Package ‘muscle’

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Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.18.0

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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

R topics documented:

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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

See Also
muscle, umax

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

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/](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**


**See Also**

`umax`

**Examples**

```r
## 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](http://www.ensembl.org/index.html)
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