

# Package ‘EGSEAdata’

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**Title** Gene set collections for the EGSEA package

**Version** 1.41.0

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**Description** This package includes gene set collections that are used for the Ensemble of Gene Set Enrichment Analyses (EGSEA) method for gene set testing. It includes Human and Mouse versions of the MSidDB (Subramanian, et al. (2005) PNAS, 102(43):15545-15550) and GeneSetDB (Araki, et al. (2012) FEBS Open Bio, 2:76-82) collections.

**biocViews** ExperimentData, Homo\_sapiens\_Data, Mus\_musculus\_Data, Rattus\_norvegicus\_Data

**Depends** R (>= 3.4)

**License** file LICENSE

**LazyLoad** yes

**NeedsCompilation** no

**Suggests** EGSEA

**RoxygenNote** 5.0.1

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|                   |   |
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| EGSEAdata-package | <i>Gene Set Collections for the EGSEA package</i> |
|-------------------|---|

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### Description

This package includes gene set collections that are used for the Ensemble of Gene Set Enrichment Analyses (EGSEA) method for gene set testing. It includes Human and Mouse versions of the MSidDB (Subramanian, et al. (2005) PNAS, 102(43):15545-15550) and GeneSetDB (Araki, et al. (2012) FEBS Open Bio, 2:76-82) collections.

### Details

While the gene set collections in MSigDB and GeneSetDB have different names and purposes, some of these collections overlap. For example, both databases contain a Gene Ontology collection but MSigDB's collection aimed for a higher level of abstraction for the GO terms.

### Author(s)

Monther Alhamdoosh, Yifang Hu and Gordon K. Smyth

### References

Monther Alhamdoosh, Milica Ng, Nicholas J. Wilson, Julie M. Sheridan, Huy Huynh, Michael J. Wilson, Matthew E. Ritchie; Combining multiple tools outperforms individual methods in gene set enrichment analyses. *Bioinformatics* 2017; 33 (3): 414-424. doi: 10.1093/bioinformatics/btw623

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|------------|--|
| egsea.data | <i>EGSEAdata databases information</i> |
|------------|--|

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### Description

It displays information about the available gene set collections in EGSEAdata for a species.

### Usage

```
egsea.data(species = "human", simple = FALSE, returnInfo = FALSE)
```

**Arguments**

|            |   |
|------------|---|
| species    | character, a species name and used to retrieve the number of gene sets for that particular species. Default is "human". Accepted values are "human", "homo sapiens", "hs", "mouse", "mus musculus", "mm", "rat", "rattus norvegicus" or "rn". |
| simple     | logical, whether to display the number of gene sets in each collection or not.  |
| returnInfo | logical, whether to print out the databases information or return it as a list.   |

**Details**

It prints out for each database: the database name, version, update/download date, data source, supported species, gene set collections, the names of the related R data objects and the number of gene sets in each collection.

**Value**

nothing.

**Examples**

```
# Example of egsea.data
egsea.data()
```

---

gsetdb.human

*GeneSetDB Human Collections*

---

**Description**

Human gene set collections from the GeneSetDB

**Format**

list

**Details**

Procedure

1. The Human GMT file was downloaded from the website.
2. The gene set sources and categories were manually compiled from the Help page.
3. An R list was created for the gene set categories.
4. An annotation data frame was created for the gene sets.
5. An R data object was written using save().

**Source**

Araki Hiromitsu, Knapp Christoph, Tsai Peter and Print Cristin (2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003 Downloaded from <http://www.genesetdb.auckland.ac.nz/>

**See Also**

Invoke egsea.data() to find out the current version and latest download/update date.

---

gsetdb.mouse

*GeneSetDB Mouse Collections*

---

### **Description**

Mouse gene set collections from the GeneSetDB

### **Format**

list

### **Details**

Procedure

1. The Mouse GMT file was downloaded from the website.
2. The gene set sources and categories were manually compiled from the Help page.
3. An R list was created for the gene set categories.
4. An annotation data frame was created for the gene sets.
5. An R data object was written using save().

### **Source**

Araki Hiromitsu, Knapp Christoph, Tsai Peter and Print Cristin (2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003 Downloaded from <http://www.genesetdb.auckland.ac.nz/>

### **See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

gsetdb.rat

*GeneSetDB Rat Collections*

---

### **Description**

Rat gene set collections from the GeneSetDB

### **Format**

list

### **Details**

Procedure

1. The Rat GMT file was downloaded from the website.
2. The gene set sources and categories were manually compiled from the Help page.
3. An R list was created for the gene set categories.
4. An annotation data frame was created for the gene sets.
5. An R data object was written using save().

**Source**

Araki Hiromitsu, Knapp Christoph, Tsai Peter and Print Cristin (2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003 Downloaded from <http://www.genesetdb.auckland.ac.nz/>

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

`il13.data`*Human IL-13 dataset*

---

**Description**

The voom object calculated from the TMM normalized count matrix of RNA-seq performed on samples of human normal PBMCs, IL-13 stimulated PBMCs and IL-13R antagonist PBMCs. It also contains the contrast matrix of this experiment.

