Package ‘muscle’

March 23, 2017

Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.16.0

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

R topics documented:

  muscle-package ................................................... 1
  muscle ............................................................ 2
  umax ............................................................... 3

Index

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)
```

---

**description**

**Usage**

```r
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)
```

---

**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)
References

Index

*Topic datasets
  umax, 3

AAMultipleAlignment, 3
AAStringSet, 2

DNAMultipleAlignment, 3
DNAStringSet, 2, 3

MultipleAlignment, 3
muscle, 2, 2
muscle-package, 1

RNAMultipleAlignment, 3
RNAStringSet, 2

umax, 2, 3, 3

XStringSet, 2