

Package ‘RNAsmc’

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Type Package

Title RNA Secondary Structure Module Mining, Comparison and Plotting

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Description Provides function for RNA secondary structure plotting, comparison and module mining. Given a RNA secondary structure, you can obtain stem regions, hairpin loops, internal loops, bulge loops and multibranch loops of this RNA structure using this program. They are the basic modules of RNA secondary structure. For each module you get, you can use this program to label the RNA structure with a specific color. You can also use this program to compare two RNA secondary structures to get a score that represents similarity. Reference: Reuter JS, Mathews DH (2010) <doi:10.1186/1471-2105-11-129>.

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bulgeLoopsPlot	<i>A function for bulge loops plotting</i>
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Description

Given a RNA secondary structure, it computes bulge loops in the RNA secondary structure and plots the RNA secondary structure.

Usage

```
bulgeLoopsPlot(ctFile)
```

Arguments

ctFile	A RNA secondary structure file containing structure information
--------	---

Value

Return a list containing base positions in bulge loops.

Examples

```
###
data(DataRNAstr)
bulgeLoopsPlot(DataRNAstr)
```

bulge_loop	<i>Internal function for getting bulge loops in a RNA secondary structure</i>
------------	---

Description

Given a RNA secondary structure,it compute bulge loops in the RNA secondary structure

Usage

```
bulge_loop(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing information of bulge loops

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataRNAstr)  
bulge_loop(DataRNAstr)
```

ct2dot	<i>ct2dot</i>
--------	---------------

Description

Given a RNA secondary structure,it compute the RNA secondary structure in dot-bracket notation

Usage

```
ct2dot(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

return a list including the RNA seqence and the RNA secondary structure in bracket dot form

Examples

```
###  
data(DataRNAstr)  
ct2dot(DataRNAstr)
```

DataCluster1 *A RNA secondary structure file containing structure information*

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCluster1)
```

Arguments

DataCluster1 A RNA secondary structure file containing structure information

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataCluster1)
```

DataCluster2 *A RNA secondary structure file containing structure information*

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCluster2)
```

Arguments

DataCluster2 A RNA secondary structure file containing structure information

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataCluster2)
```

DataCluster3	<i>A RNA secondary structure file containing structure information</i>
--------------	--

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCluster3)
```

Arguments

DataCluster3 A RNA secondary structure file containing structure information

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataCluster3)
```

DataCluster4	<i>A RNA secondary structure file containing structure information</i>
--------------	--

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCluster4)
```

Arguments

DataCluster4 A RNA secondary structure file containing structure information

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataCluster4)
```

DataCompareStr1 *A RNA secondary structure file containing structure information*

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCompareStr1)
```

Arguments

DataCompareStr1
A RNA secondary structure file containing structure information

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataCompareStr1)
```

DataCompareStr2 *A RNA secondary structure file containing structure information*

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataCompareStr2)
```

Arguments

DataCompareStr2
A RNA secondary structure file containing structure information

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataCompareStr2)
```

DataRNAstr	<i>A RNA secondary structure file containing structure information</i>
------------	--

Description

A RNA secondary structure file containing structure information

Usage

```
data(DataRNAstr)
```

Arguments

DataRNAstr A RNA secondary structure file containing structure information

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataRNAstr)
```

externalLoopsPlot	<i>A function for bulge loops plotting</i>
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Description

Given a RNA secondary structure, it compute external loops in the RNA secondary structure and plots the RNA secondary structure

Usage

```
externalLoopsPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file in CT format

Value

Return a list containing base positions in external loops and plot the given RNA secondary

Examples

```
###  
data(DataRNAstr)  
externalLoopsPlot(DataRNAstr)
```

external_loop	<i>Internal function for getting external loops in a RNA secondary structure</i>
---------------	--

Description

Given a RNA secondary structure, it compute external loops in the RNA secondary structure

Usage

```
external_loop(ctFile)
```

Arguments

ctFile A RNA secondary structure file in CT format

Value

Return a list containing information of external loops

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataRNAstr)  
external_loop(DataRNAstr)
```

getCompare	<i>Internal function for getting similarity score in a RNA secondary structure</i>
------------	--

Description

Given a substructure list, it computes similarity scores for given RNA structures.

Usage

```
getCompare(subStrList)
```

Arguments

subStrList A list comprised by the return of function getSubStr

Value

Return a similarity score

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataCluster1)  
data(DataCluster2)  
data(DataCluster3)  
data(DataCluster4)  
subStrList <- list(substr1 = getSubStr(DataCluster1),  
                  substr2 = getSubStr(DataCluster2),  
                  substr3 = getSubStr(DataCluster3),  
                  substr4 = getSubStr(DataCluster4))  
getCompare(subStrList)
```

getSubStr	<i>Internal function for getting substructure information in a RNA secondary structure</i>
-----------	--

Description

Given a RNA secondary structure, it gets all substructures of the RNA.

Usage

```
getSubStr(ctfile)
```

Arguments

ctfile A RNA secondary structure file containing structure information

Value

Return a list containing information of all substructures of the RNA

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataRNAstr)  
getSubStr(DataRNAstr)
```

hairpinLoopsPlot *A function for hairpin loops plotting*

Description

Given a RNA secondary structure, it compute hairpin loops in the RNA secondary structure and plots the RNA secondary structure

