

Package ‘Structstrings’

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Title Implementation of the dot bracket annotations with Biostrings

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Description The Structstrings package implements the widely used dot bracket annotation for storing base pairing information in structured RNA. Structstrings uses the infrastructure provided by the Biostrings package and derives the DotBracketString and related classes from the BString class. From these, base pair tables can be produced for in depth analysis. In addition, the loop indices of the base pairs can be retrieved as well. For better efficiency, information conversion is implemented in C, inspired to a large extend by the ViennaRNA package.

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'Structstrings-DotBracketDataFrame.R'
'Structstrings-DotBracketString.R'
'Structstrings-DotBracketStringSet.R'
'Structstrings-DotBracketStringSetList.R'
'Structstrings-LoopIndexList.R'
'Structstrings-StructuredXStringSet.R'
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convertAnnotation	<i>Convert between dot bracket annotations</i>
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Description

convertAnnotation converts a type of dot bracket annotation into another. This only works if the original bracket type is present and the target bracket type is not.

Usage

```
convertAnnotation(x, from, to)

## S4 method for signature 'DotBracketString'
convertAnnotation(x, from, to)

## S4 method for signature 'DotBracketStringSet'
convertAnnotation(x, from, to)

## S4 method for signature 'DotBracketStringSetList'
convertAnnotation(x, from, to)
```

Arguments

x a DotBracketString, DotBracketStringSet or DotBracketStringSetList
 from which annotation type should be converted? Must be one of the following values: 1L = '()', 2L = '<>', 3L = '[]', 4L = '{}' and must be present in the input.

to Into which annotation type should the selected one be converted? Must be one of the following values: 1L = '()', 2L = '<>', 3L = '[]', 4L = '{}'. Must not be present in the input.

Value

The modified input object, a `DotBracketString*` object.

Examples

```
str <- "((.))..[[...]]...{{...}}....."
dbs <- DotBracketString(str)
convertAnnotation(dbs, 1L, 2L)
```

dotbracket	<i>StructuredRNAStringSet for storing DotBracketAnnotation alongside nucleotide sequences</i>
------------	---

Description

The [StructuredXStringSet](#) class can be used to store structure information alongside RNA sequences. The class behaves like the [QualityScaledXStringSet](#) classes.

Please note, that this does not check for validity regarding base pairing capabilities.

Usage

```
dotbracket(x)

dotbracket(x) <- value

## S4 method for signature 'StructuredXStringSet'
dotbracket(x)

## S4 replacement method for signature 'StructuredXStringSet'
dotbracket(x) <- value

StructuredRNAStringSet(x, structure)

readStructuredRNAStringSet(filepath, nrec = -1L, skip = 0L,
  seek.first.rec = FALSE, use.names = TRUE)

writeStructuredXStringSet(x, filepath, append = FALSE,
  compress = FALSE)

## S4 method for signature 'StructuredXStringSet'
getBasePairing(x, compress = TRUE,
  return.sequence = FALSE)

## S4 method for signature 'StructuredXStringSet'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)
```

Arguments

<code>x</code>	For the Structured*StringSet constructors: Either a character vector, or an RNAString, RNAStringSet object. For writeQualityScaledXStringSet: A StructuredRNAStringSet derivative.
<code>structure, value</code>	A DotBracketStringSet
<code>use.names, type, filepath, nrec, skip, seek.first.rec, append, ...</code>	See DotBracketStringSet-io
<code>compress</code>	See getBasePairing or DotBracketStringSet-io
<code>return.sequence</code>	TRUE(default) or FALSE: Whether the sequence should be returned in the base column.
<code>bracket.type</code>	<code>getLoopIndices</code> : Which dot bracket annotation type should be converted into loop indices? Only usable, if more than one is present. (1L = '()', 2L = '<>', 3L = '[]', 4L = '{}')
<code>warn.type.drops</code>	See getLoopIndices

Details

the `dotbracket` function allows access to the included [DotBracketStringSet](#).

