

Package ‘smithWaterman’

November 4, 2022

Title Best local alignment of two nucleotide sequences according to Smith-Waterman algorithm

Version 1.0.0

Description This package serves to locally align two nucleotide sequences, by making use of Smith-Waterman algorithm.

Depends R(>= 4.2.1)

Imports Biostrings, methods

Suggests knitr, rmarkdown, BiocStyle, testthat, benchmarkme, ShortRead

License GPL-2

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

VignetteBuilder knitr

URL <https://github.com/emanuelecavalleri/Smith-Waterman>

biocViews Software, BiomedicalInformatics, BiologicalQuestion, Alignment

NeedsCompilation no

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R topics documented:

smithWaterman-package	2
build_F	2
smith_waterman	3
Smith_Waterman-class	4
smith_waterman_DNAString	5
smith_waterman_string	6
traceback	7
Index	8

smithWaterman-package *smithWaterman - Best local alignment of two nucleotide sequences according to Smith-Waterman algorithm*

Description

The smithWaterman package implements functions for the local alignment of two nucleotide sequences according to Smith-Waterman greedy algorithm.

Details

Package: smithWaterman
Type: Package
Version: 1.0.0
Date: 2022-10-03
License: GPL (>=2)

Author(s)

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References

<https://github.com/emanuelecavalleri/Smith-Waterman>

build_F *Build scoring matrix F*

Description

This function builds and returns the scoring matrix F according to Smith-Waterman greedy algorithm

Usage

build_F(F, seq_X, seq_Y, match, mismatch, d)

Arguments

F	Pre-initialized scoring matrix
seq_X	A nucleotide sequence preceeded by '0'
seq_Y	Another nucleotide sequence preceeded by '0'
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel

Value

Scoring matrix F obtained according to Smith-Waterman algorithm

Author(s)

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References

https://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm

See Also

[smith_waterman_string](#)

smith_waterman

Apply Smith-Waterman algorithm and show its output

Description

This function takes as input two strings/DNAString objects and returns one of the possible best local alignment in terms of score according to Smith-Waterman greedy algorithm.

Usage

```
smith_waterman(X, Y, match, mismatch, d)
```

Arguments

X	A nucleotide sequence or a DNAString object
Y	Another nucleotide sequence or another DNAString object
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel

Value

A Smith-Waterman object

Author(s)

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References

https://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm

See Also

[smith_waterman_string](#)
[smith_waterman_DNAString](#)

Examples

```
library(Biostrings)
smith_waterman(DNAString("TATCT"), "TTCGG", 7, -10, -7)
```

Smith_Waterman-class *Create Smith_Waterman (RefClass) object*

Description

Create Smith_Waterman (RefClass) object

Arguments

X	A nucleotide sequence
Y	Another nucleotide sequence
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel
aligned_X	The aligned nucleotide sequence obtained according to Smith-Waterman algorithm
aligned_Y	The other aligned nucleotide sequence obtained according to Smith-Waterman algorithm
alignment_score	Best alignment score obtained according to Smith-Waterman algorithm
F	Scoring matrix obtained according to Smith-Waterman algorithm

Value

A new Smith_Waterman object

Author(s)

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References

https://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm

smith_waterman_DNAString

Apply Smith-Waterman algorithm to DNAString objects

Description

This function takes as input two DNAString objects and returns one of the possible best local alignment in terms of score according to Smith-Waterman greedy algorithm.

Usage

```
smith_waterman_DNAString(X, Y, match, mismatch, d)
```

Arguments

X	A DNAString object
Y	Another DNAString object
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel

Value

A Smith_Waterman object

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References

https://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm

See Also

[smith_waterman_string](#)
[smith_waterman](#)

Examples

```
library(Biostrings)
smith_waterman_DNAString(DNAString("TATCT"), DNAString("TTCGG"), 7, -10, -7)
```

smith_waterman_string *Apply Smith-Waterman algorithm to strings*

Description

This function takes as input two strings and returns one of the possible best local alignment in terms of score according to Smith-Waterman greedy algorithm.

Usage

```
smith_waterman_string(X, Y, match, mismatch, d)
```

Arguments

X	A nucleotide sequence
Y	Another nucleotide sequence
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel

Value

A Smith_Waterman object

Author(s)

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References

https://en.wikipedia.org/wiki/Smith%E2%80%93Waterman_algorithm

See Also

[smith_waterman_DNAString](#)
[smith_waterman](#)

Examples

```
smith_waterman_string("TATCT", "TTCGG", 7, -10, -7)
```

traceback	<i>Traceback</i>
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Description

Traceback implemented according to an efficient modified version of the Needleman-Wunsch algorithm (see Wikipedia reference link)

Usage

```
traceback(F, seq_X, seq_Y, match, mismatch, d)
```

Arguments

F	Scoring matrix obtained according to Smith-Waterman algorithm
seq_X	A nucleotide sequence preceeded by '0'
seq_Y	Another nucleotide sequence preceeded by '0'
match	Score associated with a match
mismatch	Penalty associated with a mismatch
d	Penalty associated with a gap/indel

Value

A list containing the two locally aligned strings

Author(s)

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References

https://en.wikipedia.org/wiki/Needleman%E2%80%93Wunsch_algorithm#Advanced_presentation_of_algorithm

See Also

[smith_waterman_string](#)

Index

`build_F`, [2](#)

`Smith_Waterman` (`Smith_Waterman-class`), [4](#)

`smith_waterman`, [3](#), [6](#)

`Smith_Waterman-class`, [4](#)

`smith_waterman_DNAString`, [4](#), [5](#), [6](#)

`smith_waterman_string`, [3](#), [4](#), [6](#), [6](#), [7](#)

`smithWaterman` (`smithWaterman-package`), [2](#)

`smithWaterman-package`, [2](#)

`traceback`, [7](#)