

Package ‘msaR’

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Title Multiple Sequence Alignment for R Shiny

Version 0.3.0

Description Visualises multiple sequence alignments dynamically within the Shiny web application framework.

Depends R (>= 3.2.2)

License BSL-1.0

Imports ape, htmlwidgets

Suggests Biostrings, knitr, rmarkdown

LazyData true

RoxygenNote 6.0.1

VignetteBuilder knitr

NeedsCompilation no

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`as.fasta`*as.fasta*

Description

functionality to convert objects to a fasta string. Currently this can handle character objects which are interpreted as filenames or several of the popular means of storing sequence data: [DNABin](#), [DNASTringSet](#), [AAStringSet](#), [RNASTringSet](#), [BStringSet](#), [DNAMultipleAlignment](#), [RNAMultipleAlignment](#), or [AAMultipleAlignment](#).

Usage

```
as.fasta(seqs)
```

Arguments

`seqs` (Required.) the sequence/alignment to be displayed. A character vector, [DNABin](#), [DNASTringSet](#), [AAStringSet](#), or [RNASTringSet](#).

Value

A character string in fasta format.

Examples

```
seqfile <- system.file("sequences", "AHBA.aln", package="msaR")
as.fasta(seqfile)
help("as.fasta")

if (requireNamespace("Biostrings", quietly = TRUE)) {
  seqs <- Biostrings::readDNASTringSet(seqfile)
  as.fasta(seqs)
}
```

`msaR`*msaR*

Description

Dynamic Multiple Sequence Alignments in R and Shiny

Usage

```
msaR(msa, menu = TRUE, width = NULL, height = NULL, rowheight = 15,
      alignmentHeight = 225, overviewbox = TRUE, seqlogo = TRUE,
      colorscheme = "nucleotide", conservation = FALSE, markers = TRUE,
      metacell = FALSE, lefthead = TRUE, labels = TRUE, labelname = TRUE,
      labelid = TRUE, labelNameLength = 100, overviewboxWidth = "auto",
      overviewboxHeight = "fixed")
```

Arguments

<code>msa</code>	File or BioString Object representing a multiple Sequence Alignment.
<code>menu</code>	Optional. Default TRUE. Determines whether to include the interactive menu.
<code>width</code>	Optional. Default NULL. The width of the html widget element.
<code>height</code>	Optional. Default NULL. The height of the html widget element.
<code>rowheight</code>	Optional. Default 20. Height of a row in the MSA.
<code>alignmentHeight</code>	Optional. Default 225. Height of the MSA.
<code>overviewbox</code>	optional. Default TRUE. Include the overview box?
<code>seqlogo</code>	optional. Default TRUE. Include the seqlogo?
<code>colorscheme</code>	optional. Default "nucleotide". The color scheme to use. Can be one of the following: "buried", "cinema", "clustal", "clustal2", "helix", "hydro", "lesk", "mae", "nucleotide", "purine", "str
<code>conservation</code>	optional. Default TRUE. Include the conservation widget?
<code>markers</code>	optional. Default TRUE. Include the alignment markers? These are the numbers along the top that
<code>metacell</code>	optional. Default FALSE. Include the per-sequence metadata.
<code>lefthead</code>	optional. Default TRUE. Include the header information.
<code>labels</code>	optional. Default TRUE. Include all of the sequence information msa Labels.
<code>labelname</code>	optional. Default TRUE. Include sequence name?
<code>labelid</code>	optional. Default TRUE. Include the labelid?
<code>labelNameLength</code>	optional. Default 100. Width of the Label Names.
<code>overviewboxWidth</code>	optional. Default. "auto". Can also be "fixed"
<code>overviewboxHeight</code>	optional. Default. "fixed". Can also be an integer value.

Examples

```
seqfile <- system.file("sequences", "AHBA.aln", package="msaR")
msaR(seqfile)
```

msaROutput	<i>Widget output function for use in Shiny</i>
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Description

Widget output function for use in Shiny

Usage

```
msaROutput(outputId, width = "100%", height = "100%")
```

Arguments

outputId	output id
width	width
height	height

renderMsaR	<i>Widget render function for use in Shiny</i>
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Description

Widget render function for use in Shiny

Usage

```
renderMsaR(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

expr	expr
env	env
quoted	quoted

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