Value

a StructuredRNAStringSet object.

Examples

```
str <- DotBracketStringSet("((()))")
seq <- RNAStringSet("AGCU")
sdbf <- StructuredRNAStringSet(seq, str)
```

DotBracketDataFrame *DataFrame for storing base pairing information*

Description

The DotBracketDataFrame object is derived from the [DataFrame](#) class. The [DotBracketDataFrameList](#) is implemented analogous, which is also available as [CompressedSplitDotBracketDataFrameList](#). Since the names are quite long, the following short cut functions are available for object creation: `DBDF`, `DBDFL` and `SDBDFL`.

The DotBracketDataFrame can only contain 5 columns, which are named `pos`, `forward`, `reverse`, `character` and `base`. The last two columns are optional. The type of the first three has to be integer, whereas the fourth is a character and fifth is a XStringSet column.

Upon creation and modification, the validity of the contained base pairing information is checked. If the information is not correct, an error is thrown.

Usage

```

DotBracketDataFrame(...)

DBDF(...)

DotBracketDataFrameList(...)

DBDFL(...)

SplitDotBracketDataFrameList(..., compress = TRUE, cbindArgs = FALSE)

SDBDFL(..., compress = TRUE, cbindArgs = FALSE)

```

Arguments

...	for <code>DotBracketDataFrame</code> the input vectors and for <code>DotBracketDataFrameList</code> the <code>DataFrame</code> or the <code>DotBracketDataFrame</code> objects.
compress	If <code>compress = TRUE</code> , returns a <code>CompressedSplitDataFrameList</code> else returns a <code>SimpleSplitDataFrameList</code> .
cbindArgs	If <code>cbindArgs = FALSE</code> , the ... arguments are coerced to <code>DotBracketDataFrame</code> objects and concatenated to form the result. If <code>cbindArgs = TRUE</code> , the arguments are combined as columns. The arguments must then be the same length, with each element of an argument mapping to an element in the result.

Value

a `DotBracketDataFrame*` object.

Examples

```

# Manual creation
df <- DataFrame(pos = c(1,2,3,4,5,6),
                forward = c(6,5,0,0,2,1),
                reverse = c(1,2,0,0,5,6))

# Either works
dbdf <- as(df, "DotBracketDataFrame")
dbdf <- DotBracketDataFrame(df)

# With multiple input DataFrames a SplitDotBracketDataFrameList is returned
dbdf1 <- DotBracketDataFrame(df,df,df,df)

# Creation from a DotBracketString object is probably more common
data("dbs", package = "Structstrings", envir = environment())
dbdf1 <- getBasePairing(dbs)
# Elements are returned as DotBracketDataFrames
dbdf1[[1]]

```

Description

The DotBracketString extends the `BString` class. The `DotBracketStringSet` and `DotBracketStringSetList` classes are implemented accordingly.

The alphabet consists of the letters `(,), ., <, >, [,], { and }`, which describes base pairing between positions. The `.` letter describes an unpaired position. The number of opening and closing letters need to be equal within a `DotBracketString` to be a valid dot bracket annotation. This is checked upon creation and modification of the object.

The objects can also be created using the shorter function names `DB`, `DBS` and `DBSL`.

Currently, there is no distinction in base pairing strength between the different bracket types.

Usage

```
DotBracketString(x = character(), start = 1, nchar = NA)
```

```
DB(x = character(), start = 1, nchar = NA)
```

```
DotBracketStringSet(x = character())
```

```
DBS(x = character())
```

```
DotBracketStringSetList(..., use.names = TRUE)
```

```
DBSL(..., use.names = TRUE)
```

```
## S4 method for signature 'DotBracketString'
alphabet(x)
```

```
## S4 method for signature 'DotBracketString'
encoding(x)
```

Arguments

<code>x</code>	<code>DotBracketString</code> , <code>DotBracketStringSet</code> : the input, which is tried to be converted into a <code>DotBracketString*</code> .
<code>start</code>	<code>DotBracketString</code> : starting position for creating the object from the character input.
<code>nchar</code>	<code>DotBracketString</code> : number of letters are read from the input character
<code>...</code>	<code>DotBracketStringSetList</code> : the input, which converted into a list. Each element is tried to be converted into a <code>DotBracketStringSet</code> .
<code>use.names</code>	<code>DotBracketStringSetList</code> : Should names of the input be preserved.

