

# User Manual / Package Vignette

## **msa**

### **An R Package for Multiple Sequence Alignment**

**Enrico Bonatesta<sup>2</sup>, Christoph Kainrath<sup>2</sup>, and Ulrich Bodenhofer<sup>1,2</sup>**

<sup>1</sup> School of Informatics, Communication and Media  
University of Applied Sciences Upper Austria  
Softwarepark 11, 4232 Hagenberg, Austria

<sup>2</sup> previously with: Institute of Bioinformatics, Johannes Kepler University  
Altenberger Str. 69, 4040 Linz, Austria

**Version 1.42.0, September 19, 2025**

## Scope and Purpose of this Document

This document provides a gentle introduction into the R package `msa`. Not all features of the R package are described in full detail. Such details can be obtained from the documentation enclosed in the R package. Further note the following: (1) this is not an introduction to multiple sequence alignment or algorithms for multiple sequence alignment; (2) this is not an introduction to R or any of the Bioconductor packages used in this document. If you lack the background for understanding this manual, you first have to read introductory literature on the subjects mentioned above.

## Contents

<b>1</b>	<b>Introduction</b>	<b>4</b>
<b>2</b>	<b>Installation</b>	<b>4</b>
<b>3</b>	<b>msa for the Impatient</b>	<b>5</b>
<b>4</b>	<b>Functions for Multiple Sequence Alignment in More Detail</b>	<b>11</b>
4.1	ClustalW-Specific Parameters . . . . .	13
4.2	ClustalOmega-Specific Parameters . . . . .	13
4.3	MUSCLE-Specific Parameters . . . . .	14
<b>5</b>	<b>Printing Multiple Sequence Alignments</b>	<b>14</b>
<b>6</b>	<b>Processing Multiple Alignments</b>	<b>21</b>
6.1	Methods Inherited From Biostrings . . . . .	21
6.2	Consensus Sequences and Conservation Scores . . . . .	24
6.3	Interfacing to Other Packages . . . . .	31
<b>7</b>	<b>Pretty-Printing Multiple Sequence Alignments</b>	<b>34</b>
7.1	Consensus Sequence and Sequence Logo . . . . .	35
7.2	Color Shading Modes . . . . .	36
7.3	Subsetting . . . . .	37
7.4	Additional Customizations . . . . .	38
7.5	Sweave or knitr Integration . . . . .	38
7.6	Sequence Names . . . . .	39
7.7	Pretty-Printing Wide Alignments . . . . .	39
7.8	Further Caveats . . . . .	40
<b>8</b>	<b>Known Issues</b>	<b>40</b>
<b>9</b>	<b>Future Extensions</b>	<b>41</b>
<b>10</b>	<b>How to Cite This Package</b>	<b>42</b>

## 1 Introduction

Multiple sequence alignment is one of the most fundamental tasks in bioinformatics. Algorithms like ClustalW [13], ClustalOmega [12], and MUSCLE [3, 4] are well known and widely used. However, all these algorithms are implemented as stand-alone command line programs without any integration into the R/Bioconductor ecosystem. Before the `msa` package, only the `muscle` package has been available in R, but no other multiple sequence alignment algorithm, although the `Biostrings` package has provided data types for representing multiple sequence alignments for quite some time. The `msa` package aims to close that gap by providing a unified R interface to the multiple sequence alignment algorithms ClustalW, ClustalOmega, and MUSCLE. The package requires no additional software packages and runs on all major platforms. Moreover, the `msa` package provides an R interface to the powerful  $\text{\LaTeX}$  package `\text{\LaTeX}shade` [1] which allows for a highly customizable plots of multiple sequence alignments. Unless some very special features of `\text{\LaTeX}shade` are required, users can pretty-print multiple sequence alignments without the need to know the details of  $\text{\LaTeX}$  or `\text{\LaTeX}shade`.

## 2 Installation

The `msa` R package (current version: 1.42.0) is available via Bioconductor. The simplest way to install the package is the following:

```
if (!requireNamespace("BiocManager", quietly=TRUE))
  install.packages("BiocManager")
BiocManager::install("msa")
```

To test the installation of the `msa` package, enter

```
library(msa)
```

in your R session. If this command terminates without any error message or warning, you can be sure that the `msa` package has been installed successfully. If so, the `msa` package is ready for use now and you can start performing multiple sequence alignments.

To make use of all functionalities of `msaPrettyPrint()`, a  $\text{\TeX}/\text{\LaTeX}$  system [5] must be installed. To make use of  $\text{\LaTeX}$  code created by `msaPrettyPrint()` or to use the output of `msaPrettyPrint()` in Sweave [6] or knitr [15] documents, the  $\text{\LaTeX}$  package `\text{\LaTeX}shade` (file `texshade.sty`) [1] must be accessible to the  $\text{\LaTeX}$  system too. The file `texshade.sty` is shipped with the `msa` package. To determine where the file is located, enter the following command in your R session:

```
system.file("tex", "texshade.sty", package="msa")
```

Alternatively, `\text{\LaTeX}shade` can be installed directly from the Comprehensive  $\text{\TeX}$  Archive Network (CTAN).<sup>1</sup>

---

<sup>1</sup><https://www.ctan.org/pkg/texshade>

### 3 msa for the Impatient

In order to illustrate the basic workflow, this section presents a simple example with default settings and without going into the details of each step. Let us first load amino acid sequences from one of the example files that are supplied with the msa package:

```
mySequenceFile <- system.file("examples", "exampleAA.fasta", package="msa")
mySequences <- readAAStringSet(mySequenceFile)
mySequences

## AAStringSet object of length 9:
##      width seq                      names
## [1]   452 MSTAVLENPGLGRKLS...NSEIGILCSALQKIK PH4H_Homo_sapiens
## [2]   453 MAAVLENGVLSRKLS...SEVGILCNALQKIKS PH4H_Rattus_norve...
## [3]   453 MAAVLENGVLSRKLS...SEVGILCHALQKIKS PH4H_Mus_musculus
## [4]   297 MNDRADFVVPDITTRK...LNAGDRQGWADTEDV PH4H_Chromobacter...
## [5]   262 MKTTQYVARQPDDNGF...RLGLHAPLFPPKQAA PH4H_Pseudomonas...
## [6]   451 MSALVLESRALGRKLS...SSEVEILCSALQKLK PH4H_Bos_taurus
## [7]   313 MAIATPTSAAPTPAPA...LNAGTREGWADTADI PH4H_Ralstonia_so...
## [8]   294 MSGDGLSNGPPPGARP...AYATAGGRLAGAAAG PH4H_Caulobacter...
## [9]   275 MSVAEYARDCAAQGLR...VARRKDQKALDPATV PH4H_Rhizobium_loti
```

Now that we have loaded the sequences, we can run the `msa()` function which, by default, runs ClustalW with default parameters:

```
myFirstAlignment <- msa(mySequences)

## use default substitution matrix

myFirstAlignment

## CLUSTAL 2.1
##
## Call:
##      msa(mySequences)
##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln                      names
## [1] MAAVLENGVLSRKLSDF...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSDF...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDF...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [5] -----...GWADTEDV----- PH4H_Chromobacter...
## [6] -----...GWADTADI----- PH4H_Ralstonia_so...
## [7] -----...AYATAGGRLAGAAAG--- PH4H_Caulobacter...
```

```
## [8] -----...----- PH4H_Pseudomonas_...
## [9] -----...----- PH4H_Rhizobium_loti
## Con -----...??????IL??A??? Consensus
```

Obviously, the default printing function shortens the alignment for the sake of compact output. The `print()` function provided by the `msa` package provides some ways for customizing the output, such as, showing the entire alignment split over multiple blocks of sub-sequences:

```
print(myFirstAlignment, show="complete")

##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln (1..39)                                names
## [1] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAISLIF PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAVSLIF PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDFGQETSYIEDNCNQNGAISLIF PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDFGQETSYIEGNSDQN-AVSLIF PH4H_Bos_taurus
## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ----- Consensus
##
##      aln (40..78)                                names
## [1] SLKEEVGALAKVLRRLFEEENDINLTHIESRPSRLNKDEYE PH4H_Rattus_norve...
## [2] SLKEEVGALAKVLRRLFEEENEINLTHIESRPSRLNKDEYE PH4H_Mus_musculus
## [3] SLKEEVGALAKVLRRLFEEENDVNLTHIESRPSRLKKDEYE PH4H_Homo_sapiens
## [4] SLKEEVGALARVLRRLFEEENDINLTHIESRPSRLRKDEYE PH4H_Bos_taurus
## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ----- Consensus
##
##      aln (79..117)                                names
## [1] FFTYLDKRTKPVLSGIKSLRNDIGATVHELSDRDKKNT PH4H_Rattus_norve...
## [2] FFTYLDKRSKPVLSGIKSLRNDIGATVHELSDRDKKNT PH4H_Mus_musculus
## [3] FFTHLDKRSPLALTNIIKILRHDIGATVHELSDRDKKDT PH4H_Homo_sapiens
## [4] FFTNLDQRSVPALANI KILRHDIGATVHELSDRDKKDT PH4H_Bos_taurus
## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
```

```

## Con ----- Consensus
##
##      aln (118..156)                                names
## [1] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Rattus_norve...
## [2] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Mus_musculus
## [3] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Homo_sapiens
## [4] VPWFPRTIQELDNFANQVLSYGAELDADHPGFKDPVYRA PH4H_Bos_taurus
## [5] -----MNDRADFVVPD-----ITTRKNVG PH4H_Chromobacter...
## [6] -----MAIATPTSAAPTAPAGFTGTLTDKLRQ PH4H_Ralstonia_so...
## [7] -----MSG-----DGLSNG PH4H_Caulobacter_...
## [8] -----MKTTQY PH4H_Pseudomonas_...
## [9] -----MSVAEYAR-----DCAAQG PH4H_Rhizobium_loti
## Con -----????????Y????D????D???? Consensus
##
##      aln (157..195)                                names
## [1] RRKQFADIAYNYRHGQPIPRVEYTEEEKQWTGTVFRTLK PH4H_Rattus_norve...
## [2] RRKQFADIAYNYRHGQPIPRVEYTEEEKQWTGTVFRTLK PH4H_Mus_musculus
## [3] RRKQFADIAYNYRHGQPIPRVEYMEEEKQWTGTVFRTLK PH4H_Homo_sapiens
## [4] RRKQFADIAYNYRHGQPIPRVEYTEEEKQWTGTVFRTLK PH4H_Bos_taurus
## [5] LSHDAN-----DFTLPQPLDRYSAEDHATWATLYQRQC PH4H_Chromobacter...
## [6] FAEGLDGQTLRPDFTMEQPVHRYTAADHATWRTLYDRQE PH4H_Ralstonia_so...
## [7] PPPGAR-----PDWTIDQGWETYTQAEDHVWITLYERQT PH4H_Caulobacter_...
## [8] VARQPD-----DNGFIHYPETEHQVWNTLITRQL PH4H_Pseudomonas_...
## [9] LRGDYS--VCRADFTVAQDYD--YSDEEQAVWRTLCDRQT PH4H_Rhizobium_loti
## Con ?R?Q????????P?P???YTEEE??TW?TL??RQ? Consensus
##
##      aln (196..234)                                names
## [1] ALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFL PH4H_Rattus_norve...
## [2] ALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFL PH4H_Mus_musculus
## [3] SLYKTHACYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFL PH4H_Homo_sapiens
## [4] SLYKTHACYEHNHIFPLLEKYCGFREDNIPQLEEVSQFL PH4H_Bos_taurus
## [5] KLLPGRACDEFMEGL----ERLEVDADRVPDFNKLNQKL PH4H_Chromobacter...
## [6] ALLPGRACDEFQGL----STLGMSREGVPSFDRLNETL PH4H_Ralstonia_so...
## [7] DMLHGRACDEFMRGL----DALDLHRSGIPDFARINEEL PH4H_Caulobacter_...
## [8] KVIEGRACQEYLDGI----EQLGLPHERIPQLDEINRVL PH4H_Pseudomonas_...
## [9] KLTRKLAHHSYLDGV----EKLGL-LDRIPDFEDVSTKL PH4H_Rhizobium_loti
## Con ?L????AC?E???G?----??LG???D?IPQLE?VSQ?L Consensus
##
##      aln (235..273)                                names
## [1] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Rattus_norve...
## [2] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Mus_musculus
## [3] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Homo_sapiens
## [4] QSCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Bos_taurus
## [5] MAATGWKIVAVPGLIPDDVFFEHLANRRFPVTWWLREPH PH4H_Chromobacter...
## [6] MRATGWQIVAVPGLVPDEVFFEHLANRRFPASWWMRRPD PH4H_Ralstonia_so...
## [7] KRLTGWTVAVPGLVPDDVFFDHLANRRFPAGQFIRKPH PH4H_Caulobacter_...

