Package 'tRNAscanImport'

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Title Imports a tRNAscan-SE result file as GRanges object

Version 1.2.0

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Description The package imports the result of tRNAscan-SE as a GRanges object.

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Encoding UTF-8

LazyData true

Depends R (>= 3.5), GenomicRanges, tRNA

Imports methods, assertive, stringr, BiocGenerics, Biostrings, S4Vectors, GenomeInfoDb, rtracklayer

Collate 'tRNAscanImport.R' 'AllGenerics.R' 'tRNAscanImport-checks.R' 'tRNAscanImport-import.R'

Suggests BiocStyle, knitr, rmarkdown, testthat, ggplot2

RoxygenNote 6.0.1

VignetteBuilder knitr

biocViews Software, DataImport, WorkflowStep, Preprocessing, Visualization

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R topics documented:

`import.tRNAscanAsGRanges` *Importing a tRNAscan output file as a GRanges object*

Description

The function `import.tRNAscanAsGRanges` will import a tRNAscan-SE output file and return the information as a GRanges object. The reported intron sequences are spliced from the result by default, but can also returned as imported.

The function `tRNAScan2GFF` formats the output of `import.tRNAscanAsGRanges` to be GFF3 compliant.

Usage

```
import.tRNAscanAsGRanges(input, as.GFF3 = FALSE, trim.intron = TRUE,
  remove.lowerCase = FALSE)

tRNAscan2GFF(input)
```

Arguments

`input`	• `import.tRNAscanAsGRanges`: a tRNAscan-SE input file • `tRNAscan2GFF`: a compatible GRanges object such as the output of `import.tRNAscanAsGRanges`
`as.GFF3`	optional logical for `import.tRNAscanAsGRanges`: returns a gff3 compatible GRanges object directly. (default: `as.GFF3 = FALSE`)
`trim.intron`	optional logical for `import.tRNAscanAsGRanges`: remove intron sequences. This changes the tRNA length reported. To retrieve the original length fo the tRNA gene, use the `width()` function on the GRanges object. (default: `trim.intron = TRUE`)
`remove.lowerCase`	optional logical for `import.tRNAscanAsGRanges`: remove lower case characters from sequence and corresponding positions in structure annotation. Be aware, that this might lead to incorrect structures since it depends completely on how the mismatch is marked in the structure annotations. (default: `remove.lowerCase = FALSE`)

Value

a GRanges object

References

Chan, Patricia P., and Todd M. Lowe. 2016. "GtRNAdb 2.0: An Expanded Database of Transfer Rna Genes Identified in Complete and Draft Genomes." Nucleic Acids Research 44 (D1): D184–9. doi:10.1093/nar/gkv1309.

Lowe, T. M., and S. R. Eddy. 1997. "TRNAscan-Se: A Program for Improved Detection of Transfer Rna Genes in Genomic Sequence." Nucleic Acids Research 25 (5): 955–64.

Examples

```
gr <- import.tRNAscanAsGRanges(system.file("extdata",
                                file = "yeast.tRNAscan",
                                package = "tRNAscanImport"))
gff <- tRNAscan2GFF(gr)
identical(gff,import.tRNAscanAsGRanges(system.file("extdata",
                                file = "yeast.tRNAscan",
                                package = "tRNAscanImport"),
                                as.GFF3 = TRUE))
```

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istRNAscanGRanges *tRNAscan compatibility check*

Description

istRNAscanGRanges checks whether a GRanges object contains the information expected for a tRNAscan result.

Usage

```
istRNAscanGRanges(gr)

## S4 method for signature 'GRanges'
istRNAscanGRanges(gr)
```

Arguments

gr	the GRanges object to test

Value

a logical value

Examples

```
file <- system.file("extdata",
                    file = "yeast.tRNAscan",
                    package = "tRNAscanImport")
gr <- tRNAscanImport::import.tRNAscanAsGRanges(file)
istRNAscanGRanges(gr)
```

tRNAscanImport *tRNAscanImport: Importing tRNAscan-SE output as GRanges*

Description

tRNAscan-SE can be used for prediction of tRNA genes in whole genomes based on sequence context and calculated structural features. Many tRNA annotations in genomes contain or are based on information generated by tRNAscan-SE, for example the current SGD reference genome sacCer3 for Saccharomyces cerevisiae. However, not all available information from tRNAscan-SE end up in the genome annotation. Among these are for example structural information, additional scores and the information, whether the conserved CCA-end is encoded in the genomic DNA. To work with this complete set of information, the tRNAscan-SE output can be parsed into a more accessible GRanges object using 'tRNAscanImport'.

Manual

Please refer to the tRNAscanImport vignette for an example how to work and use the package: tRNAscanImport

Author(s)

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References

Chan, Patricia P., and Todd M. Lowe. 2016. "GtRNAdb 2.0: An Expanded Database of Transfer Rna Genes Identified in Complete and Draft Genomes." Nucleic Acids Research 44 (D1): D184–189.. doi:10.1093/nar/gkv1309.

Lowe, T. M., and S. R. Eddy. 1997. "TRNAscan-Se: A Program for Improved Detection of Transfer Rna Genes in Genomic Sequence." Nucleic Acids Research 25 (5): 955–964.

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