Value

a `DotBracketString*` object.

Examples

```
str <- "((.))..[[.]]...{.{.}}..<<.>>"
db <- DotBracketString(str)
dbs <- DotBracketStringSet(c("structure1" = str, "structure2" = str))
dbsl <- DotBracketStringSetList(list(first = dbs, second = dbs))
```

DotBracketStringSet-io

Reading and writing DotBracketStringSet objects

Description

`readDotBracketStringSet` and `writeDotBracketStringSet` are functions to read and write dot bracket strings from/to file. Since the `<>` is in conflict with the fasta format, saving to fastq file is sometimes the only option. Saving a string with a `<>` bracket type to a fasta file will throw an error.

The functions use the underlying Biostrings infrastructure and share most of its parameters. For a more detailed look have a look [here](#).

Usage

```
readDotBracketStringSet(filepath, format = "fasta", nrec = -1L,  
  skip = 0L, seek.first.rec = FALSE, use.names = TRUE,  
  with.qualities = FALSE)
```

```
writeDotBracketStringSet(x, filepath, append = FALSE, compress = FALSE,  
  format = "fasta", ...)
```

```
saveDotBracketStringSet(x, objname, dirpath = ".", save.dups = FALSE,  
  verbose = TRUE)
```

Arguments

<code>filepath</code>	The file name, when writing, or file name(s) when reading.
<code>format</code>	"fasta" or "fastq"
<code>nrec</code>	Single integer. The maximum of number of records to read in. Negative values are ignored.
<code>skip</code>	Single non-negative integer. The number of records of the data file(s) to skip before beginning to read in records.
<code>seek.first.rec</code> , <code>with.qualities</code> , <code>compress</code> , <code>...</code> , <code>use.names</code> , <code>objname</code> , <code>dirpath</code> , <code>save.dups</code> , <code>verbose</code>	Have a look here .
<code>x</code>	A <code>DotBracketStringSet</code> object
<code>append</code>	TRUE or FALSE. If TRUE output will be appended to file. Otherwise, it will overwrite the contents of file.

Value

`readDotBracketStringSet` returns a `DotBracketStringSet` object, `writeDotBracketStringSet` returns NULL invisibly.

Examples

```
data("dbs", package = "Structstrings", envir = environment())  
file <- tempfile()  
# works both since a DotBracketStringSet is a BStringSet  
writeXStringSet(dbs, file)  
writeDotBracketStringSet(dbs, file)
```

```
# to return immediatly a DotBracketStringSet us readDotBracketStringSet()
dbs2 <- readDotBracketStringSet(file)
```

getBasePairing

Accessing Dot Bracket annotation

Description

getBasePairing converts a dot bracket annotation from a [DotBracketString](#) into a base pair table as [DotBracketDataFrame](#). Base pairing is indicated by corresponding numbers in the forward and reverse columns.

getDotBracket converts the dot bracket annotation from a [DotBracketDataFrame](#) into a [DotBracketString](#). If the character column is populated, the information from this column will be used. If this is not desired set force = TRUE. However, beware that this will result in a dot bracket annotation, which does not necessarily matches the original dot bracket string it may have been created from. It is rather the dot bracket string with the lowest number of different loops and it will use the different dot bracket annotations one after another. Example: "(((«<>»)))" will be returned as ((((((())())))). (((<<<<)))>>> will be returned as (((<<<<)))>>>, ((([[[[]]]]]) will be returned as (((<<<<)))>>>.

getLoopIndices converts the dot bracket annotation from a [DotBracketString](#) or [DotBracketDataFrame](#) into a [LoopIndexList](#).

