Package 'muscle'

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Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.53.0

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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

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Contents

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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 through-put. *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 through-put. *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)
```

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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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