

Package: MetChem (via r-universe)

October 4, 2024

Version 0.4

Date 2023-07-05

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Title Chemical Structural Similarity Analysis

Description A new pipeline to explore chemical structural similarity across metabolite. It allows to classify metabolites in structurally-related modules and identify common shared functional groups. KODAMA algorithm is used to highlight structural similarity between metabolites. See Cacciatore S, Tenori L, Luchinat C, Bennett PR, MacIntyre DA. (2017) *Bioinformatics* <doi:10.1093/bioinformatics/btw705>, Cacciatore S, Luchinat C, Tenori L. (2014) *Proc Natl Acad Sci USA* <doi:10.1073/pnas.1220873111>, and Abdel-Shafy EA, Melak T, MacIntyre DA, Zadra G, Zerbini LF, Piazza S, Cacciatore S. (2023) *Bioinformatics Advances* <doi:10.1093/bioadv/vbad053>.

Depends R (>= 3.5.0), stats, KODAMA (>= 2.3), httr, XML, fingerprint, rcdk (>= 3.4.3)

Suggests knitr, rmarkdown, readxl, impute, pheatmap, RColorBrewer

VignetteBuilder knitr

SuggestsNote No suggestions

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

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Date/Publication 2023-07-06 07:43:05 UTC

Contents

allbranches 2

| | |
|----------------------------------|----|
| chemical.dissimilarity | 3 |
| ChemRICH | 4 |
| clusters.detection | 4 |
| diseasesMet | 5 |
| enzymesMet | 6 |
| features | 7 |
| HFD | 8 |
| KODAMA.chem.sim | 8 |
| Metabolites | 9 |
| nameMet | 10 |
| pathwaysMet | 11 |
| propertiesMet | 11 |
| readMet | 12 |
| selectionMet | 13 |
| substituentsMet | 13 |
| taxonomyMet | 14 |
| tree.cutting | 15 |
| WMCSA | 15 |
| write.cls | 16 |
| write.gct | 17 |
| write.gmt | 17 |

Index **19**

allbranches *Cut a Tree into Groups of Data*

Description

Cuts a tree as resulting from [hclust](#) function, into groups (a.k.a. modules).

Usage

```
allbranches(hh,minlen=5)
```

Arguments

| | |
|--------|--|
| hh | a tree as produced by hclust function. |
| minlen | The minimum number of elements in each module. |

Value

A list contains vectors of module memberships.

See Also

[cutree](#), [hclust](#), [clusters.detection](#)

Examples

```
data(Metabolites)

data=Metabolites$readMet$concentration
hh=hclust(dist(data),method="ward.D")
res=allbranches(hh)
```

```
chemical.dissimilarity
```

Chemical dissimilarity.

Description

This function calculates the structural dissimilarity between different metabolites using the simplified molecular-input line-entry system (SMILE) of each metabolite as input.

Usage

```
chemical.dissimilarity (smiles,method="tanimoto",type="extended")
```

Arguments

| | |
|--------|---|
| smiles | A vector of smile notations. |
| method | The method used to calculate the distance between molecular fingerprint ("tanimoto" as default). For more information see fp.sim.matrix function. |
| type | The type of fingerprint applied to the SMILES ("extended" as default). For more information see get.fingerprint function. |

Value

A list contains distance between fingerprints .

See Also

[fp.sim.matrix](#), [get.fingerprint](#),

Examples

```
data(Metabolites)
d=chemical.dissimilarity(Metabolites$SMILES[1:50])
```

ChemRICH

ChemRICH Dataset

Description

This dataset consists of a list of the metabolites names download from <https://chemrich.fiehnlab.ucdavis.edu/>. HMDB IDs were retrieved from PubChem Identifier Exchange Service (<https://pubchem.ncbi.nlm.nih.gov/idxchange/idxch>) and manually curated.

Usage

```
data(ChemRICH)
```

Value

A list with the following elements in the variable ChemRICH:

| | |
|--------|---|
| name | A vector of metabolite's names. |
| SMILES | A vector of SMILES representation of each metabolite. |
| HMDB | A vector containing HMDB IDs of each metabolite. |

Examples

```
data(ChemRICH)
```

clusters.detection

Detection of clusters.

Description

This function calculates the structural similarity between different metabolites and perform hierarchical clustering using the KODAMA algorithm and detect the optimal number of clusters. The procedure is repeated to ensure the robustness of the detection.

