

# Package ‘tRNA’

October 13, 2019

**Title** Analyzing tRNA sequences and structures

**Version** 1.3.2

**Date** 2018-06-11

**Description** The tRNA package allows tRNA sequences and structures to be accessed and used for subsetting. In addition, it provides visualization tools to compare feature parameters of multiple tRNA sets and correlate them to additional data. The tRNA package uses GRanges objects as inputs requiring only few additional column data sets.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** true

**biocViews** Software, Visualization

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**Imports** stringr, S4Vectors, methods, assertive, BiocGenerics, IRanges, XVector, Biostrings, Modstrings, ggplot2, scales

**Suggests** knitr, rmarkdown, testthat, BiocStyle, tRNAscanImport

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'tRNA-features.R' 'tRNA-plot.R' 'tRNA-sequences.R'  
'tRNA-structures.R' 'tRNA-subset.R' 'tRNA-utils.R'

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

**BugReports** <https://github.com/FelixErnst/tRNA/issues>

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gettRNABasePairing      *Accessing Dot Bracket annotation of tRNAs*

---

### Description

gettRNABasePairing converts the dot bracket annotation into a DotBracketDataFrame. Base pairing is indicated by corresponding numbers in the forward and reverse columns. For more detail have a look at [getBasePairing](#).

gettRNALoopIDs converts the dot bracket annotation into a LoopIDList. For more details have a look at [getLoopIDList](#).

### Usage

```
gettRNABasePairing(x, with.nucleotides = FALSE)
```

```
gettRNALoopIDs(x)
```

```
## S4 method for signature 'GRanges'
gettRNABasePairing(x, with.nucleotides = FALSE)
```

```
## S4 method for signature 'GRanges'
gettRNALoopIDs(x)
```

### Arguments

`x` a GRanges object created by `import.tRNAscanAsGRanges` or GRanges with equivalent information. The `tRNA_str` and `tRNA_seq` columns will be used to construct a StructuredXStringSet and used for input into `getBasePairing`.

`with.nucleotides` a single logical value: should the nucleotides be saved alongside the base pairing information in the 'base' column?

### Value

gettRNABasePairing: The result is a DotBracketDataFrame with following columns: `pos`, `forward`, `reverse`, `character` and `base`. If a position is unpaired, forward and reverse will be  $\emptyset$ , otherwise it will match the base paired positions.

gettRNALoopIDs: return a list of list of loop ids.

**Examples**

```
data("gr", package = "tRNA", envir = environment())
gettRNABasePairing(gr[1])
gettRNALoopIDs(gr[1])
```

---

gettRNAFeaturePlots     *Graphical summary of tRNA features*

---

**Description**

gettRNAFeaturePlots generates a plot for every feature found with gettRNASummary. Based on the datatype, it will generate suitable point or bar plots. Names of the GRangesList will be used as sample identifiers and used for colouring.

The options tRNA\_colour\_palette, tRNA\_colour\_yes and tRNA\_colour\_no will be used for colours.

**Usage**

```
gettRNAFeaturePlots(x, plotScores = FALSE, scores = NA,
  scoreLabel = "Score")
```

```
## S4 method for signature 'GRangesList'
gettRNAFeaturePlots(x, plotScores = FALSE,
  scores = NA, scoreLabel = "Score")
```

**Arguments**

x	a named GRangesList object.
plotScores	logical value, whether to plot scores. If scores are not provided with an additional argument, it will try to use the column "score" of the GRanges objects.
scores	a list of scores, which have to have the same dimensions as the GRangesList or GRanges object.
scoreLabel	a string to use as a label for the x axis.

**Value**

a list of ggplot2 plots. These can be customized further.