**Format**

A List object with two components: voom and contra.

**Source**

The count matrix of this experiment is available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE79027.

---

`il13.data.cnt`*Human IL-13 dataset - Raw Counts*

---

**Description**

It contains the raw count matrix of RNA-seq performed on samples of human normal PBMCs, IL-13 stimulated PBMCs and IL-13R antagonist PBMCs. It also contains the contrast and design matrices of this experiment. The gene symbols mapping is also included.

**Format**

A List object with five components: counts, group, design, contra and genes.

**Source**

The FASTQ files of this experiment are available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE79027.

---

`il13.gsa`*EGSEA analysis results on the human IL-13 dataset*

---

**Description**

EGSEA analysis was performed on the `il13.data` from the `EGSEAdata` package using the KEGG pathways, `c2` and `c5` gene set collections. Type `show(il13.gsa)` to see the version of datasets/packages that were used.

**Format**

An object of class `EGSEAResults`

**Source**

The dataset of this analysis is available in the `EGSEAdata` package.

---

`kegg.pathways`*KEGG Pathways Collections*

---

**Description**

Human, Mouse and Rat gene set collections from the KEGG database

**Format**

list

**Details**

The collections were generated using the following R script

```
library(gage)
kegg.pathways = list()
species.all = c("human", "mouse", "rat")
for (species in species.all)
  kegg = kegg.gsets(species = species, id.type = "kegg")
kegg.pathways[[species]] = kegg
```

```
save(kegg.pathways, file='kegg.pathways.rda')
```

**Source**

Luo, W., Friedman, M., Shedden K., Hankenson, K. and Woolf, P GAGE: Generally Applicable Gene Set Enrichment for Pathways Analysis. *BMC Bioinformatics* 2009, 10:161 Obtained from **gage** using the function `kegg.gsets()`

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

|          |                                   |
|----------|-----------------------------------|
| mam.data | <i>Mouse mammary cell dataset</i> |
|----------|-----------------------------------|

---

**Description**

The voom object calculated from TMM normalized count matrix of RNA-seq performed on samples of the epithelial cells of the mouse mammary glands from three populations: basal, luminal progenitor and mature luminal. It also contains the contrast matrix of this experiment.

**Format**

A List object with two components: voom and contra.

**Source**

The count matrix of this experiment is available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE63310.

---

|       |   |
|-------|---|
| Mm.c2 | <i>Mouse C2 MSigDB Gene Set Collections</i> |
|-------|---|

---

**Description**

Mouse orthologs gene set collections from the MSigDB database

**Format**

list

**Details**

Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using save().

**Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke egsea.data() to find out the current version and latest download/update date.

---

Mm.c3

*Mouse C3 MSigDB Gene Set Collections*

---

### **Description**

Mouse orthologs gene set collections from the MSigDB database

### **Format**

list

### **Details**

#### Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using save().

### **Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

### **See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

Mm.c4

*Mouse C4 MSigDB Gene Set Collections*

---

### **Description**

Mouse orthologs gene set collections from the MSigDB database

### **Format**

list

### **Details**

#### Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using save().

**Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/> Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

Mm.c5

*Mouse C5 MSigDB Gene Set Collections*

---

**Description**

Mouse orthologs gene set collections from the MSigDB database

**Format**

list

**Details**

Procedure

1. The current `msigdb_vx.xml` file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using `save()`.

**Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

Mm.c6

*Mouse C6 MSigDB Gene Set Collections*

---

### **Description**

Mouse orthologs gene set collections from the MSigDB database

### **Format**

list

### **Details**

Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using save().

### **Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

### **See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

Mm.c7

*Mouse C7 MSigDB Gene Set Collections*

---

### **Description**

Mouse orthologs gene set collections from the MSigDB database

### **Format**

list

### **Details**

Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using save().

**Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

Mm.H

*Mouse H MSigDB Gene Set Collections*

---

**Description**

Mouse orthologs gene set collections from the MSigDB database

**Format**

list

**Details**

Procedure

1. The current `msigdb_vx.xml` file was downloaded.
2. Human Entrez Gene IDs were mapped to Mouse Entrez Gene IDs, using the HGNC Comparison of Orthology Predictions (HCOP).
3. The collection was converted to a list in R, and written to a RData file using `save()`.

**Source**

Downloaded from <http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke `egsea.data()` to find out the current version and latest download/update date.

---

msigdb

*MSigDB Gene Set Collections*

---

**Description**

Gene set collections from the MSigDB database

**Format**

list

**Details**

Procedure

1. The current msigdb\_vx.xml file was downloaded.
2. It was parsed using xmlParse() and then converted to list using xmlToList() 3. The resulting list was written to an RData file using save().

This dataset is mainly used to extract MSigDB gene set annotation and the human gene set collections.

**Source**

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

**See Also**

Invoke egsea.data() to find out the current version and latest download/update date.

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