

Package ‘BioMartGOGeneSets’

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Type Package

Title Gene Ontology Gene Sets from BioMart

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Depends R (>= 4.0.0)

Imports utils, S4Vectors, GenomicRanges

Suggests biomaRt, GO.db, GenomeInfoDb, knitr, testthat, GetoptLong, DT

biocViews AnnotationData, Organism

Description It contains pre-compiled Gene Ontology gene sets for all organisms available on the Ensembl database. It also includes GO gene sets for organisms on Ensembl Plants, Ensembl Metazoa, Ensembl Fungi and Ensembl Protists. The data was collected with the biomaRt package.

VignetteBuilder knitr

URL <https://github.com/jokergoo/BioMartGOGeneSets>

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NeedsCompilation no

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Author Zuguang Gu [aut, cre] (ORCID: <<https://orcid.org/0000-0002-7395-8709>>)

Maintainer Zuguang Gu <z.gu@dkfz.de>

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BioMartGOGeneSets	<i>Version and source information</i>
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Description

Version and source information

Usage

BioMartGOGeneSets

Examples

BioMartGOGeneSets

changeSeqnameStyle	<i>Change sequence names</i>
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Description

Change sequence names

Usage

```
changeSeqnameStyle(gr, dataset, seqname_style_from, seqname_style_to,  
  reformat_from = NULL, reformat_to = NULL)
```

Arguments

gr	The input regions
dataset	A BioMart dataset or a taxon ID. For a proper value, please see supportedOrganisms .
seqname_style_from	Value should be in c("Sequence-Name", "GenBank-Accn", "RefSeq-Accn"). If you are not sure which seqname style is in gr, use getBioMartGenomeInfo to obtain list of examples.
seqname_style_to	Value should be in c("Sequence-Name", "GenBank-Accn", "RefSeq-Accn").
reformat_from	A self-defined function to reformat the seqnames. The internal seqname style can be obtained via <code>getBioMartGenomeInfo(dataset)</code> . This function converts the internal "from" seqnames to fit the user's input regions.
reformat_to	A self-defined function to reformat the seqnames.

Details

Please the conversion is not one to one. For those sequences which cannot be corrected mapped to other styles, they are just removed.

Value

A [GRanges](#) object.

Examples

```
## Not run:
gr = getBioMartGenes("giant_panda")
changeSeqnameStyle(gr, "giant_panda", "Sequence-Name", "GenBank-Accn")

## End(Not run)
```

getBioMartGenes	<i>Get genes from BioMart</i>
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Description

Get genes from BioMart

Usage

```
getBioMartGenes(dataset, add_chr_prefix = FALSE)
```

Arguments

dataset	A BioMart dataset or a taxon ID. For a proper value, please see supportedOrganisms .
add_chr_prefix	Whether to add "chr" prefix to chromosome names? If it is ture, it uses <code>GenomeInfoDb::seqlevelsStyle</code> = "UCSC" to add the prefix.

Details

Note `add_chr_prefix` is just a helper argument. You can basically do the same as:

```
gr = getBioMartGenes("hsapiens_gene_ensembl")
seqlevelsStyle(gr) = "UCSC"
```

Value

A [GRanges](#) object.

Examples

```
gr = getBioMartGenes("hsapiens_gene_ensembl")
gr
gr = getBioMartGenes("hsapiens_gene_ensembl", add_chr_prefix = TRUE)
gr
```

getBioMartGenomeInfo	<i>Get genome information</i>
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Description

Get genome information

Usage

```
getBioMartGenomeInfo(dataset)
```

Arguments

dataset A BioMart dataset or a taxon ID. For a proper value, please see [supportedOrganisms](#).

Value

A list.

Examples

```
getBioMartGenomeInfo(9606)
```

getBioMartGOGeneSets *Get GO gene sets*

Description

Get GO gene sets

Usage

```
getBioMartGOGeneSets(dataset, ontology = "BP",  
  as_table = FALSE, gene_id_type = "ensembl_gene")
```

Arguments

dataset	A BioMart dataset or a taxon ID. For a proper value, please see supportedOrganisms .
ontology	The value should be "BP", "CC", or "MF".
as_table	Whether to return the value as a data frame?
gene_id_type	Since BioMart is from Ensembl database, the default gene ID type is Ensembl gene ID. Depending on different organisms, Entrez ID ("entrez_gene") or gene symbol ("gene_symbol") can also be selected as the gene ID type.

Details

The gene sets are already compiled and are hosted on https://github.com/jokergoo/BioMartGOGeneSets_data, This function just simply retrieves data from there.

Value

A list of gene IDs or a data frame.

Examples

```
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl")  
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl", gene_id_type = "entrez")  
tb = getBioMartGOGeneSets("hsapiens_gene_ensembl", as_table = TRUE)
```

```
print.BioMartGOGeneSets_info
```

Print the BioMartGOGeneSets object

Description

Print the BioMartGOGeneSets object

Usage

```
## S3 method for class 'BioMartGOGeneSets_info'  
print(x, ...)
```

Arguments

x	A BioMartGOGeneSets_info object.
...	Other arguments

Value

No value is returned.

Examples

```
BioMartGOGeneSets
```

supportedOrganisms	<i>All supported organisms</i>
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Description

All supported organisms

Usage

```
supportedOrganisms(html = TRUE)
```

Arguments

html	Whether to open the table in the web browser?
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Value

A data frame of supported organisms.

Examples

```
if(interactive()) {  
  supportedOrganisms()  
}
```

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