Package 'mutType'

May 28, 2023

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

Version 0.0.0.9000

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

Depends R(>= 3.6)

Imports VariantAnnotation, SummarizedExperiment

Suggests knitr, rmarkdown, BiocStyle

License GPL-2

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

NeedsCompilation no

Author Alessandro Giulivo [aut, cre]

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

R topics documented:

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mutType	*Determine mutation type*

Description

This function compares a list of mutations in VCF format to a reference genome and returns the
mutation type along with context_length upstream and downstream bases

Usage

```
mutType(VCFFile, refGenome, context_length)
```

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

Value

mutation type as "UP[REF>ALT]DOWN"

Author(s)

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

Examples

```
mutType("data/inst/sample.vcf", HSapiens, 3)
```

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