Package 'SubVis'

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Version 2.0.2

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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

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RoxygenNote 5.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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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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