Package ‘SubVis’

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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
License GPL-3
Author Scott Barlowe <sabarlowe@email.wcu.edu>
Maintainer Scott Barlowe <sabarlowe@email.wcu.edu>
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Starts the SubVis app

Description

Author: Scott Barlowe Date: June 15, 2016

Usage

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