

Package ‘ChemmineR’

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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

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Imports graphics, methods, stats, RCurl

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R topics documented:

ap	3
AP-class	4
apfp	5
apset	6
APset-class	7
apset2descdb	8
atomblock	10
atomcount	11
atomprop	12
atomssubset	13
bondblock	14

bonds	15
cid	16
cluster.sizestat	17
cluster.visualize	18
cmp.cluster	21
cmp.duplicated	22
cmp.parse	24
cmp.parse1	25
cmp.search	26
cmp.similarity	28
conMA	30
datablock	31
datablock2ma	32
db.explain	33
db.subset	34
desc2fp	35
FP-class	37
fp2bit	38
FPset-class	39
fpSim	41
getIds	43
grepSDFset	43
groups	45
header	46
jarvisPatrick	47
makeUnique	48
plotStruc	49
pubchemFPencoding	51
read.AP	51
read.SDFindex	53
read.SDFset	54
read.SDFstr	55
rings	56
SDF-class	58
sdf.subset	59
sdf.visualize	60
sdf2ap	62
SDF2apcmp	63
sdf2list	64
sdf2smiles	65
sdf2str	66
sdfid	67
sdfsamples	68
SDFset-class	69
SDFset2list	71
SDFset2SDF	72
SDFstr-class	73
sdfstr2list	74
sdfStream	75
searchSim	77
searchString	78
smiles2sdf	79

<i>ap</i>	3
validSDF	79
view	81
write.SDF	82
write.SDFsplit	83
Index	85

<i>ap</i>	<i>Return atom pair component of AP/APset</i>
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Description

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

Usage

`ap(x)`

Arguments

<code>x</code>	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(sdfsampl)
sdfset <- sdfsampl[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(sdfsampl)
sdfset <- sdfsampl[1:50]
sdf <- sdfsampl[[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") # convert 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 `sdfsampl`.

Usage

```
data(apset)
```

Format

Object of class `apset`

Details

Object stores atom pairs of 100 molecules.

Source

```
apset <- sdf2ap(sdfsampl)
```

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(sdfsampl)
sdfset <- sdfsampl[1:50]
sdf <- sdfsampl[[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") # convert 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(sdfsampl)
sdfset <- sdfsampl[1:50]
sdf <- sdfsampl[[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") # convert 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(sdfsampl)
sdfset <- sdfsampl
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(sdfsampl)
sdfset <- sdfsampl

## 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,]
```

atomssubset

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

```
atomssubset(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 subsetting. 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(sdfsampl)
sdfset <- sdfsampl

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

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(sdfsampl)
sdfset <- sdfsampl
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(sdfsampl)
sdfset <- sdfsampl

## 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")
```

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(sdfsampl)
sdfset <- sdfsampl
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	<i>generate statistics on sizes of clusters</i>
------------------	---

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 indices, 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(sdfsampl); sdfset <- sdfsampl

## 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="", cluster.result=1,
```

Arguments

db	The descriptor 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 suppress 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 'cmdscales' 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.interactive' 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(sdfsampl); sdfset <- sdfsampl

## 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

<code>db</code>	The descriptor database, in the format returned by ' <code>cmp.parse</code> '.
<code>cutoff</code>	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.
<code>is.similarity</code>	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.
<code>save.distances</code>	whether to save distance for future clustering. See details below.
<code>use.distances</code>	Supply pre-computed distance matrix.
<code>quiet</code>	Whether to suppress the progress information.
<code>...</code>	Further arguments to be passed to <code>cmp.similarity</code> .

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(sdfsampl); sdfset <- sdfsampl

## 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 descriptor 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(sdfsampl); sdfset <- sdfsampl

## 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, quiet=FALSE, type="normal", dbname="")
```

Arguments

filename	The file name of the SDF file
quiet	Whether to silent the output of progress information
type	Database type. Use the default value, or set to 'file-backed' when the library is large. See below.
dbname	Database name. Only used when the type is set to 'file-backed'.

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(sdfsampl); sdfset <- sdfsampl

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

## Loads same atom pair sample data set provided by library
data(apset)
db <- apset
# (optionally) 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:NNQS2MBRHAZ
```

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	Whether to visualize the search result in a webpage.
visualize.browse	Whether to open the browser automatically if you choose to visualize the search result.
visualize.query	Filename/URL or a character string containing the SDF of the query structure if you also want to visualize the query in the search result visualization webpage.

