

Package ‘smithWaterman’

October 1, 2022

Title Applying Smith-Waterman algorithm to two nucleotidic sequences

Version 0.99.0

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

Depends R(>= 3.6)

Imports Biostrings, benchmarkme, ShortRead, methods

Suggests knitr, rmarkdown, BiocStyle, testthat

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

NeedsCompilation no

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smithWaterman-package *smithWaterman - Apply Smith-Waterman algorithm to two nucleotidic sequences*

Description

The smithWaterman package implements functions for alignment and visualization of two nucleotidic sequences according to Smith-Waterman greedy algorithm.

Details

Package: smithWaterman
Type: Package
Version: 0.99.0
Date: 2022-09-28
License: GPL (>=2)

Author(s)

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References

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

print_smith_waterman *Show Smith-Waterman algorithm output*

Description

This function take as input two strings 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 nucleotidic sequence
Y	Another nucleotidic sequence
match	Score of a match
mismatch	Penalty of a mismatch
d	Penalty of a gap/indel

Value

A visualization of the two aligned sequences with the 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 nucleotidic sequence
Y	Another nucleotidic sequence
match	Score of a match
mismatch	Penalty of a mismatch
d	Penalty of a gap/indel

Value

A list containing a possible local alignment with cost 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 with DNAStrings

Description

This function take as input two DNAString(Set) (Biostrings) 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 of a match
mismatch	Penalty of a mismatch
d	Penalty of a gap/indel

Value

A list containing a possible local alignment with cost 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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