Package ‘fmcsR’

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Type Package

Title Mismatch Tolerant Maximum Common Substructure Searching

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Description The fmcsR package introduces an efficient maximum common substructure (MCS) algorithms combined with a novel matching strategy that allows for atom and/or bond mismatches in the substructures shared among two small molecules. The resulting flexible MCSs (FMCSs) are often larger than strict MCSs, resulting in the identification of more common features in their source structures, as well as a higher sensitivity in finding compounds with weak structural similarities. The fmcsR package provides several utilities to use the FMCS algorithm for pairwise compound comparisons, structure similarity searching and clustering.

Depends R (>= 2.10.0), ChemmineR, methods

Suggests BiocStyle, knitr, knitrpackages, knitrBootstrap,rmarkdown

License Artistic-2.0

LazyLoad yes

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

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

Imports RUnit, methods, ChemmineR, BiocGenerics, parallel

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R topics documented:

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fmcsR-package A FMCS solver package.

Description

The package consists of two main functions, fmcs which computes the flexible MCS between two SDF objects. And fmcsBatch runs the FMCS algorithm on a SDFset.

Details

Package: fmcsR
Type: Package
Version: 1.0
Date: 2012-02-01

Author(s)

Yan Wang

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Examples

```
library(fmcsR)
data(sdfsample)
sdfset <- sdfsample
result1 <- fmcs(sdfset[[1]], sdfset[[2]])
result2 <- fmcs(sdfset[[1]], sdfset[[2]], au=3)
result3 <- fmcs(sdfset[[1]], sdfset[[2]], bu=3)
result4 <- fmcs(sdfset[[1]], sdfset[[2]], au=1, bu=1)
result5 <- fmcs(sdfset[[1]], sdfset[[2]], matching.mode="aromatic")
result6 <- fmcs(sdfset[[1]], sdfset[[2]], au=2, bu=1, matching.mode="aromatic")

fmcsBatch(sdfset[[1]], sdfset[1:3])
fmcsBatch(sdfset[[1]], sdfset[1:3], au=2)
fmcsBatch(sdfset[[1]], sdfset[1:3], bu=1)
fmcsBatch(sdfset[[1]], sdfset[1:3], matching.mode="aromatic", au=1, bu=1)
```

Description

R function to call the C++ implementation of the flexible common substructure (FMCS) algorithm. The FMCS algorithm provides an improved maximum common substructure (MCS) search method that allows atom and/or bond mismatches in the substructures shared among two small molecules. The resulting flexible MCSs (FMCSs) are often larger than strict MCSs, resulting in the identification of more common features in their source structures, as well as a higher sensitivity in detecting weak similarities among compounds.

Usage

```
fmcs(sdf1, sdf2, al = 0, au = 0, bl = 0, bu = 0, matching.mode = "static", fast = FALSE, timeout=60000)
```

Arguments

- `sdf1`: Input query SDF object or SDFset object with a single molecule.
- `sdf2`: Input target SDF object SDFset object with a single molecule.
- `al`: Lower bound for the number of atom mismatches.
- `au`: Upper bound for the number of atom mismatches.
- `bl`: Lower bound for the number of bond mismatches.
- `bu`: Upper bound for the number of bond mismatches.
- `matching.mode`: Three modes for bond matching are supported: "static", "aromatic", and "ring".
- `fast`: If `fast` is set to TRUE, then the fast computing mode will be turned on. In this case, the algorithm will only return the size information about the source structures and their MCSs, while omitting all structural information.
- `timeout`: The maximum amount of time to spend searching, in milliseconds. A value of 0 indicates no timeout.
Details

... 

Value

Returns object of class MCS

Author(s)

Yan Wang, Thomas Girke

References

Publication in preparation.

See Also

plotMCS, fmcsBatch, ?"MCS-class"

Examples

```r
library(fmcsR)
data(sdfsamp)  # df sample
sdfsamp <- sdfsamp
mcs1 <- fmcs(sdfsamp[[1]], sdfsamp[[2]])
mcsfast <- fmcs(sdfsamp[[1]], sdfsamp[[2]], fast=TRUE)
mcs2 <- fmcs(sdfsamp[[1]], sdfsamp[[2]], au=3)
mcs3 <- fmcs(sdfsamp[[1]], sdfsamp[[2]], bu=3)
mcs4 <- fmcs(sdfsamp[[1]], sdfsamp[[2]], au=1, bu=1)
mcs5 <- fmcs(sdfsamp[[1]], sdfsamp[[2]], matching.mode="aromatic")
mcs6 <- fmcs(sdfsamp[[1]], sdfsamp[[2]], au=2, bu=1, matching.mode="aromatic")
```

```r
## Plot MCS objects
plotMCS(mcs6)
```

```r
## Methods to return components of MCS objects
stats(mcs6)
mcs6["stats"]
mcs1(mcs6)
mcs6["mcs1"]
mcs2(mcs6)
mcs6["mcs2"]
```

```r
## Constructor method from list
mylist <- list(stats=stats(mcs6), mcs1=mcs1(mcs6), mcs2=mcs2(mcs6))
mymcs <- as(mylist, "MCS")
```
**fmcsBatch**

**FMCS Search Function**

**Description**

Compound search function that runs the FMCS algorithm for a query compound against a set of molecules stored in an SDFset container.

