

# Package ‘SubVis’

January 12, 2017

**Version** 2.0.1

**Date** 2017-01-09

**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

**Repository** CRAN

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startSubVis	<i>Starts the SubVis app</i>
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**Description**

Author: Scott Barlowe Date: June 15, 2016

**Usage**

```
startSubVis()
```

**Examples**

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startSubVis()
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