```

```

## [8] QATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPE PH4H_Pseudomonas_...
## [9] RKLTGWEIIAVPGLIPAAPFFDHLANRRFPVTNWLRTQ PH4H_Rhizobium_loti
## Con Q??TGWR??VPGL?P??FF??LA?R?FP?TQ?IR??? Consensus
##
##      aln (274..312)                                names
## [1] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Rattus_norve...
## [2] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Mus_musculus
## [3] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Homo_sapiens
## [4] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Bos_taurus
## [5] QLDYLQEPDVFHDLFHGVPLLINPVFADYLEAYGKGGVK PH4H_Chromobacter...
## [6] QLDYLQEPDGFHDIFGHVPLLINPVFADYMQAYGQGGLK PH4H_Ralstonia_so...
## [7] ELDYLQEPDIFHDVFGHVPLMTDPVFADYMQAYGEGRR PH4H_Caulobacter_...
## [8] ELDYLQEPDIFHEIFGHCPLLTNPWFAEFTHTYKGLGLK PH4H_Pseudomonas_...
## [9] ELDYIVEPDMFHDFFGHVPVLSQPVFADFMQMYGKKAGD PH4H_Rhizobium_loti
## Con ?LDY??EPDIFHELFGHVPLSDP?FA?F?Q?YG?LA?? Consensus
##
##      aln (313..351)                                names
## [1] GAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLS PH4H_Rattus_norve...
## [2] GAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLS PH4H_Mus_musculus
## [3] GAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLS PH4H_Homo_sapiens
## [4] GAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLS PH4H_Bos_taurus
## [5] AKALGALPMLARLYWYTVEFGLINTP-AGMRIYGAGILS PH4H_Chromobacter...
## [6] AARLGALDMLARLYWYTVEFGLIRTP-AGLRIYGAGIVS PH4H_Ralstonia_so...
## [7] ALGLGRLANLARLYWYTVEFGLMNTP-AGLRIYGAGIVS PH4H_Caulobacter_...
## [8] ASKE-ERVFLARLYWMTIEFGLVETD-QGKRIYGGGILS PH4H_Pseudomonas_...
## [9] IIALGGDEMITRLYWYTAEYGLVQEAGQPLKAFGAGLMS PH4H_Rhizobium_loti
## Con ?A?????E?LARLYW?TVEFGL????-???KAYGAGLLS Consensus
##
##      aln (352..390)                                names
## [1] SFGELQYCLSD-KPKLLPLELEKTACQEYSVTEFQPLYY PH4H_Rattus_norve...
## [2] SFGELQYCLSD-KPKLLPLELEKTACQEYTVTEFQPLYY PH4H_Mus_musculus
## [3] SFGELQYCLSE-KPKLLPLELEKTAIQNYTVTEFQPLYY PH4H_Homo_sapiens
## [4] SFGELQYCLSD-KPKLLPLELEKTAVQEYTITEFQPLYY PH4H_Bos_taurus
## [5] SKSESIYCLDSASPNRVGFDLMRIMNTRYRIDTFQKTYF PH4H_Chromobacter...
## [6] SKSESVYALDSASPNRIGFDVHRIMRTRYRIDTFQKTYF PH4H_Ralstonia_so...
## [7] SRTESIFALDDPSPNRIGFDLERVMRTLYRIDDFQQVYF PH4H_Caulobacter_...
## [8] SPKETVYSLSD-EPLHQAFNPLEAMRTPYRIDILQPLYF PH4H_Pseudomonas_...
## [9] SFTELQFAVEGKDAHHPFDLETVMRTGYEIDKFQRAYF PH4H_Rhizobium_loti
## Con SF?ELQYCLSD-?P???PF?LE??M?T?Y?ID?FQPLYF Consensus
##
##      aln (391..429)                                names
## [1] VAESFSDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLND PH4H_Rattus_norve...
## [2] VAESFNDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLND PH4H_Mus_musculus
## [3] VAESFNDAKEKVRNFAATIPRPFSVRYDPYTQRIEVLND PH4H_Homo_sapiens
## [4] VAESFNDAKEKVRNFAATIPRPFSVHYDPYTQRIEVLND PH4H_Bos_taurus
## [5] VIDSFQKLFDATA-PDFAPLYLQLADAQPWGAGDVAPDD PH4H_Chromobacter...

```



```
## [6] VIDSFEQLFDATR-PDFTPLYEALGTLPTFGAGDVVDGD PH4H_Ralstonia_so...
## [7] VIDSIQTLQEVTL-RDFGAIYERLASVSDIGVAEIVPGD PH4H_Caulobacter_...
## [8] VLPDLKRLFQLAQ-EDIMALVHEAMRLG-LHAPLFPPKQ PH4H_Pseudomonas_...
## [9] VLPSFDALRDAFQTADFEAIVARRKDQKALDPATV---- PH4H_Rhizobium_loti
## Con V??SF??L?E??R??D?T??????????P??????V?D? Consensus
##
##      aln (430..456)                names
## [1] TQQLKILADSINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] TQQLKILADSINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] TQQLKILADSINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] TQQLKILADSISSVEILCSALQKIK- PH4H_Bos_taurus
## [5] LVLNAGDRQGWADTEDV----- PH4H_Chromobacter...
## [6] AVLNAGTREGWADTADI----- PH4H_Ralstonia_so...
## [7] AVLTRGT-QAYATAGGRLAGAAAG--- PH4H_Caulobacter_...
## [8] AA----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ???????????????IL??A???--- Consensus
```

The `msa` package additionally offers the function `msaPrettyPrint()` which allows for pretty-printing multiple alignments using the  $\text{\LaTeX}$  package `TeXshade`. As an example, the following R code creates a PDF file `myfirstAlignment.pdf` which is shown in Figure 1:

```
msaPrettyPrint(myFirstAlignment, output="pdf", showNames="none",
               showLogo="none", askForOverwrite=FALSE, verbose=FALSE)
```

In the above call to `msaPrettyPrint()`, the printing of sequence names has been suppressed by `showNames="none"`. The settings `askForOverwrite=FALSE` and `verbose=FALSE` are necessary for building this vignette, but, in an interactive R session, they are not necessary.

Almost needless to say, the file names created by `msaPrettyPrint()` are customizable. By default, the name of the argument is taken as file name. More importantly, the actual output of `msaPrettyPrint()` is highly customizable, too. For more details, see the Section 7 and the help page of the function (`?msaPrettyPrint`).

The `msaPrettyPrint()` function is particularly useful for pretty-printing multiple sequence alignments in Sweave [6] or knitr [15] documents. More details are provided in Section 7. Here, we restrict to a teasing example:

```
msaPrettyPrint(myFirstAlignment, y=c(164, 213), output="asis",
               showNames="none", showLogo="none", askForOverwrite=FALSE)
```



Figure 1: The PDF file `myfirstAlignment.pdf` created with `msaPrettyPrint()`.

```

IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYMEEEEKKTWGTVFRTLKSLYKTHACYEYNNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKKQTWGTVFRTLKSLYKTHACYEHNHIFPLL 212
.....DFTLPQPLDRYSAEDHATWATLYQRQCKLLPGRACDEFMEGL... 67
QTLRPDFTMEQPVHRYTAADHATWRTLYDRQEALLPGRACDEFLLQGL... 83
....PDWTIDQGWETYTQAEDHVDWITLYERQTDMLHGRACDEFMRGL... 58
.....DNGFIHYPETEHQVWNTLITRQLKVIIEGRACQEYLDGI... 50
.VCRADFTVAQDYD.YSDEEQAVWRTLCDRQTKLTRKL AHHSYLDGV... 65
***** * * * * ! * * * * * * ! * * * * * * * * * ! * * * * * * * * *

```

☐ non-conserved  
☒  $\geq 50\%$  conserved

## 4 Functions for Multiple Sequence Alignment in More Detail

The example in Section 3 above simply called the function `msa()` without any additional arguments. We mentioned already that, in this case, ClustalW is called with default parameters. We can also explicitly request ClustalW or one of the two other algorithms ClustalOmega or MUSCLE:

```

myClustalWAlignment <- msa(mySequences, "ClustalW")

## use default substitution matrix

myClustalWAlignment

## CLUSTAL 2.1
##
## Call:
##   msa(mySequences, "ClustalW")
##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln                                     names
## [1] MAAVVLENGVL SRKLSDF...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] MAAVVLENGVL SRKLSDF...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDF...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [5] -----...GWADTEDV----- PH4H_Chromobacter...
## [6] -----...GWADTADI----- PH4H_Ralstonia_so...
## [7] -----...AYATAGGRLAGAAAG--- PH4H_Caulobacter...
## [8] -----...----- PH4H_Pseudomonas...
## [9] -----...----- PH4H_Rhizobium_loti
## Con -----...???????IL??A???--- Consensus

myClustalOmegaAlignment <- msa(mySequences, "ClustalOmega")

```

```
## using Gonnet

myClustalOmegaAlignment

## ClustalOmega 1.2.0
##
## Call:
##   msa(mySequences, "ClustalOmega")
##
## MsaAAMultipleAlignment with 9 rows and 467 columns
##      aln                                     names
## [1] MSALVLESRALGRKLSDF...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [2] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [3] MAAVLENGVLSRKLSDF...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [4] MAAVLENGVLSRKLSDF...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [5] -----...----- PH4H_Pseudomonas_...
## [6] -----...----- PH4H_Rhizobium_loti
## [7] -----...LAGAAAG----- PH4H_Caulobacter_...
## [8] -----...V----- PH4H_Chromobacter...
## [9] -----...I----- PH4H_Ralstonia_so...
## Con -----...???????----- Consensus

myMuscleAlignment <- msa(mySequences, "Muscle")
myMuscleAlignment

## MUSCLE 3.8.31
##
## Call:
##   msa(mySequences, "Muscle")
##
## MsaAAMultipleAlignment with 9 rows and 460 columns
##      aln                                     names
## [1] MAAVLENGVLSRKLSDF...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSDF...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDF...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [5] -----...----- PH4H_Pseudomonas_...
## [6] -----...----- PH4H_Rhizobium_loti
## [7] -----...AYATAGGRLAGAAAG--- PH4H_Caulobacter_...
## [8] -----MNDRADF...QGWADTEDV----- PH4H_Chromobacter...
## [9] MAIATPTSAAPTPAPAGF...EGWADTADI----- PH4H_Ralstonia_so...
## Con M????????????????DF...????????L??A???--- Consensus
```

Please note that the call `msa(mySequences, "ClustalW", ...)` is just a shortcut for the call `msaClustalW(mySequences, ...)`, analogously for `msaClustalOmega()` and `msaMuscle()`.

In other words, `msa()` is nothing else but a wrapper function that provides a unified interface to the three functions `msaClustalW()`, `msaClustalOmega()`, and `msaMuscle()`.

All three functions `msaClustalW()`, `msaClustalOmega()`, and `msaMuscle()` have the same parameters: The input sequences are passed as argument `inputSeqs`, and all functions have the following arguments: `cluster`, `gapOpening`, `gapExtension`, `maxiters`, `substitutionMatrix`, `order`, `type`, and `verbose`. The ways these parameters are interpreted, are largely analogous, although there are some differences, also in terms of default values. See the subsections below and the man page of the three functions for more details. All of the three functions `msaClustalW()`, `msaClustalOmega()`, and `msaMuscle()`, however, are not restricted to the parameters mentioned above. All three have a `'...'` argument through which several other algorithm-specific parameters can be passed on to the underlying library. The following subsections provide an overview of which parameters are supported by each of the three algorithms.

