

Package ‘msaR’

September 22, 2021

Title Multiple Sequence Alignment for R Shiny

Version 0.6.0

Description Visualizes 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, testthat (>= 3.0.0)

RoxygenNote 7.1.2

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-09-22 04:30:09 UTC

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`.check_lengths` *check_lengths*

Description

`check_lengths`

Usage

`.check_lengths(seqlist)`

Arguments

`seqlist` optimistic loading can lead to issues. All MSAs should have identical length. if not theres a problem.

`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](#), [DNABinStringSet](#), [AAStringSet](#), [RNAStringSet](#), [BStringSet](#), [DNAMultipleAlignment](#), [RNAMultipleAlignment](#), or [AAMultipleAlignment](#).

Usage

`as.fasta(seqs)`

Arguments

`seqs` (Required.) the sequence/alignment to be displayed. A character vector, [DNABin](#), [DNABinStringSet](#), [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")

## Not run:
if (requireNamespace("Biostrings")) {
  seqs <- readDNASTringSet(seqfile)
  as.fasta(seqs)
}

## End(Not run)
```

as.sequences

as.sequences

Description

functionality to convert sequence objects into R lists that can be serialized to JS as JSON. 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.sequences(seqs)
```

Arguments

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

Value

A list of named lists where each sublist has name, id, and seq members.

Examples

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

## Not run:
if (requireNamespace("Biostrings")) {
  seqs <- readDNASTringSet(seqfile)
  as.sequences(seqs)
}

## End(Not run)
```

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,
  leftheader = TRUE,
  labels = TRUE,
  labelname = TRUE,
  labelid = FALSE,
  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?

markers	optional. Default TRUE. Include the alignment markers? These are the numbers along the top that
metacell	optional. Default FALSE. Include the per-sequence metadata.
lefthead	optional. Default TRUE. Include the header information.
labels	optional. Default TRUE. Include all of the sequence information msa Labels.
labelname	optional. Default TRUE. Include sequence name?
labelid	optional. Default FALSE. Include the labelid?
labelNameLength	optional. Default 100. Width of the Label Names.
overviewboxWidth	optional. Default. "auto". Can also be "fixed"
overviewboxHeight	optional. Default. "fixed". Can also be an integer value.

Examples

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

msaROutput

Widget output function for use in Shiny

Description

Widget output function for use in Shiny

Usage

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

Arguments

outputId	output id
width	width
height	height

`renderMsaR`*Widget render function for use in Shiny*

Description

Widget render function for use in Shiny

Usage

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

Arguments

<code>expr</code>	<code>expr</code>
<code>env</code>	<code>env</code>
<code>quoted</code>	<code>quoted</code>

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