Package ‘muscle’

March 6, 2024

Type  Package
Title  Multiple Sequence Alignment with MUSCLE
Version  3.44.0
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  RELEASE_3_18
git_last_commit  bebb424
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Repository  Bioconductor 3.18
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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


See Also

`muscle`, `umax`

Examples

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


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)
**Umalign MAX sequences**

**Description**

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

**Usage**

*umalign*

**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**

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