#### 4.1 ClustalW-Specific Parameters

The original implementation of ClustalW offers a lot of parameters for customizing the way a multiple sequence alignment is computed. Through the `'...'` argument, `msaClustalW()` provides an interface to make use of most these parameters (see the documentation of ClustalW<sup>2</sup> for a comprehensive overview). Currently, the following restrictions and caveats apply:

- The parameters `infile`, `clustering`, `gapOpen`, `gapExt`, `numiters`, `matrix`, and `outorder` have been renamed to the standardized argument names `inputSeqs`, `cluster`, `gapOpening`, `gapExtension`, `maxiters`, `substitutionMatrix`, and `order` in order to provide a consistent interface for all three multiple sequence alignment algorithms.
- Boolean flags must be passed as logical values, e.g. `verbose=TRUE`.
- The parameter `quiet` has been replaced by `verbose` (with the exact opposite meaning).
- The following parameters are (currently) not supported: `bootstrap`, `check`, `fullhelp`, `interactive`, `maxseqlen`, `options`, and `tree`.
- For the parameter `output`, only the choice `"clustal"` is available.

#### 4.2 ClustalOmega-Specific Parameters

In the same way as ClustalW, the original implementation of ClustalOmega also offers a lot of parameters for customizing the way a multiple sequence alignment is computed. Through the `'...'` argument, `msaClustalOmega()` provides an interface to make use of most these parameters (see the documentation of ClustalOmega<sup>3</sup> for a comprehensive overview). Currently, the following restrictions and caveats apply:

- The parameters `infile`, `cluster-size`, `iterations`, and `output-order` have been renamed to the argument names `inputSeqs`, `cluster`, `maxiters`, and `order` in order to provide a consistent interface for all three multiple sequence alignment algorithms.

---

<sup>2</sup>[http://www.clustal.org/download/clustalw\\_help.txt](http://www.clustal.org/download/clustalw_help.txt)

<sup>3</sup><http://www.clustal.org/omega/README>

- ClustalOmega does not allow for setting custom gap penalties. Therefore, setting the parameters `gapOpening` and `gapExtension` currently has no effect and will lead to a warning. These arguments are only defined for future extensions and consistency with the other algorithms available in `msa`.
- ClustalOmega only allows for choosing substitution matrices from a pre-defined set of names, namely "BLOSUM30", "BLOSUM40", "BLOSUM50", "BLOSUM65", "BLOSUM80", and "Gonnet". This is a new feature — the original ClustalOmega implementation does not allow for using any custom substitution matrix. However, since these are all amino acid substitution matrices, ClustalOmega is still hardly useful for multiple alignments of nucleotide sequences.
- Boolean flags must be passed as logical values, e.g. `verbose=TRUE`.
- The following parameters are (currently) not supported: `maxSeqLength` and `help`.
- For the parameter `outFmt`, only the choice "clustal" is available.

### 4.3 MUSCLE-Specific Parameters

Finally, also MUSCLE offers a lot of parameters for customizing the way a multiple sequence alignment is computed. Through the `'...'` argument, `msaMuscle()` provides an interface to make use of most these parameters (see the documentation of MUSCLE<sup>4</sup> for a comprehensive overview). Currently, the following restrictions and caveats apply:

- The parameters `in`, `gapOpen`, `gapExtend`, `matrix`, and `seqtype` have been renamed to `inputSeqs`, `gapOpening`, `gapExtension`, `substitutionMatrix` and `type` in order to provide a consistent interface for all three multiple sequence alignment algorithms.
- Boolean flags must be passed as logical values, e.g. `verbose=TRUE`.
- The parameter `quiet` has been replaced by `verbose` (with the exact opposite meaning).
- The following parameters are currently not supported: `clw`, `clwstrict`, `fastaout`, `group`, `html`, `in1`, `in2`, `log`, `loga`, `msaout`, `msf`, `out`, `phyi`, `phyiout`, `phys`, `physout`, `refine`, `refinew`, `scorefile`, `spscore`, `stable`, `termgaps4`, `termgapsfull`, `termgapshalf`, `termgapshalflonger`, `tree1`, `tree2`, `usetree`, `weight1`, and `weight2`.

## 5 Printing Multiple Sequence Alignments

As already shown above, multiple sequence alignments can be shown in plain text format on the R console using the `print()` function (which is implicitly called if just the object name is entered on the R console). This function allows for multiple customizations, such as, enabling/disabling to display a consensus sequence, printing the entire alignment or only a subset, enabling/disabling to display sequence names, and adjusting the width allocated for sequence names. For more information, the reader is referred to the help page of the `print` function:

<sup>4</sup><http://www.drive5.com/muscle/muscle.html>

```
help("print,MsaDNAMultipleAlignment-method")
```

We only provide some examples here:

```
print(myFirstAlignment)

## CLUSTAL 2.1
##
## Call:
##   msa(mySequences)
##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln                      names
## [1] MAAVLENGVLSRKLSDF...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSDF...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDF...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [5] -----...GWADTEDV----- PH4H_Chromobacter...
## [6] -----...GWADTADI----- PH4H_Ralstonia_so...
## [7] -----...AYATAGGRLAGAAAG--- PH4H_Caulobacter_...
## [8] -----...----- PH4H_Pseudomonas_...
## [9] -----...----- PH4H_Rhizobium_loti
## Con -----...???????IL??A???--- Consensus

print(myFirstAlignment, show="complete")

##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln (1..39)                      names
## [1] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAISLIF PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAVSLIF PH4H_Mus_musculus
## [3] MSTAVLENPGLGRKLSDFGQETSYIEDNCNQNGAISLIF PH4H_Homo_sapiens
## [4] MSALVLESRALGRKLSDFGQETSYIEGNSDQN-AVSLIF PH4H_Bos_taurus
## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter_...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ----- Consensus
##
##      aln (40..78)                      names
## [1] SLKEEVGALAKVLRRLFEEENDINLTHIESRPSRLNKDEYE PH4H_Rattus_norve...
## [2] SLKEEVGALAKVLRRLFEEENEINLTHIESRPSRLNKDEYE PH4H_Mus_musculus
## [3] SLKEEVGALAKVLRRLFEEENDVNLTHIESRPSRLKKDEYE PH4H_Homo_sapiens
## [4] SLKEEVGALARVLRRLFEEENDINLTHIESRPSRLRKDEYE PH4H_Bos_taurus
```

```

## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter_...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ----- Consensus
##
##      aln (79..117)                                names
## [1] FFTYLDKRTKPVLSGSIKSLRNDIGATVHELSDKEKNT PH4H_Rattus_norve...
## [2] FFTYLDKRSPVLSGSIKSLRNDIGATVHELSDKEKNT PH4H_Mus_musculus
## [3] FFTHLDKRSLPALTNIIKILRHDIGATVHELSDKKKDT PH4H_Homo_sapiens
## [4] FFTNLDQRSVPALANI KILRHDIGATVHELSDKKKDT PH4H_Bos_taurus
## [5] ----- PH4H_Chromobacter...
## [6] ----- PH4H_Ralstonia_so...
## [7] ----- PH4H_Caulobacter_...
## [8] ----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ----- Consensus
##
##      aln (118..156)                                names
## [1] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Rattus_norve...
## [2] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Mus_musculus
## [3] VPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRA PH4H_Homo_sapiens
## [4] VPWFPRTIQELDNFANQVLSYGAELDADHPGFKDPVYRA PH4H_Bos_taurus
## [5] -----MNDRADFVVPD-----ITTRKNVG PH4H_Chromobacter...
## [6] -----MAIATPTSAAPTAPAGFTGTLTDKLEQ PH4H_Ralstonia_so...
## [7] -----MSG-----DGLSNG PH4H_Caulobacter_...
## [8] -----MKTQY PH4H_Pseudomonas_...
## [9] -----MSVAEYAR-----DCAAQG PH4H_Rhizobium_loti
## Con -----?????????Y????D?????D????? Consensus
##
##      aln (157..195)                                names
## [1] RRKQFADIAYNRYHGQPIPRVEYTEEEKQWGTVFRTLK PH4H_Rattus_norve...
## [2] RRKQFADIAYNRYHGQPIPRVEYTEEEKQWGTVFRTLK PH4H_Mus_musculus
## [3] RRKQFADIAYNRYHGQPIPRVEYMEEEKQWGTVFRTLK PH4H_Homo_sapiens
## [4] RRKQFADIAYNRYHGQPIPRVEYTEEEKQWGTVFRTLK PH4H_Bos_taurus
## [5] LSHDAN-----DFTLPQPLDRYSAEDHATWATLYQRQC PH4H_Chromobacter...
## [6] FAEGLDGQTLRPDFTMEQPVHRYTAADHATWRTLYDRQE PH4H_Ralstonia_so...
## [7] PPPGAR-----PDWTIDQGWETYTQAEDVWITLYERQT PH4H_Caulobacter_...
## [8] VARQPD-----DNGFIHYPETEHQVWNTLITRQL PH4H_Pseudomonas_...
## [9] LRGDYS--VCRADFTVAQDYD--YSDEEQAVWRTLCDRQT PH4H_Rhizobium_loti
## Con ?R?Q????????????P?P???YTEEE??TW?TL??RQ? Consensus
##
##      aln (196..234)                                names
## [1] ALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFL PH4H_Rattus_norve...
## [2] ALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFL PH4H_Mus_musculus

```



```

## [3] SLYKTHACYEYNHIFPILLEKYCGFHEDNIPQLEDVSQFL PH4H_Homo_sapiens
## [4] SLYKTHACYEHNHIFPILLEKYCGFREDNIPQLEEVSQFL PH4H_Bos_taurus
## [5] KLLPGRACDEFMEGL-----ERLEVDADRVPDFNKLNQKL PH4H_Chromobacter...
## [6] ALLPGRACDEFQLQGL-----STLGMSREGVPSFDRLNETL PH4H_Ralstonia_so...
## [7] DMLHGRACDEFMRGL----DALDLHRSRGIPDFARINEEL PH4H_Caulobacter_...
## [8] KVIEGRACQEYLDGI----EQLGLPHERIPQLDEINRVL PH4H_Pseudomonas_...
## [9] KLTRKLAHHSYLDGV----EKLGL-LDRIPDFEDVSTKL PH4H_Rhizobium_loti
## Con ?L????AC?E???G?-----??LG???D?IPQLE?VSQ?L Consensus
##
##      aln (235..273)                                names
## [1] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Rattus_norve...
## [2] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Mus_musculus
## [3] QTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Homo_sapiens
## [4] QSCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGS PH4H_Bos_taurus
## [5] MAATGWKIVAVPGLIPDDVFFFEHLANRRFPVTWWLREPH PH4H_Chromobacter...
## [6] MRATGWQIVAVPGLVPDEVFFFEHLANRRFPASWWMRRPD PH4H_Ralstonia_so...
## [7] KRLTGWTIVAVPGLVPDDVFFDHLANRRFPAGQFIRKPH PH4H_Caulobacter_...
## [8] QATTGWRVARVPALIPFQTFPELLASQQFPVATFIRTPE PH4H_Pseudomonas_...
## [9] RKLTGWEIIAVPGLIPAAPFFDHLANRRFPVTNWLRTQ PH4H_Rhizobium_loti
## Con Q???TGWR???VPGL?P???FF??LA?R?FP?TQ?IR??? Consensus
##
##      aln (274..312)                                names
## [1] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Rattus_norve...
## [2] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Mus_musculus
## [3] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Homo_sapiens
## [4] KPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-LASL PH4H_Bos_taurus
## [5] QLDYLQEPDVFHDLFGHVPLLINPVFADYLEAYGKGGVK PH4H_Chromobacter...
## [6] QLDYLQEPDGFHDIFGHVPLLINPVFADYMQAYGQGGLK PH4H_Ralstonia_so...
## [7] ELDYLQEPDIFHDVFGHVPLMTDPVFADYMQAYGEGGRR PH4H_Caulobacter_...
## [8] ELDYLQEPDIFHEIFGHCPLLTNPWFAEFTHTYKGLGLK PH4H_Pseudomonas_...
## [9] ELDYIVEPDMFHDFFGHVPVLSQPVFADFMQMYGKKAGD PH4H_Rhizobium_loti
## Con ?LDY??EPDIFHELFGHVPLLSDP?FA?F?Q?YG?LA?? Consensus
##
##      aln (313..351)                                names
## [1] GAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLS PH4H_Rattus_norve...
## [2] GAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLS PH4H_Mus_musculus
## [3] GAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLS PH4H_Homo_sapiens
## [4] GAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLS PH4H_Bos_taurus
## [5] AKALGALPMLARLYWYTVEFGLINTP-AGMRIYGAGILS PH4H_Chromobacter...
## [6] AARLGALDMLARLYWYTVEFGLIRTP-AGLRIYGAGIVS PH4H_Ralstonia_so...
## [7] ALGLGRLANLARLYWYTVEFGLMNTP-AGLRIYGAGIVS PH4H_Caulobacter_...
## [8] ASKE-ERVFLARLYWMTIEFGLVETD-QGKRIYGGGILS PH4H_Pseudomonas_...
## [9] IIALGGDEMITRLYWYTAEYGLVQEAGQPLKAFGAGLMS PH4H_Rhizobium_loti
## Con ?A?????E?LARLYW?TVEFGL????-???KAYGAGLLS Consensus
##
##      aln (352..390)                                names

