Package 'msa'

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Title Multiple Sequence Alignment

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Description The 'msa' package provides a unified R/Bioconductor interface to the multiple sequence alignment algorithms ClustalW, ClustalOmega, and Muscle. All three algorithms are integrated in the package, therefore, they do not depend on any external software tools and are available for all major platforms. The multiple sequence alignment algorithms are complemented by a function for pretty-printing multiple sequence alignments using the LaTeX package TeXshade.

URL https://github.com/UBod/msa

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`msa-package` *Multiple Sequence Alignment*

Description

The **msa** package provides a unified R/Bioconductor interface to different multiple sequence alignment algorithms. Currently, 'ClustalW', 'ClustalOmega', and 'MUSCLE' are supported. All algorithms are usable without additional software packages and on all major platforms. The multiple sequence algorithms are complemented by an R interface to the powerful LaTeX package **texshade.sty** which allows for a highly customizable plots of multiple sequence alignments.

Details

The central method of this package is msa. It provides unified access to all three multiple alignment algorithms implemented in this package. The function (like the three functions directly accessing the respective algorithm, i.e., msaClustalW, msaClustalOmega, and msaMuscle) can handle multiple types of input sequences, such as XStringSet and any subclass thereof, character vectors, and can also directly read from FASTA files. The package defines special classes for storing multiple alignments and provides several methods for manipulating, analyzing, and printing such multiple alignments. The function msaPrettyPrint provides an interface to the powerful TeXshade package that allows for powerful LaTeX-based visualization of multiple alignments.

Author(s)

Enrico Bonatesta, Christoph Kainrath, and Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* **22**(22):4673-4680. DOI: doi:10.1093/nar/22.22.4673.

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Edgar, R. C. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**(5):1792-1797. DOI: doi:10.1093/nar/gkh340.

Edgar, R. C. (2004). MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* **5**:113. DOI: doi:10.1186/147121055113.

Beitz, E. (2000). TeXshade: shading and labeling of multiple sequence alignments using LaTeX2e. *Bioinformatics* **16**(2):135-139. DOI: doi:10.1093/bioinformatics/16.2.135.

See Also

msa, msaClustalW, msaClustalOmega, msaMuscle, msaPrettyPrint

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call unified interface msa() for default method (ClustalW) and
## default parameters
msa(mySeqs)
```

msa *Unified interface to multiple sequence alignment algorithms*

Description

The msa function provides a unified interface to the three multiple sequence alignment algorithms in this package: 'ClustalW', 'ClustalOmega', and 'MUSCLE'.

Usage

```
msa(inputSeqs, method=c("ClustalW", "ClustalOmega", "Muscle"),
    cluster="default", gapOpening="default",
    gapExtension="default", maxiters="default",
    substitutionMatrix="default", type="default",
    order=c("aligned", "input"), verbose=FALSE, help=FALSE,
    ...)
```

Arguments

inputSeqs	input sequences; this argument can be a character vector, an object of class XStringSet (includes the classes AAStringSet, DNAStringSet, and RNAStringSet), or a single character string with a file name. In the latter case, the file name is required to have the suffix '.fa' or '.fasta', and the file must be in FASTA format.
method	specifies the multiple sequence alignment to be used; currently, "ClustalW", "ClustalOmega", and "Muscle" are supported.
cluster	parameter related to sequence clustering; its interpretation and default value depends on the method; see msaClustalW, msaClustalOmega, or msaMuscle for algorithm-specific information.
gapOpening	gap opening penalty; the defaults are specific to the algorithm (see msaClustalW, and msaMuscle). Note that the sign of this parameter is ignored. The sign is automatically adjusted such that the called algorithm penalizes gaps instead of rewarding them.
gapExtension	gap extension penalty; the defaults are specific to the algorithm (see msaClustalW, and msaMuscle). Note that the sign of this parameter is ignored. The sign is automatically adjusted such that the called algorithm penalizes gaps instead of rewarding them.
maxiters	maximum number of iterations; its interpretation and default value depends on the method; see msaClustalW, msaClustalOmega, or msaMuscle for algorithm-specific information.
substitutionMatrix	substitution matrix for scoring matches and mismatches; format and defaults depend on the algorithm; see msaClustalW, msaClustalOmega, or msaMuscle for algorithm-specific information.

type — type of the input sequences inputSeqs; possible values are "dna", "rna", or "protein". In the original ClustalW implementation, this parameter is also called -type; "auto" is also possible in the original ClustalW, but, in this package, "auto" is deactivated. The type argument is mandatory if inputSeqs is a character vector or the file name of a FASTA file (see above). If inputSeqs is an object of class AAStringSet, DNAStringSet, or RNAStringSet, the type of sequences is determined by the class of inputSeqs and the type parameter is not necessary. If it is nevertheless specified and the type does not match the class of inputSeqs, the function stops with an error.

order — how the sequences should be ordered in the output object; if "aligned" is chosen, the sequences are ordered in the way the multiple sequence alignment algorithm orders them. If "input" is chosen, the sequences in the output object are ordered in the same way as the input sequences. For MUSCLE, the choice "input" is not available for sequence data that is read directly from a FASTA file. Even if sequences are supplied directly via R, the sequences must have unique names, otherwise the input order cannot be recovered. If the sequences do not have names or if the names are not unique, the msaMuscle function assignes generic unique names "Seq1"-Seqn to the sequences and issues a warning.

verbose — if TRUE, the algorithm displays detailed information and progress messages.

help — if TRUE, information about algorithm-specific parameters is displayed. In this case, no multiple sequence alignment is performed and the function quits after displaying the additional help information.

... — all other parameters are passed on to the multiple sequence algorithm, i.e. to one of the functions msaClustalW, msaClustalOmega, or msaMuscle. An overview of parameters that are available for the chosen method is shown when calling msa with help=TRUE. For more details, see also the documentation of chosen multiple sequence alignment algorithm.

Details

msa is a simple wrapper function that unifies the interfaces of the three functions msaClustalW, msaClustalOmega, and msaMuscle. Which function is called, is controlled by the method argument.

Note that the input sequences may be reordered by the multiple sequence alignment algorithms in order to group together similar sequences (see also description of argument order above). So, if the input order should be preserved or if the input order should be recovered later, we strongly recommend to always assign unique names to the input sequences. As noted in the description of the inputSeqs argument above, all functions, msa(), msaClustalW, msaClustalOmega, and msaMuscle, also allow for direct reading from FASTA files. This is mainly for the reason of memory efficiency if the sequence data set is very large. Otherwise, we want to encourage users to first read the sequences into the R workspace. If sequences are read from a FASTA file directly, the order of output sequences is completely under the control of the respective algorithm and does not allow for checking whether the sequences are named uniquely in the FASTA file. The preservation of the input order works also for sequence data read from a FASTA file, but only for ClustalW and ClustalOmega; MUSCLE does not support this (see also argument order above and msaMuscle).

Value

Depending on the type of sequences for which it was called, msa returns a MsaAAMultipleAlignment, MsaDNAMultipleAlignment, or MsaRNAMultipleAlignment object. If called with help=TRUE, msa returns an invisible NULL.

Author(s)

Enrico Bonatesta and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

http://www.clustal.org/download/clustalw_help.txt

http://www.clustal.org/omega/README

http://www.drive5.com/muscle/muscle.html

Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* **22**(22):4673-4680. DOI: doi:10.1093/nar/22.22.4673.

Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., Soeding, J., Thompson, J. D., and Higgins, D. G. (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol. Syst. Biol.* **7**:539. DOI: doi:10.1038/msb.2011.75.

Edgar, R. C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**(5):1792-1797. DOI: doi:10.1093/nar/gkh340.

Edgar, R. C. (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* **5**:113. DOI: doi:10.1186/147121055113.

See Also

msaClustalW, msaClustalOmega, msaMuscle, msaPrettyPrint, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment, MsaMetaData

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call unified interface msa() for default method (ClustalW) and
## default parameters
msa(mySeqs)

## call ClustalOmega through unified interface
```

```
msa(mySeqs, method="ClustalOmega")

## call MUSCLE through unified interface with some custom parameters
msa(mySeqs, method="Muscle", gapOpening=12, gapExtension=3, maxiters=16,
    cluster="upgmamax", SUEFF=0.4, brenner=FALSE,
    order="input", verbose=FALSE)
```