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.

If 'visualize' is set to a TRUE value, [sdf.visualize](#) will be called to send the search results and the scores to ChemMine website. If 'visualize.browse' is set to a TRUE value, the browser will open to show the structures in the search result with their corresponding scores. Otherwise, a URL pointing to that webpage will be printed. By default, 'visualize.query' is not set, and the query structure will not be uploaded. If you want that to be included in the visualization webpage as well, you must set this argument to a character string containing the SDF of the query, or a filename pointing to a file containing the SDF of the query. If the character string or the file containing multiple SDFs, only the first will be considered as the SDF of the query.

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(sdfsampl); sdfset <- sdfsampl

## 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

# you may visualize the search result in ChemMine
## Not run: cmp.search(db, query, cutoff=10, visualize=TRUE, visualize.browse=FALSE, visualize.query=url)

## 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 represents 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(sdfsampl); sdfset <- sdfsampl

## 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")))
```

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 = datablock(sdfset), cleanup = "\\(.*", ...)

splitNumChar(blockmatrix = 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(sdfsampl)
sdfset <- sdfsampl

# 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(sdfsampl); sdfset <- sdfsampl

## 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	<i>Subset a descriptor database and return a sub-database for the selected compounds</i>
-----------	--

Description

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

Usage

```
db.subset(db, cmprs)
```

Arguments

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

Details

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

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(sdfsamples); sdfset <- sdfsamples

## 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))
```

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 class 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(sdfsampl)
sdfset <- sdfsampl[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)
```

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"

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

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(aset)
fpset <- desc2fp(aset)
(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 <i>vector</i> . 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 a 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

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 two 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

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, ...)
```

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.
addone	Value to add to numerator and denominator of similarity coefficient to avoid division 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.
...	arguments to be passed to/from other methods.

Details

...

Value

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

Note

...

Author(s)

Thomas Girke

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(sdfsampl); sdfset <- sdfsampl
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)
```

`getIds`*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(sdfsampl)
sdfset <- sdfsampl

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

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(sdfsampl)
sdfset <- sdfsampl

## 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	<i>Return header block</i>
--------	----------------------------

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(sdfsampl)
sdfset <- sdfsampl
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])
```

jarvisPatrick

*Jarvis-Patrick Clustering***Description**

Function to perform Jarvis-Patrick clustering. The algorithm requires a nearest neighbor table, which consists of j nearest neighbors for each item in the dataset. This information is then used to join items into clusters that share at least k nearest neighbors. The values for j and k are user-defined parameters. The `jarvisPatrick` function can generate the nearest neighbor table for `APset` and `FPset` objects and then perform Jarvis-Patrick clustering on that table. It also accepts a precomputed nearest neighbor table in form of an object of class `matrix`. The output is a cluster vector with the item labels in the name slot and the cluster IDs in the data slot. Alternatively, the function can return the nearest neighbor matrix. As third parameter the user can set a minimum similarity cutoff value for generating the nearest neighbor table. The latter is an optional setting that is not part of the original Jarvis-Patrick algorithm. It allows to generate more tight clusters and to minimize some limitations of this method, such as joining completely unrelated items when clustering small data sets.

Usage

```
jarvisPatrick(x, j, k, cutoff = NA, type = "cluster", ...)
```

Arguments

<code>x</code>	Input of class <code>FPset</code> , <code>APset</code> or <code>matrix</code> .
<code>j</code>	Number of nearest neighbors to consider when generating nearest neighbor table.
<code>k</code>	Minimum number of nearest neighbors two rows (items) in nearest neighbor table need to have in common to join them into the same cluster.
<code>cutoff</code>	Uses a minimum similarity threshold when generating the nearest neighbor table. This parameter allows to obtain tighter clustering results. It is optional and not part of the original Jarvis-Patrick algorithm. Under the default settings this behavior is turned off. If <code>cutoff</code> is set to a stringent value then it is often required to set <code>k</code> to a small value.
<code>type</code>	If <code>type = "cluster"</code> , Jarvis-Patrick clustering is performed and the result is returned in a named vector. If <code>type = "matrix"</code> , the nearest neighbors table is returned as <code>matrix</code> .
<code>...</code>	Arguments to be passed to/from other methods.

