

# Package ‘exploreSE’

September 3, 2026

**Title** Explorer for Your Bulk RNA Seq Analyses

**Version** 0.99.6

**Description** Interactive exploration of a Summarized experiment and associated DE analyses. A shiny app to inspect and interact with pre-calculated differential expression and functional enrichment results, and to facilitate comparisons between multiple models. This is meant to be a tool for exploration and discussion, rather than analysis.

**License** MIT + file LICENSE

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**Depends** R (>= 4.6.0)

**Imports** BiocGenerics, clusterProfiler, colourpicker, DeeDeeExperiment, DESeq2, dplyr, DT, forcats, ggplot2, htmltools, magrittr, matrixStats, methods, msigdb, org.Hs.eg.db, org.Mm.eg.db, plotly, purrr, readr, rlang, S4Vectors, shiny, shinyWidgets, stats, stringr, SummarizedExperiment, tibble, tidyr, tidyselect

**Suggests** airway, BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

**URL** <https://github.com/jaspitzer/exploreSE>

**BugReports** <https://github.com/jaspitzer/exploreSE/issues>

**biocViews** ShinyApps, RNASeq, Visualization, GeneExpression, Pathways, GO

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|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| exploreSE-package | <i>exploreSE: Explorer for Your Bulk RNA Seq Analyses</i> |
|-------------------|-----------------------------------------------------------|

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Description

Interactive exploration of a Summarized experiment and associated DE analyses. A shiny app to inspect and interact with pre-calculated differential expression and functional enrichment results, and to facilitate comparisons between multiple models. This is meant to be a tool for exploration and discussion, rather than analysis.

Author(s)

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See Also

Useful links:

- <https://github.com/jaspitzer/exploreSE>
- Report bugs at <https://github.com/jaspitzer/exploreSE/issues>

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|          |                                         |
|----------|-----------------------------------------|
| baseline | <i>DE results for airway - baseline</i> |
|----------|-----------------------------------------|

---

**Description**

Example DE results for airway data set

**Format**

A DESeqResults

**Details**

This is a DESeqResults object, with the simplest model, using ~dex as the design. Data is from the airway package, DE results are generated with DESeq2.

**Value**

A DESeqResults

---

|                  |                                                      |
|------------------|------------------------------------------------------|
| baseline_down_go | <i>Example GO enrichments for the baseline model</i> |
|------------------|------------------------------------------------------|

---

**Description**

GO enrichments based on the baseline DE results

**Format**

A EnrichResults

**Details**

GO enrichments are generated with clusterProfiler, filtered on down-regulated genes only; genes that underwent DE testing were taken as the universe.

The code to create said object can be found in the folder /inst/scripts in the exploreSE package, the file is called creating\_dataset\_examples.R.

**Value**

A EnrichResults object

---

`baseline_up_go`*Example GO enrichments for the baseline model*

---

**Description**

GO enrichments based on the baseline DE results

**Format**

A `EnrichResults`

**Details**

GO enrichments are generated with `clusterProfiler`, filtered on up-regulated genes only; genes that underwent DE testing were taken as the universe.

The code to create said object can be found in the folder `/inst/scripts` in the `exploreSE` package, the file is called `creating_dataset_examples.R`.

**Value**

A `EnrichResults` object

---

`cell_controlled`*DE results for airway - cell-controlled*

---

**Description**

Example DE results for airway data set

**Format**

A `DESeqResults`

**Details**

This is a `DESeqResults` object, using `~ cell + dex` as the design. Data is from the `airway` package, DE results are generated with `DESeq2`, using the `dex untrt vs trt` contrast

**Value**

A `DESeqResults`

---

|                    |                                                             |
|--------------------|-------------------------------------------------------------|
| controlled_down_go | <i>Example GO enrichments for the cell_controlled model</i> |
|--------------------|-------------------------------------------------------------|

---

**Description**

GO enrichments based on the cell\_controlled DE results

**Format**

A EnrichResults

**Details**

GO enrichments are generated with clusterProfiler, filtered on down-regulated genes only; genes that underwent DE testing were taken as the universe.

The code to create said object can be found in the folder /inst/scripts in the exploreSE package, the file is called creating\_dataset\_examples.R.

**Value**

A EnrichResults object

---

|                  |                                                             |
|------------------|-------------------------------------------------------------|
| controlled_up_go | <i>Example GO enrichments for the cell controlled model</i> |
|------------------|-------------------------------------------------------------|

---

**Description**

GO enrichments based on the cell\_controlled DE results

**Format**

A EnrichResults

**Details**

GO enrichments are generated with clusterProfiler, filtered on up-regulated genes only; genes that underwent DE testing were taken as the universe.