Usage

```
hairpinLoopsPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in hairpin loops

Examples

```
###  
data(DataRNAstr)  
hairpinLoopsPlot(DataRNAstr)
```

hairpin_loop	<i>Internal function for getting hairpin loops</i>
--------------	--

Description

Given a RNA secondary structure,it compute hairpin loops in the RNA secondary structure

Usage

```
hairpin_loop(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in hairpin loops,and the length of the number of hairpin loops

Examples

```
###  
data(DataRNAstr)  
hairpin_loop(DataRNAstr)
```

internalLoopsPlot	<i>A function for internal loops plotting</i>
-------------------	---

Description

Given a RNA secondary structure,it compute internal loops in the RNA secondary structure and plots the RNA secondary structure

Usage

```
internalLoopsPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file without the first line of free energy information

Value

Return a list containing base positions in internal loops

Examples

```
###  
data(DataRNAstr)  
internalLoopsPlot(DataRNAstr)
```

internal_loop	<i>Internal function for getting internal loops</i>
---------------	---

Description

Given a RNA secondary structure,it compute internal loops in the RNA secondary structure

Usage

```
internal_loop(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in internal loops,and the length of the number of internal loops

Examples

```
###  
data(DataRNAstr)  
internal_loop(DataRNAstr)
```

multiBranchLoopsPlot	<i>A function for multi-branch loops plotting</i>
----------------------	---

Description

Given a RNA secondary structure,it compute multi-branch loops in the RNA secondary structure and plots the RNA secondary structure

Usage

```
multiBranchLoopsPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in multi-branch loops

Examples

```
###  
data(DataRNAstr)  
multiBranchLoopsPlot(DataRNAstr)
```

multi_branch_loop	<i>Internal function for getting multi-branch loops</i>
-------------------	---

Description

Given a RNA secondary structure,it compute multi-branch loops in the RNA secondary structure

Usage

```
multi_branch_loop(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in multi-branch loops,and the length of the number of multi-branch loops

Examples

```
###  
data(DataRNAstr)  
multi_branch_loop(DataRNAstr)
```

RNAstrCluster *A function for RNAs clustering by their structure similarites*

Description

Given a RNA secondary structure,it compute simility of these RNAs and cluster them

Usage

```
RNAstrCluster(ctFiles)
```

Arguments

ctFiles A list contain RNA structures needed to cluster

Value

Return simility matrix and cluster tree

Author(s)

Zheng Hewei

Examples

```
#####  
data(DataCluster1)  
data(DataCluster2)  
data(DataCluster3)  
data(DataCluster4)  
###  
a <- list(str1=DataCluster1,str2=DataCluster2,str3=DataCluster3,str4=DataCluster4)  
RNAstrCluster(a)
```

RNAstrPlot *A function for whole RNA secondary structure plotting*

Description

Given a RNA secondary structure,it plots RNA structure and specify strucutre units by different colors

Usage

```
RNAstrPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing structure information

Author(s)

Zheng Hwei

Examples

```
#####  
data(DataRNAstr)  
RNAstrPlot(DataRNAstr)
```

stem *Internal function for getting stems*

Description

Given a RNA secondary structure,it compute stem in the RNA secondary structure

Usage

```
stem(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in stems

Examples

```
###  
data(DataRNAstr)  
stem(DataRNAstr)
```

stemPlot *A function for stems plotting*

Description

Given a RNA secondary structure,it compute stems in the RNA secondary structure and plots the RNA secondary structure

Usage

```
stemPlot(ctFile)
```

Arguments

ctFile A RNA secondary structure file containing structure information

Value

Return a list containing base positions in stems

Examples

```
###  
data(DataRNAstr)  
stemPlot(DataRNAstr)
```

strCompare *strCompare*

Description

return similarity score of two RNA secondary structures

Usage

```
strCompare(ctFile1,ctFile2)
```

Arguments

ctFile1 A RNA secondary structure file containing structure information
ctFile2 A RNA secondary structure file containing structure information

Value

Returns a numerical value which represent the similarity of the two RNA secondary structures.The larger the value, the more similar the two RNA structures are.The maximum value is 10, representing the two RNA secondary structures exactly the same,and 0 is the minnum value.

Examples

```
###  
data(DataCluster1)  
data(DataCluster2)  
#####RNAstrPlot(DataCluster1)  
#####RNAstrPlot(DataCluster2)  
strCompare(DataCluster1,DataCluster2)
```

strComparePlot	<i>strComparePlot</i>
----------------	-----------------------

Description

return similarity score of two RNA secondary structures

Usage

```
strComparePlot(ctFile1,ctFile2)
```

Arguments

ctFile1	A RNA secondary structure file containing structure information
ctFile2	A RNA secondary structure file containing structure information

Value

Returns a numerical value which represent the similarity of the two RNA secondary structures. The larger the value, the more similar the two RNA structures are. The maximum value is 10, representing the two RNA secondary structures exactly the same, and 0 is the minimum value.

Examples

```
###  
data(DataCluster1)  
data(DataCluster2)  
#####RNAstrPlot(DataCluster1)  
#####RNAstrPlot(DataCluster2)  
strComparePlot(DataCluster1,DataCluster2)
```

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