Package ‘seq2pathway.data’

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Type Package
Title data set for R package seq2pathway
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Depends R (>= 2.10.0)
bioCViews ExperimentData
Description Supporting data for the seq2pathway package. Includes modified gene sets from MsigDB and org.Hs.eg.db; gene locus definitions from GENCODE project.
License GPL (>= 2)
NeedsCompilation no

R topics documented:

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```
dat_gene2path_chip

demo result of gene2pathway function from chip seq data

Description
demo result of gene2pathway function from chip seq data

Usage
data("dat_gene2path_chip")

Format
A list with 2 elements.
gene2pathway_result.2 a list of gene2pathway test result, with 3 data frames (3 GO terms)
gene2pathway_result.FET a list of fisher’s test result, with 3 data frames (3 GO terms)

Value
A list, with two sub lists. The name of one sub list is "gene2pathway_result.2", with 3 data frames of GO_BP, GO_MF, and GO_CC, another is "gene2pathway_result.FET", with 3 data frames of GO_BP, GO_MF, and GO_CC.

dat_gene2path_RNA
demo result of gene2pathway function from RNA seq data

Description
demo result of gene2pathway function from RNA seq data

Usage
data("dat_gene2path_RNA")

Format
A list with 2 elements.
gene2pathway_result.2 a data frame of gene2pathway test result
gene2pathway_result.FET a data frame of fisher’s test result

Value
A list, with two elements. one element is a data frame about "gene2pathway_result.2"", another data frame is about "gene2pathway_result.FET".
dat_seq2pathway_GOterms

demo result of seq2pathway function from chip seq data

Description
demo result of seq2pathway function from chip seq data

Usage
data("dat_seq2pathway_GOterms")

Format
A list with 3 elements.

seq2gene_result  a list with 2 annotation table
gene2pathway_result.FAIME  a list of gene2pathway test result, with 3 data frames(3 GO terms)
gene2pathway_result.FET  a list of fisher's test result, with 3 data frames(3 GO terms)

Value
A list, with three sub lists. The name of first sub list is seq2gene_result, with 2 data frames of full
and coding gene annotation respectively, the name of second sub list is "gene2pathway_result.FAIME",
with 3 data frames of GO_BP, GO_MF, and GO_CC, the third is "gene2pathway_result.FET", with
3 data frames of GO_BP, GO_MF, and GO_CC.

dat_seq2pathway_Msig  demo result of seq2pathway function from chip seq data

Description
demo result of seq2pathway function from chip seq data

Usage
data("dat_seq2pathway_Msig")

Format
A list with 3 elements.

seq2gene_result  a list with 2 annotation table
gene2pathway_result.FAIME  a data frame of gene2pathway test result by MsigDB C5 terms
gene2pathway_result.FET  a data frame of fisher's test resulby MsigDB C5 terms

Value
A list, with three elements. The name of first element is seq2gene_result, with 2 data frames of full
and coding gene annotation respectively, the second element is a data frame of "gene2pathway_result.FAIME",
the third is a data frame of "gene2pathway_result.FET".
Des_BP_list

**Description**

Description of GO term BP

**Usage**

```
data("Des_BP_list")
```

**Format**

A list, list names are Go term BP’s IDs, list elements are GO term BP’s description respectively.

**Value**

A list, list names are Go term BP’s IDs, list elements are GO term BP’s description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(Des_BP_list)
head(names(Des_BP_list))
head(Des_BP_list)
```

Des_CC_list

**Description**

Description of GO term CC

**Usage**

```
data("Des_CC_list")
```

**Format**

A list, list names are Go term CC’s IDs, list elements are GO term CC’s description respectively.

**Value**

A list, list names are Go term CC’s IDs, list elements are GO term CC’s description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.
Des_MF_list

**Examples**

