

# Package: CleanBSequences (via r-universe)

September 7, 2024

**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 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** pwalign, Biostrings

**RoxygenNote** 7.3.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2024-05-09 18:10:02 UTC

## Contents

DNASetOPR . . . . .	2
DNASetTPR . . . . .	2
OnePrimerRemove . . . . .	3
TwoPrimerRemove . . . . .	4
<b>Index</b>	<b>5</b>

---

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

---

**Description**

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

**Usage**

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

**Arguments**

SEQs dnastring 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 and Silvina A. Felitti

**Examples**

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

---

TwoPrimerRemove      *Clean biological sequences*

---

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

# Index

DNAStrngSetOPR, [2](#)

DNAStrngSetTPR, [2](#)

OnePrimerRemove, [3](#)

TwoPrimerRemove, [4](#)