Package ‘muscle’

July 12, 2025

Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.51.0

Date 2012-10-05

Author Algorithm by Robert C. Edgar. R port by Alex T. Kalinka.

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Description MUSCLE performs multiple sequence alignments of nucleotide or amino acid sequences.

biocViews MultipleSequenceAlignment, Alignment, Sequencing, Genetics, SequenceMatching, DataImport

Depends Biostrings

License Unlimited

URL `http://www.drive5.com/muscle/`

LazyLoad yes

LazyData yes

NeedsCompilation yes

git_url https://git.bioconductor.org/packages/muscle

git_branch devel

git_last_commit fb6df83

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-11

Contents

`muscle-package` *Multiple Sequence Alignment*

Description

MUSCLE performs multiple sequence alignments of nucleotide and amino acid sequences.

Details

Details about the algorithm can be found on the MUSCLE website:
`http://www.drive5.com/muscle/`

Author(s)

Algorithm: Robert C. Edgar

R port: Alex T. Kalinka `<alex.t.kalinka@gmail.com>`

References

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* **32**, 1792-1797.

See Also

`muscle`, `umax`

Examples

```
## Align sequences in an XStringSet object.
## Not run:
aln <- muscle(stringset = umax)

## End(Not run)
```

`muscle` *Multiple Sequence Alignment*

Description

MUSCLE performs multiple sequence alignments of nucleotide or amino acid sequences.

Usage

```
muscle(stringset, quiet = FALSE, ...)
```

Arguments

`stringset`	An object of class `XStringSet`: `DNAStringSet`, `RNAStringSet`, or `AAStringSet`.
`quiet`	Logical, whether to prevent printing of the progress of the algorithm to the screen. Defaults to FALSE.
`...`	Arguments (options and flags) for the MUSCLE algorithm (see Details).

Details

Arguments for the MUSCLE algorithm are either options or flags. Options take a variety of values, but flags are always logicals (TRUE or FALSE). All options and flags are explained in detail on the MUSCLE website: `http://www.drive5.com/muscle/muscle_userguide3.8.html`

Value

Output is an object of class `MultipleAlignment`: `DNAMultipleAlignment`, `RNAMultipleAlignment`, or `AAMultipleAlignment`.

Note

For further details see the MUSCLE website: `http://www.drive5.com/muscle/`

Author(s)

Algorithm by Robert C. Edgar. Ported into R by Alex T. Kalinka `<alex.t.kalinka@gmail.com>`

References

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* **32**, 1792-1797.

See Also

`umax`

Examples

```
## Align sequences in an XStringSet object.
aln <- muscle(stringset = umax)

## Switch on the diags flag.
aln <- muscle(stringset = umax, diags = TRUE)
```

`umax` *Unaligned MAX sequences*

Description

Unaligned DNA sequences of the MAX gene for 31 mammalian species.

Usage

```
umax
```

Format

An object of class `DNAStringSet`.

Value

An object of class `DNAStringSet`.

Source

`http://www.ensembl.org/index.html`

References

Wagner, AJ et al. (1992) Expression, regulation, and chromosomal localization of the Max gene. *Proc Natl Acad Sci USA* **89**: 3111-3115.

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