Package: tRNA (via r-universe)

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Title Analyzing tRNA sequences and structures

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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

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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()
```

`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 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 structure 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 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 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)]
```

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)
```

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.

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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