```

```

## [1] SFGELQYCLSD-KPKLLPLELEKTACQEYSVTEFQPLY PH4H_Rattus_norve...
## [2] SFGELQYCLSD-KPKLLPLELEKTACQEYTVTEFQPLY PH4H_Mus_musculus
## [3] SFGELQYCLSE-KPKLLPLELEKTAIQNYTVTEFQPLY PH4H_Homo_sapiens
## [4] SFGELQYCLSD-KPKLLPLELEKTAVQEYTITEFQPLY PH4H_Bos_taurus
## [5] SKSESIYCLDSASPNRVGFDLMRIMNTRYRIDTFQKTYF PH4H_Chromobacter...
## [6] SKSESVYALDSASPNRIGFDVHRIMRTRYRIDTFQKTYF PH4H_Ralstonia_so...
## [7] SRTESIFALDDPSPNRIGFDLVRMRTLYRIDDFQQVYF PH4H_Caulobacter_...
## [8] SPKETVYSLSD-EPLHQAFNPLEAMRTPYRIDILQPLYF PH4H_Pseudomonas_...
## [9] SFTELQFAVEGKDAHHVPFDLETVMRTGYEIDKFQRAYF PH4H_Rhizobium_loti
## Con SF?ELQYCLSD-?P???PF?LE??M?T?Y?ID?FQPLYF Consensus
##
##      aln (391..429)                      names
## [1] VAESFSDAKEKVRTFAATIPRPFVRYDPYTQRVEVLN PH4H_Rattus_norve...
## [2] VAESFNDAKEKVRTFAATIPRPFVRYDPYTQRVEVLN PH4H_Mus_musculus
## [3] VAESFNDAKEKVRNFAATIPRPFVRYDPYTQRIEVLN PH4H_Homo_sapiens
## [4] VAESFNDAKEKVRNFAATIPRPFVHYDPYTQRIEVLN PH4H_Bos_taurus
## [5] VIDSFQKLFDATA-PDFAPLYLQLADAQPWGAGDVAPDD PH4H_Chromobacter...
## [6] VIDSFQKLFDATR-PDFTPLYEALGTLPTFGAGDVVDGD PH4H_Ralstonia_so...
## [7] VIDSIQTLQEVTL-RDFGAIYERLASVSDIGVAEIVPGD PH4H_Caulobacter_...
## [8] VLPDLKRLFQLAQ-EDIMALVHEAMRLG-LHAPLFPKQ PH4H_Pseudomonas_...
## [9] VLPSFDALRDAFQTADFEAIVARRKDQKALDPATV---- PH4H_Rhizobium_loti
## Con V??SF??L?E??R??D?T?????????P??????V?D? Consensus
##
##      aln (430..456)                      names
## [1] TQQLKILADSINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] TQQLKILADSINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] TQQLKILADSINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] TQQLKILADSISSVEILCSALQKIK- PH4H_Bos_taurus
## [5] LVLNAGDRQGWADTEDV----- PH4H_Chromobacter...
## [6] AVLNAGTREGWADTADI----- PH4H_Ralstonia_so...
## [7] AVLTRGT-QAYATAGGRLAGAAAG--- PH4H_Caulobacter_...
## [8] AA----- PH4H_Pseudomonas_...
## [9] ----- PH4H_Rhizobium_loti
## Con ????????????????IL??A???--- Consensus

print(myFirstAlignment, showConsensus=FALSE, halfNrow=3)

## CLUSTAL 2.1
##
## Call:
##      msa(mySequences)
##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln                      names
## [1] MAAVLENGVLSRKLSD...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] MAAVLENGVLSRKLSD...SINSEVGILCHALQKIKS PH4H_Mus_musculus

```

```

## [3] MSTAVLENPGLGRKLSDF...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## ... ...
## [7] -----...AYATAGGRLAGAAAG--- PH4H_Caulobacter_...
## [8] -----...----- PH4H_Pseudomonas_...
## [9] -----...----- PH4H_Rhizobium_loti

print(myFirstAlignment, showNames=FALSE, show="complete")

##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##     aln (1..60)
## [1] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAISLIFSLKEEVGALAKVLRRLFENDI
## [2] MAAVLENGVLSRKLSDFGQETSYIEDNSNQNGAVSLIFSLKEEVGALAKVLRRLFENEI
## [3] MSTAVLENPGLGRKLSDFGQETSYIEDNCNQNNGAISLIFSLKEEVGALAKVLRRLFENDV
## [4] MSALVLESRALGRKLSDFGQETSYIEGNSDQN-AVSLIFSLKEEVGALARVLRRLFENDI
## [5] -----
## [6] -----
## [7] -----
## [8] -----
## [9] -----
## Con -----
##
##     aln (61..120)
## [1] NLTHIESRPSRLNKDEYEFFTYLDKRTKPVLSGSIKSLRNDIGATVHELSDKEKNTVPW
## [2] NLTHIESRPSRLNKDEYEFFTYLDKRSKPVLSGSIKSLRNDIGATVHELSDKEKNTVPW
## [3] NLTHIESRPSRLKKDEYEFFTHLDRSLPALTNIKILRHDIGATVHELSDKKKDTVPW
## [4] NLTHIESRPSRLRKDEYEFFTNLDQRSVPALANI IKILRHDIGATVHELSDKKKDTVPW
## [5] -----
## [6] -----
## [7] -----
## [8] -----
## [9] -----
## Con -----
##
##     aln (121..180)
## [1] FPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYT
## [2] FPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYT
## [3] FPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYM
## [4] FPRTIQELDNFANQVLSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYT
## [5] -----MNDRADFVVPD-----ITTRKNVGLSHDAN-----DFTLPQPLDRYS
## [6] -----MAIATPTSAAPTAPAGFTGTLTDKLREQFAEGLDGQTLRPDFTMEQPVHRYT
## [7] -----MSG-----DGLSNGPPPGAR-----PDWTIDQGWEITYT
## [8] -----MKTQYVARQPD-----DNGFIHYP
## [9] -----MSVAEYAR-----DCAAQGLRGDYS--VCRADFTVAQDYD-YS
## Con -----????????Y????D???????D?????R?Q???????????P?P???YT
##

```

```

##      aln (181..240)
## [1] EEEKQWGTVFRTLKALYKTHACYEHNHIFPILLEKYCGFREDNIPQLEDVVSQFLQTCTGF
## [2] EEERKTWGTVFRTLKALYKTHACYEHNHIFPILLEKYCGFREDNIPQLEDVVSQFLQTCTGF
## [3] EEEKKTWGTVFKTLKSLYKTHACYEYNNHIFPILLEKYCGFHEDNIPQLEDVVSQFLQTCTGF
## [4] EEEKKTWGTVFRTLKSLYKTHACYEHNHIFPILLEKYCGFREDNIPQLEEVVSQFLQSCTGF
## [5] AEDHATWATLYQRQCKLLPGRACDEFMEGL-----ERLEVDADRVPDFNKNLQKLMAATGW
## [6] AADHATWRTLYDRQEALLPGRACDEFQLGL-----STLGMSREGVPSFDRLNETLMRATGW
## [7] QAEHDVWITLYERQTDMLHGRACDEFMRGL-----DALDLHRSGIPDFARINEELKRLTGW
## [8] ETEHQVWNTLITRQLKVIEGRACQEYLDGI-----EQLGLPHERIPQLDEINRVLQATTGW
## [9] DEEQAVWRTLCDRQTKLTRKLAHHSYLDGV-----EKLGL-LDRIPDFEDVSTKLRLKTGW
## Con EEE??TW?TL??RQ??L????AC?E???G?-----??LG???D?IPQLE?VSQ?LQ??TGW
##
##      aln (241..300)
## [1] RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA
## [2] RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA
## [3] RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA
## [4] RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA
## [5] KIVAVPGLIPDDVFFEHLANRRFPVTWWLREPHQLDYLQEPDVFDLFGHVPLLINPVFA
## [6] QIVAVPGLVPDEVFFEHLANRRFPASWMMRRPDQLDYLQEPDGFHDIFGHVPLLINPVFA
## [7] TVVAVPGLVPDDVFFDHLANRRFPAGQFIRKPHELDYLQEPDIFHDVFGHVPMLTDPVFA
## [8] RVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHCPLLTNPWFA
## [9] EIIAVPGLIPAAPFFDHLANRRFPVTNWLRTREQELDYIVEPDMFHDFFGHVPVLSQPVFA
## Con R???VPGL?P???FF??LA?R?FP?TQ?IR????LDY??EPDIFHELFGHVPLLSDP?FA
##
##      aln (301..360)
## [1] QFSQEIG-LASLGAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLSSFGEQYCL
## [2] QFSQEIG-LASLGAPDEYIEKLATIIYWFTVEFGLCKEG-DSIKAYGAGLLSSFGEQYCL
## [3] QFSQEIG-LASLGAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLSSFGEQYCL
## [4] QFSQEIG-LASLGAPDEYIEKLATIIYWFTVEFGLCKQG-DSIKAYGAGLLSSFGEQYCL
## [5] DYLEAYGKGGVKAKALGALPMLARLYWYTVEFGLINTP-AGMRIYGAGILSSKSESIYCL
## [6] DYMQAYGQGGKKAARLGALDMLARLYWYTVEFGLIRTP-AGLRIYGAGIVSSKSESIVYAL
## [7] DYMQAYGEGRRALGLGRLANLARLYWYTVEFGLMNT-AGLRIYGAGIVSSRTESIFAL
## [8] EFTHTYKGLGLKASKE-ERVFLARLYWMTIEFGLVETD-QGKRIYGGGILSSPKETVYSL
## [9] DFMQMYGKKAGDIIALGGDEMITRLYWYTAEYGLVQEAGQPLKAFGAGLMSSFTTELQFAV
## Con ?F?Q?YG?LA???A?????E?LARLYW?TVEFGL????-???KAYGAGLLSSF?ELQYCL
##
##      aln (361..420)
## [1] SD-KPKLLPLELEKTACQEYSVTEFQPLYYVAESFSDAKEKVRTFAATIPRPFVRYDPY
## [2] SD-KPKLLPLELEKTACQEYTVTEFQPLYYVAESFNDAKEKVRTFAATIPRPFVRYDPY
## [3] SE-KPKLLPLELEKTAIQNYTVTEFQPLYYVAESFNDAKEKVRNFAATIPRPFVRYDPY
## [4] SD-KPKLLPLELEKTAVQEYTTITEFQPLYYVAESFNDAKEKVRNFAATIPRPFVHYDPY
## [5] DSASPNRVGFDLMRIMNTRYRIDTFQKTYFVIDSFKQLFDATA-PDFAPLYLQLADAQPW
## [6] DSASPNRIGFDVHRIMRTRYRIDTFQKTYFVIDSFEQLFDATR-PDFTPLYEALGTLPTF
## [7] DDPSPNRIGFDLERVMRTLYRIDDFQQVYFVIDSIQTLQEVTL-RDFGAIYERLASVSDI
## [8] SD-EPLHQAFNPLEAMRTPYRIDILQPLYFVLPDLKRLFQLAQ-EDIMALVHEAMRLG-L
## [9] EGKDAHHPFDLETVMRTGYEIDKFQRAYFVLPSPFDALRDAFQTADFEAIVARRKDQKAL

```

```
## Con SD-?P???PF?LE?M?T?Y?ID?FQPLYFV??SF??L?E??R??D?T??????????P?
##
##      aln (421..456)
## [1] TQRVEVLDNTQQLKILADSINSEVGILCNALQKIKS
## [2] TQRVEVLDNTQQLKILADSINSEVGILCHALQKIKS
## [3] TQRIEVLDTNTQQLKILADSINSEIGILCSALQKIK-
## [4] TQRIEVLDTNTQQLKILADSSISSEVEILCSALQKLK-
## [5] GAGDVAPDDLVLNAGDRQGWADTEDV-----
## [6] GAGDVVDGDAVLNAGTREGWADTADI-----
## [7] GVAEIVPGDAVLTRGT-QAYATAGGRLAGAAAG---
## [8] HAPLFPPKQAA-----
## [9] DPATV-----
## Con ?????V?D?????????????????IL??A???---
```

## 6 Processing Multiple Alignments

### 6.1 Methods Inherited From Biostrings

The classes defined by the `msa` package for storing multiple alignment results have been derived from the corresponding classes defined by the `Biostrings` package. Therefore, all methods for processing multiple alignments are available and work without any practical limitation. In this section, we highlight some of these.

