

SDFset2SDF<- signature(x = "SDFset"): replacement method for SDFset component in SDFset using accessor method

show signature(object = "SDFset"): prints summary of SDFset

view signature(x = "SDFset"): prints extended summary of SDFset

SDFset SDFset(SDF, ID): interface to SDFset constructor

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Related classes: SDF, SDFstr, AP, APset

Import function: read.SDFset("some_SDF_file")

Export function: write.SDF(sdfset, "some_file.sdf")

Examples

```
showClass("SDFset")

## Instances of SDFset class
data(sdfsample); sdfset <- sdfsample
sdfset; view(sdfset[1:4])
sdfset[[1]]

## Import and store SD File in SDFset container
# sdfset <- read.SDFset("some_SDF_file")

## Miscellaneous accessor methods
header(sdfset[1:4])
atomblock(sdfset[1:4])
atomcount(sdfset[1:4])
bondblock(sdfset[1:4])
datablock(sdfset[1:4])

## Assigning compound IDs and keeping them unique
cid(sdfset); sdfid(sdfset)
unique_ids <- makeUnique(sdfid(sdfset))
```

```
cid(sdfset) <- unique_ids

## Convert data block to matrix
blockmatrix <- datablock2ma(datablocklist=datablock(sdfset)) # Converts data block to matrix
numchar <- splitNumChar(blockmatrix=blockmatrix) # Splits to numeric and character matrix
numchar[[1]][1:4,]; numchar[[2]][1:4,]

## Compute atom frequency matrix, molecular weight and formula
propma <- data.frame(MF=MF(sdfset), MW=MW(sdfset), atomcountMA(sdfset))
propma[1:4, ]

## Assign matrix data to data block
datablock(sdfset) <- propma
view(sdfset[1:4])

## String Searching in SDFset
grepSDFset("650001", sdfset, field="datablock", mode="subset") # To return index, set mode="index")

## Export SDFset to SD file
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE)

## Plot molecule structure of SDF
plot(sdfset[1:4]) # plots to R graphics device
# sdf.visualize(sdfset[1:4]) # viewing in browser
```

SDFset2list	SDFset *to* list

Description

Returns object of class SDFset as list where each component conists of a list of the four SDF sub-components: header block, atom block, bond block and data block.

Usage

```
SDFset2list(x)
```

Arguments

x   object of class SDFset

Details

...

Value

list	containing one or many lists each with following components:
character	SDF header block
matrix	SDF bond block
matrix	SDF atom block
character	SDF data block

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: `sdfstr2list`, `sdf2str`, `sdf2list`, `SDFset2SDF`

Examples

```
## Instance of SDFset class
data(sdfsample); sdfset <- sdfsample
sdfset

## Returns sdfset as list
SDFset2list(sdfset[1:4])
as(sdfset, "list")[1:4] # similar result
```

SDFset2SDF   SDFset *to list with many* SDF

Description

Returns object of class `SDFset` as `list` were each component consists of an SDF object.

Usage

```
SDFset2SDF(x)
```

Arguments

x   object of class `SDFset`

Details

...

Value

list   containing one or many SDF objects

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: sdfstr2list, sdf2str, sdf2list, SDFset2list

Examples

```
## Instance of SDFset class
data(sdfsample); sdfset <- sdfsample
sdfset

## Returns sdfset as list
SDFset2SDF(sdfset[1:4])
as(sdfset, "SDF")[1:4] # similar result
view(sdfset[1:4]) # same result
```

SDFstr-class   *Class "SDFstr"*

Description

List-like container for storing one or many molecules from an SD (or MOL) file. Each component of an SDFstr object stores the SD data line by line from a single molecule in a character vector. The SDFstr class is an intermediate container to import SD files into the more important SDFset object or to export the data back from an SDFset container to a valid SD file.

