BioMartGOGeneSets

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Version and source information

Description

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Usage

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Examples

BioMartGOGeneSets

changeSeqnameStyle

Change sequence names

Description

Change sequence names

Usage

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

**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 `getBioMartGenomeInfo(dataset)`. 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**

```r
## Not run:
gr = getBioMartGenes("giant panda")
changeSeqnameStyle(gr, "giant panda", "Sequence-Name", "GenBank-Accn")
## End(Not run)
```

---

**Description**

Get GO gene sets

**Usage**

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

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)

getBioMartGenes Get genes from BioMart

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 true, it uses GenomeInfoDb::seqlevelsStyle(gr) = "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"
print.BioMartGOGeneSets_info

Value

A GRanges object.

Examples

```r
gr <- getBioMartGenes("hsapiens_gene_ensembl")
gr <- getBioMartGenes("hsapiens_gene_ensembl", add_chr_prefix = TRUE)
gr
```

getBioMartGenomeInfo Get genome information

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

```r
geneInfo <- getBioMartGenomeInfo(9606)
```

print.BioMartGOGeneSets_info Print the BioMartGOGeneSets object

Description

Print the BioMartGOGeneSets object.

Usage

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

Arguments

x A BioMartGOGeneSets_info object.

... Other arguments

Value

No value is returned.

Examples

BioMartGOGeneSets

<table>
<thead>
<tr>
<th>supportedOrganisms</th>
<th>All supported organisms</th>
</tr>
</thead>
</table>

Description

All supported organisms

Usage

supportedOrganisms(html = TRUE)

Arguments

html Whether to open the table in the web browser?

Value

A data frame of supported organisms.

Examples

if(interactive()) {
  supportedOrganisms()
}
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