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.daylight.com/dayhtml/doc/cluster/index.pdf>

See Also

Functions: `cmp.cluster`

Examples

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

## Standard Jarvis-Patrick clustering on APset/FPset objects
jarvisPatrick(apset, j=6, k=5)
jarvisPatrick(fpset, j=6, k=5)

## Modified Jarvis-Patrick clustering with minimum similarity 'cutoff'
## value (here Tanimoto coefficient)
jarvisPatrick(fpset, j=6, k=2, cutoff=0.6, method="Tanimoto")

## Output nearest neighbor table (matrix)
nmm <- jarvisPatrick(fpset, j=6, k=5, type="matrix")

## Perform clustering on precomputed nearest neighbor table
jarvisPatrick(nmm, j=6, k=5)
```

makeUnique

Uniquify CMP names

Description

Creates unique CMP names by appending a counter to each duplication 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])
```

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", ...)
```

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.
...	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=FALSE`.

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)
```

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,]
```

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)
```

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

Details

...

Value

object of class APset or FPset

Author(s)

Thomas Girke

References

...

See Also

sdf2ap, sdfStream

Examples

```
## Load sample data
library(ChemmineR)
data(sdfsampl); sdfset <- sdfsampl
## 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(sdfsampl); sdfset <- sdfsampl
## 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.

Usage

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

Arguments

sdfstr path/name to an SD file; alternatively an SDFstr object can be provided
 ... option to pass on additional arguments

Details

...

Value

SDFset for details see ?"SDFset-class"

Author(s)

Thomas Girke

References

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

See Also

Functions: read.SDFstr

Examples

```
## Write instance of SDFset class to SD file
data(sdfsampl); sdfset <- sdfsampl
# 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	<i>SD file to SDFstr</i>
-------------	--------------------------

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

ReferencesSDF format definition: <http://www.symyx.com/downloads/public/ctfile/ctfile.jsp>**See Also**

Functions: read.SDFset

Examples

```
## Write instance of SDFstr class to SD file
data(sdfsampl); sdfset <- sdfsampl
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)
```

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.

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 sp ² 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 sp ² hybridized atom. (ii) In addition, Hueckel's rule ' $4n + 2$ ' needs to be true, where 'n' is either zero or any positive integer.
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 limit 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(sdfsampl)
sdfset <- sdfsampl

## 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 aromatic
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"

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
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(sdfsamples); sdfset <- sdfsamples
(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 segments 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, cmprs)
```

Arguments

db	The database generated by 'cmp.parse'
cmprs	An array of indices 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 contain the 2 SDFs for those 2 compounds
```

sdf.visualize

Subset a SDFset and visualize selected compounds in a webpage

Description

'sdf.visualize' will take a descriptor database generated by 'cmp.parse' and an array of indices, send an SDF consisting structure information of compounds indexed by this array to ChemMine (<http://bioweb.ucr.edu/ChemMineV2>), and open a webpage that shows the structures of these compounds. It returns the URL of that page.

Usage

```
sdf.visualize(db, cmps, extra=NULL, reference.sdf=NULL, reference.note=NULL, browse=TRUE, quiet=TRUE)
```

Arguments

db	The database generated by 'cmp.parse'
cmps	A vector of indices that correspond to a set of selected compounds from the database
extra	A vector or list of character strings or matrices or data frames, each entry of which gives extra description on the compounds being visualized.
reference.sdf	A character string of SDF or a filename of an SDF file for the reference compound.

reference.note	Note to be displayed with the reference compound.
browse	Whether to open the webpage automatically after the upload is finished
quiet	Whether to display the progress information

Details

'sdf.visualize' uses [sdf.subset](#) to extract the SDF for the selected compounds. Therefore, 'sdf.visualize' also depends on information embedded in the descriptor database returned by 'cmp.parse'. It also relies on the availability of the original SDF file 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.visualize' cannot function properly.