Objects from the Class

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

Slots

a: Object of class "list" with character components

Methods

[signature(x = "SDFstr"): subsetting of class with bracket operator

[[signature(x = "SDFstr"): returns single component as character vector

[[<- signature(x = "SDFstr"): replacement method for single SDFstr component

[<- signature(x = "SDFstr"): replacement method for several SDFstr components

coerce signature(from = "character", to = "SDFstr"): as(character,"SDFstr")

coerce signature(from = "list", to = "SDFstr"): as(list,"SDFstr")

coerce signature(from = "SDF", to = "SDFstr"): as(sdf,"SDFstr")

coerce signature(from = "SDFset", to = "SDFstr"): as(sdfset,"SDFstr")

coerce signature(from = "SDFstr", to = "list"): as(sdfstr,"list")

coerce signature(from = "SDFstr", to = "SDFset"): as(sdfstr,"SDFset")

length signature(x = "SDFstr"): returns length of SDFstr

sdfstr2list signature(x = "SDFstr"): accessor method to return SDFstr as list

sdfstr2list<- signature(x = "SDFstr"): replacement method for several SDFstr components

show signature(object = "SDFstr"): prints summary of SDFstr

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Related classes: SDFset, AP, APset

Import function: read.SDFstr("some_SDF_file")

Examples

```
showClass("SDFstr")

## Instances of SDFstr class
data(sdfsample); sdfset <- sdfsample
sdfstr <- as(sdfset, "SDFstr")
sdfstr[1:4] # print summary of container content
sdfstr[[1]] # returns character vector

## Import: sdfstr <- read.SDFstr("some_SDF_file")
## Export: write.SDF(sdfstr, "some_file.sdf")
```

---

sdfstr2list   SDFstr *to* list

Description

Returns objects of class SDFstr as list.

Usage

```
sdfstr2list(x)
```

Arguments

x   object of class SDFstr

Details

...

Value

list   with many of the following components:

character   SDF content of one molecule vectorized line by line

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Functions: sdf2list, sdf2str, SDFset2list, SDFset2SDF

Examples

```
## Instance of SDFstr class
data(sdfsample); sdfset <- sdfsample
sdfstr <- as(sdfset, "SDFstr")

## Return as list
sdfstr2list(sdfstr)
as(sdfstr, "list") # similar result
```

---

sdfStream   *Streaming through large SD files*

Description

Streaming function to compute descriptors for large SD Files without consuming much memory. In addition to descriptor values, it returns a line index that defines the positions of each molecule in the source SD File. This line index can be used by the read.SDFindex function to retrieve specific compounds of interest from large SD Files without reading the entire file into memory.

Usage

```
sdfStream(input, output, append=FALSE, fct, Nlines = 10000, startline=1, restartNlines=10000, silen
```

Arguments

input	file name of input SD file
output	file name of tabular descriptor file
append	if append=FALSE, a new output file will be created, if one with the same name exists it will be overwritten; whereas append=TRUE will appended to this file.
fct	Function to select descriptor sets; any combination of descriptors, supported by ChemmineR, can be chosen here, as long as they can be represented in tabular format.
Nlines	Number of lines to read from input SD File at a time; the memory consumption will be proportional to this value.
startline	For restarting sdfStream at specific line assigned to startline argument. If assigned startline value does not match the first line of a molecule in the SD file then it will be reset to the start position of the next molecule in the SD file.
restartNlines	Number of lines to parse when startline > 1 in order to identify proper molecule start position. The default value of 10,000 is usually a good choice.
silent	if silent=FALSE, the processing status will be printed to the screen, while silent=TRUE suppresses this output.
...	Arguments to be passed to/from other methods.

Details

...

Value

Writes a descriptor matrix to a tabular file. The first and last line number (position index) of each molecule is specified in the first two columns of the tabular output file, respectively.

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Import/export functions: `read.AP`, `read.SDFset`, `read.SDFstr`, `read.SDFstr`, `read.SDFset`, `write.SDFsplit`

