

# Package ‘carnation’

February 26, 2026

**Title** Shiny App to Explore RNA-Seq Analysis

**Version** 0.99.8

**Description** Interactive Shiny dashboard app that can be used to explore RNA-Seq analysis results including differential expression (DE), functional enrichment and pattern analysis. Several visualizations are implemented to provide a wide-ranging view of data sets. For DE analysis, we provide PCA plot, MA plot, Upset plot & heatmaps, in addition to a highly customizable gene plot. Seven different visualizations are available for functional enrichment analysis, and we also support gene pattern analysis. In addition, the app provides a platform to manage multiple projects and user groups that can be run on a central server.

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**BugReports** <https://github.com/NICHD-BSPC/carnation/issues>

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| carnation-package | <i>carnation</i> |
|-------------------|------------------|

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**Description**

carnation is an interactive Shiny dashboard that makes complex bulk RNA-Seq data more accessible and intuitive, integrating all facets of bulk RNA-Seq analysis using three modules - differential expression analysis, functional enrichment and pattern analysis.

## Details

- Deeply explore analysis results from complex experiments using interactive plots.
- Easily keep track of genes of interest using the 'Gene scratchpad'.
- Use fuzzy search to filter and search functional enrichment results.
- Visualize complex patterns using highly customizable gene plot.
- Manage local data in single-user mode or deploy on a server to share with collaborators using in-built user management system.

Main function to run the app: `run_carnation()`

## Author(s)

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- Ryan Dale <ryan.dale@nih.gov> ([ORCID](#)) [funder]

## See Also

Useful links:

- <https://nichd-bspc.github.io/carnation/>
- Report bugs at <https://github.com/NICHD-BSPC/carnation/issues>

---

add.set.column

*Add set column to UpSet plot matrix*

---

## Description

This function adds a column denoting set number to a matrix generated for an upset plot with `fromList.with.names()`

## Usage

```
add.set.column(df)
```

## Arguments

`df` binary matrix where row = genes & columns are gene sets, with 1 indicating that a gene is present in that gene set and vice-versa

## Value

data.frame with added set column

**Examples**

```
# list of genes
lst <- list(group1 = c(a = "gene1", b = "gene2", c = "gene3", d = "gene4"),
            group2 = c(c = "gene3", d = "gene4"))

# binarized matrix with group membership
df <- fromList.with.names(lst)

# matrix with added set column
ldf <- add.set.column(df)
```

---

|              |  |
|--------------|--|
| add_metadata | <i>Add metadata to counts data frame</i> |
|--------------|--|

---

**Description**

Add metadata to counts data frame

**Usage**

```
add_metadata(df, coldata, exclude.intgroups)
```

**Arguments**

|                   |                             |
|-------------------|-----------------------------|
| df                | data.frame with gene counts |
| coldata           | data.frame with metadata    |
| exclude.intgroups | metadata columns to ignore  |

**Value**

counts data frame with added metadata

**Examples**

```
library(DESeq2)

# make example DESeq data set
dds <- makeExampleDESeqDataSet()

# extract counts and metadata
df <- assay(dds)
coldata <- colData(dds)

# get gene counts df
counts_df <- get_gene_counts(dds, paste0('gene', seq_len(10)))

# add metadata
```

```
counts_df <- add_metadata(counts_df, coldata, exclude.intgroups=NULL)
```

---

|             |                             |
|-------------|-----------------------------|
| alluvialmod | <i>Alluvial plot module</i> |
|-------------|-----------------------------|

---

## Description

UI & module to generate alluvial plots.

## Usage

```
alluvialUI(id, panel)
```

```
alluvialServer(id, obj, res_obj, config)
```

## Arguments

|         |   |
|---------|---|
| id      | Module id   |
| panel   | string, can be 'sidebar' or 'main'                |
| obj     | reactiveValues object containing GeneTonic object |
| res_obj | reactive, dataframe containing enrichment results |
| config  | reactive list with config settings                |

## Value

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

## Examples

```
library(shiny)

# get DESeqResults object
data(res_dex, package='carnation')

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object

gt <- GeneTonic::shake_enrichResult(eres_dex)

obj <- reactive({
  list(l_gs = gt$l_gs,
       anno_df = gt$anno_df,
       label = 'comp1')
})
```

```
res_obj <- reactive({ res })

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(alluvialUI('p', 'sidebar')),
      mainPanel(alluvialUI('p', 'main'))
    ),
    server = function(input, output, session){
      alluvialServer('p', obj, res_obj, config)
    }
  )
}
```

