Package ‘muscle’

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Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.16.0

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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.

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

muscle  

Description
MUSCLE performs multiple sequence alignments of nucleotide or amino acid sequences.

Usage
muscle(stringset, quiet = FALSE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>stringset</td>
<td>An object of class XStringSet: DNAStringSet, RNAStringSet, or AAStringSet.</td>
</tr>
<tr>
<td>quiet</td>
<td>Logical, whether to prevent printing of the progress of the algorithm to the screen. Defaults to FALSE.</td>
</tr>
<tr>
<td>...</td>
<td>Arguments (options and flags) for the MUSCLE algorithm (see Details).</td>
</tr>
</tbody>
</table>

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

```r
## Align sequences in an XStringSet object.
aln <- muscle(stringset = umax)

## Switch on the diags flag.
aln <- muscle(stringset = umax, diags = TRUE)
```

### umax

**Unaligned MAX sequences**

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

**Usage**

```r
umax
```

**Format**
An object of class `DNAStringSet`.

**Value**
An object of class `DNAStringSet`.

**Source**
http://www.ensembl.org/index.html
References

*Proc Natl Acad Sci USA* **89**: 3111-3115.
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