

Package: msaR (via r-universe)

September 5, 2024

Title Multiple Sequence Alignment for R Shiny

Version 0.6.0

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, testthat (>= 3.0.0)

LazyData true

RoxygenNote 7.1.1

VignetteBuilder knitr

Config/testthat/edition 3

Repository <https://zachcp.r-universe.dev>

RemoteUrl <https://github.com/zachcp/msar>

RemoteRef HEAD

RemoteSha bea35f214a4634d3cf34d216990b772d6d1e8c88

Contents

| | |
|------------------------|---|
| as.fasta | 2 |
| as.sequences | 2 |
| msaR | 3 |
| msaROutput | 5 |
| renderMsaR | 5 |

| | |
|--------------|----------|
| Index | 6 |
|--------------|----------|

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,
    lefthead = 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? |
| <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 FALSE. 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> |
|------------|--|

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> |
|------------|--|

Description

Widget render function for use in Shiny

Usage

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

Arguments

| | |
|--------|--------|
| expr | expr |
| env | env |
| quoted | quoted |

Index

AAMultipleAlignment, [2](#)

AAStringSet, [2](#), [3](#)

as.fasta, [2](#)

as.sequences, [2](#)

BStringSet, [2](#)

DNAbin, [2](#), [3](#)

DNAMultipleAlignment, [2](#)

DNAStrngSet, [2](#), [3](#)

msaR, [3](#)

msaROutput, [5](#)

renderMsaR, [5](#)

RNAMultipleAlignment, [2](#)

RNAStrngSet, [2](#), [3](#)