Examples

```
## Load sample data
library(ChemmineR)
data(sdfsample); sdfset <- sdfsample
## Not run: write.SDF(sdfset, "test.sdf")

## Define descriptor set in a simple function
desc <- function(sdfset) {
        cbind(SDFID=sdfid(sdfset),
              # datablock2ma(datablocklist=datablock(sdfset)),
              MW=MW(sdfset),
              groups(sdfset),
              # AP=sdf2ap(sdfset, type="character"),
              rings(sdfset, type="count", upper=6, arom=TRUE)
        )
}

## Run sdfStream with desc function and write results to a file called 'matrix.xls'
sdfStream(input="test.sdf", output="matrix.xls", append=FALSE, fct=desc, Nlines=1000)

## Same as before but starting in SD file at line number 950
sdfStream(input="test.sdf", output="matrix.xls", append=FALSE, fct=desc, Nlines=1000, startline=950)

## Select molecules from SD File using line index from sdfStream
indexDF <- read.delim("matrix.xls", row.names=1)[,1:4]
indexDFsub <- indexDF[indexDF$MW < 400, ] # Selects molecules with MW < 400
sdfset <- read.SDFindex(file="test.sdf", index=indexDFsub, type="SDFset")

## Write result directly to SD file without storing larger numbers of molecules in memory
read.SDFindex(file="test.sdf", index=indexDFsub, type="file", outfile="sub.sdf")

## Read atom pair string representation from file into APset
apset <- read.AP(file="matrix.xls", colid="AP")
cid(apsdf) <- as.character(indexDF$SDFID)
```

```
## End(Not run)
```

---

searchSim-deprecated   *PubChem Similarity (Fingerprint) Search*

Description

Accepts one `SDFset` container and performs a >0.9 similarity PubChem fingerprint search, returning up to 200 hits in an `SDFset` container. The ChemMine Tools web service is used as an intermediate, to translate queries from plain HTTP POST to a PubChem Power User Gateway (PUG) query. If the input object contains multiple items, only the first is used as a query.

Usage

```
searchSim(sdf)
```

Arguments

sdf   A `SDFset` object which contains one compound

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Tyler Backman

References

PubChem PUG SOAP: http://pubchem.ncbi.nlm.nih.gov/pug_soap/pug_soap_help.html

Chemmine web service: http://chemmine.ucr.edu

PubChem help: http://pubchem.ncbi.nlm.nih.gov/search/help_search.html

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## get a sample compound
data(sdfsample); sdfset <- sdfsample[2]
## search a compound on PubChem
compounds <- searchSim(sdfset)
## End(Not run)
```

searchString-deprecated

PubChem Similarity (Fingerprint) SMILES Search

Description

Accepts one SMILES string (Simplified Molecular Input Line Entry Specification) and performs a >0.95 similarity PubChem fingerprint search, returning the hits in an `SDFset` container. The ChemMine Tools web service is used as an intermediate, to translate queries from plain HTTP POST to a PubChem Power User Gateway (PUG) query.

Usage

```
searchString(smiles)
```

Arguments

smiles   A `character` object which contains one SMILES string

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Tyler Backman

References

PubChem PUG SOAP: http://pubchem.ncbi.nlm.nih.gov/pug_soap/pug_soap_help.html

Chemmine web service: http://chemmine.ucr.edu

PubChem help: http://pubchem.ncbi.nlm.nih.gov/search/help_search.html

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## search a compound on PubChem
compounds <- searchString("CC(=O)OC1=CC=CC=C1C(=O)O")
## End(Not run)
```

| selectInBatches | *Select in Batches* |

Description

When doing a select were the condition is a large number of ids it is not always possible to include them in a single SQL statement. This function will break the list of ids into chunks and send the query for each batch. The resutls are appended and returned as one data frame.

Usage

```
selectInBatches(conn, allIndices, genQuery, batchSize = 1e+05)
```

Arguments

conn	Database connection object
allIndices	A vector of indices to pass to the genQuery function in batches.
genQuery	A function which takes a vector of indices and constructs an SQL SELECT statement returning records for the given indicies.
batchSize	How many indicies to put in each batch.

Value

A data frame with the results of the query as if all inidices had been included in a single SELEcT statement.