The classes used for storing multiple alignments allow for defining masks on sequences and sequence positions via their row and column mask slots. They can be set by `rowmask()` and `colmask()` functions which serve both as setter and getter functions. To set row or column masks, an `IRanges` object must be supplied:

```
myMaskedAlignment <- myFirstAlignment
colM <- IRanges(start=1, end=100)
colmask(myMaskedAlignment) <- colM
myMaskedAlignment

## CLUSTAL 2.1
##
## Call:
##      msa(mySequences)
##
## MsaAAMultipleAlignment with 9 rows and 456 columns
##      aln                                     names
## [1] #####...SINSEVGILCNALQKIKS PH4H_Rattus_norve...
## [2] #####...SINSEVGILCHALQKIKS PH4H_Mus_musculus
## [3] #####...SINSEIGILCSALQKIK- PH4H_Homo_sapiens
## [4] #####...SISSEVEILCSALQKLK- PH4H_Bos_taurus
## [5] #####...GWADTEDV----- PH4H_Chromobacter...
```

```
## [6] #####...GWADTADI----- PH4H_Ralstonia_so...
## [7] #####...AYATAGGRLAGAAAG--- PH4H_Caulobacter...
## [8] #####...----- PH4H_Pseudomonas...
## [9] #####...----- PH4H_Rhizobium_loti
## Con #####...???????IL??A???--- Consensus
```

The `unmasked()` allows for removing these masks, thereby casting the multiple alignment to a set of aligned Biostrings sequences (class `AAStringSet`, `DNAStringSet`, or `RNAStringSet`):

```
unmasked(myMaskedAlignment)
```

```
## AAStringSet object of length 9:
##      width seq                                names
## [1]   456 MAAVLENGVLSRKLS...SEVGILCNALQKIKS PH4H_Rattus_norve...
## [2]   456 MAAVLENGVLSRKLS...SEVGILCHALQKIKS PH4H_Mus_musculus
## [3]   456 MSTAVLENPGLGRKLS...SEIGILCSALQKIK- PH4H_Homo_sapiens
## [4]   456 MSALVLESRALGRKLS...SEVEILCSALQKLK- PH4H_Bos_taurus
## [5]   456 -----...DTEDV----- PH4H_Chromobacter...
## [6]   456 -----...DTADI----- PH4H_Ralstonia_so...
## [7]   456 -----...TAGGRLAGAAAG--- PH4H_Caulobacter...
## [8]   456 -----...----- PH4H_Pseudomonas...
## [9]   456 -----...----- PH4H_Rhizobium_loti
```

Consensus matrices can be computed conveniently as follows:

```
conMat <- consensusMatrix(myFirstAlignment)
dim(conMat)

## [1] 30 456

conMat[, 101:110]

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## A      0    0    0    4    0    0    0    0    0    0
## R      0    0    0    0    0    0    0    0    0    0
## N      0    0    0    0    0    0    0    0    0    0
## D      4    0    0    0    0    0    0    0    0    0
## C      0    0    0    0    0    0    0    0    0    0
## Q      0    0    0    0    0    0    0    0    0    0
## E      0    0    0    0    0    0    0    4    0    0
## G      0    0    4    0    0    0    0    0    0    0
## H      0    0    0    0    0    0    4    0    0    0
## I      0    4    0    0    0    0    0    0    0    0
## L      0    0    0    0    0    0    0    0    4    0
```

```
## K    0    0    0    0    0    0    0    0    0    0
## M    0    0    0    0    0    0    0    0    0    0
## F    0    0    0    0    0    0    0    0    0    0
## P    0    0    0    0    0    0    0    0    0    0
## S    0    0    0    0    0    0    0    0    0    4
## T    0    0    0    0    4    0    0    0    0    0
## W    0    0    0    0    0    0    0    0    0    0
## Y    0    0    0    0    0    0    0    0    0    0
## V    0    0    0    0    0    4    0    0    0    0
## U    0    0    0    0    0    0    0    0    0    0
## D    0    0    0    0    0    0    0    0    0    0
## B    0    0    0    0    0    0    0    0    0    0
## J    0    0    0    0    0    0    0    0    0    0
## Z    0    0    0    0    0    0    0    0    0    0
## X    0    0    0    0    0    0    0    0    0    0
## *    0    0    0    0    0    0    0    0    0    0
## -    5    5    5    5    5    5    5    5    5    5
## +    0    0    0    0    0    0    0    0    0    0
## .    0    0    0    0    0    0    0    0    0    0
```

If called on a masked alignment, `consensusMatrix()` only uses those sequences/rows that are not masked. If there are masked columns, the matrix contains NA's in those columns:

```
conMat <- consensusMatrix(myMaskedAlignment)
conMat[, 95:104]

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## A     NA  NA  NA  NA  NA  NA    0    0    0     4
## R     NA  NA  NA  NA  NA  NA    0    0    0     0
## N     NA  NA  NA  NA  NA  NA    0    0    0     0
## D     NA  NA  NA  NA  NA  NA    4    0    0     0
## C     NA  NA  NA  NA  NA  NA    0    0    0     0
## Q     NA  NA  NA  NA  NA  NA    0    0    0     0
## E     NA  NA  NA  NA  NA  NA    0    0    0     0
## G     NA  NA  NA  NA  NA  NA    0    0    4     0
## H     NA  NA  NA  NA  NA  NA    0    0    0     0
## I     NA  NA  NA  NA  NA  NA    0    4    0     0
## L     NA  NA  NA  NA  NA  NA    0    0    0     0
## K     NA  NA  NA  NA  NA  NA    0    0    0     0
## M     NA  NA  NA  NA  NA  NA    0    0    0     0
## F     NA  NA  NA  NA  NA  NA    0    0    0     0
## P     NA  NA  NA  NA  NA  NA    0    0    0     0
## S     NA  NA  NA  NA  NA  NA    0    0    0     0
## T     NA  NA  NA  NA  NA  NA    0    0    0     0
## W     NA  NA  NA  NA  NA  NA    0    0    0     0
## Y     NA  NA  NA  NA  NA  NA    0    0    0     0
```

## V	NA	NA	NA	NA	NA	NA	0	0	0	0
## U	NA	NA	NA	NA	NA	NA	0	0	0	0
## O	NA	NA	NA	NA	NA	NA	0	0	0	0
## B	NA	NA	NA	NA	NA	NA	0	0	0	0
## J	NA	NA	NA	NA	NA	NA	0	0	0	0
## Z	NA	NA	NA	NA	NA	NA	0	0	0	0
## X	NA	NA	NA	NA	NA	NA	0	0	0	0
## *	NA	NA	NA	NA	NA	NA	0	0	0	0
## -	NA	NA	NA	NA	NA	NA	5	5	5	5
## +	NA	NA	NA	NA	NA	NA	0	0	0	0
## .	NA	NA	NA	NA	NA	NA	0	0	0	0

Multiple alignments also inherit the `consensusString()` method from the `Biostrings` package. However, for more flexibility and consistency, we rather advise users to use the `msaConsensusSequence()` method (see below).

## 6.2 Consensus Sequences and Conservation Scores

With version 1.7.1 of `msa`, new methods have been provided that allow for the computation of consensus sequences and conservation scores. By default, the `msaConsensusSequence()` method is a wrapper around the `consensusString()` method from the `Biostrings`:

```
printSplitString <- function(x, width=getOption("width") - 1)
{
  starts <- seq(from=1, to=nchar(x), by=width)

  for (i in 1:length(starts))
    cat(substr(x, starts[i], starts[i] + width - 1), "\n")
}

printSplitString(msaConsensusSequence(myFirstAlignment))

## -----
## -----?
## ?????????Y????D??????D??????R?Q????????????P?P???YTEEE??TW?TL??
## RQ??L????AC?E???G?----??LG???D?IPQLE?VSQ?LQ??TGWR???VPGL?P???FF?
## ?LA?R?FP?TQ?IR????LDY??EPDIFHELFGHVPLLSDP?FA?F?Q?YG?LA???A?????E
## ?LARLYW?TVEFGL????-???KAYGAGLLSSF?ELQYCLSD-?P???PF?LE??M?T?Y?ID?
## FQPLYFV??SF??L?E??R??D?T????????P??????V?D????????????????IL?
## ?A???---
```

However, there is also a second method for computing consensus sequence that has been implemented in line with a consensus sequence method implemented in `TeXshade` that allows for specify an upper and a lower conservation threshold (see example below). This method can be accessed via the argument `type="upperlower"`. Additional customizations are available, too:



```
printSplitString(msaConsensusSequence(myFirstAlignment, type="upperlower",
                                     thresh=c(40, 20)))

## .....-.....
## .....
## .....d.....p...y..ee..tw.t...
## ....l...ac.e.....g...d.ip.....l...tg....v.gl.....f..
## .la.r.f..t..ir.....y..epdi.h...ghvpl.....fa.f.q..g.....
## .la.yw.tvefgl....-....ygag.lss..e..y.l....p.....le.....y.i..
## fq.y.v..sf.....v.....
## .....-
```

Regardless of which method is used, masks are taken into account: masked rows/sequences are neglected and masked columns are shown as “#” in the consensus sequence:

```
printSplitString(msaConsensusSequence(myMaskedAlignment, type="upperlower",
                                     thresh=c(40, 20)))

## #####
## #####.....
## .....d.....p...y..ee..tw.t...
## ....l...ac.e.....g...d.ip.....l...tg....v.gl.....f..
## .la.r.f..t..ir.....y..epdi.h...ghvpl.....fa.f.q..g.....
## .la.yw.tvefgl....-....ygag.lss..e..y.l....p.....le.....y.i..
## fq.y.v..sf.....v.....
## .....-
```

