

# Package ‘indel.shiny’

October 24, 2018

**Type** Package

**Title** Analyze heterozygous and homozygous indels

**Version** 1.0

**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 sequence files and reference sequence in fasta format as a .txt file.

**License** MIT License

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

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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.

## Details

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

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Use start\_indel\_shiny() to start the shiny application.

**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 | <i>Start Shiny App</i> |
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**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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