`msaCheckNames` *Check and fix sequence names*

Description

This function checks and fixed sequence names of multiple alignment objects if they contain characters that might lead to LaTeX problems when using `msaPrettyPrint`.

Usage

```
msaCheckNames(x, replacement=" ", verbose=TRUE)
```

Arguments

`x`	an object of class `MultipleAlignment` (which includes objects of classes `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, and `MsaRNAMultipleAlignment`)
`replacement`	a character string specifying with which character(s) potentially problematic characters should be replaced.
`verbose`	if `TRUE` (default), a warning message is shown if potentially problematic characters are found. Otherwise, the function silently replaces these characters (see details below).

Details

The **Biostrings** package does not impose any restrictions on the names of sequences. Consequently, **msa** also allows all possible ASCII strings as sequence (row) names in multiple alignments. As soon as `msaPrettyPrint` is used for pretty-printing multiple sequence alignments, however, the sequence names are interpreted as plain LaTeX source code. Consequently, LaTeX errors may arise because of characters or words in the sequence names that LaTeX does not or cannot interpret as plain text correctly. This particularly includes appearances of special characters and backslash characters in the sequence names.

The `msaCheckNames` function takes a multiple alignment object and checks sequence names for possibly problematic characters, which are all characters but letters (upper and lower case), digits, spaces, commas, colons, semicolons, periods, question and exclamation marks, dashes, braces, single quotes, and double quotes. All other characters are considered problematic. The function allows for both checking and fixing the sequence names. If called with `verbose=TRUE` (default), the function prints a warning if a problematic character is found. At the same time, regardless of the `verbose` argument, the function invisibly returns a copy of `x` in whose sequence names all problematic characters have been replaced by the string that is supplied via the `replacement` argument (the default is a single space).

In any case, the best solution is to check sequence names carefully and to avoid problematic sequence names from the beginning.

Value

The function invisibly returns a copy of the argument x (therefore, an object of the same class as x), but with modified sequence/row names (see details above).

Author(s)

Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

msaPrettyPrint, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment

Examples

```
## create toy example
mySeqs <- DNAStringSet(c("ACGATCGATC", "ACGACGATC", "ACGATCCCCC"))
names(mySeqs) <- c("Seq. #1", "Seq. \2", "Seq. ~3")

## perform multiple alignment
myAlignment <- msa(mySeqs)
myAlignment

## check names
msaCheckNames(myAlignment)

## fix names
myAlignment <- msaCheckNames(myAlignment, replacement="", verbose=FALSE)
myAlignment
```

---

msaClustalOmega *Multiple Sequence Alignment with ClustalOmega*

Description

This function calls the multiple sequence alignment algorithm ClustalOmega.