Author(s)

Kevin Horan

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (conn, allIndices, genQuery, batchSize = 1e+05)
{
    batchByIndex(allIndices, function(indexBatch) {
        df = dbGetQuery(conn, genQuery(indexBatch))
        result = rbind(result, df)
    }, batchSize)
    result
  }
```

---

setPriorities | *Set Priorities*

Description

This function should be run after loading a complete set of data. It will find each group of compounds which share the same descriptor and call the given function, `priorityFn`, with the compound_id numbers of the group. This function should then assign priorities to each compound-descriptor pair, however it wishes. Priorities are integer values with lower values being used in preference of higher values.

It is important that this function be called after all data is loaded. It may be that a compound loaded at the beginning of a data set shares a descriptor with a compound loaded near the end of the data set. If the priorities were set at some point in between these then it would not see all the compounds for that one descriptor.

If a SNOW cluster and connection source function are given, it will run in parallel.

Some pre-defined functions that can be use for `priorityFn` are:

`randomPriorities`: Set the priorities of compounds within a descriptor group randomly.

`forestSizePriorities`: Set the priority based on the number of disconnected components (trees) within the compound. Compounds with fewer trees will have a higher priority (lower numerical value) than compounds with more trees.

Usage

```
setPriorities(conn,priorityFn,descriptorIds=c(),cl=NULL,connSource=NULL)
forestSizePriorities(conn,compIds)
randomPriorities(conn,compIds)
```

Arguments

conn	A database connection object.
priorityFn	This function will be called with the compound_id numbers associated with the same descriptor. It should use the id numbers to lookup whatever data it wants to assign a priority to each compound. These priority values will be used to pick a compound to represent the group in cases where only one compound is needed for each descriptor.
	The function should return a data.frame with the fields "compound_id" and "priority". The order of the rows is not important.
descriptorIds	If given then only re-compute priorities for groups involving descriptors in this list. This is useful for updating priorities after adding new compounds to an existing database.
cl	A SNOW cluster on which to run jobs on.
connSource	A function to create a new database connection with. This will be run once for each new job created. It must return a newly created connection, not a reference to an existing connection.
compIds	The compound_id values for each group.

Value

For setPriorities, no value is returned. randomPriorities and forestSizePriorities return a data.frame with columns "compound_id" and "priority".

Author(s)

Kevin Horan

Examples

```
## Not run:
data(sdfsample)
conn = initDb("sample.db")
sdfLoad(conn,sdfsample)
setPriorities(conn,forestSizePriorities)

## End(Not run)
```

---

smartsSearchOB   *SMARTS Search OB*

Description

Perform searches for SMARTS patterns using Open Babel (requires ChemmineOB package to be installed).

Usage

```
smartsSearchOB(sdfset, smartsPattern, uniqueMatches = TRUE)
```

Arguments

sdfset	An SDFset of the compounds you want to search
smartsPattern	The SMARTS pattern as a string.
uniqueMatches	If true, only return the number of distinct matches, otherwise return the number of all matches.

Value

Returns a vector of counts, one for each input compound.

Author(s)

Kevin Horan

Examples

```
## Not run:
library(ChemmineOB)
data(sdfsample)
#look for rotable bonds
rotableBonds = smartsSearchOB(sdfsample[1:5],"[!$(*#*)&!D1]-!@[!$(*#*)&!D1]",uniqueMatches=FALSE)

## End(Not run)
```

SMI-class *Class* "SMI"

Description

Container for storing the SMILES string of a single molecule.

Objects from the Class

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

Slots

smiles: Object of class "character" of length one

Methods

as.character signature(x = "SMI"): returns content as character vector

coerce signature(from = "character",to = "SMI"): as(smi,"SMI")

coerce signature(from = "SMIset",to = "SMI"): as(smiset,"SMI")

show signature(object = "SMI"): prints summary of SMI

Author(s)

Thomas Girke

References

SMILES (Simplified molecular-input line-entry system) format definition: http://en.wikipedia.org/wiki/Simplified_molec
input_line-entry_system

See Also

Related classes: SMIset, SDF, SDFset

Examples

```
showClass("SMI")

## Instances of SMI class
data(smisample); smiset <- smisample
(smi <- smiset[[1]]) # returns first molecule in smiset as SMI object
```

---

smiles2sdf   *Convert SMILES (*`character`*) to* `SDFset`

Description

Accepts a named vector or `SMIset` of SMILES (Simplified Molecular Input Line Entry Specification) strings and returns its equivalent as an `SDFset` container.

This function runs in two modes. If ChemmineOB is available then it will use OpenBabel to convert all the given smiles into an SDFset with 2D coordinates. Otherwise the compound is submitted to the ChemMine Tools web service for conversion with the Open Babel Open Source Chemistry Toolbox. In this case only the first element will be used since this is a very slow operation.

Usage