```r
data(Des_CC_list)
head(names(Des_CC_list))
head(Des_CC_list)
```

<table>
<thead>
<tr>
<th>Des_MF_list</th>
<th>Description of GO term MF</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Description of GO term MF</td>
</tr>
</tbody>
</table>

**Description**

Description of GO term MF

**Usage**

```r
data("Des_MF_list")
```

**Format**

A list, list names are Go term MF’s IDs, list elements are GO term MF’s description respectively.

**Value**

A list, list names are Go term MF’s IDs, list elements are GO term MF’s description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```r
data(Des_MF_list)
head(names(Des_MF_list))
head(Des_MF_list)
```

<table>
<thead>
<tr>
<th>gencode_coding</th>
<th>Coding gene list in GENCODE 20.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Coding gene list in GENCODE 20.</td>
</tr>
</tbody>
</table>

**Description**

Coding gene list in GENCODE 20.

**Usage**

```r
data("gencode_coding")
```

**Format**

A vector including all coding gene symbols in GENCODE version20.
**Value**

A character vector including all coding gene symbols in GENCODE version20.

**Source**

GENCODE 20

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```r
data(gencode_coding)
head(gencode_coding)
```

---

<table>
<thead>
<tr>
<th>gene_description</th>
<th>demo data of adding gene description</th>
</tr>
</thead>
</table>

**Description**

demo data of adding gene description

**Usage**

```r
data("gene_description")
```

**Format**

A data frame with 561 observations on the following 2 variables.

- `hgnc_symbol` a characteristic vector
- `description` a characteristic vector

**Value**

A characteristic matrix of gene symbols and descriptions.
\textbf{GO\_BP\_list} \hspace{1cm} \textit{Gene symbol list of GO term BP}

\begin{itemize}
\item \textbf{Description} \\
\hspace{1cm} Gene symbol list of GO term BP
\item \textbf{Usage} \\
\hspace{1cm} \texttt{data("GO\_BP\_list")}
\item \textbf{Format} \\
\hspace{1cm} A list, list names are Go term BP’s IDs, list elements are gene symbols in GO term BP.
\item \textbf{Value} \\
\hspace{1cm} A list, list names are Go term BP’s IDs, list elements are gene symbols in GO term BP.
\item \textbf{Source} \\
\hspace{1cm} Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.
\item \textbf{Examples} \\
\hspace{1cm} \texttt{data(GO\_BP\_list)} \\
\hspace{1cm} \texttt{head(GO\_BP\_list)}
\end{itemize}

\textbf{GO\_CC\_list} \hspace{1cm} \textit{Gene symbol list of GO term CC}

\begin{itemize}
\item \textbf{Description} \\
\hspace{1cm} Gene symbol list of GO term CC
\item \textbf{Usage} \\
\hspace{1cm} \texttt{data("GO\_CC\_list")}
\item \textbf{Format} \\
\hspace{1cm} A list, list names are Go term CC’s IDs, list elements are gene symbols in GO term CC.
\item \textbf{Value} \\
\hspace{1cm} A list, list names are Go term CC’s IDs, list elements are gene symbols in GO term CC.
\item \textbf{Source} \\
\hspace{1cm} Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.
\end{itemize}
Examples

data(GO_CC_list)
head(GO_CC_list)

GO_GENCODE_df_hg_v19  intersection genes of GO terms and GENCODE 19

Description

intersection genes of GO terms and GENCODE 19

Usage

data("GO_GENCODE_df_hg_v19")

Format

A data frame.

Value

A data frame.

Source

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

References

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

Examples

data(GO_GENCODE_df_hg_v19)
head(GO_GENCODE_df_hg_v19)
**GO_GENCODE_df_hg_v20**  
**intersection genes of GO terms and GENCODE 20**

**Description**

intersection genes of GO terms and GENCODE 20

**Usage**

data("GO_GENCODE_df_hg_v20")

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

data(GO_GENCODE_df_hg_v20)  
head(GO_GENCODE_df_hg_v20)

---

**GO_GENCODE_df_mm_vM1**  
**intersection genes of GO terms and GENCODE vM1**

**Description**

intersection genes of GO terms and GENCODE vM1

**Usage**

data("GO_GENCODE_df_mm_vM1")

**Format**

A data frame.

**Value**

A data frame.
GO_GENCODE_df_mm_vM3

Source

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

References

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

Examples

