Package: muscle (via r-universe)

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Type Package

Title Multiple Sequence Alignment with MUSCLE

Version 3.55.0

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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

Config/pak/sysreqs zlib1g-dev

Repository https://bioc.r-universe.dev

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RemoteUrl https://github.com/bioc/muscle

RemoteRef HEAD

RemoteSha 2446ca4ab6e585b3aca01b365cfff217f3953ec8

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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 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)
```

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 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)
```

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.

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