Usage

```
msaClustalOmega(inputSeqs, cluster="default",
                gapOpening="default", gapExtension="default",
                maxiters="default",  substitutionMatrix="default",
                type="default", order=c("aligned", "input"),
                verbose=FALSE, help=FALSE, ...)
```

Arguments

`inputSeqs`	input sequences; see `msa`. In the original ClustalOmega implementation, this parameter is called `infile`.
`cluster`	The cluster size which should be used. The default is 100. In the original ClustalOmega implementation, this parameter is called `cluster-size`.
`gapOpening, gapExtension`	ClustalOmega currently does not allow to adjust gap penalties; these arguments are only for future extensions and consistency with the other algorithms and `msa`. However, setting these parameters to values other than `"default"` will result in a warning.
`maxiters`	maximum number of iterations; the default value is 0 (no limitation). In the original ClustalOmega implementation, this parameter is called `iterations`.
`substitutionMatrix`	name of substitution matrix for scoring matches and mismatches; can be one of the choices `"BLOSUM30"`, `"BLOSUM40"`, `"BLOSUM50"`, `"BLOSUM65"`, `"BLOSUM80"`, and `"Gonnet"`. This parameter is a new feature - the original ClustalOmega implementation does not allow for using a custom substitution matrix.
`type`	type of the input sequences `inputSeqs`; see `msa`.
`order`	how the sequences should be ordered in the output object (see `msa`); in the original ClustalW implementation, this parameter is called `output-order`.
`verbose`	if `TRUE`, the algorithm displays detailed information and progress messages.
`help`	if `TRUE`, information about algorithm-specific parameters is displayed. In this case, no multiple sequence alignment is performed and the function quits after displaying the additional help information.
`...`	further parameters specific to ClustalOmega; An overview of parameters that are available in this interface is shown when calling `msaClustalOmega` with `help=TRUE`. For more details, see also the documentation of ClustalOmega.

Details

This is a function providing the ClustalOmega multiple alignment algorithm as an R function. It can be used for various types of sequence data (see `inputSeqs` argument above). Parameters that are common to all multiple sequences alignments provided by the **msa** package are explicitly provided by the function and named in the same for all algorithms. Most other parameters that are specific to ClustalOmega can be passed to ClustalOmega via additional arguments (see argument `help` above).

Since ClustalOmega only allows for using built-in amino acid substitution matrices, it is hardly useful for multiple alignments of nucleotide sequences.

For a note on the order of output sequences and direct reading from FASTA files, see `msa`.

Value

Depending on the type of sequences for which it was called, `msaClustalOmega` returns a `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, or `MsaRNAMultipleAlignment` object. If called with `help=TRUE`, `msaClustalOmega` returns an invisible `NULL`.

Author(s)

Enrico Bonatesta and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

http://www.clustal.org/omega/README

Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., Soeding, J., Thompson, J. D., and Higgins, D. G. (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol. Syst. Biol.* **7**:539. DOI: doi:10.1038/msb.2011.75.

See Also

`msa`, `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, `MsaRNAMultipleAlignment`, `MsaMetaData`

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call msaClustalOmega with default values
msaClustalOmega(mySeqs)

## call msaClustalOmega with custom parameters
msaClustalOmega(mySeqs, auto=FALSE, cluster=120, dealign=FALSE,
                useKimura=FALSE, order="input", verbose=FALSE)
```

`msaClustalW` *Multiple Sequence Alignment with ClustalW*

Description

This function calls the multiple sequence alignment algorithm ClustalW.

Usage

```
msaClustalW(inputSeqs, cluster="default", gapOpening="default",
            gapExtension="default", maxiters="default",
            substitutionMatrix="default", type="default",
            order=c("aligned", "input"), verbose=FALSE,
            help=FALSE, ...)
```

Arguments

inputSeqs	input sequences; see msa. In the original ClustalW implementation, this parameter is called infile.
cluster	The clustering method which should be used. Possible values are "nj" (default) and "upgma". In the original ClustalW implementation, this parameter is called clustering. Please note that cluster="upgma" leads to an unidentified error on Windows with R 4.0.x that even crashes the entire R session.
gapOpening	gap opening penalty; the default value for nucleotide sequences is 15.0, the default value for amino acid sequences is 10.0.
gapExtension	gap extension penalty; the default value for nucleotide sequences is 6.66, the default value for amino acid sequences is 0.2.
maxiters	maximum number of iterations; the default value is 16. In the original ClustalW implementation, this parameter is called numiters.
substitutionMatrix	substitution matrix for scoring matches and mismatches; can be a real matrix, a file name, or the name of a built-in substitution matrix. In the latter case, the choices "blosum", "pam", "gonnet", and "id" are supported for amino acid sequences. For aligning nucleotide sequences, the choices "iub" and "clustalw" are possible. The parameter dnamatrix can also be used instead for the sake of backwards compatibility. The valid choices for this parameter are "iub" and "clustalw". In the original ClustalW implementation, this parameter is called matrix.
type	type of the input sequences inputSeqs; see msa.
order	how the sequences should be ordered in the output object (see msa); in the original ClustalW implementation, this parameter is called outorder.
verbose	if TRUE, the algorithm displays detailed information and progress messages.
help	if TRUE, information about algorithm-specific parameters is displayed. In this case, no multiple sequence alignment is performed and the function quits after displaying the additional help information.
...	further parameters specific to ClustalW; An overview of parameters that are available in this interface is shown when calling msaClustalW with help=TRUE. For more details, see also the documentation of ClustalW.

Details

This is a function providing the ClustalW multiple alignment algorithm as an R function. It can be used for various types of sequence data (see inputSeqs argument above). Parameters that are

common to all multiple sequences alignments provided by the **msa** package are explicitly provided by the function and named in the same for all algorithms. Most other parameters that are specific to ClustalW can be passed to ClustalW via additional arguments (see argument `help` above).

For a note on the order of output sequences and direct reading from FASTA files, see `msa`.

Value

Depending on the type of sequences for which it was called, `msaClustalW` returns a `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, or `MsaRNAMultipleAlignment` object. If called with `help=TRUE`, `msaClustalW` returns an invisible `NULL`.

Author(s)

Enrico Bonatesta and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

http://www.clustal.org/download/clustalw_help.txt

Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* **22**(22):4673-4680. DOI: doi:10.1093/nar/22.22.4673.

See Also

`msa`, `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, `MsaRNAMultipleAlignment`, `MsaMetaData`

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call msaClustalW with default values
msaClustalW(mySeqs)

## call msaClustalW with custom parameters
msaClustalW(mySeqs, gapOpening=1, gapExtension=1, maxiters=16,
            kimura=FALSE, order="input", maxdiv=23)
```

msaConsensusSequence *Computation of Consensus Sequence from Multiple Alignment*

Description

This method computes a consensus sequence from a multiple alignment or a previously computed consensus matrix. Currently, two different ways of these computations are available.