**Examples**

```
data("gr", package = "tRNA", envir = environment())
data("gr_eco", package = "tRNA", envir = environment())
grl <- GRangesList(Sce = gr,
  Eco = gr_eco)
plots <- gettRNAFeaturePlots(grl)

# customized plots
plots$length$layers <- plots$length$layers[c(-1,-2)]
plots$length + ggplot2::geom_boxplot()
```

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 gettRNAstructureGRanges

*tRNA structures and sequences*


---

## Description

gettRNAstructureGRanges returns a list of GRanges describing the boundaries of tRNA structures as extracted from the dot bracket annotation. The dot bracket annotation is parsed using gettRNABasePairing, which internally uses getBasePairing.

gettRNAstructureSeq returns split or partial tRNA sequences based on the structure information. Variations in the length of structure features can be padded to retrieve sequences of equal length. If sequences are joined by setting joinCompletely = FALSE, the boundaries of the tRNA structure are stored in the result as metadata. They can be accessed as an IRanges object by using metadata(seq)[["tRNA\_structures"]].

## Usage

```
gettRNAstructureGRanges(x, structure = "")

gettRNAstructureSeqs(x, structure = "", joinCompletely = FALSE,
  joinFeatures = FALSE, padSequences = TRUE)

## S4 method for signature 'GRanges'
gettRNAstructureSeqs(x, structure = "",
  joinCompletely = FALSE, joinFeatures = FALSE, padSequences = TRUE)

## S4 method for signature 'GRanges'
gettRNAstructureGRanges(x, structure = "")
```

## Arguments

- |                |  |
|----------------|--|
| x              | a GRanges object with tRNA information. It has to pass the istRNAGRanges function.   |
| structure      | optional parameter for returning just partial sequences. The following values are accepted: anticodonStem, Dprime5, DStem, Dloop, Dprime3, acceptorStem, anticodonloop, variableLoop, TStem, Tloop, discriminator. (default: structure = "")                           |
| joinCompletely | Should the sequence parts, which are to be returned, be joined into one sequence? (default: joinCompletely = FALSE) Setting this to TRUE excludes joinFeatures be set to TRUE as well. In addition, joinCompletely = TRUE uses automatically all sequence structures.  |
| joinFeatures   | Should the sequence parts, which are to be returned and are from the same structure type, be joined into one sequence? (default: joinCompletely = FALSE) Setting this to TRUE excludes joinCompletely be set to TRUE as well. joinCompletely takes precedence.         |
| padSequences   | parameter whether sequences of the same type should be returned with the same length. For stems missing positions will be filled up in the middle, for loops at the ends. (default: padSequences = TRUE). If joinCompletely == TRUE this is set to TRUE automatically. |

**Value**

a list of GRanges or DNASTringSet objects. In case joinCompletely is set to TRUE a single DNASTringSet is returned.

**Examples**

```
data("gr", package = "tRNA", envir = environment())
gettRNAstructureGRanges(gr, structure = "anticodonLoop")
gettRNAstructureSeqs(gr, structure = "anticodonLoop")
gettRNABasePairing(gr[1:10])
```

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gettRNASummary	<i>Summary of tRNA features</i>
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---

**Description**

gettRNAsummary prepares a DataFrame with the aggregated features of tRNAs from a GRanges object. Logical values are converted to numeric values.

**Usage**

```
gettRNAsummary(x)

## S4 method for signature 'GRangesList'
gettRNAsummary(x)

## S4 method for signature 'GRanges'
gettRNAsummary(x)
```

**Arguments**

x a GRanges or a GRangesList object. All elements have to pass the isRNAGRanges test.

**Value**

a DataFrame object

**Examples**

```
data("gr", package = "tRNA", envir = environment())
gettRNAsummary(gr)
```

---

hasTStem

*Subsetting tRNAs*


---

### Description

The functions `has*` can be used to subset the `GRanges` object containing information about tRNAs.

Please note that the settings `mismatches` and `bulged` take precedence before `unpaired` or `paired`. This means that by setting either `mismatches` or `bulged` to either `TRUE` or `FALSE`, `unpaired = TRUE` or `paired = TRUE` are automatically set to allow specific subsetting. If this removes elements from the results, please consider constructing a logical vector with two calls as suggested in the examples.