```r
data(GO_GENCODE_df_mm_vM1)
head(GO_GENCODE_df_mm_vM1)
```

Description

intersection genes of GO terms and GENCODE vM3

Usage

```r
data("GO_GENCODE_df_mm_vM3")
```

Format

A data frame.

Value

A data frame.

Source

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

References

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

Examples

```r
data(GO_GENCODE_df_mm_vM3)
head(GO_GENCODE_df_mm_vM3)
```
**GO_GENCODE_df_mm_vM4**

**Description**

intersection genes of GO terms and GENCODE vM4 simply by gene symbol match

**Usage**

```r
data("GO_GENCODE_df_mm_vM4")
```

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```r
data(GO_GENCODE_df_mm_vM4)
head(GO_GENCODE_df_mm_vM4)
```

---

**GO_MF_list**

Gene symbol list of GO term MF

**Description**

Gene symbol list of GO term MF

**Usage**

```r
data("GO_MF_list")
```

**Format**

A list, list names are Go term MF’s IDs, list elements are gene symbols in GO term MF.

**Value**

A list, list names are Go term MF’s IDs, list elements are gene symbols in GO term MF.
**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```r
data(GO_MF_list)
head(GO_MF_list)
```

---

**MsigDB_C5**

*MsigDB data set*

**Description**

_.gsa format data_

**Usage**

```r
data("MsigDB_C5")
```

**Format**

A list with 3 sub lists.
- `genesets` a list of gene names
- `geneset.names` a list of geneset names
- `geneset.descriptions` a list of geneset descriptions

**Value**

A "GSA.genesets" object from GSA package.

---

**Msig_GENCODE_df_hg_v19**

*intersection genes of MSigDB collection and GENCODE 19*

**Description**

intersection genes of MSigDB collection and GENCODE 19

**Usage**

```r
data("Msig_GENCODE_df_hg_v19")
```

**Format**

A data frame.
Value

A data frame.

References


Examples

data(Msig_GENCODE_df_hg_v19)
head(Msig_GENCODE_df_hg_v19)

---

**Msig_GENCODE_df_hg_v20**

*intersection genes of MSigDB collection and GENCODE 20*

Description

intersection genes of MSigDB collection and GENCODE 20

Usage

data("Msig_GENCODE_df_hg_v20")

Format

A data frame.

Value

A data frame.

References


Examples

data(Msig_GENCODE_df_hg_v20)
head(Msig_GENCODE_df_hg_v20)
Msig_GENCODE_df_mm_vM1

Description
intersection genes of MSigDB collection and GENCODE vM1

Usage
data("Msig_GENCODE_df_mm_vM1")

Format
A data frame.

Value
A data frame.

References

Examples
data(Msig_GENCODE_df_mm_vM1)
head(Msig_GENCODE_df_mm_vM1)

Msig_GENCODE_df_mm_vM3

Description
intersection genes of MSigDB collection and GENCODE vM3

Usage
data("Msig_GENCODE_df_mm_vM3")

Format
A data frame.

Value
A data frame.
References


Examples

data(Msig_GENCODE_df_mm_vM3)
head(Msig_GENCODE_df_mm_vM3)

---

**Msig_GENCODE_df_mm_vM4**

*intersection genes of MSigDB collection and GENCODE vM4*

Description

intersection genes of MSigDB collection and GENCODE vM4 simply by gene symbol match

Usage

data("Msig_GENCODE_df_mm_vM4")

Format

A data frame.

Value

A data frame.

References


Examples

data(Msig_GENCODE_df_mm_vM4)
head(Msig_GENCODE_df_mm_vM4)
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