Usage

```
clusters.detection (smiles,  
                    repetition=10,  
                    k=50,  
                    seed=12345,  
                    max_nc = 30,  
                    dissimilarity.parameters=list(),  
                    kodama.matrix.parameters=list(),  
                    kodama.visualization.parameters=list(),
```

```
hclust.parameters=list(method="ward.D"),  
verbose = TRUE)
```

Arguments

| | |
|---------------------------------|--|
| smiles | A list of smile notations for the study metabolites dataset. |
| repetition | The number of time the KODAMA analysis is repeated. |
| k | A number of components of multidimensional scaling. |
| seed | Seed for the generation of random numbers. |
| max_nc | Maximum number of clusters. |
| dissimilarity.parameters | Optional parameters for chemical.dissimilarity function. |
| kodama.matrix.parameters | Optional parameters for KODAMA.matrix function. |
| kodama.visualization.parameters | Optional parameters for KODAMA.visualization function. |
| hclust.parameters | Optional parameters for hclust function. |
| verbose | If verbose is TRUE, it displays the progress for each iteration. |

Value

A list contains all results of KODAMA chemical similarity analysis and hierarchical clustering.

See Also

[KODAMA.matrix](#)

Examples

```
data(Metabolites)  
  
res=clusters.detection(Metabolites$SMILES)
```

diseasesMet

Metabolite-associated Diseases

Description

This function correlates metabolites to associated diseases.

Usage

```
diseasesMet(doc)
```

Arguments

doc A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the diseases associated with each metabolite.

See Also

[pathwaysMet](#), [taxonomyMet](#), [enzymesMet](#)

Examples

```
data(Metabolites)
dis=diseasesMet(Metabolites$readMet)
```

enzymesMet

Metabolite-associated Enzymes

Description

This function finds the metabolite related enzymes.

Usage

```
enzymesMet(doc)
```

Arguments

doc A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the enzymes associated with each metabolite.

See Also

[pathwaysMet](#) , [taxonomyMet](#), [diseasesMet](#)

Examples

```
data(Metabolites)
enz=enzymesMet(Metabolites$readMet)
```

| | |
|----------|------------------------------------|
| features | <i>Cluster features extraction</i> |
|----------|------------------------------------|

Description

This function finds features associated with each cluster.

Usage

```
features(doc, cla, cl, HMDB_ID)
```

Arguments

| | |
|---------|--|
| doc | The output of the readMet function. |
| cla | The output of diseasesMet , enzymesMet , pathwaysMet , propertiesMet , substituentsMet , or taxonomyMet functions. |
| cl | The output of the allbranches function containing the module memberships. |
| HMDB_ID | A vector of HMDB IDs associated with their chemical name. |

Value

A list of p-value calculated using Fisher test for cluster associated features.

See Also

[KODAMA.chem.sim](#), [tree.cutting](#), [substituentsMet](#)

Examples

```
data(Metabolites)
SMILES=Metabolites$SMILES
names(SMILES)=Metabolites$name
HMDB=Metabolites$HMDB
names(HMDB)=Metabolites$name
res=KODAMA.chem.sim(SMILES)
cl=allbranches(res$hclust)
cla=substituentsMet(Metabolites$readMet)
f=features(Metabolites$readMet, cla, cl, HMDB)
```

HFD

HFD Dataset

Description

This dataset is dataframe of metabolite dataset contains only chemical information.

Usage

```
data(HFD)
```

Value

A list with the following elements in the variable HFD:

| | |
|-------------|--|
| SMILES | A vector of SMILES representation of each metabolite. |
| CHEMICAL_ID | A vector of chemical ID number or each metabolite. |
| PUBCHEM | A vector of identifier ID number from PUBCHEM database for chemical molecules and their activities in biological assays. |
| CHEMSPIDER | A vector of a unique identifier from CHEMSPIDER database each molecule. |
| HMDB | A vector containing HMDB IDs of each metabolite. |

Examples

```
data(HFD)
```

KODAMA.chem.sim

KODAMA chemical similarity.

Description

This function calculates the structural similarity between different metabolites and perform hierarchical clustering using the KODAMA algorithm.

Usage

```
KODAMA.chem.sim (smiles,  
                 d=NULL,  
                 k=50,  
                 dissimilarity.parameters=list(),  
                 kodama.matrix.parameters=list(),  
                 kodama.visualization.parameters=list(),  
                 hclust.parameters=list(method="ward.D"))
```


Arguments

| | |
|---------------------------------|---|
| smiles | A list of smile notations for the study metabolites dataset. |
| d | A distance structure such as that returned by <code>dist</code> or a full symmetric matrix containing the dissimilarities. If <code>NULL</code> (default), then the dissimilarity matrix will be generated by <code>chemical.dissimilarity</code> function. Otherwise, <code>d</code> will be considered as the dissimilarity matrix. |
| k | A number of components of multidimensional scaling. |
| dissimilarity.parameters | Optional parameters for <code>chemical.dissimilarity</code> function. |
| kodama.matrix.parameters | Optional parameters for <code>KODAMA.matrix</code> function. |
| kodama.visualization.parameters | Optional parameters for <code>KODAMA.visualization</code> function. |
| hclust.parameters | Optional parameters for <code>hclust</code> function. |

Value

A list contains all results of KODAMA chemical similarity analysis and hierarchical clustering for the KODAMA dimensions.

