Package ‘muscle’

November 21, 2016

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

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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

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high through-

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 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
**umax**

**Value**

Output is an object of class `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)
```

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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](http://www.ensembl.org/index.html)
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