

Package ‘smithWaterman’

October 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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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>

print_smith_waterman *Apply Smith-Waterman algorithm and show its output*

Description

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

Usage

```
print_smith_waterman(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 visualization of the local alignment with scoring matrix and best score

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References

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

See Also

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

Examples

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

smith_waterman

Apply Smith-Waterman algorithm

Description

This function take 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(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 list containing the local alignment with scoring matrix and best score

Author(s)

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References

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

See Also

[smith_waterman_DNAString](#)
[print_smith_waterman](#)

Examples

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

smith_waterman_DNAString

Apply Smith-Waterman algorithm to DNAString objects

Description

This function take 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 list containing the local alignment with scoring matrix and best score

Author(s)

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References

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

See Also

[smith_waterman](#)
[print_smith_waterman](#)

Examples

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

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