See Also

[KODAMA.matrix](#)

Examples

```
data(Metabolites)

res=KODAMA.chem.sim(Metabolites$SMILES)
plot(res$kodama$visualization)
```

Metabolites

Metabolomic Dataset

Description

This dataset consists of a list of the metabolites as returned by the function `readMet` and concentration value of each metabolites.

Usage

```
data(Metabolites)
```

Value

A list with the following elements in the variable `Metabolites`:

| | |
|----------------------------|---|
| <code>concentration</code> | A matrix containing the concentration of each metabolites. |
| <code>name</code> | A vector of metabolite's names. |
| <code>SMILES</code> | A vector of SMILES representation of each metabolite. |
| <code>HMDB</code> | A vector containing HMDB IDs of each metabolite. |
| <code>readMet</code> | A list of metabolites information produced by readMet function. |

Examples

```
data(Metabolites)
```

| | |
|----------------------|----------------------------|
| <code>nameMet</code> | <i>Name of metabolites</i> |
|----------------------|----------------------------|

Description

This function extracts the metabolite's names from the list generated by [readMet](#) function.

Usage

```
nameMet(doc)
```

Arguments

`doc` A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the names of each metabolite.

See Also

[readMet](#)

Examples

```
data(Metabolites)
nam=nameMet(Metabolites$readMet)
```

pathwaysMet

Metabolic Pathways

Description

This function finds the metabolite related pathways.

Usage

```
pathwaysMet(doc)
```

Arguments

doc A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the pathways associated with each metabolite.

See Also

[readMet](#), [taxonomyMet](#), [enzymesMet](#), [diseasesMet](#)

Examples

```
data(Metabolites)
pat=pathwaysMet(Metabolites$readMet)
```

propertiesMet

Physical Proprieties of metabolites

Description

This function finds the Physical Proprieties of metabolites.

Usage

```
propertiesMet(doc)
```

Arguments

doc A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the properties associated with each metabolite.

See Also

[readMet](#), [taxonomyMet](#), [substituentsMet](#), [propertiesMet](#)

Examples

```
data(Metabolites)
pro=propertiesMet(Metabolites$readMet)
```

readMet

Metabolite Cards Reading

Description

This function extract metabocards of your metabolites dataset from <http://www.hmdb.ca/metabolites/> database and store all of this information in a list.

Usage

```
readMet(ID, address = c("http://www.hmdb.ca/metabolites/"), remove=TRUE)
```

Arguments

| | |
|---------|--|
| ID | A vector containing the HMDBcodes (i.e., metabolite IDs) of metabolites dataset. |
| address | Optional address where the MetaboCards are located. The default address is http://www.hmdb.ca/metabolites/ . |
| remove | A logic value. If true, missing and wrong HMDB IDs are removed. |

Value

A list containing all the information related to the metabocards.

See Also

[nameMet](#)

Examples

```
ID=c("HMDB0000122", "HMDB0000124", "HMDB0000243", "HMDB0000263")
doc=readMet(ID)
```

| | |
|--------------|------------------------------|
| selectionMet | <i>Metabolites selection</i> |
|--------------|------------------------------|

Description

This function select metabolites from the list generated by [readMet](#) function.

Usage

```
selectionMet(doc, sel)
```

Arguments

| | |
|-----|---|
| doc | A list of metabolites information produced by readMet function. |
| sel | A vector of metabolite's HMDBcode that will be selected |

Value

| | |
|-----|---|
| doc | A doc list contains only the selcted metabolites. |
|-----|---|

See Also

[readMet](#), [nameMet](#)

Examples

```
data(Metabolites)
doc=selectionMet(Metabolites$readMet,c("HMDB0000299", "HMDB0000881"))
nameMet(doc)
```

| | |
|-----------------|--------------------------------|
| substituentsMet | <i>Metabolite substituents</i> |
|-----------------|--------------------------------|

Description

This function finds the metabolite related substituents.

Usage

```
substituentsMet(doc)
```

Arguments

| | |
|-----|--|
| doc | A list of metabolites information produced by readMet function |
|-----|--|

Value

A data frame contains the substituents of each metabolite.

See Also

[readMet](#), [nameMet](#), [propertiesMet](#)

Examples

```
data(Metabolites)
sub=substituentsMet(Metabolites$readMet)
```

taxonomyMet

Metabolite Taxonomy

Description

This function finds the metabolite related taxonomy.

