Package 'EDIRquery'

November 11, 2026

Title Query the EDIR Database For Specific Gene

Version 1.12.0

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

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Encoding UTF-8

biocViews Genetics, SequenceMatching

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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

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`gene_chr` *Gene chromosome location*

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

`gene_lookup` *Look Up a Gene in EDIR Dataset*

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
)
```

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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