# Package 'tRNAscanImport'

October 16, 2019

**Title** Importing a tRNAscan-SE result file as GRanges object

**Version** 1.4.2

**Date** 2019-06-11

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

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5), GenomicRanges, tRNA

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

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

**Suggests** BiocStyle, knitr, rmarkdown, testthat, ggplot2

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

**biocViews** Software, DataImport, WorkflowStep, Preprocessing, Visualization

**BugReports** https://github.com/FelixErnst/tRNAscanImport/issues

**git_url** https://git.bioconductor.org/packages/tRNAscanImport

**git_branch** RELEASE_3_9

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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.

tRNAscanID generates a unique tRNA ID, which is like the format used in the SGD annotation

t*AminoAcidSingleLetter*(*Anticodon*)*ChromosomeIdentifier**optionalNumberIfOnTheSameChromosome*

Example: tP(UGG)L or tE(UUC)E1.

## Usage

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

tRNAscan2GFF(input)

tRNAscanID(input)
```

## Arguments

| | |
|---|---|
| input | • import.tRNAscanAsGRanges: a tRNAscan-SE input file<br>• 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*

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## 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)

Felix G M Ernst [aut]

## 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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