### Usage

```
hasTStem(x, length = NA, unpaired = NA, mismatches = NA,
        bulged = NA)
```

```
hasDStem(x, length = NA, unpaired = NA, mismatches = NA,
        bulged = NA)
```

```
hasAcceptorStem(x, length = NA, unpaired = NA, mismatches = NA,
                bulged = NA)
```

```
hasAnticodonStem(x, length = NA, unpaired = NA, mismatches = NA,
                 bulged = NA)
```

```
hasTloop(x, length = NA)
```

```
hasDloop(x, length = NA)
```

```
hasAnticodonLoop(x, length = NA)
```

```
hasVariableLoop(x, length = NA, paired = NA, mismatches = NA,
                bulged = NA)
```

```
## S4 method for signature 'GRanges'
hasTStem(x, length = NA, unpaired = NA,
        mismatches = NA, bulged = NA)
```

```
## S4 method for signature 'GRanges'
hasDStem(x, length = NA, unpaired = NA,
        mismatches = NA, bulged = NA)
```

```
## S4 method for signature 'GRanges'
hasAcceptorStem(x, length = NA, unpaired = NA,
                mismatches = NA, bulged = NA)
```

```
## S4 method for signature 'GRanges'
hasAnticodonStem(x, length = NA, unpaired = NA,
                 mismatches = NA, bulged = NA)
```

```
## S4 method for signature 'GRanges'
hasTloop(x, length = NA)

## S4 method for signature 'GRanges'
hasDloop(x, length = NA)

## S4 method for signature 'GRanges'
hasAnticodonLoop(x, length = NA)

## S4 method for signature 'GRanges'
hasVariableLoop(x, length = NA, paired = NA,
  mismatches = NA, bulged = NA)
```

### Arguments

x	a GRanges object from a tRNAscan import or with equivalent information
length	the length as integer
unpaired	logical: has unpaired nucleotides
mismatches	logical: has mismatched nucleotides
bulged	logical: has mismatched nucleotides of different length creating a bulge
paired	logical: has paired nucleotides (only used for loops)

### Value

a logical vector of the length of input GRanges object

### Examples

```
data("gr", package = "tRNA", envir = environment())
hasTstem(gr, length = 5, mismatches = TRUE)
gr[hasTstem(gr, length = 5, mismatches = TRUE)]
gr[hasDstem(gr, unpaired = FALSE) & hasDstem(gr, mismatches = FALSE)]
```

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istRNAGRanges	<i>tRNA compatibility check</i>
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### Description

istRNAGRanges checks whether a GRanges object contains the information expected for a tRNA result. This is used internally to ensure the the required data is present in the input.

### Usage

```
istRNAGRanges(x)

## S4 method for signature 'GRanges'
istRNAGRanges(x)
```

**Arguments**

x                      the GRanges object to test for compatibility.

**Value**

a logical value

**Examples**

```
data("gr", package = "tRNA", envir = environment())
istrNAGRanges(gr)
```

---

tRNA

*tRNA: analyzing tRNA sequences and structures*


---

**Description**

The tRNA package allows feature information of tRNAs to be accessed and list of tRNA to be subset based on these features. The main purpose is to unify overlapping functions from the tRNAscanImport and tRNAdbImport packages. The functionality is currently under development and may change. The package expects a GRanges object with certain columns as input. The following columns are a requirement: tRNA\_length, tRNA\_type, tRNA\_anticodon, tRNA\_seq, tRNA\_str, tRNA\_CCA.end. Outputs of tRNAscanImport and tRNAdbImport meet these requirements.

Have a look at the vignette for an overview of the functionality. Additional functions are planned to be added in the future.

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tRNA-data

*tRNA example data*


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**Description**

Example data for using the tRNA package

**Usage**

tRNA

gr\_human

gr\_human2

gr\_eco

**Format**

object of class GRanges

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