BioMartGOGeneSets

November 11, 2026

`BioMartGOGeneSets` *Version and source information*

Description

Version and source information

Usage

```
BioMartGOGeneSets
```

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)
```

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

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

## End(Not run)
```

---

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)
```

---

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 ture, it uses GenomeInfoDb::seqlevelsStyle = "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` *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

```
getBioMartGenomeInfo(9606)
```

`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 *All supported organisms*

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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