Usage

```
## S4 method for signature 'matrix'
msaConsensusSequence(x, type=c("Biostrings", "upperlower"),
    thresh=c(80, 20), ignoreGaps=FALSE, ...)
## S4 method for signature 'MultipleAlignment'
msaConsensusSequence(x, ...)
```

Arguments

x	an object of class MultipleAlignment (which includes objects of classes MsaAAMultipleAlignment, MsaDNAMultipleAlignment, and MsaRNAMultipleAlignment) or a previously computed consensus matrix (see details below).
type	a character string specifying how to compute the consensus sequence. Currently, types "Biostrings" and "upperlower" are available (see details below).
thresh	a decreasing two-element numeric vector of numbers between 0 and 100 corresponding to the two conservation thresholds. Only relevant for type="upperlower" (see details below), otherwise ignored.
ignoreGaps	a logical (default: FALSE) indicating whether gaps should be considered when computing the consensus sequence. Only relevant for type="upperlower" (see details below), otherwise ignored.
...	when the method is called for a MultipleAlignment object, the consensus matrix is computed and, including all further arguments, passed passed on to the msaConsensusSequence method with signature matrix. The method with signature matrix forwards additional arguments to the consensusString method from the **Biostrings** package if type="Biostrings".

Details

The method takes a MultipleAlignment object or a previously computed consensus matrix and computes a consensus sequence. For type="Biostrings", the method consensusString from the **Biostrings** package is used to compute the consensus sequence. For type="upperlower", two thresholds (argument thresh, see above) are used to compute the consensus sequence:

- If the relative frequency of the most frequent letter at a given position is at least as large as the first threshold (default: 80%), then this most frequent letter is used for the consensus sequence at this position as it is.

- If the relative frequency of the most frequent letter at a given position is smaller than the first threshold, but at least as large as the second threshold (default: 20%), then this most frequent letter is used for the consensus sequence at this position, but converted to lower case.
- If the relative frequency of the most frequent letter in a column is even smaller than the second threshold, then a dot is used for the consensus sequence at this position.
- If `ignoreGaps=FALSE` (which is the default), gaps are treated like all other letters except for the fact that obviously no lowercase conversion takes place in case that the relative frequency is between the two thresholds. If `ignoreGaps=TRUE`, gaps are ignored completely, and the consensus sequence is computed from the non-gap letters only.

If the consensus matrix of a multiple alignment of nucleotide sequences contains rows labeled '+' and/or '.', these rows are ignored.

Value

The function returns a character string with the consensus sequence.

Author(s)

Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

msa, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment, MsaMetaData, MultipleAlignment, consensusString

Examples

```
## read sequences
filepath <- system.file("examples", "HemoglobinAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## perform multiple alignment
myAlignment <- msa(mySeqs)

## regular consensus sequence using consensusString() method from the
## 'Biostrings' package
msaConsensusSequence(myAlignment)

## use the other method
msaConsensusSequence(myAlignment, type="upperlower")

## use the other method with custom parameters
```

```
msaConsensusSequence(myAlignment, type="upperlower", thresh=c(50, 20),
                     ignoreGaps=TRUE)

## compute a consensus matrix first
conMat <- consensusMatrix(myAlignment)
msaConsensusSequence(conMat)
```

`msaConservationScore` *Computation of Conservation Scores from Multiple Alignment*

Description

This method computes a vector of conservation scores from a multiple alignment or a previously computed consensus matrix.

Usage

```
## S4 method for signature 'matrix'
msaConservationScore(x, substitutionMatrix, gapVsGap=NULL,
    ...)
## S4 method for signature 'MultipleAlignment'
msaConservationScore(x, ...)
```

Arguments

`x`	an object of class `MultipleAlignment` (which includes objects of classes `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, and `MsaRNAMultipleAlignment`) or a previously computed consensus matrix (see details below).
`substitutionMatrix`	substitution matrix (see details below).
`gapVsGap`	score to use for aligning gaps versus gaps (see details below).
`...`	when the method is called for a `MultipleAlignment` object, the consensus matrix is computed and, including all further arguments, passed on to the `msaConservationScore` method with signature `matrix`. This method passes all further arguments on to the `msaConsensusSequence` method to customize the way the consensus sequence is computed.

Details

The method takes a `MultipleAlignment` object or a previously computed consensus matrix and computes the sum of pairwise scores for all positions of the alignment. For computing these scores, it is compulsory to specify a substitution/scoring matrix. This matrix must be provided as a `matrix` object. This can either be one of the ready-made matrices provided by the **pwalign** package (e.g. `BLOSUM62`) or any other hand-crafted matrix. In the latter case, the following restrictions apply:

- The matrix must be quadratic.
- For reasonable results, the matrix should be symmetric (note that this is not checked).

- Rows and columns must be named and the order of letters/symbols in row names and column names must be identical.
- All letters/symbols occurring in the multiple alignment, including gaps '-', must also be found in the row/column names of the substitution matrix. For consistency with the matrices from the **pwalign** package, the row/column corresponding to gap penalties may also be labeled '*' instead of '-'.

So, nucleotide substitution matrices created by `nucleotideSubstitutionMatrix` can be used for multiple alignments of nucleotide sequences, but must be completed with gap penalty rows and columns (see example below).

If the consensus matrix of a multiple alignment of nucleotide sequences contains rows labeled '+' and/or '.', these rows are ignored.

The parameter `gapVsGap` can be used to control how pairs of gaps are scored. If `gapVsGap=NULL` (default), the corresponding diagonal entry of the substitution matrix is used as is. In the BLOSUM matrices, this is usually a positive value, which may not make sense under all circumstances. Therefore, the parameter `gapVsGap` can be set to an alternative value, e.g. 0 for ignoring gap-gap pairs.

