# Package 'mutType'

June 5, 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, tidyr, dplyr

**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

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## R topics documented:

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mutType                    *Determine mutation type*

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## 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

data.frame object of mutations as "UP[REF>ALT]DOWN" and mutation types as "[REF>ALT]" where "REF" is always either "C" or "T"..

[REF>ALT]: R:REF%3EALT%5C

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## Examples

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

mutType(sample, Hs, 7)
```

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| mutTypeTable | *Summarize Mutation Types* |
|---|---|

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## 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

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## Examples

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

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

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