The main purpose of consensus sequences is to get an impression of conservation at individual positions/columns of a multiple alignment. The `msa` package also provides another means of analyzing conservation: the method `msaConservationScore()` computes sums of pairwise scores for a given substitution/scoring matrix. Thereby, conservation can also be analyzed in a more sensible way than by only taking relative frequencies of letters into account as `msaConsensusSequence()` does.

```
library(pwalign) # for the BLOSUM62 matrix

##
## Attaching package: 'pwalign'
## The following objects are masked from 'package:Biostrings':
##
## PairwiseAlignments, PairwiseAlignmentsSingleSubject,
## aligned, alignedPattern, alignedSubject,
## compareStrings, deletion, errorSubstitutionMatrices,
## indel, insertion, mismatchSummary, mismatchTable,
## nedit, nindel, nucleotideSubstitutionMatrix,
```

```
## pairwiseAlignment, pattern, pid,  
## qualitySubstitutionMatrices, stringDist, unaligned,  
## writePairwiseAlignments  
  
data(BLOSUM62)  
msaConservationScore(myFirstAlignment, BLOSUM62)
```

```

## 324 216 199 86 86 42 486 214 125 108 324 324 92
## R ? F P ? T Q ? I R ? ? ?
## 341 45 486 223 172 184 106 343 233 405 117 117 100
## ? L D Y ? ? E P D I F H E
## 209 92 110 567 124 132 405 567 486 149 214 648 301
## L F G H V P L L S D P ? F
## 186 214 486 648 249 567 249 196 108 239 175 27 486
## A ? F ? Q ? Y G ? L A ? ?
## 324 213 387 90 286 70 199 486 -73 7 196 3 26
## ? A ? ? ? ? ? E ? L A R L
## 124 83 76 29 49 40 71 108 71 292 261 165 244
## Y W ? T V E F G L ? ? ? ?
## 567 891 301 405 244 405 439 486 324 173 157 129 97
## - ? ? ? K A Y G A G L L S
## 6 92 143 140 285 124 502 486 262 486 244 217 324
## S F ? E L Q Y C L S D - ?
## 324 52 93 405 77 81 451 261 276 171 183 -117 131
## P ? ? ? P F ? L E ? ? M ?
## 436 104 45 137 163 214 254 175 131 175 120 149 8
## T ? Y ? I D ? F Q P L Y F
## 165 0 567 102 288 190 73 388 405 169 108 567 382
## V ? ? S F ? ? L ? E ? ? R
## 324 100 182 262 306 118 82 124 62 264 64 95 129
## ? ? D ? T ? ? ? ? ? ? ? ?
## -75 -10 134 92 87 44 68 51 56 18 41 44 61
## ? ? P ? ? ? ? ? ? ? V ? D ?
## 79 83 91 161 56 69 51 12 42 66 -40 78 116
## ? ? ? ? ? ? ? ? ? ? ? ? ?
## 43 1 -40 -71 -11 -86 -70 -67 37 -8 -41 -38 -11
## ? ? ? I L ? ? A ? ? ? - -
## -28 -87 -7 -5 -44 4 -110 -44 -84 -68 -74 -83 -55
## -
## -47

```

As the above example shows, a substitution matrix must be provided. The result is obviously a vector as long as the alignment has columns. The entries of the vector are labeled by the consensus sequence. The way the consensus sequence is computed can be customized:

```

msaConservationScore(myFirstAlignment, BLOSUM62, gapVsGap=0,
                     type="upperlower", thresh=c(40, 20))

## - - - - - - - - - - - - -
## -80 -120 -119 -134 -96 -96 -80 -96 -144 -146 -96 -120 -80
## - - - - - - - - - - - - -
## -80 -96 -96 -64 -64 -64 -80 -80 -80 -96 -48 -96 -80
## - - - - - - - - - - - - -

```

```

## -106 -64 -121 -94 -80 -64 -90 -96 -104 -96 -96 -96 -64
## - - - - - - - - - - - - -
## -96 -96 -80 -80 -80 -96 -64 -96 -96 -96 -98 -96 -96
## - - - - - - - - - - - - -
## -80 -96 -64 -80 -80 -64 -89 -102 -64 -96 -80 -32 -96
## - - - - - - - - - - - - -
## -80 -96 -80 -48 -96 -80 -96 -122 -80 -64 -80 -48 -80
## - - - - - - - - - - - - -
## -64 -64 -80 -116 -96 -64 -104 -80 -113 -146 -48 -128 -96
## - - - - - - - - - - - - -
## -135 -112 -96 -96 -80 -144 -96 -80 -96 -64 -96 -64 -96
## - - - - - - - - - - - - -
## -80 -96 -32 -80 -96 -96 -80 -64 -80 -112 -80 -104 -80
## - - - - - - - - - - . . .
## -96 -48 16 -64 -48 -80 -80 -96 -80 -80 -75 -76 -129
## . . . . . . . y . . . . d
## -76 -91 8 43 -48 -63 -15 14 -49 -62 -80 -100 -10
## . . . . . . . d . . . . .
## -90 -82 -43 -58 -75 -36 -60 246 52 74 52 97 74
## . r . q . . . . . . . .
## -5 100 77 125 60 51 -66 -115 -71 -45 -28 -36 48
## . . . p . p . . . Y t e e
## 95 48 -3 166 30 218 6 21 33 567 141 160 165
## e . . t W . T l . . r q .
## 325 179 71 216 891 38 405 204 208 79 165 109 42
## . l . . . . A c . e . . .
## 79 249 113 106 93 172 324 536 109 324 261 72 157
## g . - - - - . . l g . . .
## 54 156 -48 -96 -96 -80 163 60 204 267 153 -20 60
## d . i P q l e . v s q . L
## 288 141 296 567 183 196 181 145 228 236 189 20 324
## q . . T G w r . . . V p g
## 171 74 145 405 486 411 167 216 36 125 324 199 388
## L . p . . . F f . . L A .
## 324 216 199 86 86 42 486 214 125 108 324 324 92
## r . F p . t q . i R . . .
## 341 45 486 223 172 184 106 343 233 405 117 117 100
## . l d Y . . E P D i f H e
## 209 92 110 567 124 132 405 567 486 149 214 648 301
## l f G H v P l l s d p . F
## 186 214 486 648 249 567 249 196 108 239 175 27 486
## A . f . q . y G . l a . .
## 324 213 387 90 286 70 199 486 -89 7 196 3 26
## . a . . . . . e . l a r l
## 124 83 76 29 48 40 71 108 71 292 261 165 244
## Y W . T v E f G L . . . .

```

[illegible]

##	NA	NA	NA	NA	NA	NA	NA	NA	NA	-64	-96	-64	-96
##	-	-	-	-	-	-	-	-	-	-	-	-	-
##	-80	-96	-32	-80	-96	-96	-80	-64	-80	-112	-80	-104	-80
##	-	-	-	-	-	-	-	-	-	-	.	.	.
##	-96	-48	16	-64	-48	-80	-80	-96	-80	-80	-75	-76	-129
##	.	.	.	.	.	.	.	y	.	.	.	.	d
##	-76	-91	8	43	-48	-63	-15	14	-49	-62	-80	-100	-10
##	.	.	.	.	.	.	.	d	.	.	.	.	.
##	-90	-82	-43	-58	-75	-36	-60	246	52	74	52	97	74
##	.	r	.	q	.	.	.	.	.	.	.	.	.
##	-5	100	77	125	60	51	-66	-115	-71	-45	-28	-36	48
##	.	.	.	p	.	p	.	.	.	Y	t	e	e
##	95	48	-3	166	30	218	6	21	33	567	141	160	165
##	e	.	.	t	W	.	T	l	.	.	r	q	.
##	325	179	71	216	891	38	405	204	208	79	165	109	42
##	.	l	.	.	.	.	A	c	.	e	.	.	.
##	79	249	113	106	93	172	324	536	109	324	261	72	157
##	g	.	-	-	-	-	.	.	l	g	.	.	.
##	54	156	-48	-96	-96	-80	163	60	204	267	153	-20	60
##	d	.	i	P	q	l	e	.	v	s	q	.	L
##	288	141	296	567	183	196	181	145	228	236	189	20	324
##	q	.	.	T	G	w	r	.	.	.	V	p	g
##	171	74	145	405	486	411	167	216	36	125	324	199	388
##	L	.	p	.	.	.	F	f	.	.	L	A	.
##	324	216	199	86	86	42	486	214	125	108	324	324	92
##	r	.	F	p	.	t	q	.	i	R	.	.	.
##	341	45	486	223	172	184	106	343	233	405	117	117	100
##	.	l	d	Y	.	.	E	P	D	i	f	H	e
##	209	92	110	567	124	132	405	567	486	149	214	648	301
##	l	f	G	H	v	P	l	l	s	d	p	.	F
##	186	214	486	648	249	567	249	196	108	239	175	27	486
##	A	.	f	.	q	.	y	G	.	l	a	.	.
##	324	213	387	90	286	70	199	486	-89	7	196	3	26
##	.	a	.	.	.	.	.	e	.	l	a	r	l
##	124	83	76	29	48	40	71	108	71	292	261	165	244
##	Y	W	.	T	v	E	f	G	L	.	.	.	.
##	567	891	301	405	244	405	439	486	324	173	157	129	97
##	-	.	.	.	k	a	y	G	a	G	l	l	S
##	-58	92	143	140	285	124	502	486	262	486	244	217	324
##	S	f	.	E	l	q	y	c	l	s	d	-	.
##	324	52	93	405	77	81	451	261	276	171	183	-142	131
##	p	.	.	.	p	f	.	l	e	.	.	m	.
##	436	104	45	137	163	214	254	175	131	175	120	149	8
##	t	.	Y	.	i	d	.	f	Q	p	l	Y	f
##	165	0	567	102	288	190	73	388	405	169	108	567	382
##	V	.	.	s	f	.	.	l	.	e	.	.	r

```
## 324 100 182 262 306 118 82 124 62 264 64 95 129
## . . d . t . . . . . . .
## -91 -10 134 92 87 44 68 51 56 18 41 44 61
## . . p . . . . . . v . d .
## 79 83 90 161 56 69 51 12 42 65 -41 77 115
## . . . . . . . . . . . .
## 42 0 -44 -75 -15 -90 -74 -76 33 -12 -45 -42 -15
## . . . i l . . a . . . - -
## -32 -91 -11 -9 -60 -12 -126 -60 -100 -84 -90 -108 -80
## -
## -96
```

### 6.3 Interfacing to Other Packages

There are also other sequence analysis packages that use or make use of multiple sequence alignments. The `msa` package does not directly interface to these packages in order to avoid dependencies and possible incompatibilities. However, `msa` provides a function `msaConvert()` that allows for converting multiple sequence alignment objects to other types/classes. Currently, five such conversions are available, namely to the classes `alignment` (`seqinr` package [2]), `align` (`bios2mds` package [14]), `AABin/DNABin` (`ape` package [10]), and `phyDat` (`phangorn` package [11]). Except for the conversion to the class `phyDat`, these conversion are performed without loading or depending on the respective packages.

In the following example, we perform a multiple alignment of Hemoglobin alpha example sequences and convert the result for later processing with the `seqinr` package:

```
hemoSeq <- readAAStringSet(system.file("examples/HemoglobinAA.fasta",
                                         package="msa"))
hemoAln <- msa(hemoSeq)

## use default substitution matrix

hemoAln

## CLUSTAL 2.1
##
## Call:
##   msa(hemoSeq)
##
## MsaAAMultipleAlignment with 17 rows and 143 columns
##      aln                                     names
## [1] -VLSPADKTNVKAAGKV...LDKFLASVSTVLTISKYR HBA1_Homo_sapiens
## [2] MVLSPADKTNVKAAGKV...LDKFLASVSTVLTISKYR HBA1_Pan_troglodytes
## [3] -VLSPADKSNVKAAGKV...LDKFLASVSTVLTISKYR HBA1_Macaca_mulatta
## [4] -VLSAADKGNVKAAGKV...LDKFLANVSTVLTISKYR HBA1_Bos_taurus
```

```
## [5] -VLSPADKTNVKGTWSKI...LDKFLASVSTVLTSKYR HBA1_Tursiops_tru...
## [6] -VLSGEDKSNIAAWGKI...LDKFLASVSTVLTSKYR HBA1_Mus_musculus
## [7] MVLSADDKTNIKNCWGKI...LDKFLASVSTVLTSKYR HBA1_Rattus_norve...
## [8] -VLSATDKANVKTFWGL...LDKFLATVATVLTSKYR HBA1_Erinaceus_eu...
## [9] -VLSAADKSNVKACWGKI...LDKFFSAVSTVLTSKYR HBA1_Felis_silves...
## [10] -VLSPADKTNIKSTWDKI...LDKFFTAVSTVLTSKYR HBA1_Chrysocyon_b...
## [11] -VLSDNDKTNVKATWSKV...LDKFLSNVSTVLTSKYR HBA1_Loxodonta_af...
## [12] -VLSAADKTNVKAWSKV...LDKFLALLSTVLTSKYR HBA1_Monodelphis_...
## [13] -MLTDAEKKEVTALWGKA...MDKFLSKVATVLTSKYR HBA1_Ornithorhync...
## [14] -VLSAADKNNVKGIFTKI...LDKFLCAVGTVLTAKYR HBA1_Gallus_gallus
## [15] -HLTADKKHKHIAIWPSV...LDKFLVSVSNVLTSKYR HBA1_Xenopus_trop...
## [16] -VLTEEDKARVRVAWVPV...VDKFLGQISKVLASRYR HBA1_Microcephalo...
## [17] -SLSDTDKAVVKAIWAKI...VDKFFNNLALALSEKYR HBA1_Danio_rerio
## Con -VLS?ADK?NVKA?WGK?...LDKFLA?VSTVLTSKYR Consensus
```

```
hemoAln2 <- msaConvert(hemoAln, type="seqinr::alignment")
```

