Package: SubVis (via r-universe)

August 20, 2024

Version 2.0.2

Date 2017-05-08

Title Visual Exploration of Protein Alignments Resulting from Multiple Substitution Matrices

Description Substitution matrices are important parameters in protein alignment algorithms. These matrices represent the likelihood that an amino acid will be substituted for another during mutation. This tool allows users to apply predefined and custom matrices and then explore the resulting alignments with interactive visualizations. 'SubVis' requires the availability of a web browser.

Depends R (>= 3.3.0), shiny, Biostrings

License GPL-3

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RoxygenNote 5.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository https://sabarlowe.r-universe.dev

RemoteUrl https://github.com/cran/SubVis

RemoteRef HEAD

RemoteSha f822cbf16662a997d5646bfdaa76f7d6294ea7c1

Contents

`startSubVis` *Starts the SubVis app*

Description

Author: Scott Barlowe Date: June 15, 2016

Usage

```
startSubVis()
```

Examples

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startSubVis()
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