Package 'indel.shiny'

December 13, 2018

Type Package

Title Analyze heterozygous and homozygous indels

Version 1.3

Date 2018-08-20

Author Who wrote it

Maintainer Who to complain to <yourfault@somewhere.net>

Description Shiny app for analysis of heterozygous and homozygous indels using .ab1 Sanger sequnce files and reference sequence in fasta format as a .txt file.

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Imports BiocGenerics, Biostrings, crayon, knitr, msa, readr, sangerseqR, shiny

R topics documented:

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indel.shiny-package   *Analyze heterozygous and homozygous indels*

Description

Shiny app for analysis of heterozygous and homozygous indels using .ab1 Sanger sequnce files and reference sequence in fasta format as a .txt file.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.
Use start_indel_shiny() to start the shiny application.

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Author(s)

Who wrote it

Maintainer: Who to complain to <yourfault@somewhere.net>

Examples

```
## Not run:
start_indel_shiny()

## End(Not run)
```

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start_indel_shiny   *Start Shiny App*

Description

Start the shiny indel application

Usage

```
start_indel_shiny()
```

Value

The running shiny app

Author(s)

Anastasia Eskova

Examples

```
## Not run:
start_indel_shiny()

## End(Not run)
```

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