Now we compute a distance matrix using the `dist.alignment()` function from the `seqinr` package:

```
library(seqinr)

d <- dist.alignment(hemoAln2, "identity")
as.matrix(d)[2:5, "HBA1_Homo_sapiens", drop=FALSE]
```

	HBA1_Homo_sapiens
HBA1_Pan_troglodytes	0.0000000
HBA1_Macaca_mulatta	0.1684304
HBA1_Bos_taurus	0.3472281
HBA1_Tursiops_truncatus	0.4038819

Now we can construct a phylogenetic tree with the neighbor joining algorithm using the `nj()` function from the `ape` package:

```
library(ape)

hemoTree <- nj(d)
plot(hemoTree, main="Phylogenetic Tree of Hemoglobin Alpha Sequences")
```



### Phylogenetic Tree of Hemoglobin Alpha Sequences



The following example shows how to convert a multiple alignment object in an object of class `align` as defined by the `bios2mds` package:

```
hemoAln3 <- msaConvert(hemoAln, type="bios2mds::align")
str(hemoAln3)

## List of 17
## $ HBA1_Homo_sapiens      : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Pan_troglodytes   : chr [1:143] "M" "V" "L" "S" ...
## $ HBA1_Macaca_mulatta    : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Bos_taurus        : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Tursiops_truncatus : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Mus_musculus      : chr [1:143] "-" "V" "L" "S" ...
```

```
## $ HBA1_Rattus_norvegicus      : chr [1:143] "M" "V" "L" "S" ...
## $ HBA1_Erinaceus_europaeus   : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Felis_silvestris_catus : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Chrysocyon_brachyurus  : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Loxodonta_africana     : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Monodelphis_domestica  : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Ornithorhynchus_anatinus : chr [1:143] "-" "M" "L" "T" ...
## $ HBA1_Gallus_gallus          : chr [1:143] "-" "V" "L" "S" ...
## $ HBA1_Xenopus_tropicalis     : chr [1:143] "-" "H" "L" "T" ...
## $ HBA1_Microcephalophis_gracilis: chr [1:143] "-" "V" "L" "T" ...
## $ HBA1_Danio_rerio           : chr [1:143] "-" "S" "L" "S" ...
## - attr(*, "class")= chr "align"
```

The conversions to the standard Biostrings classes are straightforward using `standard as()` methods and not provided by the `msaConvert()` function. The following example converts a multiple alignment object to class `BStringSet` (e.g. the `msaplot()` function from the `ggtree` package [16] accepts `BStringSet` objects):

```
hemoAln4 <- as(hemoAln, "BStringSet")
hemoAln4

## BStringSet object of length 17:
##      width seq                      names
## [1]   143 -VLSPADKTNVKA AW...KFLASVSTVLTSKYR HBA1_Homo_sapiens
## [2]   143 MVLSPADKTNVKA AW...KFLASVSTVLTSKYR HBA1_Pan_troglodytes
## [3]   143 -VLSPADKSNVKA AW...KFLASVSTVLTSKYR HBA1_Macaca_mulatta
## [4]   143 -VLSAADKGNVKA AW...KFLANVSTVLTSKYR HBA1_Bos_taurus
## [5]   143 -VLSPADKTNVKG TW...KFLASVSTVLTSKYR HBA1_Tursiops_tru...
## ...   ...   ...
## [13]  143 -MLTDAEKKEVTALW...KFLSKVATVLTSKYR HBA1_Ornithorhync...
## [14]  143 -VLSAADKNNVKGIF...KFLCAVGTVLTA KYR HBA1_Gallus_gallus
## [15]  143 -HLTADDKKHIAIW...KFLVSVSNVLT SKYR HBA1_Xenopus_trop...
## [16]  143 -VLTEEDKARVRVAW...KFLGQISKVLAS RYR HBA1_Microcephalo...
## [17]  143 -SLSDTDKAVVKAIW...KFFNNLALALSE KYR HBA1_Danio_rerio
```

**Note:** The `msaConvert()` function has been introduced in version 1.3.3 of the `msa` package. So, to have this function available, at least Bioconductor 3.3 is required, which requires at least R 3.3.0.

## 7 Pretty-Printing Multiple Sequence Alignments

As already mentioned above, the `msa` package offers the function `msaPrettyPrint()` which allows for pretty-printing multiple sequence alignments using the  $\text{\LaTeX}$  package `TeXshade` [1].

The `msaPrettyPrint()` function writes a multiple sequence alignment to an alignment (`.aln`) file and then creates  $\text{\LaTeX}$  code for pretty-printing the multiple sequence alignment on the basis of the  $\text{\LaTeX}$  package `TeXshade`. Depending on the choice of the output argument, the function `msaPrettyPrint()` either prints a  $\text{\LaTeX}$  fragment to the R session (choice `output="asis"`) or writes a  $\text{\LaTeX}$  source file (choice `output="tex"`) that it processes to a DVI file (choice `output="dvi"`) or PDF file (choice `output="pdf"`). Note that no extra software is needed for choices `output="asis"` and `output="tex"`. For `output="dvi"` and `output="pdf"`, however, a  $\text{\TeX}/\text{\LaTeX}$  distribution must be installed in order to translate the  $\text{\LaTeX}$  source file into the desired target format (DVI or PDF).

## 7.1 Consensus Sequence and Sequence Logo

```
msaPrettyPrint(myFirstAlignment, output="asis", y=c(164, 213),
               subset=c(1:6), showNames="none", showLogo="none",
               consensusColor="ColdHot", showLegend=FALSE,
               askForOverwrite=FALSE)
```

TAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213  
IAYNYRHGQPIPRVEYTEEEERKTWGTVFRTLKALYKTHACYEHNHIFPLL 213  
IAYNYRHGQPIPRVEYMEEEKKTWGTVFKTLKS LYKTHACYEYNHIFPLL 213  
IAYNYRHGQPIPRVEYTEEEKKTWGTVFRTLSLYKTHACYEHNHIFPLL 212

. . . . DFTLPQPLDRYSAE DHATWATLYQRCKLLPGRACDEFMEGL... 67  
QTLRPDFTMEQGVPVHYRTAADHATWRITLYDRQEAL LPGRACDEF LQGL... 83

\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*

In the above example, an exclamation mark ‘!’ in the consensus sequence stands for a conserved letter, i.e. a sequence positions in which all sequences agree, whereas an asterisk ‘\*’ stands for positions in which there is a majority of sequences agreeing. Positions in which the sequences disagree are left blank in the consensus sequence. For a more advanced example how to customize the consensus sequence, see the example in Subsection 7.4 below.

---

<sup>5</sup><https://www.ctan.org/pkg/texshade>

The color scheme of the consensus sequence can be configured with the `consensusColors` parameter. Possible values are "ColdHot", "HotCold", "BlueRed", "RedBlue", "GreenRed", "RedGreen", or "Gray". The above example uses the color scheme "RedGreen".

Additionally, `msaPrettyPrint()` also offers a more sophisticated visual representation of the consensus sequence — sequence logos. Sequence logos can be displayed either on top of the multiple sequence alignment (`showLogo="top"`), below the multiple sequence alignment (`showLogo="bottom"`), or omitted at all (`showLogo="none"`):

```
msaPrettyPrint(myFirstAlignment, output="asis", y=c(164, 213),
               subset=c(1:6), showNames="none", showLogo="top",
               logoColors="rasmol", shadingMode="similar",
               showLegend=FALSE, askForOverwrite=FALSE)
```



The color scheme of the sequence logo can be configured with the `logoColors` parameter. Possible values are "chemical", "rasmol", "hydropathy", "structure", "standard area", and "accessible area". The above example uses the color scheme "rasmol".

Note that a consensus sequence and a sequence logo can be displayed together, but only on opposite sides.

Finally, a caveat: for computing consensus sequences, `msaPrettyPrint()` uses the functionality provided by `TeXshade`, therefore, the results need not match to the results of the methods described in Section 6 above.

## 7.2 Color Shading Modes

`TeXshade` offers different shading schemes for displaying the multiple sequence alignment itself. The following schemes are available: "similar", "identical", and "functional". Moreover, there are five different color schemes available for shading: "blues", "reds", "greens", "grays", or "black". The following example uses the shading mode "similar" along with the color scheme "blues":

```
msaPrettyPrint(myFirstAlignment, output="asis", y=c(164, 213),
               showNames="none", shadingMode="similar",
               shadingColors="blues", showLogo="none",
               showLegend=FALSE, askForOverwrite=FALSE)
```

```

IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYMEEKKTWGTVFRTLKSLYKTHACYEYNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKSLYKTHACYEHNHIFPLL 212
.....DFTLPQPLDRYSAEDHATWATLYQRQCKLLPGRACDEFMEGL... 67
QTLRPDFTMEQPVHRYTAADHATWRTL YDRQEALLPGRACDEFLLQGL... 83
....PDWTIDQGWEYTYTQAEDHVWITLYERQTDMLHGRACDEFMRGL... 58
.....DNGFIHYPETEHQVWNTLITRQLKVIIEGRACQEYLDGI... 50
.VCRADFTVAQDYD.YSDEEQAVWRTLCDRQTKLTKLAHHSYLDGV... 65
***** * *****!***** *!* ***** * *!*****

```

If the shading modes "similar" or "identical" are used, the `shadingModeArg` argument allows for setting a similarity threshold (a numerical value between 0 and 100). For shading mode "functional", the following settings of the `shadingModeArg` argument are possible: "charge", "hydropathy", "structure", "hemical", "rasmol", "standard area", and "accessible area". The following example uses shading mode "functional" along with `shadingModeArg` set to "structure":

```

msaPrettyPrint(myFirstAlignment, output="asis", y=c(164, 213),
               showNames="none", shadingMode="functional",
               shadingModeArg="structure",
               askForOverwrite=FALSE)

```

```

IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL 213
IAYNYRHGQPIPRVEYMEEKKTWGTVFRTLKSLYKTHACYEYNHIFPLL 213
IAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKSLYKTHACYEHNHIFPLL 212
.....DFTLPQPLDRYSAEDHATWATLYQRQCKLLPGRACDEFMEGL... 67
QTLRPDFTMEQPVHRYTAADHATWRTL YDRQEALLPGRACDEFLLQGL... 83
....PDWTIDQGWEYTYTQAEDHVWITLYERQTDMLHGRACDEFMRGL... 58
.....DNGFIHYPETEHQVWNTLITRQLKVIIEGRACQEYLDGI... 50
.VCRADFTVAQDYD.YSDEEQAVWRTLCDRQTKLTKLAHHSYLDGV... 65

```

```

X external
X ambivalent
X internal

```

In the above example, a legend is shown that specifies the meaning of the color codes with which the letters are shaded. In some of the other examples above, we have suppressed this legend with the option `showLegend=FALSE`. The default, however, is that a legend is printed underneath the multiple sequence alignment like in the previous example.

### 7.3 Subsetting

In case that not the complete multiple sequence alignment should be printed, `msaPrettyPrint()` offers two ways of sub-setting. On the one hand, the `subset` argument allows for selecting only a

subset of sequences. Not surprisingly, `subset` must be a numeric vector with indices of sequences to be selected. On the other hand, it is also possible to slice out certain positions of the multiple sequence alignment using the `y` argument. In the simplest case, `y` can be a numeric vector with two elements in ascending order which correspond to the left and right bounds between which the multiple sequence alignment should be displayed. However, it is also possible to slice out multiple windows. For this purpose, the argument `y` must be an `IRanges` object containing the starts and ends of the windows to be selected.