After extracting the SDF segments for the selected compounds, 'sdf.visualize' will send the SDF to ChemMine (<http://bioweb.ucr.edu/ChemMineV2>) using HTTP POST method. ChemMine will generate the 2D images for the selected compounds and a webpage containing these images as well as the SDFs. The URL is returned by 'sdf.visualize'. If 'browse' is set to TRUE, the URL will be opened by your default browser.

If the argument 'extra' is given, it must be a vector or list of character strings or data frames or matrices. The length of the vector or list must be the same as that of the indices. Each entry may be named or not. Each entry of this vector is a character string giving extra description on a compound. This vector will be sent to ChemMine, and the extra description for a compound will be listed at the right hand side of the compound. Data frames or matrices will be formatted and displayed as they would be formatted by the 'print' function.

The 'reference.sdf' argument is given when you want to upload an extra compound as a reference compound. This compound will be displayed at the top of the visualization web page. This argument can be a character string of SDF(s), or it can be a filename or URL that points to an SDF file. If the string or the file contains multiple SDFs, this function will use the first one.

If a reference compound is uploaded, note about this compound can be set via the 'reference.note' argument. This note will be displayed next to the structure of the compound on the resulting webpage.

Value

Returns the URL of the webpage containing all the SDFs and 2D images corresponding to the selected compounds.

See Also

[cmp.parse](#), [sdf.subset](#), [plotStruc](#)

Examples

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

## Not run:
## Plot structures using web service ChemMine Tools
sdf.visualize(sdfset[1:4])

## Add extra annotation as vector
sdf.visualize(sdfset[1:4], extra=month.name[1:4])
```

```
## Add extra annotation as matrix
extra <- apply(propma[1:4,], 1, function(x) data.frame(Property=colnames(propma), Value=x))
sdf.visualize(sdfset[1:4], extra=extra)

## Add extra annotation as list
sdf.visualize(sdfset[1:4], extra=bondblock(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")
```

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.

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(sdfsampl)
sdfset <- sdfsampl[1:50]
sdf <- sdfsampl[[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") # convert 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(sdfsampl)
sdf <- sdfsampl[[1]]

## Return list
SDF2apcmp(sdf)
```

sdf2list	SDF <i>to</i> 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

ReferencesSDF format definition: <http://www.symyx.com/downloads/public/ctfile/ctfile.jsp>**See Also**

Functions: sdfstr2list, sdf2str, SDFset2list, SDFset2SDF

Examples

```
## Instance of SDF class
data(sdfsampl); sdfset <- sdfsampl
sdf <- sdfset[[1]]

## Return as list
sdf2list(sdf)
as(sdf, "list") # similar result
```

`sdf2smiles`SDFset to character *Convert SDFset to SMILES* (character)

Description

Accepts one compound in an SDFset container and returns the corresponding SMILES string (Simplified Molecular Input Line Entry Specification). 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 contains one compound

Value

character for details see ?"character"

Author(s)

Tyler Backman

ReferencesChemmine 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(sdfsamples); sdfset <- sdfsamples[1]  
## convert to smiles  
smiles <- sdf2smiles(sdfset)  
## 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(sdfsamples); sdfset <- sdfsamples
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)
```

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(sdfsamples)
sdfset <- sdfset
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])
```

sdfsamples

SD file in SDFset object

Description

First 100 compounds from PubChem SD file: Compound_00650001_00675000.sdf.gz

Usage

```
data(sdfsamples)
```

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(sdfsampl)
sdfset <- sdfsampl
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 ChemmineR 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

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(sdfsamples); sdfset <- sdfsamples
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 consists 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(sdfsampl); sdfset <- sdfsampl
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 where 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(sdfsampl); sdfset <- sdfsampl
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

