BioMartGOGeneSets

May 27, 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::seqlevelsSt` `= "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()
}
```

Index