Package 'mutType'

June 9, 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

URL https://github.com/AlessandroGiulivo/sciprog/tree/main/RProj

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*

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".

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References

https://github.com/AlessandroGiulivo/sciprog/tree/main/RProj

See Also

mutTypeTable

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*

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 data.frame as obtained from the mutType function

Value

a table along with a histogram summarizing mutation types

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References

https://github.com/AlessandroGiulivo/sciprog/tree/main/RProj

See Also

mutType

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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