## 7.4 Additional Customizations

The `msaPrettyPrint()` function provides an interface to the most common functionality of `TeXshade` in a way that the user does not need to know the specific commands of `TeXshade`. `TeXshade`, however, provides a host of additional customizations many of which are not covered by the interface of the `msaPrettyPrint()` function. In order to allow users to make use of all functionality of `TeXshade`, `msaPrettyPrint()` offers the `furtherCode` argument through which users can add `LaTeX` code to the `texshade` environment that is created by `msaPrettyPrint()`. Moreover, the code argument can be used to bypass all of `msaPrettyPrint()`'s generation of `TeXshade` code.

Here is an example how to use the `furtherCode` argument in order to customize the consensus sequence and to show a ruler on top:

```
msaPrettyPrint(myFirstAlignment, output="asis", y=c(164, 213),
               subset=c(1:6), showNames="none", showLogo="none",
               consensusColor="ColdHot", showLegend=FALSE,
               shadingMode="similar", askForOverwrite=FALSE,
               furtherCode=c("\\defconsensus{.}{lower}{upper}",
                             "\\showruler{1}{top}"))
```

170	180	190	200	210	
IAYNYRHGQPIPRVEYTEEEKQ	TWGT	VFRTLKALYKTHACYEHNHIFPLL			213
IAYNYRHGQPIPRVEYTEEEK	RKTWGT	VFRTLKALYKTHACYEHNHIFPLL			213
IAYNYRHGQPIPRVEYMEEEK	KKTWGT	VFRTLKSLYKTHACYEYHNHIFPLL			213
IAYNYRHGQPIPRVEYTEEEK	KKTWGT	VFRTLKSLYKTHACYEHNHIFPLL			212
.....DFTLPQPLDRYS	AEDHATW	ATLYQRQCKLLPGRACDEFMEGL...			67
QTLRPDFTMEQPVHRYTA	ADHATW	RTLYDRQEALLPGRACDEFLLQGL...			83
iaynyrhggpi	PrveYteeek	TWgTvf	rtlkaLykthACyEhnhifpll		

## 7.5 Sweave or knitr Integration

The function `msaPrettyPrint()` is particularly well-suited for pretty-printing multiple alignments in Sweave [6] or knitr [15] documents. The key is to set `output` to "asis" when calling `msaPrettyPrint()` and, at the same time, to let the R code chunk produce output that is directly included in the resulting `LaTeX` document as it is. This can be accomplished with the code chunk option `results="tex"` in Sweave and with the code chunk option `results="asis"` in

knitr. Here is an example of a Sweave code chunk that displays a pretty-printed multiple sequence alignment inline:

```
<<AnyChunkName,results="tex">>=
msaPrettyPrint(myFirstAlignment, output="asis")
@
```

The same example in knitr:

```
<<AnyChunkName,results="asis">>=
msaPrettyPrint(myFirstAlignment, output="asis")
@
```

Note that, for processing the resulting  $\text{\LaTeX}$  source document, the  $\text{\TeXshade}$  package must be installed (see Section 2) and the  $\text{\TeXshade}$  package must be loaded in the preamble:

```
\usepackage{texshade}
```

## 7.6 Sequence Names

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  $\text{\LaTeX}$  source code. Consequently,  $\text{\LaTeX}$  errors may arise because of characters or words in the sequence names that  $\text{\LaTeX}$  does not or cannot interpret as plain text correctly. This particularly includes appearances of special characters and backslash characters in the sequence names.

The `msa` package offers a function `msaCheckNames()` which allows for finding and replacing potentially problematic characters in the sequence names of multiple alignment objects (see `?msaCheckNames`). However, the best solution is to check sequence names carefully and to avoid problematic sequence names from the beginning. Note, moreover, that too long sequence names will lead to less appealing outputs, so users are generally advised to consider sequence names carefully.

## 7.7 Pretty-Printing Wide Alignments

If the alignment to be printed with `msaPrettyPrint()` is wide (thousands of columns or wider),  $\text{\LaTeX}$  may terminate prematurely because of exceeded  $\text{\TeX}$  capacity. Unfortunately, this problem remains opaque to the user, since `texi2dvi()` and `texi2pdf()` do not convey much details about  $\text{\LaTeX}$  problems when typesetting a document. We recommend the following if a user encounters problems with running `msaPrettyPrint()`'s output with `texi2dvi()` and `texi2pdf()`:

1. Run `pdflatex` on the generated `.tex` file to see whether it is actually a problem with  $\text{\TeX}$  capacity.

2. If so, split the alignment into multiple chunks and run `msaPrettyPrint()` on each chunk separately.

The following example demonstrates this approach for a multiple alignment object ‘aln’:

```
chunkSize <- 300 ## how much fits on one page depends on the length of
                 ## names and the number of sequences;
                 ## change to what suits your needs

for (start in seq(1, ncol(aln), by=chunkSize))
{
  end <- min(start + chunkSize - 1, ncol(aln))
  alnPart <- DNAMultipleAlignment(subseq(unmasked(aln), start, end))

  msaPrettyPrint(x=alnPart, output="pdf", subset=NULL,
                 file=paste0("aln_", start, "-", end, ".pdf"))
}
```

This creates multiple PDF files all of which show one part of the alignment. Please note, however, that the numbering of columns is restarted for each chunk.

## 7.8 Further Caveats

- Note that `texi2dvi()` and `texi2pdf()` always save the resulting DVI/PDF files to the current working directory, even if the  $\text{\LaTeX}$  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.
- `TeXshade` has a wide array of functionalities. Only the most common ones have been tested for interoperability with R. So the use of the arguments `furtherCode` and `code` is the user’s own risk!

## 8 Known Issues

### Memory Leaks

The original implementations of ClustalW, ClustalOmega, and MUSCLE are stand-alone command line programs which are only run once each time a multiple sequence alignment is performed. During the development of the `msa` package, we performed memory management checks using Valgrind [8] and discovered multiple memory leaks in ClustalW and MUSCLE. These memory leaks have no effect for the command line tools, since the program is closed each time the alignment is finished. In the implementation of the `msa` package, however, these memory leaks may have an effect if the same algorithm is run multiple times.

For MUSCLE, we managed to eliminate all memory leaks by deactivating the two parameters `weight1` and `weight2`. ClustalOmega did not show any memory leaks. ClustalW indeed has



several memory leaks which are benign if the algorithm is run only a few times, but which may have more severe effects if the algorithm is run many times. ClustalOmega also has a minor memory leak, but the loss of data is so small that no major problems are to be expected except for thousands of executions of ClustalOmega.

### **ClustalOmega vs. Older GCC Versions on Linux/Unix**

We have encountered peculiar behavior of ClustalOmega if the package was built using an older GCC version: if we built the package on an x86\_64 Linux system with GCC 4.4.7, ClustalOmega built smoothly and could be executed without any errors. However, the resulting multiple sequence alignment was more than sub-optimal. We could neither determine the source of this problem nor which GCC versions show this behavior. We therefore recommend Linux/Unix users to use an up-to-date GCC version (we used 4.8.2 during package development, which worked nicely) or, in case they encounter dubious results, to update to a newer GCC version and re-install the package.

### **ClustalOmega: OpenMP Support on Mac OS**

ClustalOmega is implemented to make use of OpenMP (if available on the target platform). Due to issues on one of the Bioconductor build servers running Mac OS, we had to deactivate OpenMP generally for Mac OS platforms. If a Mac OS user wants to re-activate OpenMP, he/she should download the source package tarball, untar it, comment/uncomment the corresponding line in `msa/src/ClustalOmega/msaMakefile` (see first six lines), and build/install the package from source.

### **Build/installation issues**

Some users have reported compiler and linker errors when building `msa` from source on Linux systems. In almost all cases, these could have been tracked down to issues with the R setup on those systems (e.g. a `Rprofile.site` file that makes changes to the R environment that are not compatible with `msa`'s Makefiles).<sup>6</sup> In most cases, these issues can be avoided by installing `msa` in a “vanilla R session”, i.e. starting R with option `--vanilla` when installing `msa`.

On some systems (e.g. FreeBSD), the required Gnu make command is installed under a different name, e.g., `gmake`. The `msa` package installation can handle this under the condition that an environment variable `MAKE` is defined beforehand that contains the name of the Gnu make binary.

## **9 Future Extensions**

We envision the following changes/extensions in future versions of the package:

- Integration of more multiple sequence alignment algorithms, such as, T-Coffee [9] or DIALIGN [7]
- Support for retrieving guide trees from the multiple sequence alignment algorithms

---

<sup>6</sup>See, e.g., <https://support.bioconductor.org/p/90735/>

- Interface to methods computing phylogenetic trees (e.g. as contained in the original implementation of ClustalW)
- Elimination of memory leaks described in Section 8 and re-activation of parameters that have been deactivated in order to avoid memory leaks
- More tolerant handling of custom substitution matrices (MUSCLE interface)

## 10 How to Cite This Package

If you use this package for research that is published later, you are kindly asked to cite it as follows:

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

To obtain a BibTeX entries of the reference, enter the following into your R session:

```
toBibtex(citation("msa"))
```

Moreover, we insist that, any time you cite the package, you also cite the original paper in which the original algorithm has been introduced (see bibliography below).

## References

- [1] E. Beitz. T<sub>E</sub>Xshade: shading and labeling of multiple sequence alignments using L<sup>A</sup>T<sub>E</sub>X2<sub>ε</sub>. *Bioinformatics*, 16(2):135–139, 2000.
- [2] D. Charif and J. R. Lobry. SeqinR 1.0-2: a contributed package to the R project for statistical computing devoted to biological sequences retrieval and analysis. In U. Bastolla, M. Porto, H. E. Roman, and M. Vendruscolo, editors, *Structural approaches to sequence evolution: Molecules, networks, populations*, Biological and Medical Physics, Biomedical Engineering, pages 207–232. Springer, New York, 2007.
- [3] R. C. Edgar. MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics*, 5(5):113, 2004.
- [4] R. C. Edgar. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.*, 32(5):1792–1797, 2004.
- [5] L. Lamport. *L<sup>A</sup>T<sub>E</sub>X — A Document Preparation System. User's Guide and Reference Manual*. Addison-Wesley Longman, Amsterdam, 1999.
- [6] F. Leisch. Sweave: dynamic generation of statistical reports using literate data analysis. In W. Härdle and B. Rönz, editors, *Compstat 2002 — Proceedings in Computational Statistics*, pages 575–580, Heidelberg, 2002. Physica-Verlag.

- [7] B. Morgenstern. DIALIGN 2: improvement of the segment-to-segment approach to multiple sequence alignment. *Bioinformatics*, 15(3):211–218, 1999.
- [8] N. Nethercote and J. Seward. Valgrind: A framework for heavyweight dynamic binary instrumentation. In *Proc. of the ACM SIGPLAN 2007 Conf. on Programming Language Design and Implementation*, San Diego, CA, 2007.
- [9] C. Notredame, D. G. Higgins, and J. Heringa. T-Coffee: A novel method for fast and accurate multiple sequence alignment. *J. Mol. Biol.*, 302(1):205–217, 2000.
- [10] E. Paradis, J. Claude, and K. Strimmer. APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20:289–290, 2004.
- [11] K. P. Schliep. phangorn: phylogenetic analysis in R. *Bioinformatics*, 27(4):592–593, 2011.
- [12] F. Sievers, A. Wilm, D. Dineen, T. J. Gibson, K. Karplus, W. Li, R. Lopez, H. McWilliam, M. Remmert, J. Söding, J. D. Thompson, and D. G. Higgins. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol. Syst. Biol.*, 7:539, 2011.
- [13] J. D. Thompson, D. G. Higgins, and T. J. Gibson. 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, 2004.
- [14] J. Pele with J.-M. Becu, H. Abdi, and M. Chabbert. *bios2mds: From BIOlogical Sequences to MultiDimensional Scaling*, 2012. R package version 1.2.2.
- [15] Y. Xie. *Dynamic Documents with R and knitr*. Chapman & Hall/CRC, 2014.
- [16] G. Yu, D. Smith, H. Zhu, Y. Guan, and T. T. Y. Lam. ggtree: an R package for visualization and annotation of phylogenetic tree with different types of meta-data. submitted.