The method, in any case, returns a vector of scores that is as long as the alignment/consensus matrix has columns. The names of the vector entries are the corresponding positions of the consensus sequence of the alignment. How this consensus sequence is computed, can be controlled with additional arguments that are passed on to the `msaConsensusSequence` method.

Value

The function returns a vector as long as the alignment/consensus matrix has columns. The vector is named with the consensus sequence (see details above).

Author(s)

Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

`msa`, `MsaAAMultipleAlignment`, `MsaDNAMultipleAlignment`, `MsaRNAMultipleAlignment`, `MsaMetaData`, `MultipleAlignment`, `msaConsensusSequence`

Examples

```
## load 'pwalign' package which provides substitution matrices
library(pwalign)

## read sequences
```

```
filepath <- system.file("examples", "HemoglobinAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## perform multiple alignment
myAlignment <- msa(mySeqs)

## compute consensus scores using the BLOSUM62 matrix
data(BLOSUM62)
msaConservationScore(myAlignment, BLOSUM62)

## compute consensus scores using the BLOSUM62 matrix
## without scoring gap-gap pairs and using a different consensus sequence
msaConservationScore(myAlignment, BLOSUM62, gapVsGap=0,
                     type="upperlower")

## compute a consensus matrix first
conMat <- consensusMatrix(myAlignment)
data(PAM250)
msaConservationScore(conMat, PAM250, gapVsGap=0)


## DNA example
filepath <- system.file("examples", "exampleDNA.fasta", package="msa")
mySeqs <- readDNAStringSet(filepath)

## perform multiple alignment
myAlignment <- msa(mySeqs)

## create substitution matrix with gap penalty -8
mat <- nucleotideSubstitutionMatrix(4, -1)
mat <- cbind(rbind(mat, "-"=-8), "-"=-8)

## compute consensus scores using this matrix
msaConservationScore(myAlignment, mat, gapVsGap=0)
```

---

msaConvert *Convert Multiple Sequence Alignment for Other Packages*

Description

This function converts a multiple sequence alignment object to formats used in other sequence analysis packages.

Usage

```
msaConvert(x,
           type=c("seqinr::alignment", "bios2mds::align",
                  "ape::AAbin", "ape::DNAbin",
                  "phangorn::phyDat", "bio3d::fasta"))
```

Arguments

x	an object of class MultipleAlignment (which includes objects of classes MsaAAMultipleAlignment, MsaDNAMultipleAlignment, and MsaRNAMultipleAlignment)
type	a character string specifying to which type of object x should be converted; currently, the values "seqinr::alignment", "bios2mds::align", "ape::AAbin", "ape::DNAbin", "phangorn::phyDat", and "bio3d::fasta".

Details

The function converts x to the class of object as specified by the type argument. The values possible for the type argument follow the same principle *pkg*::*cl*, i.e. x is converted to class *cl* as defined in the *pkg* package.

The conversions for usage by the packages **seqinr**, **bios2mds**, and **ape** work independently of these packages and do not strictly require these packages. They need not even be installed. This approach has been chosen to avoid abundant dependencies and possible incompatibilities. That is also why the standard S3/S4 mechanism of as/as.class functions is not used.

The conversion to the phyDat class can be done easily using the as.phyDat function from the **phangorn** package. The msaConvert function still provides this conversion for the sake of consistency. However, this conversion is just a wrapper function around the as.phyDat function from the **phangorn** package. Thus, the **phangorn** package needs to be installed.

The conversion "ape::AAbin" only works for multiple alignments of amino acid sequences, while the conversions "ape::DNAbin" and "phangorn::phyDat" only work for multiple alignments of DNA sequences. When converting to "ape::AAbin", gaps/dashes are replaced by 'X'. Moreover, conversions to "ape::DNAbin" also convert all characters to lowercase and replace gaps/dashes by 'n'.

Value

The function returns an object of the class as specified by the type argument.

Author(s)

Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

msa, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment, MsaMetaData

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## perform multiple alignment
myAlignment <- msa(mySeqs)

## convert to an object of class 'alignment' (package 'seqinr')
msaConvert(myAlignment, "seqinr::alignment")

## convert to an object of class 'align' (package 'bios2mds')
msaConvert(myAlignment, "bios2mds::align")
```

MsaMetaData-class *Class* MsaMetaData

Description

S4 class for storing metadata about multiple sequence alignment results

Objects

Objects of this virtual class are not be created and used directly. This is an auxiliary class used by the classes MsaAAMultipleAlignment, MsaDNAMultipleAlignment, and MsaRNAMultipleAlignment

Slots

The following slots are defined for MsaMetaData objects:

`version`: slot in which information is stored with which algorithm the multiple alignment has been computed along with its version number.

`params`: list in which the parameters are stored with which the multiple alignment algorithm has been executed.

`call`: the matched call with which the object was created

Methods

`version(object)`: accessor to the `version` slot

`params(x)`: accessor to the `params` slot

Author(s)

Enrico Bonatesta and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

msa, msaClustalW, msaClustalOmega, msaMuscle, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## simple call with default values
myAlignment <- msaClustalOmega(mySeqs)

## show the algorithm version with which the results were created
version(myAlignment)

## show the results
show(myAlignment)

## print the results
print(myAlignment, show="alignment")
print(myAlignment, show=c("alignment", "version"))
print(myAlignment, show="standardParams")
print(myAlignment, show="algParams")
print(myAlignment, show=c("call", "version"))

## show the params
params(myAlignment)
```

MsaMultipleAnlignmentClasses

Classes MsaAAMultipleAlignment, MsaDNAMultipleAlignment, *and* MsaRNAMultipleAlignment

---

Description

S4 classes for storing multiple alignments of amino acid, DNA, and RNA sequences along with algorithm metadata

Objects

Objects of these classes are returned by the multiple sequence alignment algorithms `msaClustalW`, `msaClustalOmega`, `msaMuscle`, and the wrapper function `msa`, all of which are provided by the **msa** package.

