Package ‘CleanBSequences’

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Type Package

Title Clean Biological Sequences

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Description Cleans biological sequences massively, quickly, without errors and without internet connection. Biological sequences cleaning 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 (2016, ISSN:2314-1484).

License GPL-3

Encoding UTF-8

LazyData true

Depends Biostrings

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

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R topics documented:

`OnePrimerRemove` *Clean biological secuences of one primer*

Description

Cleans biological sequences of one primer.

Usage

```
OnePrimerRemove(SEQ, PrimerOPR)
```

Arguments

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

Value

clean biological sequences

Author(s)

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Examples

```
SEQ4 = DNAString("AATCG")
SEQ5 = DNAString("CG")
OnePrimerRemove (SEQ4,SEQ5)
```

`TwoPrimerRemove` *Clean biological secuences of two primers*

Description

Clean biological sequences of two restriction enzyme primers or cloning vectors.

Usage

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

Arguments

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

Value

clean biological sequences

Author(s)

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Examples

```
SEQ1 = DNAString("AATCG")
SEQ2 = DNAString("TT")
SEQ3 = DNAString("CG")
TwoPrimerRemove (SEQ1,SEQ2,SEQ3)
```

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