ReferencesSDF 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(sdfsampl); sdfset <- sdfsampl
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(sdfsampl); sdfset <- sdfsampl
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, silent = FALSE)
```

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 be 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(sdfsampl); sdfset <- sdfsampl
## 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

PubChem Similarity (Fingerprint) Search

Description

Accepts one SDFset container 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. 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(sdfsamples); sdfset <- sdfsamples[1]  
## search a compound on PubChem  
compounds <- searchSim(sdfset)  
## End(Not run)
```

searchString	<i>PubChem Similarity (Fingerprint) SMILES Search</i>
--------------	---

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)
```

`smiles2sdf`*Convert SMILES (character) to SDFset*

Description

Accepts one compound as a SMILES string (Simplified Molecular Input Line Entry Specification) and returns its equivalent as an SDFset container. The compound is submitted to the ChemMine Tools web service for conversion with the Open Babel Open Source Chemistry Toolbox.

Usage

```
smiles2sdf(smiles)
```

Arguments

`smiles` A character object which contains one SMILES string

Value

SDFset for details see `?"SDFset-class"`

Author(s)

Tyler Backman

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  
sdf <- smiles2sdf("CC(=O)OC1=CC=CC=C1C(=O)O\tname")  
## End(Not run)
```

`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, Nabc col = 3, Nbbcol = 3, logic = "&", checkNA=TRUE)
```

Arguments

x	x object of class SDFset
Nabc col	minimum number of columns in atom block
Nbbcol	minimum number of columns in bond block
logic	logical connection (& or) among Nabc col 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(sdfsampl e)
sdfset <- sdfsampl e

## 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	<i>Viewing of complex objects</i>
------	-----------------------------------

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(sdfsampl); sdfset <- sdfsampl
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(sdfsampl); sdfset <- sdfsampl

## 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	<i>SDF split function</i>
----------------	---------------------------

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(sdfsampl)

## Not run: ## Create sample SD File with 100 molecules
write.SDF(sdfsampl, "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=sdfsampl, filetag="myfile", nmol=10)  
  
## End(Not run)
```

Index

- *Topic **aplot**
 - plotStruc, 49
- *Topic **classes**
 - AP-class, 4
 - APset-class, 7
 - FP-class, 37
 - FPset-class, 39
 - SDF-class, 58
 - SDFset-class, 69
 - SDFstr-class, 73
- *Topic **datasets**
 - apfp, 5
 - apset, 6
 - atomprop, 12
 - pubchemFPencoding, 51
 - sdfsamples, 68
- *Topic **utilities**
 - ap, 3
 - apset2descdb, 8
 - atomblock, 10
 - atomcount, 11
 - atomssubset, 13
 - bondblock, 14
 - bonds, 15
 - cid, 16
 - cluster.sizestat, 17
 - cluster.visualize, 18
 - cmp.cluster, 21
 - cmp.duplicated, 22
 - cmp.parse, 24
 - cmp.parse1, 25
 - cmp.search, 26
 - cmp.similarity, 28
 - conMA, 30
 - datablock, 31
 - datablock2ma, 32
 - db.explain, 33
 - db.subset, 34
 - desc2fp, 35
 - fp2bit, 38
 - fpSim, 41
 - getIds, 43
 - grepSDFset, 43
 - groups, 45
 - header, 46
 - jarvisPatrick, 47
 - makeUnique, 48
 - plotStruc, 49
 - read.AP, 51
 - read.SDFindex, 53
 - read.SDFset, 54
 - read.SDFstr, 55
 - rings, 56
 - sdf.subset, 59
 - sdf.visualize, 60
 - sdf2ap, 62
 - SDF2apcmp, 63
 - sdf2list, 64
 - sdf2smiles, 65
 - sdf2str, 66
 - sdfid, 67
 - SDFset2list, 71
 - SDFset2SDF, 72
 - sdfstr2list, 74
 - sdfStream, 75
 - searchSim, 77
 - searchString, 78
 - smiles2sdf, 79
 - validSDF, 79
 - view, 81
 - write.SDF, 82
 - write.SDFsplit, 83
 - [,APset-method (APset-class), 7
 - [,FPset-method (FPset-class), 39
 - [,SDF-method (SDF-class), 58
 - [,SDFset-method (SDFset-class), 69
 - [,SDFstr-method (SDFstr-class), 73
 - [<-,APset-method (APset-class), 7
 - [<-,FPset-method (FPset-class), 39
 - [<-,SDF-method (SDF-class), 58
 - [<-,SDFset-method (SDFset-class), 69
 - [<-,SDFstr-method (SDFstr-class), 73
 - [[,APset-method (APset-class), 7
 - [[,FPset-method (FPset-class), 39
 - [[,SDF-method (SDF-class), 58
 - [[,SDFset-method (SDFset-class), 69

