Package: remart (via r-universe)

May 17, 2026

Title Reimplementation of the 'biomaRt' Package Using Modern Ensembl APIs

Version 0.0.0.9000

Description This package aims to offer a drop-in replacement to biomaRt using the same interface but the more modern and better maintained APIs provided by Ensembl.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

Imports httr2

URL `https://huber-group-embl.github.io/remart/`, `https://github.com/Huber-group-EMBL/remart`

BugReports `https://github.com/Huber-group-EMBL/remart/issues`

Config/pak/sysreqs libssl-dev

Repository https://bisaloo.r-universe.dev

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RemoteUrl https://github.com/Huber-group-EMBL/remart

RemoteRef HEAD

RemoteSha 18249389aad2109e82cbc02769c53f1ef421ba28

Contents

`getGene` *Retries gene annotation information from Ensembl.*

Description

Retries gene annotation information from Ensembl.

Usage

```
getGene(id, type = "ensembl_gene_id", ...)
```

Arguments

`id`	vector of gene identifiers one wants to annotate
`type`	type of identifier, possible values can be obtained by the listFilters function. Examples are entrezgene_id, hgnc_symbol (for hugo gene symbol), ensembl_gene_id, unigene, agilentprobe, affy_hg_u133_plus_2, refseq_dna, etc.
`...`	Ignored. Used to catch no longer necessary parameters such as `mart` from **biomaRt** functions.

Examples

```
remart::getGene(
  "ENSG00000157764",
  type = "ensembl_gene_id"
)

ids <- c(
 "ENSG00000003987",
 "ENSG00000004939"
)
remart::getGene(
  id = ids,
  type = "ensembl_gene_id"
)
```

`getSequence` *Get Sequences from Ensembl*

Description

Get Sequences from Ensembl

Usage

```
getSequence(
  chromosome,
  start,
  end,
  id,
  type,
  seqType,
  upstream,
  downstream,
  ...
)
```

Arguments

`chromosome`	Chromosome name
`start`	start position of sequence on chromosome
`end`	end position of sequence on chromosome
`id`	An identifier or vector of identifiers.
`type`	The type of identifier used. Supported types are hugo, ensembl, embl, entrezgene, refseq, ensemblTrans and unigene. Alternatively one can also use a filter to specify the type. Possible filters are given by the `listFilters()` function.
`seqType`	Type of sequence that you want to retrieve. Allowed seqTypes are given in the details section.
`upstream`	To add the upstream sequence of a specified number of basepairs to the output.
`downstream`	To add the downstream sequence of a specified number of basepairs to the output.
`...`	Ignored. Used to catch no longer necessary parameters such as `mart` from **biomaRt** functions.

Examples

```
remart::getSequence(
  seqType = "gene_exon_intron",
  type = "ensembl_gene_id",
  id = "ENSG00000001497"
)

ids <- c(
 "ENSG00000003987",
 "ENSG00000004939"
)
remart::getSequence(
  seqType = "gene_exon_intron",
  type = "ensembl_gene_id",
  id = ids
)
```

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