---

check\_user\_access

*Get data areas a user has access to*

---

## Description

This function takes a username and returns a list with two elements:

## Usage

```
check_user_access(al, u, admin = "admin")
```

## Arguments

|       |  |
|-------|--|
| al    | list with access settings; should have two elements - user_group & data_area |
| u     | user name  |
| admin | Admin user group   |

## Details

user\_group: one element vector data\_area: vector of data areas

## Value

list of user groups and data areas

## Examples

```
# save access details to file
home <- Sys.getenv('HOME')

# create carnation data area if it doesn't exist
carnation_home <- file.path(home, 'carnation/data')
if(!dir.exists(carnation_home)) dir.create(carnation_home)

create_access_yaml(user = 'admin',
                  user_group = 'admin',
                  data_area = carnation_home)

# get current user access details
al <- read_access_yaml()

lst <- check_user_access(al, u='admin')
```

---

cnetmod

*Cnetplot module*

---

## Description

UI & module to generate Cnetplots.

## Usage

```
cnetPlotUI(id, panel)

cnetPlotServer(id, obj, config)
```

## Arguments

|        |   |
|--------|---|
| id     | Module id   |
| panel  | string, can be 'sidebar' or 'main'                |
| obj    | reactive, dataframe containing enrichment results |
| config | reactive list with config settings                |

## Value

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

## Examples

```
library(shiny)

# get DESeqResults object
data(res_dex, package='carnation')

obj <- reactive({ res })

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(cnetPlotUI('p', 'sidebar')),
      mainPanel(cnetPlotUI('p', 'main'))
    ),
    server = function(input, output, session){
      cnetPlotServer('p', obj, config)
    }
  )
}
```

---

create\_access\_yaml      *Create access yaml*

---

## Description

This function creates an access yaml file. This is primarily intended for the first run.

## Usage

```
create_access_yaml(user, user_group, data_area)
```

## Arguments

|            |  |
|------------|--|
| user       | User name                              |
| user_group | User group                             |
| data_area  | Path to data area containing RDS files |

## Value

Invisibly returns NULL. This function is primarily used for its side effect of saving a yaml file with access settings

**Examples**

```
# save access details to file
home <- Sys.getenv('HOME')

# create carnation data area if it doesn't exist
carnation_home <- file.path(home, 'carnation/data')
if(!dir.exists(carnation_home)) dir.create(carnation_home)

create_access_yaml(user = 'admin',
                  user_group = 'admin',
                  data_area = carnation_home)
```

---

degmod

*Pattern plot module*


---

**Description**

Module UI & server to generate pattern plots.

**Usage**

```
patternPlotUI(id, panel, tab)
```

```
patternPlotServer(id, obj, coldata, plot_args, config)
```

**Arguments**

|           |   |
|-----------|---|
| id        | Module id   |
| panel     | string, can be 'sidebar' or 'main'  |
| tab       | string, if 'plot' show plot settings, if 'table' show table settings; if 'both', show settings for both.                          |
| obj       | reactiveValues object containing carnation object   |
| coldata   | reactiveValues object containing object metadata  |
| plot_args | reactive containing 'gene_scratchpad' (genes selected in scratchpad) & 'upset_data' (list containing data from upset plot module) |
| config    | reactive list with config settings  |

**Value**

UI returns tagList with module UI server invisibly returns NULL (used for side effects)

**Examples**

```

library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

cdata <- lapply(oobj$rld, function(x) colData(x))

coldata <- reactiveValues( all=cdata, curr=cdata )

plot_args <- reactive({
  list(
    gene_scratchpad=c('gene1', 'gene2'),
    upset_data=list(genes=NULL, labels=NULL)
  )
})

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(
      patternPlotUI('p', 'sidebar', 'both'),
      conditionalPanel(condition = "input.pattern_mode == 'Plot'",
        patternPlotUI('p', 'sidebar', 'plot')
      ),
      conditionalPanel(condition = "input.pattern_mode == 'Table'",
        patternPlotUI('p', 'sidebar', 'table')
      )
    ),
    mainPanel(
      tabsetPanel(id='pattern_mode',
        tabPanel('Plot',
          patternPlotUI('p', 'plot')
        ), # tabPanel plot

        tabPanel('Cluster membership',
          patternPlotUI('p', 'table')
        ) # tabPanel cluster_membership

      ) # tabsetPanel pattern_mode
    ) # tabPanel pattern_analysis
  )

