

Package: CleanBSequences (via r-universe)

October 16, 2026

Type Package

Title Curing of Biological Sequences

Version 2.3.0

Author Florencia I. Pozzi, Silvina A. Felitti

Maintainer Florencia I. Pozzi <florenciapoz@hotmail.com>

Description Curates biological sequences massively, quickly, without errors and without internet connection. Biological sequences curing is performed by aligning the forward and / or reverse primers or ends of cloning vectors with the sequences to be cleaned. After the alignment, new subsequences are generated without biological fragment not desired by the user. Pozzi et al (2020) <[doi:10.1007/s00438-020-01671-z](https://doi.org/10.1007/s00438-020-01671-z)>.

License GPL (>= 2)

Encoding UTF-8

Depends pwalign, Biostrings

RoxygenNote 7.3.1

NeedsCompilation no

Config/pak/sysreqs zlib1g-dev

Repository <https://cran.r-universe.dev>

Date/Publication 2024-05-10 02:40:17 UTC

RemoteUrl <https://github.com/cran/CleanBSequences>

RemoteRef HEAD

RemoteSha d380c92ecb8b2dcddd28eaac9c37018c5a14ad32

Contents

DNAStrngSetOPR	2
DNAStrngSetTPR	2
OnePrimerRemove	3
TwoPrimerRemove	4

Index	5
--------------	----------

DNASetOPR	<i>Curing of biological sequences</i>
-----------	---------------------------------------

Description

Curates biological sequences of primer reverse. This cleaning is required for techniques such as cDNA-AFLP.

Usage

```
DNASetOPR(SEQs, PrimerR)
```

Arguments

SEQs	file with fasta format containing biological sequences that are to be cleaned.
PrimerR	dnastring containing the reverse primer/vector sequences to be removed.

Value

clean biological sequences and visualization of the alignments

Author(s)

Florencia I Pozzi, Silvina A. Felitti

Examples

```
SEQs = readDNASet(system.file("sequences", "SeqInputOPR.fasta", package = "CleanBSequences"))
PrimerR= DNASet ("GACTGCGTACCATGC")
DNASetOPR (SEQs,PrimerR)
```

DNASetTPR	<i>Curing of biological sequences</i>
-----------	---------------------------------------

Description

Curates biological sequences of two restriction enzyme primers or cloning vectors. This cleaning is required for techniques such as cDNA-AFLP. This cleaning is required for techniques such as cDNA-AFLP.

Usage

```
DNASetTPR(SEQs, PrimerF, PrimerR)
```

Arguments

SEQs	file with fasta format containing biological sequences that are to be cleaned.
PrimerF	dnasttring containing the foward primer/vector sequences to be removed.
PrimerR	dnasttring containing the reverse primer/vector sequences to be removed.

Value

clean biological sequences and visualization of the alignments

Author(s)

Florescia I Pozzi, Silvina A. Felitti

Examples

```
SEQs = readDNASTringSet(system.file("sequences", "SeqInputTPR.fasta", package = "CleanBSequences"))
PrimerR= DNASTring ("GACTGCGTACCATGC")
PrimerF = DNASTring("GATGAGTCCTGACCGAA")
DNASTringSetTPR (SEQs,PrimerF,PrimerR)
```

OnePrimerRemove	<i>Clean biological sequeces</i>
-----------------	----------------------------------

Description

Curates biological sequences of primer reverse.This cleaning is required for techniques such as cDNA-AFLP.

Usage

```
OnePrimerRemove(SEQs, PrimerR)
```

Arguments

SEQs	dnasttring containing biological sequences that are to be cleaned.
PrimerR	dnasttring containing the reverse primer/vector sequences to be removed.

Value

clean biological sequences and visualization of the alignments

Author(s)

Florescia I Pozzi and Silvina A. Felitti

Examples

```
SEQs = DNASTring(paste("GCCTCGCCTCCCTCTTTGATCAGCTTCGCATATCAGGCAACAGCTCAATTT",
"GGTACTTGTTCAAATAAGCATTTAGACCATCTGTTCCAAGAACCTTTGCAATCTT",
"CACAAGGTGGTCATGGTACGCAGTC", sep=""))
PrimerR= DNASTring("GACTGCGTACCATGC")
OnePrimerRemove (SEQs,PrimerR)
```

TwoPrimerRemove	<i>Clean biological sequences</i>
-----------------	-----------------------------------

Description

Curates biological sequences of two restriction enzyme primers or cloning vectors. This cleaning is required for techniques such as cDNA-AFLP.

Usage

```
TwoPrimerRemove(SEQs, PrimerF, PrimerR)
```

Arguments

SEQs	DNASTring containing biological sequences that are to be cleaned.
PrimerF	dnasttring containing the foward primer/vector sequences to be removed.
PrimerR	dnasttring containing the reverse primer/vector sequences to be removed.

Value

clean biological sequences and visualization of the alignments

Author(s)

Florencia I Pozzi, Silvina A. Felitti

Examples

```
SEQs = DNASTring(paste("ACTTTCTGCTGCTTGTGGTCGCAATCAGAGTCCTGATGATGAGTCCTGA",
"CCGAACCCTTTTCTCCGTCATCCGTTGGTCCATGGTACGCAATCAGAG", sep = ""))
PrimerF = DNASTring("GATGAGTCCTGACCGAA")
PrimerR = DNASTring("GACTGCGTACCATGC")
TwoPrimerRemove (SEQs,PrimerF,PrimerR)
```

Index

DNAStringSetOPR, [2](#)

DNAStringSetTPR, [2](#)

OnePrimerRemove, [3](#)

TwoPrimerRemove, [4](#)