Package 'tRNAscanImport'

October 16, 2018

Title Imports a tRNAscan-SE result file as GRanges object

Version 1.0.1

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

Depends R (>= 3.5), GenomicRanges

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Encoding UTF-8

LazyData true

biocViews Software, DataImport, WorkflowStep, Preprocessing, Visualization

Imports methods, assertive, stringr, reshape2, BiocGenerics, Biostrings, S4Vectors, GenomicRanges, GenomeInfoDb, rtracklayer

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

RoxygenNote 6.0.1

Suggests BiocStyle, knitr, rmarkdown, testthat, graphics, ggplot2, scales

VignetteBuilder knitr

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R topics documented:

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gettRNAscanSummary   *tRNAscanImport summary functions*

Description

gettRNAscanSummary(): creates an DataFrame with aggregated information from the tRNAscan information.

gettRNAscanPlots(): If ggplot2 is installed a plot of the data is generated and returned.

plottRNAscan(): If ggplot2 is installed a plot of the data is generated and ploted directly.

Usage

```
gettRNAscanSummary(gr)

plottRNAscan(grl)

gettRNAscanPlots(grl)

## S4 method for signature 'GRanges'
gettRNAscanSummary(gr)

## S4 method for signature 'GRangesList'
plottRNAscan(grl)

## S4 method for signature 'GRangesList'
gettRNAscanPlots(grl)
```

Arguments

gr	a GRanges object created by import.tRNAscanAsGRanges or GRanges with equivalent information.
grl	a GRangesList object created with GRanges created by import.tRNAscanAsGRanges or GRanges with equivalent information.

Value

gettRNAscanSummary(): returns a DataFrame with the summarized results used for plotting internally.

gettRNAscanPlots(): returns a list of ggplots per column of data returned by gettRNAscanSummary().

plottRNAscan(): the function plots the output of gettRNAscanPlots directly to the current plotting device.

Examples

```
library(GenomicRanges, quietly = TRUE)
sce <- import.tRNAscanAsGRanges(system.file("extdata",
                         file = "sacCer3-tRNAs.ss.sort",
                         package = "tRNAscanImport"))
eco <- import.tRNAscanAsGRanges(system.file("extdata",
                      file = "eschColi_K_12_MG1655-tRNAs.ss.sort",
```

```
                                    package = "tRNAscanImport"))
gettRNAscanSummary(sce)
plots <- gettRNAscanPlots(GRangesList(Sce = sce,
                                      Eco = eco))
```

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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)

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: FALSE)
trim.intron	optional logical for `import.tRNAscanAsGRanges`: remove intron sequences (default: 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 = "sacCer3-tRNAs.ss.sort",
                               package = "tRNAscanImport"))
gff <- tRNAscan2GFF(gr)
identical(gff,import.tRNAscanAsGRanges(system.file("extdata",
                               file = "sacCer3-tRNAs.ss.sort",
                               package = "tRNAscanImport"),
                               as.GFF3 = TRUE))
```

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