Package: tRNAdbImport (via r-universe)

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Title Importing from tRNAdb and mitotRNAdb as GRanges objects

Version 1.31.0

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Description tRNAdbImport imports the entries of the tRNAdb and mtRNAdb (http://trna.bioinf.uni-leipzig.de) as GRanges object.

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Encoding UTF-8

LazyData false

biocViews Software, Visualization, DataImport

Depends R (>= 3.6), GenomicRanges, Modstrings, Structstrings, tRNA

Imports Biostrings, stringr, httr2, xml2, S4Vectors, methods, IRanges, utils

Suggests BiocGenerics, knitr, rmarkdown, testthat, httptest, BiocStyle, rtracklayer

Collate 'tRNAdbImport.R' 'AllGenerics.R' 'tRNAdbImport-checks.R' 'tRNAdbImport-import.R' 'tRNAdbImport-open.R' 'utils.R'

VignetteBuilder knitr

RoxygenNote 7.2.3

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

Config/pak/sysreqs libicu-dev libxml2-dev libssl-dev zlib1g-dev

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

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`import.tRNAdb` *Importing information from the tRNA db as GRanges object*

Description

title

Usage

```
TRNA_DB_URL

TRNA_DB_URL_MT

import.tRNAdb.id(
  tdbID,
  database = c("DNA", "RNA"),
  origin = c("allothers", "plastid", "mitochondrial"),
  dbURL = TRNA_DB_URL,
  verbose = FALSE
)

import.mttRNAdb.id(mtdbID, dbURL = TRNA_DB_URL_MT, verbose = FALSE)

import.tRNAdb.blast(
  blastSeq,
  database = c("DNA", "RNA"),
  origin = c("allothers", "plastid", "mitochondrial"),
  dbURL = TRNA_DB_URL,
  verbose = FALSE
)

import.tRNAdb(
  organism = "",
  strain = "",
  taxonomyID = "",
  aminoacids = "",
  anticodons = "",
  sequences = list(),
  structures = list(),
```

```
  reference = "",
  comment = "",
  pubmed = "",
  genes = "",
  database = c("DNA", "RNA"),
  origin = c("allothers", "plastid", "mitochondrial"),
  dbURL = TRNA_DB_URL,
  verbose = FALSE
)

import.mttRNAdb(
  organism = "",
  strain = "",
  taxonomyID = "",
  aminoacids = "",
  anticodons = "",
  sequences = list(),
  structures = list(),
  reference = "",
  comment = "",
  pubmed = "",
  genes = "",
  dbURL = TRNA_DB_URL_MT,
  verbose = FALSE
)

tRNAdb2GFF(input)
```

Arguments

tdbID	a tRNAdb ID
database	"RNA" or "DNA"
origin	one ore more of "plastid", "mitochondrial" or "allothers"
dbURL	the URL of the tRNA db
verbose	whether to report verbose information from the httr2 calls
mtdbID	a mtRNAdb ID
blastSeq	a sequence to use for a blast search
organism	a organism name as a character string
strain	a strain information as a character string
taxonomyID	organism and strain information as a taxonom ID
aminoacids	a character vector of amino acids as a three letter code
anticodons	a character vector of anticodon sequences
sequences	a named (1-15) list of sequences, which are used for the search
structures	a named (1-15) list of structures, which are used for the search. Please use the \(\) or >< dot bracket annotation.

reference	a reference as a character string
comment	a comment as a character string
pubmed	a pubmed ID
genes	a gene name as a character string
input	a GRanges object which passes the istRNAdbGRanges check

Format

An object of class character of length 1.

An object of class character of length 1.

Value

a GRanges object containing the information from the tRNA db

Examples

```
import.tRNAdb(organism = "Saccharomyces cerevisiae",
              aminoacids = c("Phe","Ala"))
import.tRNAdb.id(tdbID = "tdbD00000785")
import.tRNAdb.blast(blastSeq =
"GCGGATTTAGCTCAGTTGGGAGAGCGCCAGACTGAAGATCTGGAGGTCCTGTGTTCGATCCACAGAATTCGCA")
import.mttRNAdb(organism = "Bos taurus",
                aminoacids = c("Phe","Ala"))
import.mttRNAdb.id(mtdbID = "mtdbD00000900")
```

---

istRNAdbGRanges *tRNAdb compatibility check*

Description

istRNAdbGRanges checks whether a GRanges object contains the information expected for a tRNAdb result.

Usage

```
istRNAdbGRanges(x)

## S4 method for signature 'GRanges'
istRNAdbGRanges(x)
```

Arguments

x	the GRanges object to test

Value

a logical value

Examples

```
gr <- import.tRNAdb(organism = "Saccharomyces cerevisiae",
              aminoacids = c("Phe","Ala"),
              anticodons = c("GAA"))
istRNAdbGRanges(gr)
```

`open_tdbID` *Open a tRNA db entry in a browser*

Description

`open.tdbID` is a wrapper for `browseURL` and opens a tab for a tRNAdb entry in a browser. Please note, that the tRNAdb server does not show the entry right away without a session ID. open twice upon first use.

Usage

```
open_tdbID(tdbID, dbURL = TRNA_DB_URL)

open_mtdbID(mtdbID, dbURL = TRNA_DB_URL_MT)
```

Arguments

`tdbID`	a tRNA db
`dbURL`	the URL for the tRNAdb
`mtdbID`	a mtRNA db

Value

opens a window in a default browser for tRNAdb entry selected

Examples

```
if(interactive()){
  open_tdbID("tdbD00000785")
  open_mtdbID("mtdbD00000907")
}
```

tRNAdbImport *tRNAdbImport: Importing from to tRNAdb and mitotRNAdb as GRanges*

Description

The tRNAdb and mttRNAdb (Jühling et al. 2009) is a compilation of tRNA sequences and tRNA genes. It is a follow up version of the database of Sprinzl et al. 2005.

Using ‘tRNAdbImport‘ the tRNAdb can be accessed as outlined on the website http://trna.bioinf.uni-leipzig.de/ and the results are returned as a ‘GRanges‘ object.

Manual

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

Author(s)

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References

Jühling F, Mörl M, Hartmann RK, Sprinzl M, Stadler PF, Pütz J. 2009. "tRNAdb 2009: compilation of tRNA sequences and tRNA genes." Nucleic Acids Research, Volume 37 (suppl_1): D159–162. doi:10.1093/nar/gkn772.

See Also

[import.tRNAdb()] for examples

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