```
smiles2sdf(smiles)
```

Arguments

smiles   A named vector of SMILES strings. The names will be used to name the SDF
                    objects.

Value

SDFset   for details see ?"SDFset-class"

Author(s)

Tyler Backman, Kevin Horan

References

Chemmine web service: http://chemmine.ucr.edu

Open Babel: http://openbabel.org

SMILES Format: http://en.wikipedia.org/wiki/Chemical_file_format#SMILES

Examples

```
## Not run:
## convert to sdf
data(smisample)
(sdf <- smiles2sdf(smisample[1:4]))

## End(Not run)
```

---

smisample | *SMILES file in* SMIset *object*

Description

First 100 compounds from PubChem SD file (Compound_00650001_00675000.sdf.gz) converted to SMILES format

Usage

```
data(smisample)
```

Format

Object of class smiset

Details

Object stores 100 molecules from a sample SMILES file.

Source

ftp://ftp.ncbi.nih.gov/pubchem/Compound/CURRENT-Full/SDF/Compound_00650001_00675000.sdf.gz

References

SMILES (Simplified molecular-input line-entry system) format definition: http://en.wikipedia.org/wiki/Simplified_mole
input_line-entry_system

Examples

```
data(smisample)
smiset <- smisample
view(smiset[1:4])
```

SMIset-class | *Class* "SMIset"

Description

List-like container for storing SMILES strings of many compounds.

Objects from the Class

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

Slots

smilist: Object of class "list" with compound identifiers stored in name slots

Methods

[signature(x = "SMIset"): subsetting of class with bracket operator

[[signature(x = "SMIset"): returns single component as SMI object

[<- signature(x = "SMIset"): replacement method for one or many entries

as.character signature(x = "SMIset"): returns content as named character vector

c signature(x = "SMIset"): concatenates two SMIset containers

cid signature(x = "SMIset"): returns compound identifiers

cid<- signature(x = "SMIset"): replacement method for compound identifiers

coerce signature(from = "character", to = "SMIset"): as(character, "SMIset")

coerce signature(from = "list", to = "SMIset"): as(list, "SMIset")

coerce signature(from = "SMIset", to = "SMI"): as(smiset, "SMI")

length signature(x = "SMIset"): returns number of entries stored in object

show signature(object = "SMIset"): prints summary of SMIset

view signature(x = "SMIset"): prints extended summary of SMIset

Author(s)

Thomas Girke

References

SMILES (Simplified molecular-input line-entry system) format definition: http://en.wikipedia.org/wiki/Simplified_mole
input_line-entry_system

See Also

Related classes: SMI, SDF, SDFset

Import function: read.SMIset("some_SMILES_file")

Export function: write.SMI(smiset, "some_file.smi")

Examples

```
showClass("SMIset")

## Instances of SMIset class
data(smisample); smiset <- smisample
smiset; view(smiset[1:4])
smiset[[1]]

## Import and store SMILES file in SMIset container
# smiset <- read.SMIset("some_SMILES_file")

## Miscellaneous accessor methods
cid(smiset[1:4])
(smivec <- as.character(smiset[1:4]))

## Construct SMIset from named vector
as(smivec, "SMIset")

## Assigning compound IDs and keeping them unique
```

```
unique_ids <- makeUnique(cid(smiset))
cid(smiset) <- unique_ids

## Export SMIset to SMILES file
# write.SMI(smiset[1:4], file="sub.smi", cid=TRUE)
```

---

status   *Get Status of a ChemMine Tools Job*

Description

Returns the status of a launched ChemMine Tools job as represented by a `jobToken` object.

Usage

```
status(object)
```

Arguments

object   A `jobToken` job as returned by the function `launchCMTool`

Value

The status of the specified job is returned as a string. Possible values include "RUNNING", "FIN-ISHED", or "FAILED".

Author(s)

Tyler William H Backman

References

See ChemMine Tools at <http://chemmine.ucr.edu>.

See Also

Functions: `toolDetails`, `listCMTools`, `launchCMTool`, `browseJob`, `result`

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")

## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
status(job1)
result1 <- result(job1)
```

```
## End(Not run)
```

---

toolDetails	*Detailed instructions for each ChemMine Tools web tool*

Description

Connects to the ChemMine Tools web service, and provides detailed instructions and example function calls for any tool.