Details

The class `MsaAAMultipleAlignment` extends the `AAMultipleAlignment` class, the class `MsaDNAMultipleAlignment` extends the `DNAMultipleAlignment` class, and the class `MsaRNAMultipleAlignment` extends the `RNAMultipleAlignment` class. All three classes extend their parent classes by the slots contained in the `MsaMetaData`, i.e. all three classes are class unions of the aforementioned parent classes and the class `MsaMetaData`.

Methods

`print(x, show=c("alignment", "version", "call"), showNames=TRUE, showConsensus=TRUE, halfNrow=9, nameWi`
: prints information about the object `x`; the `show` argument allows for determining what should be printed. The `show` must be a character vector and may contain any combination of the following strings: if `show` contains `"alignment"`, the multiple sequence alignment is printed in a way similar to the corresponding method from the **Biostrings** package (except for the consensus sequence, see below). If `show` contains `"complete"`, the entire width of the alignment is printed by splitting it over multiple blocks of lines if necessary. This overrules `"alignment"` if both are contained in the `show` argument. If `show` contains `"version"`, the `version` slot is shown. If `show` contains `"call"`, the `call` slot is shown. If `show` contains `"standardParams"`, the settings of the parameters that are common to all three multiple sequence alignment algorithms are shown. If `show` contains `"algParams"`, the algorithm-specific parameters are shown. The order in which the strings are placed in the `show` argument does not have an effect on the order in which data are printed. The default is `show=c("alignment", "version", "call")`, i.e. by default, the multiple sequence alignment is shown along with version and call information. If `show` contains `"all"`, the complete alignment is shown along with version information, call, and the complete set of parameters. As said above, by default, printing alignments is similar to the standard `print` method provided by the **Biostrings** package, whereas including `"complete"` in the argument `show` prints the entire width of the alignment. Unlike the method from the **Biostrings** package, the appearance can be customized: by default, the consensus sequence is appended below the alignment. To switch this off, use `showConsensus=FALSE`. Whether or not sequence names should be printed can be controlled via the `showNames` argument. The width reserved for the sequence names can be adjusted using the `nameWidth` argument; the default is 20 like in the **Biostrings** method. If the number of sequences in the alignment is large, output can become quite lengthy. That is why only the first `halfNrow` and the last `halfNrow` sequences are shown. To show all sequences, set `halfNrow` to `NA` or -1. Note that `print` can also handle masked objects, where the masked sequences/positions are shown as hash marks. However, the consensus sequences are computed from the complete, unmasked alignment and displayed as such. Additional arguments are passed on to `msaConsensusSequence` for customizing how the consensus sequence is computed.

`show(object)`**:** displays the alignment along with metadata; synonymous to calling `print` with default arguments.

`version(object)`: displays the algorithm with which the multiple alignment has been computed along with its version number (see also `MsaMetaData`).

`params(x)`: accessor to the `params` slot (see also `MsaMetaData`)

Author(s)

Enrico Bonatesta, Christoph Kainrath, and Ulrich Bodenhofer

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

See Also

`msa`, `msaClustalW`, `msaClustalOmega`, `msaMuscle`, `MsaMetaData`

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## simple call with default values
myAlignment <- msaClustalOmega(mySeqs)

## show the algorithm version with which the results were created
version(myAlignment)

## show the results
show(myAlignment)

## print the results
print(myAlignment, show="alignment")
print(myAlignment, show="alignment", showConsensus=FALSE)
print(myAlignment, show=c("alignment", "version"))
print(myAlignment, show="standardParams")
print(myAlignment, show="algParams")
print(myAlignment, show=c("call", "version"))

## print results with custom consensus sequence
print(myAlignment, show="complete", type="upperlower", thresh=c(50, 20))

## show the params
params(myAlignment)
```

msaMuscle *Multiple Sequence Alignment with MUSCLE*

Description

This function calls the multiple sequence alignment algorithm MUSCLE.

Usage