The code to create said object can be found in the folder /inst/scripts in the exploreSE package, the file is called creating\_dataset\_examples.R.

**Value**

A EnrichResults object

---

 exploreSE

*exploreSE*


---

### Description

This runs the explorer app. You can add a path to a .rds file or a the relevant R object as an argument to load it on start-up. The app looks for DE results in the metadata of the `metadata(object)$de_results` and, if it is a `DeeDeeExperiment`, in the DEA slots of the object. Similarly, the enrichment results are looked for in the `metadata(object)$fe_results` or FEA slots (`DeeDeeExperiment`). As the `DeeDeeExperiment` structure does a lot of work to clean and standardize the inputs and outputs for both DE and enrichment results, using it is highly recommended.

### Usage

```
exploreSE(file = NULL, object = NULL)
```

### Arguments

|                     |                                                                                           |
|---------------------|-------------------------------------------------------------------------------------------|
| <code>file</code>   | a string leading to a file you want loaded as a default                                   |
| <code>object</code> | a <code>summarizedExperiment</code> object (or <code>DeeDeeExperiment</code> ) to load in |

### Value

an application

### Examples

```
app <- exploreSE()
if(interactive()){
  shiny::runApp(app, port = 1234)
}
```

---

 get.gos

*Calculate GO Enrichments for a given comparison*


---

### Description

A function to calculate GO term enrichments from a given `summarizedExperiment` or `DeeDeeExperiment`. By default, it calculates separate enrichments for up- downregulated genes, at the cutoffs of  $|\log\text{FC}| > 1$  and adjusted p- value  $< 0.05$ . It utilises the `clusterProfiler::enrichGO()` function.

### Usage

```
get.gos(NAME, obj, species = "hs", gene_type = "SYMBOL")
```

**Arguments**

|           |                                                      |
|-----------|------------------------------------------------------|
| NAME      | character, name of the DE comparison                 |
| obj       | DeeDeeExperiment or SummarizedExperiment, the object |
| species   | character, the species hs/mm                         |
| gene_type | character, the type of gene identifier               |

**Value**

a DeeDeeExperiment or SummarizedExperiment

**Examples**

```
library(airway)
library(DeeDeeExperiment)
data(airway)
data("baseline_de", package = "exploreSE")

se_with_de <- addDEA(DeeDeeExperiment(airway), baseline)
se_with_go <- get.gos(obj = se_with_de,
                      NAME = "baseline",
                      gene_type = "ENSEMBL")
```

---

get.gsea

---

*Calculate GSEA Enrichments for a given comparison*


---

**Description**

Calculates the GSEA enrichments with the counts within a summarizedExperiment or DeeDeeExperiment and adds them in the respective slots. It follows the **original signal-to-noise ratio of the method**; other approaches for ranking of genes are available in other implementations, such as the `clusterProfiler::GSEA()` implementation which calls for logFC ranked genes.

**Usage**

```
get.gsea(
  NAME,
  obj,
  type = "HALLMARK",
  conditions,
  species = "hs",
  condition_var = "condition",
  gene_type = "SYMBOL"
)
```

**Arguments**

|      |                                                       |
|------|-------------------------------------------------------|
| NAME | character, name of the DE comparison                  |
| obj  | DeeDeeExperiment or SummarizedExperiment, the object  |
| type | character, the type of gene set, HALLMARK or REACTOME |

|               |                                                                                  |
|---------------|----------------------------------------------------------------------------------|
| conditions    | a vector of length 2, which levels of the condition variable are being compared, |
| species       | character, supported values are "hs" and "mm"                                    |
| condition_var | symbol or character, the variable name for this comparison                       |
| gene_type     | character, the type of gene identifier                                           |

**Value**

a DeeDeeExperiment or SummarizedExperiment

**Examples**

```
library(airway)
library(DeeDeeExperiment)
data(airway)
data("baseline_de", package = "exploreSE")

se_with_de <- addDEA(DeeDeeExperiment(airway), baseline)
se_with_gsea <- get.gsea(NAME = "baseline",
  obj = se_with_de,
  type = "HALLMARK",
  condition_var = "dex",
  conditions = c("trt", "untrt"),
  gene_type = "ENSEMBL")
```

---

|     |                      |
|-----|----------------------|
| %>% | <i>Pipe operator</i> |
|-----|----------------------|

---

**Description**

See `magrittr::%>%` for details.

**Usage**

lhs %>% rhs

**Arguments**

|     |                                               |
|-----|-----------------------------------------------|
| lhs | A value or the magrittr placeholder.          |
| rhs | A function call using the magrittr semantics. |

**Value**

The result of calling `rhs(lhs)`.

**Examples**

TRUE

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