Package ‘tRNAdbImport’

January 27, 2024

Title Importing from tRNAdb and mitotRNAdb as GRanges objects
Version 1.20.1
Date 2020-01-13
Description tRNAdbImport imports the entries of the tRNAdb and mtRNAdb (http://trna.bioinf.uni-leipzig.de) as GRanges object.
License GPL-3 + file LICENSE
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
git_url https://git.bioconductor.org/packages/tRNAdbImport
git_branch RELEASE_3_18
git_last_commit c5a12a3
git_last_commit_date 2024-01-15
Repository Bioconductor 3.18
Date/Publication 2024-01-26
Author Felix G.M. Ernst [aut, cre] (https://orcid.org/0000-0001-5064-0928)
Maintainer Felix G.M. Ernst <felix.gm.ernst@outlook.com>
import.tRNAdb

**R topics documented:**

import.tRNAdb .......................................................... 2
istRNAdbGRanges ...................................................... 4
open_tdbID .............................................................. 5
tRNAdbImport .......................................................... 6

Index 7

---

import.tRNAdb  

*Importing information from the tRNA db as GRanges object*

**Description**

title

**Usage**

```r
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(mttdbID, 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(),
)```
import.tRNAdb

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

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

tRNAdb2GFF(input)

Arguments

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

**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**

```r
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")
```

---

**Description**

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

**Usage**

```r
istRNAdbGRanges(x)
```

## S4 method for signature 'GRanges'

**istRNAdbGRanges(x)**

**Arguments**

- `x` : the GRanges object to test

**Value**

A logical value
**Examples**

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

**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**

```r
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**

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

Felix G M Ernst [aut]

References


See Also

[import.tRNAdb()] for examples
Index

* datasets
  import.tRNAdb, 2

import.mtrRNAdb (import.tRNAdb), 2
import.tRNAdb, 2
istRNAdbGRanges, 4
istRNAdbGRanges, GRanges-method
  (istRNAdbGRanges), 4

open_mtdbID (open_tdbID), 5
open_tdbID, 5

TRNA_DB_URL (import.tRNAdb), 2
TRNA_DB_URL_MT (import.tRNAdb), 2
tRNAdb2GFF (import.tRNAdb), 2
tRNAdbImport, 6