Package ‘muscle’

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Type Package
Title Multiple Sequence Alignment with MUSCLE
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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.
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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

```r
## 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 AMultipleAlignment.

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


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
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