Package: tRNAscanImport (via r-universe)

November 1, 2026

Title Importing a tRNAscan-SE result file as GRanges object

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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 false

Depends R (>= 3.5), GenomicRanges, tRNA

Imports methods, stringr, BiocGenerics, Biostrings, Structstrings, S4Vectors, IRanges, XVector, Seqinfo, rtracklayer, BSgenome, Rsamtools

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

Suggests BiocStyle, knitr, rmarkdown, testthat, ggplot2, BSgenome.Scerevisiae.UCSC.sacCer3

RoxygenNote 7.1.1

VignetteBuilder knitr

biocViews Software, DataImport, WorkflowStep, Preprocessing, Visualization

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

URL https://github.com/FelixErnst/tRNAscanImport

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository https://bioc.r-universe.dev

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`get.tRNAprecursor` *Get tRNA precursor sequences*

Description

`get.tRNAprecursor` retrieves tRNA precursor sequences from genomic sequences. The length of 5'- and 3'-overhangs can be specifid individually. The output is checked for validity against the tRNA sequences as reported by tRNAscan.

The chromosomes names of tRNAscan input and genome sequences must be compatible.

Usage

```
get.tRNAprecursor(
  input,
  genome,
  add.5prime = 50L,
  add.3prime = add.5prime,
  trim.intron = FALSE
)
```

Arguments

`input`	a compatible `GRanges` object
`genome`	a `BSgenome` object, a `DNAStringSet` object, a `FaFile` object or a character vector with a single value referncing a file, which can be coerced to a `FaFile` object.
`add.5prime`, `add.3prime`	the length of overhangs as a single integer value each. (default `add.5prime = 50L`)
`trim.intron`	`TRUE` or `FALSE`: Should intron sequences be included in the precursor sequences? (default `trim.intron = FALSE`)

Value

a `DNAStringSet` object, containing the precursor sequences.

Examples

```
library(BSgenome.Scerevisiae.UCSC.sacCer3)
file <- system.file("extdata",
                    file = "yeast.tRNAscan",
                    package = "tRNAscanImport")
gr <- tRNAscanImport::import.tRNAscanAsGRanges(file)
genome <- getSeq(BSgenome.Scerevisiae.UCSC.sacCer3)
names(genome) <- c(names(genome)[-17],"chrmt")
get.tRNAprecursor(gr, genome)
# this produces an error since the seqnames do not match
## Not run:
genome <- BSgenome.Scerevisiae.UCSC.sacCer3
names(genome) <- c(names(genome)[-17],"chrmt")
get.tRNAprecursor(gr, genome)

## End(Not run)
# ... but it can also be fixed
genome <- BSgenome.Scerevisiae.UCSC.sacCer3
seqnames(genome) <- c(seqnames(genome)[-17],"chrmt")
get.tRNAprecursor(gr, genome)
```

`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)

tRNAscan2GFF(input)

tRNAscanID(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)

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))
```

---

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)
```

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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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