BioMartGOGeneSets
January 31, 2024

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**BioMartGOGeneSets**

**Description**

Version and source information

**Usage**

BioMartGOGeneSets

**Examples**

BioMartGOGeneSets

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**changeSeqnameStyle**

*Change sequence names*

**Description**

Change sequence names

**Usage**

```r
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 \texttt{c("Sequence-Name", "GenBank-Accn", "RefSeq-Accn")}. If you are not sure which seqname style is in \texttt{gr}, use `getBioMartGenomeInfo` to obtain list of examples.
- **seqname_style_to**: Value should be in \texttt{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 \texttt{GRanges} object.

Examples

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

getBioMartGOGeneSets  \hspace{1cm} 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")
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl", gene_id_type = "entrez")
tb = getBioMartGOGeneSets("hsapiens_gene_ensembl", as_table = TRUE)
```

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 ture, 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 \texttt{GRanges} object.

Examples

\begin{verbatim}
gr = getBioMartGenes("hsapiens_gene_ensembl")
gr
gr = getBioMartGenes("hsapiens_gene_ensembl", add_chr_prefix = TRUE)
gr
\end{verbatim}

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\textbf{getBioMartGenomeInfo} \hspace{1cm} \textit{Get genome information}

Description

Get genome information

Usage

\begin{verbatim}
getBioMartGenomeInfo(dataset)
\end{verbatim}

Arguments

dataset \hspace{1cm} A BioMart dataset or a taxon ID. For a proper value, please see \texttt{supportedOrganisms}.

Value

A list.

Examples

\begin{verbatim}
getBioMartGenomeInfo(9606)
\end{verbatim}

---

\textbf{print.BioMartGOGeneSets_info} \hspace{1cm} \textit{Print the BioMartGOGeneSets object}

Description

Print the BioMartGOGeneSets object

Usage

\begin{verbatim}
## S3 method for class 'BioMartGOGeneSets_info'
print(x, ...)
\end{verbatim}
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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