Usage

```
toolDetails(tool_name)
```

Arguments

tool_name   A tool name matching verbatim an existing tool name as listed by listCMTools.

Details

Prints instructions to console.

Author(s)

Tyler William H Backman

References

See ChemMine Tools at http://chemmine.ucr.edu.

See Also

Functions: launchCMTool, listCMTools, result, browseJob, status

Examples

```
## Not run:
## list available tools
listCMTools()

## get detailed instructions on using a tool
toolDetails("Fingerprint Search")

## download compound 2244 from PubChem
job1 <- launchCMTool("pubchemID2SDF", 2244)

## check job status and download result
status(job1)
result1 <- result(job1)

## End(Not run)
```

---

trimNeighbors *Trim Neighbors*

Description

Further reduce the cutoff value of a nearest neighbor (NN) table, as produced by nearestNeighbors. This allows one to compute a very relaxed NN table initially, and then quickly restrict it later without having to re-compute all the similarities.

Usage

```
trimNeighbors(nnm, cutoff)
```

Arguments

nnm   A nearest neighbor table, as produced by nearestNeighbors.

cutoff   The new similarities cutoff value. All pairs with a similarity less than this value
                will be removed from the table.

Value

The return value has the same structure as nnm, with some neighbors removed from the indexes
and similarties entries.

Author(s)

Kevin Horan

See Also

jarvisPatrick nearestNeighbors

Examples

```
data(sdfsample)
ap = sdf2ap(sdfsample)
nnm = nearestNeighbors(ap,numNbrs=20)
nnm = trimNeighbors(nnm,cutoff=0.5)
clustering = jarvisPatrick(nnm,k=2,mode="a1b")
```

---

validSDF	*Validity check of SDFset*

Description

Performs validity check of SDFs stored in `SDFset` objects. Currently, the function tests whether the atom block and the bond block in each `SDF` component of an `SDFset` have at least `Nabcol` and `Nbbcol` columns (default is 3 for both). In additions, it tests for the presence of NA values in the atom and bond blocks. The function returns a logical vector with `TRUE` values for valid compounds and `FALSE` values for invalid ones.

Usage

```
validSDF(x, Nabcol = 3, Nbbcol = 3, logic = "&", checkNA=TRUE)
```

Arguments

x	x object of class `SDFset`
Nabcol	minimum number of columns in atom block
Nbbcol	minimum number of columns in bond block
logic	logical connection (& or |) among Nabcol and Nbbcol cutoffs
checkNA	checks for NA values in atom and bond blocks

Details

The function is important to remove invalid compounds from `SDFset` containers.

Value

`logical` vector of length x with `TRUE` for valid compounds and `FALSE` for invalid compounds.

Author(s)

Thomas Girke

References

...

See Also

Functions: `read.SDFset`

Examples

```
## SDFset instance
data(sdfsample)
sdfset <- sdfsample

## Detect and remove invalid SDFs in SDFset.
valid <- validSDF(sdfset)
which(!valid) # Returns index for invalid SDFs
sdfset <- sdfset[valid] # Returns only valid SDFs.
```

view   *Viewing of complex objects*

Description

Convenience function for viewing the content of complex objects like SDFset and APset containers.
The function is a shorthand wrapper for as(sdfset,"SDF") and as(apset,"AP").

Usage

```
view(x)
```

Arguments

x   object of class SDFset or APset

Details

...

Value

List populated with SDF and AP components.

Author(s)

Thomas Girke

References

...

