

Package ‘CleanBSequences’

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Type Package

Title Curing of Biological Sequences

Version 1.4.0

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Description Curates biological sequences massively, quickly, without errors and without internet connection. Biological sequences curing is performed by aligning the forward and / or revers 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 Biostrings

RoxygenNote 7.1.2

NeedsCompilation no

Repository CRAN

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DNAStrngSetOPR *Curing of biological sequences*

Description

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

Usage

```
DNAStrngSetOPR(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 = readDNAStrngSet(system.file("sequences", "SeqInputOPR.fasta", package = "CleanBSequences"))
PrimerR = DNAStrng ("GACTGCGTACCATGC")
DNAStrngSetOPR (SEQs, PrimerR)
```

DNAStrngSetTPR *Curing of biological sequences*

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

```
DNAStrngSetTPR(SEQs, PrimerF, PrimerR)
```

Arguments

SEQs file with fasta format containing biological sequences that are to be cleaned.
 PrimerF dnastring containing the forward primer/vector sequences to be removed.
 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 = readDNASTringSet(system.file("sequences", "SeqInputTPR.fasta", package = "CleanBSequences"))
PrimerR= DNASTring ("GACTGCGTACCATGC")
PrimerF = DNASTring("GATGAGTCCTGACCGAA")
DNASTringSetTPR (SEQs,PrimerF,PrimerR)
```

OnePrimerRemove *Clean biological sequences*

Description

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

Usage

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

Arguments

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

Value

clean biological sequences and visualization of the alignments

Author(s)

Florencia I Pozzi and Silvina A. Felitti

Examples

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

TwoPrimerRemove *Clean biological secuenes*

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	dnastring containing the foward primer/vector sequences to be removed.
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 = DNASTring(paste("ACTTTCTGCTGCTTGTGGTCGCAATCAGAGTCCTGATGATGAGTCCTGA",
"CCGAACCCTTTTCTCCGTATCCGTTGGTCCATGGTACGCAATCAGAG", sep = ""))
PrimerF = DNASTring("GATGAGTCCTGACCGAA")
PrimerR = DNASTring("GACTGCGTACCATGC")
TwoPrimerRemove (SEQs,PrimerF,PrimerR)
```

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