Package ‘muscle’

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Type Package

Title Multiple Sequence Alignment with MUSCLE

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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:

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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


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/](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

`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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