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:

dat_gene2path_chip .......................................................... 2
dat_gene2path_RNA ......................................................... 2
dat_seq2pathway.GOterms ................................................. 3
dat_seq2pathway.Msig ..................................................... 3
Des_BP_list ................................................................. 4
Des_CC_list ................................................................. 4
Des_MF_list ................................................................. 5
gencode_coding ............................................................. 5
gene_description ........................................................... 6
GO_BP_list ................................................................. 7
GO_CC_list ................................................................. 7
GO_GENCODE_df_hg_v19 ................................................... 8
GO_GENCODE_df_hg_v20 ................................................... 9
GO_GENCODE_df_mm_vM1 .................................................. 9
GO_GENCODE_df_mm_vM3 .................................................. 10
GO_GENCODE_df_mm_vM4 .................................................. 11
GO_MF_list ................................................................. 11
MsigDB.C5 ................................................................. 12
Msig_GENCODE_df_hg_v19 ............................................... 12
Msig_GENCODE_df_hg_v20 ............................................... 13
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.

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 tables
- 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 tables
- gene2pathway_result.FAIME: a data frame of gene2pathway test result by MsigDB C5 terms
- gene2pathway_result.FET: a data frame of fisher’s test result by 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 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 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)
```

---

### Des_MF_list

**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)
```

---

**gencode_coding**

**Coding gene list in GENCODE 20.**

**Description**

Coding gene list in GENCODE 20.

**Usage**

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

**Format**

A vector including all coding gene symbols in GENCODE version 20.
**gene_description**

**Value**

A character vector including all coding gene symbols in GENCODE version 20.

**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.
### GO_BP_list

**Description**

Gene symbol list of GO term BP

**Usage**

```r
data("GO_BP_list")
```

**Format**

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

**Value**

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

**Source**

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

**Examples**

```r
data(GO_BP_list)
head(GO_BP_list)
```

### GO_CC_list

**Description**

Gene symbol list of GO term CC

**Usage**

```r
data("GO_CC_list")
```

**Format**

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

**Value**

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

**Source**

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

```r
data(GO_CC_list)
head(GO_CC_list)
```

---

**Description**

intersection genes of GO terms and GENCODE 19

**Usage**

```r
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**

```r
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.
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_mm_vM1)
head(GO_GENCODE_df_mm_vM1)

---

GO_GENCODE_df_mm_vM3 intersection genes of GO terms and GENCODE vM3

Description
intersection genes of GO terms and GENCODE vM3

Usage
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
data(GO_GENCODE_df_mm_vM3)
head(GO_GENCODE_df_mm_vM3)
**GO_GENCODE_df_mm_vM4**

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

**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

data(GO_MF_list)
head(GO_MF_list)

MsigDB_C5

MsigDB data set

Description

.gsa format data

Usage

data("MsigDB_C5")

Format

A list with 3 sub lists.

genesets a list of gene names
geneseet.names a list of geneset names
geneseet.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

data("Msig_GENCODE_df_hg_v19")

Format

A data frame.
Value

A data frame.

References


Examples

data(Msig_GENCODE_df_hg_v20)
head(Msig_GENCODE_df_hg_v20)

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)
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)

Description

intersection genes of MSigDB collection and GENCODE vM3

Usage

data("Msig_GENCODE_df_mm_vM3")

Format

A data frame.

Value

A data frame.
Msig_GENCODE_df_mm_vM4

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)
Index

Topic datasets

dat_gene2path_chip, 2
dat_gene2path_RNA, 2
dat_seq2pathway_GOterms, 3
dat_seq2pathway_Msig, 3
Des_BP_list, 4
Des_CC_list, 4
Des_MF_list, 5
gencode_coding, 5
gene_description, 6
GO_BP_list, 7
GO_CC_list, 7
GO_GENCODE_df_hg_v19, 8
GO_GENCODE_df_hg_v20, 9
GO_GENCODE_df_mm_vM1, 9
GO_GENCODE_df_mm_vM3, 10
GO_GENCODE_df_mm_vM4, 11
GO_MF_list, 11
Msig_GENCODE_df_hg_v19, 12
Msig_GENCODE_df_hg_v20, 13
Msig_GENCODE_df_mm_vM1, 14
Msig_GENCODE_df_mm_vM3, 14
Msig_GENCODE_df_mm_vM4, 15
MsigDB_C5, 12

Msig_GENCODE_df_hg_v19, 12
Msig_GENCODE_df_hg_v20, 13
Msig_GENCODE_df_mm_vM1, 14
Msig_GENCODE_df_mm_vM3, 14
Msig_GENCODE_df_mm_vM4, 15
MsigDB_C5, 12

dat_gene2path_chip, 2
dat_gene2path_RNA, 2
dat_seq2pathway_GOterms, 3
dat_seq2pathway_Msig, 3
Des_BP_list, 4
Des_CC_list, 4
Des_MF_list, 5
gencode_coding, 5
gene_description, 6
GO_BP_list, 7
GO_CC_list, 7
GO_GENCODE_df_hg_v19, 8
GO_GENCODE_df_hg_v20, 9
GO_GENCODE_df_mm_vM1, 9
GO_GENCODE_df_mm_vM3, 10
GO_GENCODE_df_mm_vM4, 11
GO_MF_list, 11

Msig_GENCODE_df_hg_v19, 12
Msig_GENCODE_df_hg_v20, 13
Msig_GENCODE_df_mm_vM1, 14
Msig_GENCODE_df_mm_vM3, 14
Msig_GENCODE_df_mm_vM4, 15
MsigDB_C5, 12

16