Package 'smithWaterman'

November 8, 2022

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

Version 0.99.0

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

Author Emanuele Cavalleri [aut, cre]

Maintainer Emanuele Cavalleri <emanuele.cavalleri@mail.polimi.it>

R topics documented:

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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:	0.99.0
Date:	2022-12-19
License:	GPL (>=2)

Author(s)

Emanuele Cavalleri [aut, cre]
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

References

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

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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 preceded by '0'
seq_Y	Another nucleotide sequence preceded 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)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

References

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

See Also

smith_waterman_string

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

Description

This function takes as input one string and one DNAString object or two strings or 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(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)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

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)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

References

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

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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

Author(s)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

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)

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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)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

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)
```

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traceback	*Traceback*

Description

Traceback implemented according to an efficient modified version of the Needleman-Wunsch algorithm (see Wikipedia reference link). This function returns a list containing the two locally aligned strings

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 preceded by '0'
seq_Y	Another nucleotide sequence preceded 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)

Emanuele Cavalleri
Politecnico di Milano
Maintainer: Emanuele Cavalleri
E-Mail: emanuele.cavalleri@mail.polimi.it

References

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

See Also

smith_waterman_string

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