Package ‘EDIRquery’

May 17, 2024

Title  Query the EDIR Database For Specific Gene

Version  1.4.0

Description  
EDIRquery provides a tool to search for genes of interest within the Exome Database of Inter-
spersed Repeats (EDIR). A gene name is a required input, and users can additionally specify re-
peat sequence lengths, minimum and maximum distance between sequences, and whether to al-
low a 1-bp mismatch. Outputs include a summary of results by re-
peat length, as well as a dataframe of query results. Example data provided includes a sub-
set of the data for the gene GAA (ENSG00000171298). To query the full database requires pro-
viding a path to the downloaded database files as a parameter.

License  GPL-3

Encoding  UTF-8

biocViews  Genetics, SequenceMatching

Roxygen  list(markdown = TRUE)

RoxygenNote  7.2.3

Depends  R (>= 4.2.0)

Imports  tibble (>= 3.1.6), tictoc (>= 1.0.1), utils (>= 4.1.3), stats
         (>= 4.1.3), readr (>= 2.1.2), InteractionSet (>= 1.22.0),
         GenomicRanges (>= 1.46.1)

Suggests  knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder  knitr

Config/testthat/edition  3

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Description

A dataset containing two formats of gene names and associated chromosome number.

Usage

gene_chr

Format

A data frame with 60571 rows and 3 variables:

- **chromosome_name** chromosome
- **ensembl_gene_id** Ensembl gene ID of gene
- **hgnc_symbol** HGNC symbol of gene

Description

This function searches for a specified gene in the EDIR dataset. A gene name is a required parameter.

Usage

gene_lookup(
  gene,
  length = NA,  
  mindist = 0,  
  maxdist = 1000,  
  format = "data.frame",  
  summary = FALSE,  
  mismatch = TRUE,  
  path = NA
)
gene_lookup

Arguments

gene
The gene name (ENSEMBL ID or HGNC symbol)

length
Repeat sequence length, must be between 7 and 20. Defaults to NA. If NA, results will include all available lengths in dataset for queried gene.

mindist
Minimum spacer distance between repeats. Defaults to 0.

maxdist
Maximum spacer distance between repeats. Defaults to 1000.

format
Output table format. One of 'data.frame', 'GInteractions'. Defaults to 'data.frame'.

summary
Logical value indicating whether to store summary. Defaults to FALSE.

mismatch
Logical value indicating whether to allow 1 mismatch in sequences. Defaults to TRUE.

path
String containing path to directory holding downloaded dataset files. Defaults to NA. If not provided (path = NA), gene_lookup() will use subset of data provided as example.

Details

Summary of results printed to console includes gene name, gene length (bp), Ensembl transcript ID, queried distance between repeats (default: 0-1000 bp), and an overview of total results for the given repeat length. Console outputs include runtime.

Value

A data.frame of the results from the EDIR database. If summary = TRUE, returns a tibble containing the summary ($summary), and query results ($results).

Examples

## With given repeat length,
gene_lookup("GAA", length = 7, mindist = 10, maxdist = 1000, mismatch = TRUE)

## Without specified repeat length
gene_lookup("GAA", mindist = 0, maxdist = 1000, mismatch = TRUE)

## To access query results, store in variable
output <- gene_lookup("GAA", length = 7, mindist = 10, maxdist = 1000, mismatch = FALSE)
head(output)

## With summary = TRUE
output <- gene_lookup("GAA", length = 10, mindist = 10, maxdist = 1000, summary = TRUE, mismatch = TRUE)
output$summary
head(output$results)
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