```
msaMuscle(inputSeqs, cluster="default", gapOpening="default",
          gapExtension="default", maxiters="default",
          substitutionMatrix="default",
          type="default", order=c("aligned", "input"),
          verbose=FALSE, help=FALSE, ...)
```

Arguments

inputSeqs	input sequences; see msa. In the original MUSCLE implementation, this parameter is called -in.
cluster	The clustering method which should be used. Possible values are "upgma", "upgmamax", "upgmamin", "upgmb", and "neighborjoining".
gapOpening	gap opening penalty; the default is 400 for DNA sequences and 420 for RNA sequences. The default for amino acid sequences depends on the profile score settings: for the setting le=TRUE, the default is 2.9, for sp=TRUE, the default is 1,439, and for sv=TRUE, the default is 300. Note that these defaults may not be suitable if custom substitution matrices are being used. In such a case, a sensible choice of gap penalties that fits well to the substitution matrix must be made.
gapExtension	gap extension penalty; the default is 0.
maxiters	maximum number of iterations; the default is 16. In the original MUSCLE implementation, it is also possible to set maxiters to 0 which leads to an (out of memory) error. Therefore, maxiters=0 is not allowed in msaMuscle.
substitutionMatrix	substitution matrix for scoring matches and mismatches; can be a real matrix or a file name If the file interface is used, matrices have to be in NCBI-format. The original MUSCLE implementation also accepts matrices in WU_BLAST (AB_BLAST) format, but, due to copyright restrictions, this format is not supported by msaMuscle.
type	type of the input sequences inputSeqs; see msa.
order	how the sequences should be ordered in the output object (see msa for more details); the original MUSCLE implementation does not allow for preserving the order of input sequences. The msaMuscle function realizes this functionality by reverse matching of sequence names. Therefore, the sequences need to have unique names. If the sequences do not have names or if the names are not unique, the msaMuscle function assignes generic unique names "Seq1"-Seqn to the sequences and issues a warning. The choice "input" is not available at all for sequence data that is read directly from a FASTA file.

verbose	if TRUE, the algorithm displays detailed information and progress messages.
help	if TRUE, information about algorithm-specific parameters is displayed. In this case, no multiple sequence alignment is performed and the function quits after displaying the additional help information.
...	further parameters specific to MUSCLE; An overview of parameters that are available in this interface is shown when calling msaMuscle with help=TRUE. For more details, see also the documentation of MUSCLE.

Details

This is a function providing the MUSCLE multiple alignment algorithm as an R function. It can be used for various types of sequence data (see inputSeqs argument above). Parameters that are common to all multiple sequences alignments provided by the **msa** package are explicitly provided by the function and named in the same for all algorithms. Most other parameters that are specific to MUSCLE can be passed to MUSCLE via additional arguments (see argument help above).

For a note on the order of output sequences and direct reading from FASTA files, see msa.

Value

Depending on the type of sequences for which it was called, msaMuscle returns a MsaAAMultipleAlignment, MsaDNAMultipleAlignment, or MsaRNAMultipleAlignment object. If called with help=TRUE, msaMuscle returns an invisible NULL.

Author(s)

Enrico Bonatesta and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

http://www.drive5.com/muscle/muscle.html

Edgar, R. C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**(5):1792-1797. DOI: doi:10.1093/nar/gkh340.

Edgar, R. C. (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* **5**:113. DOI: doi:10.1186/147121055113.

See Also

msa, MsaAAMultipleAlignment, MsaDNAMultipleAlignment, MsaRNAMultipleAlignment, MsaMetaData

Examples

```
## load 'pwalign' package which provides substitution matrices
library(pwalign)

## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call msaMuscle with default values
msaMuscle(mySeqs)

## call msaMuscle with custom parameters
msaMuscle(mySeqs, gapOpening=12, gapExtension=3, maxiters=16,
          cluster="upgmamax", SUEFF=0.4, brenner=FALSE,
          order="input", verbose=FALSE)

## call msaMuscle with a custom substitution matrix
data(PAM120)
msaMuscle(mySeqs, substitutionMatrix=PAM120)
```

`msaPrettyPrint` *Pretty-Printing of Multiple Sequence Alignments*

Description

The `msaPrettyPrint` function provides an R interface to the powerful LaTeX package **texshade.sty** which allows for a highly customizable plots of multiple sequence alignments.

Usage

```
msaPrettyPrint(x, y, output=c("pdf", "tex", "dvi", "asis"),
               subset=NULL, file=NULL, alFile=NULL,
               askForOverwrite=TRUE,  psFonts=FALSE, code=NA,
               paperWidth=11, paperHeight=8.5, margins=c(0.1, 0.3),
               shadingMode=c("identical", "similar", "functional"),
               shadingModeArg=NA,
               shadingColors=c("blues", "reds", "greens", "grays",
                               "black"),
               showConsensus=c("bottom", "top", "none"),
               consensusColors=c("ColdHot", "HotCold", "BlueRed",
                                 "RedBlue", "GreenRed",
                                 "RedGreen", "Gray"),
               consensusThreshold=50,
               showLogo=c("top", "bottom", "none"),
               logoColors=c("chemical", "rasmol", "hydropathy",
                            "structure", "standard area",
                            "accessible area"),
               showLogoScale=c("none", "leftright", "left",
```