- [[,SDFstr-method (SDFstr-class), 73
- [[<-,APset-method (APset-class), 7
- [[<-,SDF-method (SDF-class), 58
- [[<-,SDFset-method (SDFset-class), 69
- [[<-,SDFstr-method (SDFstr-class), 73
- ap, 3
- ap,AP-method (AP-class), 4
- ap,APset-method (APset-class), 7
- AP-class, 4
- ap-methods (ap), 3
- apfp, 5
- apset, 6
- APset-class, 7
- apset2descdb, 8
- as.character,FP-method (FP-class), 37
- as.character,FPset-method (FPset-class), 39
- as.matrix,FPset-method (FPset-class), 39
- as.numeric,FP-method (FP-class), 37
- as.vector,FP-method (FP-class), 37
- atomblock, 10
- atomblock,SDF-method (SDF-class), 58
- atomblock,SDFset-method (SDFset-class), 69
- atomblock-methods (atomblock), 10
- atomblock<- (atomblock), 10
- atomblock<- ,SDFset-method (SDFset-class), 69
- atomcount, 11
- atomcount,SDF-method (SDF-class), 58
- atomcount,SDFset-method (SDFset-class), 69
- atomcountMA (atomcount), 11
- atomprop, 12
- atomssubset, 13
- bondblock, 14
- bondblock,SDF-method (SDF-class), 58
- bondblock,SDFset-method (SDFset-class), 69
- bondblock-methods (bondblock), 14
- bondblock<- (bondblock), 14
- bondblock<- ,SDFset-method (SDFset-class), 69
- bonds, 15
- c,APset-method (APset-class), 7
- c,FPset-method (FPset-class), 39
- c,SDFset-method (SDFset-class), 69
- cid, 16
- cid,APset-method (APset-class), 7
- cid,FPset-method (FPset-class), 39
- cid,SDFset-method (SDFset-class), 69
- cid<- (cid), 16
- cid<- ,APset-method (APset-class), 7
- cid<- ,FPset-method (FPset-class), 39
- cid<- ,SDFset-method (SDFset-class), 69
- cluster.sizestat, 17, 20
- cluster.visualize, 18, 18
- cmp.cluster, 18, 20, 21, 25, 26, 28, 29
- cmp.duplicated, 22
- cmp.parse, 20, 22, 23, 24, 26, 28, 29, 34, 35, 60, 61
- cmp.parse1, 22, 25, 25, 28, 29
- cmp.search, 22, 23, 25, 26, 26, 28, 29
- cmp.similarity, 22, 25, 26, 28, 28
- coerce,APset,AP-method (APset-class), 7
- coerce,APset,list-method (APset-class), 7
- coerce,character,FPset-method (FPset-class), 39
- coerce,character,SDF-method (SDF-class), 58
- coerce,character,SDFstr-method (SDFstr-class), 73
- coerce,FPset,FP-method (FPset-class), 39
- coerce,list,APset-method (APset-class), 7
- coerce,list,SDF-method (SDF-class), 58
- coerce,list,SDFset-method (SDFset-class), 69
- coerce,list,SDFstr-method (SDFstr-class), 73
- coerce,matrix,FPset-method (FPset-class), 39
- coerce,numeric,FP-method (FP-class), 37
- coerce,SDF,character-method (SDF-class), 58
- coerce,SDF,list-method (SDF-class), 58
- coerce,SDF,SDFset-method (SDF-class), 58
- coerce,SDF,SDFstr-method (SDF-class), 58
- coerce,SDFset,list-method (SDFset-class), 69
- coerce,SDFset,SDF-method (SDFset-class), 69
- coerce,SDFset,SDFstr-method (SDFset-class), 69
- coerce,SDFstr,list-method (SDFstr-class), 73
- coerce,SDFstr,SDFset-method (SDFstr-class), 73
- conMA, 30
- datablock, 31
- datablock,SDF-method (SDF-class), 58
- datablock,SDFset-method (SDFset-class), 69