See Also

Classes: SDF, SDFset, AP, APset

Examples

```
## Viewing content of SDFset
data(sdfsample); sdfset <- sdfsample
view(sdfset[1:4])

## Viewing content of APset
apset <- sdf2ap(sdfset[1:10])
view(apset)
```

---

write.SDF   *SDF export function*

Description

Writes one or many molecules stored in a `SDFset`, `SDFstr` or SDF object to SD file.

Usage

```
write.SDF(sdf, file, cid = FALSE, ...)
```

Arguments

`sdf`	object of class `SDFset`, `SDFstr` or SDF
`file`	name of SD file to write to
`cid`	if `cid` = TRUE and an `SDFset` object is provide as input, then the compound IDs in the ID slot of the `SDFset` are used for compound naming
`...`	the optional arguments of the `sdf2str` function can be provided here, including `head, ab, bb, db`; details are provided in the help page for the `sdf2str` function

Details

If the `write.SDF` function is supplied with an `SDFset` object, then it uses internally the `sdf2str` function to allow customizing the resulting SD file. For this all optional arguments of the `sdf2str` function can be passed on to `write.SDF`.

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Import function: `read.SDFset`, `read.SDFstr`

Examples

```
## Instance of SDFset class
data(sdfsample); sdfset <- sdfsample

## Write objects of classes SDFset/SDFstr/SDF to file
# write.SDF(sdfset[1:4], file="sub.sdf")

## Example for writing customized SDFset to file containing
## ChemmineR signature, IDs from SDFset and no data block
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE, cid=TRUE, db=NULL)

## Example for injecting a custom matrix/data frame into the data block of an
## SDFset and then writing it to an SD file
```

```
props <- data.frame(MF=MF(sdfset), MW=MW(sdfset), atomcountMA(sdfset))
datablock(sdfset) <- props
view(sdfset[1:4])
# write.SDF(sdfset[1:4], file="sub.sdf", sig=TRUE, cid=TRUE)
```

---

write.SDFsplit	*SDF split function*

Description

Splits SD Files into any number of smaller SD Files

Usage

```
write.SDFsplit(x, filetag, nmol)
```

Arguments

x	object of class `SDFset`, `SDFstr`
filetag	string to prepend to file names
nmol	integer specifying number of molecules in split SD files

Details

To split an SD File into smaller ones, one can read the source file into R with `read.SDFstr` and write out smaller ones with `write.SDFsplit`. Note: when importing big SD Files, `read.SDFstr` will be much faster than `read.SDFset`, and there is no need to go through an SDFset object instance in this case.

Author(s)

Thomas Girke

References

SDF format definition: http://www.symyx.com/downloads/public/ctfile/ctfile.jsp

See Also

Import/export functions: `read.SDFset`, `read.SDFstr`, `read.SDFstr`, `read.SDFset`

Examples

```
## Load sample data
library(ChemmineR)
data(sdfsample)

## Not run: ## Create sample SD File with 100 molecules
write.SDF(sdfsample, "test.sdf")

## Read in sample SD File
sdfstr <- read.SDFstr("test.sdf")
```

```
## Run export on SDFstr object
write.SDFsplit(x=sdfstr, filetag="myfile", nmol=10)

## Run export on SDFset object
write.SDFsplit(x=sdfsample, filetag="myfile", nmol=10)


## End(Not run)
```

---

write.SMI   *SMI export function*

Description

Writes one or many molecules stored in a `SMIset` object to a SMILES file.

Usage

```
write.SMI(smi, file, cid = TRUE, ...)
```

Arguments

smi	object of class `SMIset`
file	name of SMILES file to write to
cid	if `cid = TRUE` the compound identifiers will be exported by appending them in tab-separated format to each SMILES string
...	option to pass on additional arguments

Details

...

Author(s)

Thomas Girke

References

SMILES (Simplified molecular-input line-entry system) format definition: http://en.wikipedia.org/wiki/Simplified_mole
input_line-entry_system

See Also

Functions: `write.SDF`

Examples

```
## Instance of SMIset class
data(smisample); smiset <- smisample

## Write objects of classes SMIset to file with and
## without compound identifiers
# write.SMI(smiset[1:4], file="sub.smi", cid=TRUE)
# write.SMI(smiset[1:4], file="sub.smi", cid=FALSE)
```

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