BioMartGOGeneSets

May 1, 2024

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BioMartGOGeneSets  
Version and source information

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Description

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Usage

BioMartGOGeneSets

Examples

BioMartGOGeneSets

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changeSeqnameStyle  
Change sequence names

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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 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)
```

getBioMartGOGeneSets

Get GO gene sets

Description

Get GO gene sets

Usage

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](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**

```r
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl")
tt = 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**

```r
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:

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

A `GRanges` object.

Examples

```r
g = getBioMartGenes("hsapiens_gene_ensembl")
g
```

```r
g = getBioMartGenes("hsapiens_gene_ensembl", add_chr_prefix = TRUE)
g
```

---

**getBioMartGenomeInfo**  
*Get genome information*

Description

Get genome information

Usage

```r
getBioMartGenomeInfo(dataset)
```

Arguments

- `dataset`  
  A BioMart dataset or a taxon ID. For a proper value, please see `supportedOrganisms`.

Value

A list.

Examples

```r
g = 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

| 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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