# Package ‘muscle’

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**Type** Package

**Title** Multiple Sequence Alignment with MUSCLE

**Version** 3.55.0

**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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**git_last_commit_date** 2026-04-28

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## Contents

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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>`

## 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)
```

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`muscle` *Multiple Sequence Alignment*

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## 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)
```

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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.

# Index