Package 'msaR'

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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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R topics documented:

.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, 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")

## 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

msa	File or BioString Object representing a multiple Sequence Alignment.
menu	Optional. Default TRUE. Determines whether to include the interactive menu.
width	Optional. Default NULL. The width of the html widget element.
height	Optional. Default NULL. The height of the html widget element.
rowheight	Optional. Default 20. Height of a row in the MSA.
alignmentHeight	Optional. Default 225. Height of the MSA.
overviewbox	optional. Default TRUE. Include the overview box?
seqlogo	optional. Default TRUE. Include the seqlogo?
colorscheme	optional. Default "nucleotide". The color scheme to use. Can be one of the following: "buried","cinema","clustal","clustal2","helix","hydro","lesk","mae","nucleotide","purine","st
conservation	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.
leftheader	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

expr	expr
env	env
quoted	quoted

Index