Usage

```
taxonomyMet(doc)
```

Arguments

doc A list of metabolites information produced by [readMet](#) function.

Value

A data frame contains the taxonomy of each metabolite.

See Also

[readMet](#), [propertiesMet](#), [enzymesMet](#), [diseasesMet](#)

Examples

```
data(Metabolites)
tax=taxonomyMet(Metabolites$readMet)
```

| | |
|--------------|--|
| tree.cutting | <i>Optimal cluster number calculation.</i> |
|--------------|--|

Description

This function helps to estimate the optimal cluster number that fit the metabolites dataset. It applies different optimal cluster number calculating algorithms to cut clustering tree of `hclust` function. and return a list contains index corresponding to each cluster number.

Usage

```
tree.cutting (res,max_nc=20)
```

Arguments

| | |
|--------|---|
| res | A list produced by <code>KODAMA.chem.sim</code> function. |
| max_nc | The maximum number of cluster (default = 20). |

Value

A list contains the calculation for each clustering of Rousseeuw's Silhouette index.

See Also

[KODAMA.chem.sim](#), [WMCSA](#)

Examples

```
data(Metabolites)

res=KODAMA.chem.sim(Metabolites$SMILES)
clu=tree.cutting(res,max_nc = 30)
plot(clu$min_nc:clu$max_nc,clu$res.S)
```

| | |
|-------|---|
| WMCSA | <i>Weighted Metabolite Chemical Structural Analysis</i> |
|-------|---|

Description

Summarize metabolites concentration in each of identified clusters using the module eigenvalue (eigen-metabolite) for calculating module membership measures.

Usage

```
WMCSA(data,cl)
```

Arguments

data dataset of different metabolite concentration in differnt samples.
cl The output of the [allbranches](#) function containing the module memberships.

Value

This function returns a matrix as output represent similarity score of metabolites within the same module among different samples.

See Also

[KODAMA.chem.sim](#), [tree.cutting](#)

Examples

```
data(Metabolites)

SMILES=Metabolites$SMILES
names(SMILES)=Metabolites$name
res=KODAMA.chem.sim(SMILES)
cl=allbranches(res$hclust)
ww=WMCSA(Metabolites$concentration,cl)
```

write.cls

Write a CLS file

Description

This function write a file in the format CLS defined by GenePattern.

Usage

```
write.cls(es, address)
```

Arguments

es A matrix.
address The address of the file should be saved.

Value

No return value. If an invalid address is inserted, the function will generate an error.

See Also[write.gmt](#), [write.gct](#)

`write.gct`*Write a GCT file*

Description

This function write a file in the format GCT defined by GenePattern.

Usage

```
write.gct(es, address)
```

Arguments

| | |
|----------------------|--|
| <code>es</code> | A matrix. |
| <code>address</code> | The address of the file should be saved. |

Value

No return value. If an invalid address is inserted, the function will generate an error.

See Also[write.gmt](#), [write.cls](#)

`write.gmt`*Write a GMT file*

Description

This function write a file containing the Metabolite Set information in the format GMT defined by GenePattern.

Usage

```
write.gmt(sub, address, min_entry=2, max_entry=50)
```

Arguments

| | |
|------------------------|--|
| <code>sub</code> | A matrix. |
| <code>address</code> | The address of the file should be saved. |
| <code>min_entry</code> | The minimum number of metabolites for each metabolite set. |
| <code>max_entry</code> | The maximum number of metabolites for each metabolite set. |

Value

No return value. If an invalid address is inserted, the function will generate an error.

See Also

[write.gct](#), [write.cls](#)

Index

* datasets

ChemRICH, 4
HFD, 8
Metabolites, 9

allbranches, 2, 7, 16

chemical.dissimilarity, 3, 5, 9
ChemRICH, 4
clusters.detection, 2, 4
cutree, 2

diseasesMet, 5, 6, 7, 11, 14

enzymesMet, 6, 6, 7, 11, 14

features, 7
fp.sim.matrix, 3

get.fingerprint, 3

hclust, 2, 5, 9, 15
HFD, 8

KODAMA.chem.sim, 7, 8, 15, 16
KODAMA.matrix, 5, 9
KODAMA.visualization, 5, 9

Metabolites, 9

nameMet, 10, 12–14

pathwaysMet, 6, 7, 11
propertiesMet, 7, 11, 12, 14

readMet, 6, 7, 10–12, 12, 13, 14

selectionMet, 13
substituentsMet, 7, 12, 13

taxonomyMet, 6, 7, 11, 12, 14
tree.cutting, 7, 15, 16

WMCSA, 15, 15
write.cls, 16, 17, 18
write.gct, 17, 17, 18
write.gmt, 17, 17