Usage

```
getBasePairing(x, compress = TRUE, return.sequence = FALSE)
```

```
getDotBracket(x, force = FALSE)
```

```
getLoopIndices(x, bracket.type, warn.type.drops = TRUE)
```

```
## S4 method for signature 'DotBracketString'
getBasePairing(x)
```

```
## S4 method for signature 'DotBracketStringSet'
getBasePairing(x, compress = TRUE)
```

```
## S4 method for signature 'DotBracketDataFrame'
getDotBracket(x, force = FALSE)
```

```
## S4 method for signature 'DotBracketDataFrameList'
getDotBracket(x, force = FALSE)
```

```
## S4 method for signature 'CompressedDotBracketDataFrameList'
getDotBracket(x,
  force = FALSE)
```

```
## S4 method for signature 'DotBracketString'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)
```



```

## S4 method for signature 'DotBracketStringSet'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)

## S4 method for signature 'DotBracketDataFrame'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)

## S4 method for signature 'DotBracketDataFrameList'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)

## S4 method for signature 'SplitDotBracketDataFrameList'
getLoopIndices(x, bracket.type,
  warn.type.drops = TRUE)

## S4 method for signature 'CompressedSplitDotBracketDataFrameList'
getLoopIndices(x,
  bracket.type, warn.type.drops = TRUE)

```

Arguments

x	a DotBracketString or DotBracketStringSet object
compress	getBasePairing: whether to return a CompressedDotBracketDataFrameList or a SplitDotBracketDataFrameList
return.sequence	if the input is a StructuredXStringSet : TRUE(default) or FALSE: Whether the sequence should be returned in the base column.
force	getDotBracket: Should the dot bracket string be generated from the base pairing, if the character column is present?
bracket.type	getLoopIndices: Which dot bracket annotation type should be converted into loop indices? Only usable, if more than one is present. (1L = '()', 2L = '<>', 3L = '[]', 4L = '{}')
warn.type.drops	getLoopIndices: TRUE(default) or FALSE: Warn if more than one dot bracket annotation type is present in the input?

Value

getBasePairing: The result is a [DotBracketDataFrame](#) with following columns: pos, forward, reverse, character (and optionally the base column). If a position is unpaired, forward and reverse will be \emptyset , otherwise it will match the base paired positions.

getLoopIndices: returns a [LoopIndexList](#).

Examples

```

data("dbs", package = "Structstrings", envir = environment())
# conversion
dbdf <- getBasePairing(dbs)
# ... and the round trip
dbs <- getDotBracket(dbdf)

```

```
# loop indices per bracket type
loopids <- getLoopIndices(dbs)
# choose the bracket type manually, if necessary
loopids <- getLoopIndices(dbs, bracket.type = 1L)
# do not show warning if multiple bracket types are present
loopids <- getLoopIndices(dbs, bracket.type = 1L, warn.type.drops = FALSE)
```

LoopIndexList	<i>LoopIndexList: base pairing information as a list of integer values</i>
---------------	--

Description

With loop indices base pairing information can be represented by giving each base pair a number and increasing/decreasing it with each opened/closed base pair. This information can be used for further analysis of the represented structure.

Usage

```
LoopIndexList(...)
```

Arguments

... the integer input vectors.

Value

a LoopIndexList object.

Examples

```
# if the object is create manually make sure it is a valid structure
# information. Otherwise an error is thrown.
lil <- LoopIndexList(list(c(1L,2L,3L,3L,3L,2L,1L,0L,5L,6L,6L,5L),
                        c(1L,2L,2L,2L,2L,2L,1L,0L,5L,6L,6L,5L)))
```

Structstrings	<i>Structstrings: implementation of the dot bracket annotations with Biostrings</i>
---------------	---

Description

The Structstrings package implements the widely used to bracket annotation for storing base pairing information in structured RNA. For example it is used in the ViennaRNA package (Lorenz et al. 2011), the tRNAscan-SE software (Lowe et al. 1997) and the tRNAdb (Jühling et al. 2009).

