

Package ‘mutType’

June 3, 2023

Title Determine the mutation type for a set of single nucleotide variants in a genome with mutType package

Version 0.0.1

Description The mutType package takes a set of mutations (single nucleotide variants, SNVs) in VCF format, and determines for each mutation the corresponding mutation type.

Depends R(>= 3.6)

Imports utils, VariantAnnotation, SummarizedExperiment, IRanges, Biostrings, ggplot2, BSgenome.Hsapiens.UCSC.hg19

Suggests knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

License GPL-2

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

biocViews Software, SNV, GenomicVariation, MutationTypes, VCF

NeedsCompilation no

Author Alessandro Giulivo [aut, cre]

Maintainer Alessandro Giulivo <alessandro.giulivo@mail.polimi.it>

R topics documented:

mutType	1
mutTypeTable	2
Index	4

mutType	<i>Determine mutation type</i>
---------	--------------------------------

Description

The mutType function compares a list of mutations in VCF format to a reference genome and returns the mutation type along with upstream and downstream bases for a total length = context_length

Usage

```
mutType(VCFFile, refGenome, context_length, graphics = TRUE)
```

Arguments

VCFFile	a set of mutations in VCF Format
refGenome	Full reference genome sequences as provided by UCSC in Biostrings objects
context_length	an odd integer representing the length of region around the mutation
graphics	default = TRUE; if TRUE, saves a barplot of mutation type frequencies in a pdf file

Value

vector of mutation types as "UP[REF>ALT]DOWN"

Author(s)

Alessandro Giulivo
 Politecnico di Milano
 Maintainer: Alessandro Giulivo
 E-Mail: alessandro.giulivo@mail.polimi.it

Examples

```
library(BSgenome.Hsapiens.UCSC.hg19)
Hs <- Hsapiens
sample <- system.file("extdata", "sample.vcf", package = "mutType")

mutType(sample, Hs, 7)
```

mutTypeTable

Summarize Mutation Types

Description

The mutTypeTable function summarizes the mutations obtained from mutType function into a counts table and produces a pdf image plotting the results. It is automatically run when calling mutType function when parameter graphics = T

Usage

```
mutTypeTable(mutTypeResult)
```

Arguments

mutTypeResult	a vector as obtained from the mutType function
---------------	--

Value

a table along with a histogram summarizing mutation types

Author(s)

Alessandro Giulivo
Politecnico di Milano
Maintainer: Alessandro Giulivo
E-Mail: alessandro.giulivo@mail.polimi.it

Examples

```
library(BSgenome.Hsapiens.UCSC.hg19)
Hs <- Hsapiens
sample <- system.file("extdata", "sample.vcf", package = "mutType")

mutts <- mutType(sample, Hs, 7, graphics = FALSE)
mutTypeTable(mutts)
```

Index

`mutType`, [1](#)
`mutTypeTable`, [2](#)