**Usage**

```r
fmcsBatch(querySdf, sdfset, al = 0, au = 0, bl = 0, bu = 0,
matching.mode = "static",timeout=60000,numParallel=1)
```

**Arguments**

- `querySdf`: Input query SDF object or SDFset object of length one.
- `sdfset`: Input target SDFset object.
- `al`: Lower bound for the number of atom mismatches.
- `au`: Upper bound for the number of atom mismatches.
- `bl`: Lower bound for the number of bond mismatches.
- `bu`: Upper bound for the number of bond mismatches.
- `matching.mode`: Three matching mode are supported, "static", "aromatic", and "ring".
- `timeout`: The maximum amount of time to spend on each pair of comparisons, in milliseconds. A value of 0 indicates no timeout.
- `numParallel`: The number of comparisons to run in parallel, using local cores.

**Details**

This function runs the FMCS algorithm in fast computing mode. Thus, it will only return the similarity scores and size information about the source structures and their MCSs, while omitting all structural information.

**Value**

Returns a matrix with compound IDs as row names and the following columns: Query_Size, Target_Size, MCS_Size, Tanimoto_Coefficient and Overlap_Coefficient. For details see vignette of this package.

**Author(s)**

Yan Wang, Thomas Girke

**See Also**

`plotMCS, fmcs, "MCS-class"`
Examples

```r
library(fmcsR)
data(sdfsample)
sdfset <- sdfsample
fmcsBatch(sdfset[[1]], sdfset[1:3])
fmcBatch(sdfset[[1]], sdfset[1:3], au=2)
fmcBatch(sdfset[[1]], sdfset[1:3], bu=1)
fmcBatch(sdfset[[1]], sdfset[1:3], matching.mode="aromatic", au=1, bu=1)
```

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**fmcstest**

*SD file stored in SDFset object*

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**Description**

Sample compound structures stored in SDF format.

**Usage**

```r
data(fmcstest)
```

**Format**

Object of class `SDFset`

**Details**

Object stores X molecules from a sample SD file.

**Source**


**References**


**Examples**

```r
data(fmcstest)
sdfset <- fmcstest
view(sdfset)
```
Description

List-like container for storing results from `fmcs` function.

Objects from the Class

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

Slots

- `stats`: Object of class "numeric" 
- `mcs1`: Object of class "SDFset" 
- `mcs2`: Object of class "SDFset" 

Methods

- `[[ signature(x = "MCS")`: ... 
- `coerce signature(from = "list", to = "MCS")`: ... 
- `mcs1 signature(x = "MCS")`: ... 
- `mcs2 signature(x = "MCS")`: ... 
- `stats signature(x = "MCS")`: ...

Note

...

Author(s)

Yan Wang

References

...

See Also

Related classes: SDF, SDFstr
mcs2sdfset

**Examples**

```r
## Create MCS instance
showClass("MCS")
data(sdfsample)
sdfset <- sdfsample
mcs <- fmcs(sdfset[[1]], sdfset[[2]], au=2, bu=2)

## Methods to return components of MCS
stats(mcs)
mcs[["stats"]]
mcs1(mcs)
mcs[["mcs1"]]
mcs2(mcs)
mcs[["mcs2"]]

## Constructor method from list
mylist <- list(stats=stats(mcs), mcs1=mcs1(mcs), mcs2=mcs2(mcs))
mymcs <- as(mylist, "MCS")
```

---

**mcs2sdfset**  
*Return MCS object as SDFset*

**Description**

Helper function to run atomsubset from ChemmineR library on MCS objects in order to obtain their results in SDFset format.

**Usage**

```r
mcs2sdfset(x, ...)
```

**Arguments**

- `x`  
  Object of class MCS
- `...`  
  Arguments to be passed to/from other methods.

**Details**

Returns MCS data in form of a list containing two SDFset objects, one for the query and one for the target structure.

**Value**

List with two SDFset objects.

**Note**

...
Author(s)
Thomas Girke

References
...

See Also
fmcs

Examples
library(fmcsR)
data(sdfsamples)
sdfs <- sdfsamples
mcs <- fmcs(sdfs[[1]], sdfs[[2]], au=2, bu=1, matching.mode="aromatic")

mcs2sdfs(x=mcs, type="new")
mcs2sdfs(x=mcs, type="old")
plot(mcs2sdfs(x=mcs, type="new"))

Description
Convenience plotting function to visualize and compare MCSs generated by fmcs function.

Usage
plotMCS(x, mcs = 1, print = FALSE, ...)

Arguments

x MCS object
mcs Selection of MCS solution by position number, default is 1.
print print=FALSE turns of printing behavior of class.
... Arguments to be passed to/from other methods.

details
The two structures, target and query, used to generate x with a call to fmcs are plotted next to each other, and the corresponding MCS substructures are highlighted in color.

Value
Prints summary of MCS to screen and plots their structures to graphics device.
Note

... 

Author(s)

Yan Wang

References

...

See Also

sdf.visualize

Examples

library(fmcsR)
data(sdfsampl)
sdfset <- sdfsampl
mcs <- fmcs(sdfset[[1]], sdfset[[2]], au=2, bu=1, matching.mode="aromatic")
plotMCS(mcs, mcs=1)
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