

Package ‘MINTplates’

January 20, 2025

Title Encode ``License-Plates" from Sequences and Decode Them Back

Version 1.0.1

Description It can be used to create/encode molecular ``license-plates" from sequences and to also decode the ``license-plates" back to sequences. While initially created for transfer RNA-derived small fragments (tRFs), this tool can be used for any genomic sequences including but not limited to: tRFs, microRNAs, etc. The detailed information can reference to Pliatsika V, Loher P, Telonis AG, Rigoutsos I (2016) <[doi:10.1093/bioinformatics/btw194](https://doi.org/10.1093/bioinformatics/btw194)>. It can also be used to annotate tRFs. The detailed information can reference to Loher P, Telonis AG, Rigoutsos I (2017) <[doi:10.1038/srep41184](https://doi.org/10.1038/srep41184)>.

Depends R (>= 3.2.3)

License GPL (>= 2)

RoxygenNote 7.1.1

URL <http://www.bio-inf.cn/>

NeedsCompilation no

Author Shanliang Zhong [aut, cre]

Maintainer Shanliang Zhong <slzhong@foxmail.com>

Repository CRAN

Date/Publication 2021-09-03 06:50:07 UTC

Contents

annotate_tRF	2
deseqs	2
enseqs	3
exclusive	4
source_tRNA	4
source_tRNA2	5
tRFtype	6

Index	7
--------------	----------

annotate_tRF	<i>Annotate a tRF sequence</i>
--------------	--------------------------------

Description

Obtain tRF ID, type, whether exclusive to tRNA space, and tRNA sources of the tRF with its sequence.

Usage

```
annotate_tRF(sequence)
```

Arguments

sequence tRF sequence.

Value

tRF ID, type, whether exclusive to tRNA space, and tRNA sources of the tRF.

References

Loher P, Telonis AG, Rigoutsos I. Sci Rep (2017) <doi: 10.1038/srep41184>

Examples

```
sequence='TCCCTGGTGGTCTAGTGGTTAGGATTCGGC'  
annotate_tRF(sequence)
```

deseqs	<i>Decode license-plates</i>
--------	------------------------------

Description

Decode the license-plates using the lookup table.

Usage

```
deseqs(plates)
```

Arguments

plates The license plates being decoded.

Value

The sequences they decodes to.

References

Pliatsika V, Loher P, Telonis AG, Rigoutsos I. Bioinformatics (2016) <doi: 10.1093/bioinformatics/btw194>

Examples

```
plates=c('tRF-18-BS6PDFD2', 'tRF-20-51K36D26')
deseqs(plates)
```

enseqs	<i>Encode sequences</i>
--------	-------------------------

Description

Encode the sequences into their corresponding license plates with given prefix (if given one).

Usage

```
enseqs(sequences, prefix = "")
```

Arguments

sequences	The sequences being encoded.
prefix	The prefix to use for the license plate.

Value

The license plates they encode to.

References

Pliatsika V, Loher P, Telonis AG, Rigoutsos I. Bioinformatics (2016) <doi: 10.1093/bioinformatics/btw194>

Examples

```
seqs=c('AACCGGCAGAACACCA', 'GAGCCCCAGTGAACACCA')
enseqs(seqs, 'tRF')
```

exclusive

Determine whether the tRFs are exclusive to tRNA space

Description

Determine whether the tRFs are exclusive to tRNA space with the tRF sequences.

Usage

```
exclusive(sequences)
```

Arguments

sequences tRF sequences.

Value

Whether the tRFs are exclusive to tRNA space.

References

Loher P, Telonis AG, Rigoutsos I. Sci Rep (2017) <doi: 10.1038/srep41184>

Examples

```
sequences=c('TCCCTGGTGGTCTAGTGGTTAGGATTCGGC', 'TCCCTGGTGGTCTAGTGGTTAGGATTCGGCG')
exclusive(sequences)
```

source_tRNA

Obtain the tRNA source of a tRF

Description

Obtain the tRNA source of a tRF with the tRF sequence.

Usage

```
source_tRNA(sequence)
```

Arguments

sequence tRF sequence.

Value

Sources of the tRF.

References

Loher P, Telonis AG, Rigoutsos I. Sci Rep (2017) <doi: 10.1038/srep41184>

Examples

```
sequence='TCCCTGGTGGTCTAGTGGTTAGGATTCGGC'  
source_tRNA(sequence)
```

source_tRNA2	<i>Obtain the tRNA sources of tRFs</i>
--------------	--

Description

Obtain the tRNA sources of tRFs with the tRF sequences.

Usage

```
source_tRNA2(sequences)
```

Arguments

sequences tRF sequences.

Value

Sources of the tRFs.

References

Loher P, Telonis AG, Rigoutsos I. Sci Rep (2017) <doi: 10.1038/srep41184>

Examples

```
sequences=c('TCCCTGGTGGTCTAGTGGTTAGGATTCGGC', 'TCCCTGGTGGTCTAGTGGCT', 'TCCCTGGTGGTCTAATGGTTA')  
source_tRNA2(sequences)
```

tRFtype

Obtain the type of tRFs

Description

Obtain the type of tRFs with the tRF sequences.

Usage

```
tRFtype(sequences)
```

Arguments

sequences tRF sequences.

Value

The type of tRFs.

References

Loher P, Telonis AG, Rigoutsos I. Sci Rep (2017) <doi: 10.1038/srep41184>

Examples

```
sequences=c('TCCCTGGTGGTCTAGTGGTTAGGATTCGGC', 'AAAAATTTTGGTGCAACTCAAATAAAA')
tRFtype(sequences)
```

Index

annotate_tRF, [2](#)

deseqs, [2](#)

enseqs, [3](#)

exclusive, [4](#)

source_tRNA, [4](#)

source_tRNA2, [5](#)

tRFtype, [6](#)