

# Package ‘muscle’

May 9, 2024

**Type** Package

**Title** Multiple Sequence Alignment with MUSCLE

**Version** 3.47.0

**Date** 2012-10-05

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

**Maintainer** Alex T. Kalinka <alex.t.kalinka@gmail.com>

**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

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**Repository** Bioconductor 3.20

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muscle-package

*Multiple Sequence Alignment*

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### 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](mailto: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 <code>XStringSet</code> : <code>DNAStrngSet</code> , <code>RNAStringSet</code> , or <code>AAStringSet</code> .
quiet	Logical, whether to prevent printing of the progress of the algorithm to the screen. Defaults to <code>FALSE</code> .
...	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](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](mailto: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)
```

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umax

*Unaligned MAX sequences*

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**Description**

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

**Usage**

umax

**Format**

An object of class [DNAStrngSet](#).

**Value**

An object of class [DNAStrngSet](#).

**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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