

# Package ‘RNAsmc’

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**Type** Package

**Title** RNA Secondary Structure Module Mining, Comparison and Plotting

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**Depends** RRNA,stats,graphics,circlize

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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](https://doi.org/10.1186/1471-2105-11-129)>.

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bulgeLoopsPlot      *A function for bulge loops plotting*

### Description

Given a RNA secondary structure, it compute 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 sequece 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 Hwei

**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 Hwei

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

---

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

---

**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 Hwei

**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 Hwei

**Examples**

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

---

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

---

**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)
```

---

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

---

**Description**

Internal function for getting similarity score in a RNA secondary structure

**Usage**

```
getScore(h1, i1, b1, m1, s1, e1,
         seqA, seqCode1, h1Num, i1Num, b1Num, m1Num, s1Num, e1Num,
         h2, i2, b2, m2, s2, e2,
         seqB, seqCode2, h2Num, i2Num, b2Num, m2Num, s2Num, e2Num)
```

**Arguments**

h1	hairpin_loop result A
i1	internal_loop result A
b1	bulge_loop result A
m1	multi_branch_loop result A
s1	stem result A
e1	external_loop result A
seqA	sequence A
seqCode1	coding sequence A
h1Num	hairpin_loop number A
i1Num	internal_loop number A
b1Num	bulge_loop number A
m1Num	multi_branch_loop number A
s1Num	stem number A
e1Num	external_loop number A
h2	hairpin_loop result B
i2	internal_loop result B
b2	bulge_loop result B
m2	multi_branch_loop result B
s2	stem result B
e2	external_loop result B
seqB	sequence B
seqCode2	coding sequence B
h2Num	hairpin_loop number B
i2Num	internal_loop number B
b2Num	bulge_loop number B
m2Num	multi_branch_loop number B
s2Num	stem number B
e2Num	external_loop number B

**Value**

Return a list contains similarity score and other information

**Author(s)**

Zheng Hewei

**Examples**

```
#####  
#nothing
```

---

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 Hewei

**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              *Internal function for getting hairpin loops*

---

**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      *A function for internal loops plotting*

---

**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            *Internal function for getting internal loops*

---

**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 *A function for multi-branch loops plotting*

---

**Description**

Given a RNA secondary structure, it computes 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)
```

---

RNAcirPlot	<i>function for plotting RNA secondary structure in a circos style</i>
------------	--

---

**Description**

Given a RNA secondary structure,it plots RNA secondary structure in a circos style

**Usage**

```
RNAcirPlot(ctFile,cex = 1,posNum = 2.5,ifNum = FALSE,  
          ifBulge = FALSE,ifExternalLoops = FALSE,ifHairpin = FALSE,  
          ifInternalLoops = FALSE,ifMultiBranchLoops = FALSE)
```

**Arguments**

ctFile	A RNA secondary structure file containing structure information
cex	The size of base or number in plotting
posNum	The position of number in plotting. Change the position of number if number is plotted
ifNum	Whether to draw number
ifBulge	Whether to emphasize bulge loops
ifExternalLoops	Whether to emphasize external loops
ifHairpin	Whether to emphasize hairpin loops
ifInternalLoops	Whether to emphasize internal loops
ifMultiBranchLoops	Whether to emphasize multi branch loops

**Value**

Return a RNA secondary structure in a circos style

**Author(s)**

Zheng Hewei

**Examples**

```
#####
data(DataRNAstr)
RNAcirPlot(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 Hewei

**Examples**

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

---

stem	<i>Internal function for getting stems</i>
------	--

---

**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	<i>A function for stems plotting</i>
----------	--------------------------------------

---

**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	<i>strCompare</i>
------------	-------------------

---

**Description**

return similarity score of two RNA secondary structures

**Usage**

```
strCompare(ctFile1,ctFile2,randomTime = 1000)
```

**Arguments**

ctFile1	A RNA secondary structure file containing structure information
ctFile2	A RNA secondary structure file containing structure information
randomTime	random times of permutation test to get P value

**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 minmum value.

**Examples**

```
###  
data(DataCluster1)  
data(DataCluster2)  
#####RNAstrPlot(DataCluster1)  
#####RNAstrPlot(DataCluster2)  
strCompare(DataCluster1,DataCluster2,randomTime = 100)
```

---

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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