Package ‘SubVis’

May 23, 2017

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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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Suggests knitr, rmarkdown
VignetteBuilder knitr
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Starts the SubVis app

Description
Author: Scott Barlowe Date: June 15, 2016

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