Structstrings uses the infrastructure provided by the Biostrings package and derives the class [DotBracketString](#) and such from the equivalent [BString](#) class. From these base pair table can be produced for in depth analysis. For this purpose the [DotBracketDataFrame](#) class is derived from the [DataFrame](#) class. In addition the loop IDs of the base pairs can be retrieved as a [LoopIndexList](#), a derivative of the [IntegerList](#). Generally, it checks automatically for the validity of the dot bracket annotation.

The conversion of the `DotBracketString` to the base pair table and the loop indices is implemented in C for efficiency. The C implementation to a large extent inspired by the `ViennaRNA` package.

This package was developed as a requirement for the `tRNA` package. However, other projects might benefit as well, so it was split of and improved upon.

Manual

Please refer to the Structstrings vignette for an example how to work and use the package: [Structstrings](#).

Author(s)

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References

Lorenz, Ronny; Bernhart, Stephan H.; Höner zu Siederdisen, Christian; Tafer, Hakim; Flamm, Christoph; Stadler, Peter F.; Hofacker, Ivo L. (2011): "ViennaRNA Package 2.0". *Algorithms for Molecular Biology* 6:26. doi:[10.1186/1748-7188-6-26](https://doi.org/10.1186/1748-7188-6-26)

Lowe, T.M.; Eddy, S.R.(1997): "tRNAscan-SE: A program for improved detection of transfer RNA genes in genomic sequence". *Nucl. Acids Res.* 25: 955-964. doi:[10.1093/nar/25.5.955](https://doi.org/10.1093/nar/25.5.955)

Jühling, Frank; Mörl, Mario; Hartmann, Roland K.; Sprinzl, Mathias; Stadler, Peter F.; Pütz, Joern (2009): "TRNAdb 2009: Compilation of tRNA Sequences and tRNA Genes." *Nucleic Acids Research* 37 (suppl_1): D159–D162. doi:[10.1093/nar/gkn772](https://doi.org/10.1093/nar/gkn772).

Structstrings-data *Structstrings example data*

Description

Example data for using the Structstrings package

Usage

`dbs`

`seq`

Format

object of class `DotBracketStringSet` and `DNAStrngSet`

Source

sequence and dot bracket annotation of tRNAscan-SE output for *S. cerevisiae** imported using `tRNAscanImport`. The example file is part of the `tRNAscanImport` package.

Structstrings-internals

Structstrings internals

Description

Analog to Biostrings there are a few objects, which should only be used internally, but may be of use to other package developers. Otherwise take care.

Usage

```
DOTBRACKET_CHAR_VALUES
```

```
DOTBRACKET_ALPHABET
```

```
STRUCTURE_NEUTRAL_CHR
```

```
STRUCTURE_OPEN_CHR
```

```
STRUCTURE_CLOSE_CHR
```

```
## S4 replacement method for signature 'DotBracketDataFrame'  
x[i, j, ...] <- value
```

```
## S4 replacement method for signature 'CompressedSplitDotBracketDataFrameList'  
colnames(x) <- value
```

Arguments

```
x, i, j, ..., value
```

See [DataFrame](#).

Format

An object of class integer of length 9.

Examples

```
DOTBRACKET_CHAR_VALUES  
DOTBRACKET_ALPHABET  
STRUCTURE_NEUTRAL_CHR  
STRUCTURE_OPEN_CHR  
STRUCTURE_CLOSE_CHR
```

```
# the replace method for a DotBracketDataFrame had to be reimplemented  
# because of the requirement of columns for a DotBracketDataFrameList and  
# DotBracketDataFrame  
data("dbs", package = "Structstrings", envir = environment())  
dbdf1 <- getBasePairing(dbs)  
# Elements are returned as DotBracketDataFrames  
dbdf <- dbdf1[[1]]  
dbdf1[[1]] <- dbdf  
dbdf1[1] <- dbdf1[1]
```

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