- datablock-methods (datablock), 31
- datablock2ma, 32
- datablock<- (datablock), 31
- datablock<-,SDFset-method (SDFset-class), 69
- datablocktag (datablock), 31
- datablocktag,SDF-method (SDF-class), 58
- datablocktag,SDFset-method (SDFset-class), 69
- db.explain, 33
- db.subset, 34
- desc2fp, 35
- FP-class, 37
- fp2bit, 38
- FPset-class, 39
- fpSim, 41
- getIds, 43
- grepSDFset, 43
- groups, 45
- header, 46
- header,SDF-method (SDF-class), 58
- header,SDFset-method (SDFset-class), 69
- header-methods (header), 46
- header<- (header), 46
- header<-,SDFset-method (SDFset-class), 69
- jarvisPatrick, 47
- length,APset-method (APset-class), 7
- length,FPset-method (FPset-class), 39
- length,SDFset-method (SDFset-class), 69
- length,SDFstr-method (SDFstr-class), 73
- makeUnique, 48
- MF (atomcount), 11
- MW (atomcount), 11
- plot (plotStruc), 49
- plot,SDF-method (SDF-class), 58
- plot,SDFset-method (SDFset-class), 69
- plotStruc, 49, 61
- pubchemFPencoding, 51
- read.AP, 51
- read.SDFindex, 53
- read.SDFset, 54
- read.SDFstr, 55
- rings, 56
- SDF-class, 58
- sdf.subset, 35, 59, 61
- sdf.visualize, 27, 28, 60, 60
- sdf2ap, 62
- SDF2apcmp, 63
- sdf2list, 64
- sdf2list,SDF-method (SDF-class), 58
- sdf2smiles, 65
- sdf2str, 66
- sdf2str,SDF-method (SDF-class), 58
- sdf2str-methods (sdf2str), 66
- sdfid, 67
- sdfid,SDF-method (SDF-class), 58
- sdfid,SDFset-method (SDFset-class), 69
- sdfsamples, 68
- SDFset (SDFset-class), 69
- SDFset-class, 69
- SDFset2list, 71
- SDFset2list,SDFset-method (SDFset-class), 69
- SDFset2list-methods (SDFset2list), 71
- SDFset2SDF, 72
- SDFset2SDF,SDFset-method (SDFset-class), 69
- SDFset2SDF-methods (SDFset2SDF), 72
- SDFset2SDF<- (SDFset2SDF), 72
- SDFset2SDF<-,SDFset-method (SDFset-class), 69
- SDFstr-class, 73
- sdfstr2list, 74
- sdfstr2list,SDFstr-method (SDFstr-class), 73
- sdfstr2list-methods (sdfstr2list), 74
- sdfstr2list<- (sdfstr2list), 74
- sdfstr2list<-,SDFstr-method (SDFstr-class), 73
- sdfStream, 75
- searchSim, 77
- searchString, 78
- show,AP-method (AP-class), 4
- show,APset-method (APset-class), 7
- show,FP-method (FP-class), 37
- show,FPset-method (FPset-class), 39
- show,SDF-method (SDF-class), 58
- show,SDFset-method (SDFset-class), 69
- show,SDFstr-method (SDFstr-class), 73
- smiles2sdf, 79
- splitNumChar (datablock2ma), 32
- validSDF, 79
- view, 81
- view,APset-method (APset-class), 7
- view,FPset-method (FPset-class), 39
- view,SDFset-method (SDFset-class), 69
- view-methods (view), 81

write.SDF, [82](#)

write.SDFsplit, [83](#)