```
                        "right"),
    showNames=c("left", "right", "none"),
    showNumbering=c("right", "left", "none"),
    showLegend=TRUE, furtherCode=NA, verbose=FALSE, index=TRUE)
```

Arguments

x	an object of class MultipleAlignment, which includes the classes MsaAAMultipleAlignment, MsaDNAMultipleAlignment, and MsaRNAMultipleAlignment.
y	argument for restricting the output to a subset of columns; can be a numeric vector of length 2 with a lower and an upper bound or an object of class IRanges. If missing, the entire multiple alignment is printed.
output	type of output to be generated (see details below)
subset	can be used to specify a subset of sequences in the multiple alignment x if not all sequences should be printed.
file	name of output file; if no name is given, the name of the output file defaults to name of the object provided as argument x along with the proper suffix which depends on the type of output specified with the output argument. Note that this might lead to invalid file names if not the name of an object, but an R expression is passed as argument x.
alFile	name of alignment file to be created; msaPrettyPrint first writes the multiple alignment x to a .fasta file. The name of this file can be determined with the alFile argument. If no name is given, the name of the output file defaults to name of the object provided as argument x along with the suffix .fasta. Note that this might lead to invalid file names if not the name of an object, but an R expression is passed as argument x.
askForOverwrite	if TRUE (default), msaPrettyPrint asks whether existing files should be overwritten or not. If askForOverwrite is set to FALSE, files are overwritten without further notice.
psFonts	if TRUE, msaPrettyPrint produces LaTeX code that includes the LaTeX package **times.sty**; if FALSE, msaPrettyPrint produces LaTeX code based on the standard LaTeX fonts (default). Ignored for output="asis".
code	this argument can be used to specify the entire LaTeX code in the texshade environment. This overrides all arguments that customize the appearance of the output. Instead, all customizations must be done as LaTeX commands provided by the package **texshade.sty** directly. This option should only be used by expert users and for special applciations in which the possibilities of the customizations of the msaPrettyPrint function turn out to be insufficient.
paperWidth, paperHeight	paper format to be used in the resulting document; defaults to 11in x 8.5in (US letter in landscape orientation). Ignored for output="asis".
margins	a numeric vector of length 2 with the horizontal and vertical margins, respectively; the default is 0.1in for the horizontal and 0.3in for the vertical margin.
shadingMode	shading mode; currently the shading modes "identical", "similar", and "functional" are supported (see documentation of **texshade.sty** for details).

shadingModeArg — for shading modes "identical" and "similar", shadingModeArg must be a single numeric threshold between 0 and 100 or two thresholds between 0 and 100 in increasing order. For shading mode "functional", valid shadingModeArg arguments are "charge", "hydropathy", "structure", "chemical", "rasmol", "standard area", and "accessible area" (see documentation of **texshade.sty** for details).

shadingColors — color scheme for shading; valid "shadingColors" arguments are "blues", "reds", "greens", "grays", and "black" (see documentation of **texshade.sty** for details).

showConsensus — where to show the consensus sequence; possible values are "bottom", "top", and "none" (the latter option suppresses printing of the consensus sequence).

consensusColors — color scheme for printing the consensus sequence; the following choices are possible: "ColdHot", "HotCold", "BlueRed", "RedBlue", "GreenRed", "RedGreen", and "Gray" (see documentation of **texshade.sty** for details).

consensusThreshold — one or two numbers between 0 and 100, where the second one is optional and must be larger than the first one (see documentation of **texshade.sty** for details)

showLogo — where to show a sequence logo; possible values are "top", "bottom", or "none" (the latter option suppresses printing of the consensus sequence). If a sequence logo and a consensus sequence should be shown together, they can only be located at opposite sides.

logoColors — color scheme for printing the sequence logo; the following choices are possible: "chemical", "rasmol", "hydropathy", "structure", "standard area", and "accessible area" (see documentation of **texshade.sty** for details).

showLogoScale — where to plot the vertical axis of the sequence logo; possible values are "left", "right", "leftright", and "none" (the latter option suppresses that the axis is displayed).

showNames — where to print sequence names; possible values are "left", "right", and "none" (the latter option suppresses that names are displayed).

showNumbering — where to print sequence numbers; possible values are "left", "right", and "none" (the latter option suppresses that numbers are displayed). If sequence names and numbers should be shown together, they can only be located at opposite sides.

showLegend — if TRUE (default), a legend is printed at the end of the alignment.

furtherCode — additional LaTeX code to be included in the texshade environment; all text passed as furtherCode is placed between the commands created by msaPrettyPrint and the end of the texshade environment. Note the difference to the code argument: while the code argument replaces all LaTeX code in the texshade environment, the code passed as furtherCode argument is added to the LaTeX code in the texshade environment.

verbose — if TRUE (default), progress messages are printed and also the output of running (PDF)LaTeX (if applicable) is printed to the R session.

index — argument to be forwarded to texi2dvi; normally, index=FALSE would be sufficient, but this might create problems in conjunction with verbose=FALSE.

Details

The msaPrettyPrint function writes a multiple alignment to a .fasta file and creates LaTeX code for pretty-printing the multiple alignment on the basis of the LaTeX package **texshade.sty**. If output="asis", msaPrettyPrint prints a LaTeX fragment consisting of the texshade environment to the console. The parameters described above can be used to customize the way the multiple alignment is formatted. If output="tex", a complete LaTeX file including preamble is created. For output="dvi" and output="pdf", the same kind of LaTeX file is created, but processed using (PDF)LaTeX to produce a final DVI or PDF file, respectively. The file argument be used to determine the file name of the final output file (except for the output="asis" which does not create an output file).

The choice output="asis" is particularly useful for Sweave or knitr documents. If msaPrettyPrint is called with output="asis" in a code chunk with results="tex" (Sweave) or results="asis" (knitr), then the resulting LaTeX fragment consisting of the texshade environment is directly included in the LaTeX document that is created from the Sweave/knitr document.

As noted above, if they are not specified explicitly, output file names are determined automatically. It is important to point out that all file names need to be LaTeX-compliant, i.e. no special characters and spaces (!) are allowed. If a file name would be invalid, msaPrettyPrint makes a default choice.

Moreover, if sequence names are to be printed, there might be names that are not LaTeX-compliant and lead to LaTeX errors. In order to check that in advance, the function msaCheckNames is available.

Note that texi2dvi and texi2pdf always save the resulting DVI/PDF files to the current working directory, even if the LaTeX source file is in a different directory. That is also the reason why the temporary file is created in the current working directory in the example below.

Value

msaPrettyPrint returns an invisible character vector consisting of the LaTeX fragment with the texshade environment.

Author(s)

Ulrich Bodenhofer, Enrico Bonatesta, and Christoph Kainrath

References

https://github.com/UBod/msa

Bodenhofer, U., Bonatesta, E., Horejs-Kainrath, C., and Hochreiter, S. (2015). msa: an R package for multiple sequence alignment. *Bioinformatics* **31**(24):3997-3999. DOI: doi:10.1093/bioinformatics/btv494.

https://www.ctan.org/pkg/texshade

Beitz, E. (2000). TeXshade: shading and labeling of multiple sequence alignments using LaTeX2e. *Bioinformatics* **16**(2):135-139. DOI: doi:10.1093/bioinformatics/16.2.135.

See Also

msaCheckNames

Examples

```
## read sequences
filepath <- system.file("examples", "exampleAA.fasta", package="msa")
mySeqs <- readAAStringSet(filepath)

## call unified interface msa() for default method (ClustalW) and
## default parameters
myAlignment <- msa(mySeqs)

## show resulting LaTeX code with default settings
msaPrettyPrint(myAlignment, output="asis", askForOverwrite=FALSE)

## create PDF file according to some custom settings
## Not run:
tmpFile <- tempfile(pattern="msa", tmpdir=".", fileext=".pdf")
tmpFile
msaPrettyPrint(myAlignment, file=tmpFile, output="pdf",
               showNames="left", showNumbering="none", showLogo="top",
               showConsensus="bottom", logoColors="rasmol",
               verbose=FALSE, askForOverwrite=FALSE)

library(Biobase)
openPDF(tmpFile)
## End(Not run)
```

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