Package 'indel.shiny'

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Type Package	tage
itle Analyze heterozygous and homozygous indels ersion 1.5	
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Description Shiny app for analysis of heterozygous and homozygous indels using .ab1 Sanger sequence files and reference sequence in fasta format as a .txt file.	
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Imports BiocGenerics, Biostrings, crayon, knitr, msa, readr, sangerseqR, shiny	
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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. 2 calculate.indel

Author(s)

Robert Deibel

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Examples

```
## Not run:
start_indel_shiny()
## End(Not run)
```

calculate.indel

Calculates Indels for Base strings

Description

Calculates and prints the found indels for a given String of IUPAC bases

Usage

```
calculate.indel(sequence, max.shift)
```

Arguments

sequence A String of IUPAC bases

max.shift An integer stating the prefered maximum shift length. Is 15 by default

Value

Calculated indel Strings with marked indel positions

Author(s)

Robert Deibel

Examples

```
## Not run:
calculate.indel("AAAGGGTTTTCCCGCT", 12)
## 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)
```

test.data

Test Data for the indel script

Description

Can be used to test the calculate.indel() function.

Usage

rivers

Format

A string of bases in IUPAC notation

Source

Anastasia Eskova

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