Package 'tRNA'

January 20, 2026

Title Analyzing tRNA sequences and structures

Version 1.28.0

Date 2025-07-28

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.

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Encoding UTF-8

LazyData true

biocViews Software, Visualization

Depends R (>= 3.5), GenomicRanges, Structstrings

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

Suggests knitr, rmarkdown, testthat, BiocStyle, tRNAscanImport

Collate 'tRNA.R' 'AllGenerics.R' 'tRNA-checks.R' 'tRNA-dotbracket.R' 'tRNA-features.R' 'tRNA-plot.R' 'tRNA-sequences.R' 'tRNA-structures.R' 'tRNA-subset.R' 'tRNA-utils.R' 'utils.R'

VignetteBuilder knitr

RoxygenNote 7.3.1

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

git_url https://git.bioconductor.org/packages/tRNA

git_branch RELEASE_3_22

git_last_commit 3266a22

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-19

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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 cosrresponding 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 0, otherwise it will match the base paired positions.

gettRNALoopIDs: return a list of list of loop ids.

Examples

```
data("gr", package = "tRNA")
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")
data("gr_eco", package = "tRNA")
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 struc-
tures 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 ength 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 struc-
ture are stored in the result as metadata. They can be accessesed 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 struc-
                 ture 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 joinCompletly is set to TRUE a single `DNAStringSet`
is returned.

Examples

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

---

gettRNASummary   *Summary of tRNA features*

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 `istRNAGRanges`
                 test.

Value

a DataFrame object

Examples

```
data("gr", package = "tRNA")
gettRNASummary(gr)
```

---

hasTStem   *Subsetting tRNAs*

Description

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

Please not 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 vectors 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 or input GRanges object

Examples

```
data("gr", package = "tRNA")
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   *tRNA compatibility check*

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")
istRNAGRanges(gr)
```

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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 tR-NAscanImport 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.

Author(s)

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See Also

Useful links:

  • Report bugs at <https://github.com/FelixErnst/tRNA/issues>

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tRNA-data   *tRNA example data*

Description

Example data for using the tRNA package

Usage

```
data(gr)

data(gr_human)

data(gr_human2)

data(gr_eco)
```

Format

object of class `GRanges`

An object of class `GRanges` of length 596.

An object of class `GRanges` of length 631.

An object of class `GRanges` of length 89.

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