```

```

    ),
    server = function(input, output, session){
      patternPlotServer('deg_plot', obj, coldata,
        plot_args, config)
    }
  )

```

---

|                 |   |
|-----------------|---|
| degpatterns_dex | <i>A degPatterns object for differentially expressed genes in the dexamethasone treatment comparison.</i> |
|-----------------|---|

---

### Description

A degPatterns object for differentially expressed genes in the dexamethasone treatment comparison.

### Format

A degPatterns object, generated with the degPatterns function from the DEGreport package.

### Details

This degPatterns object was created to test for groups of coexpressed genes in the top 100 differentially expressed genes from the dexamethasone treatment comparison.

Details on how this object has been created are included in the create\_carnation\_data.R script, included in the scripts folder of the Carnation package.

### References

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderma B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778

---

|           |                          |
|-----------|--------------------------|
| dendromod | <i>Dendrogram module</i> |
|-----------|--------------------------|

---

### Description

UI & module to generate dendrograms.

**Usage**

```
dendrogramUI(id, panel)

dendrogramServer(id, obj, config)
```

**Arguments**

|        |   |
|--------|---|
| id     | Module id   |
| panel  | string, can be 'sidebar' or 'main'                |
| obj    | reactiveValues object containing GeneTonic object |
| config | reactive list with config settings                |

**Value**

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

**Examples**

```
library(shiny)

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

obj <- reactive({
  list(l_gs = gt$l_gs,
       anno_df = gt$anno_df,
       label = 'comp1')
})

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(dendrogramUI('p', 'sidebar')),
      mainPanel(dendrogramUI('p', 'main'))
    ),
    server = function(input, output, session){
      dendrogramServer('p', obj, config)
    }
  )
}
```

---

`distillmod`*Distilled enrichment map module*

---

## Description

UI & module to generate distill enrichment map plots.

## Usage

```
distillPlotUI(id, panel)
```

```
distillPlotServer(id, obj, args, config)
```

## Arguments

|                     |   |
|---------------------|---|
| <code>id</code>     | Module id   |
| <code>panel</code>  | string, can be 'sidebar' or 'main'  |
| <code>obj</code>    | reactive containing 'distilled' enrichment results                          |
| <code>args</code>   | reactive, list with plot arguments, 'numcat' (number of categories to plot) |
| <code>config</code> | reactive list with config settings  |

## Value

UI returns tagList with plot UI server returns reactive with number of plotted terms

## Examples

```
library(GeneTonic)
library(shiny)

# get DESeqResults object
data(res_dex, package='carnation')

# get enrichResult object
data(eres_dex, package='carnation')

# preprocess & convert to GeneTonic object
eres2 <- GeneTonic::shake_enrichResult(eres_dex)
gt <- enrich_to_genetonic(eres_dex, res_dex)

# get distilled results
df <- distill_enrichment(
  eres2,
  res_dex,
  gt$anno_df,
  n_gs = 10,
  cluster_fun = "cluster_markov"
)
```

```

# number of plotted terms
args <- reactive({ list(numcat=10) })

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(distillPlotUI('p', 'sidebar')),
      mainPanel(distillPlotUI('p', 'main'))
    ),
    server = function(input, output, session){
      numcat <- observe({
        distillPlotServer('p',
                          reactive({ df }),
                          args,
                          config)
      })
    }
  )
}

```

---

dlmod

*Download button module*


---

## Description

Module UI & server for download buttons.

## Usage

```
downloadButtonUI(id)
```

```
downloadButtonServer(id, outplot, plot_type)
```

## Arguments

|           |  |
|-----------|--|
| id        | Module id                                      |
| outplot   | reactive plot handle                           |
| plot_type | reactive/static value used for output filename |

## Value

UI returns tagList with download button UI. Server invisibly returns NULL (used for side effects).

**Examples**

```
library(shiny)
library(ggplot2)

# get example object
obj <- make_example_carnation_object()
res <- as.data.frame(obj$res[[1]])

# make MA plot
p <- ggplot(res, aes(x=baseMean, y=log2foldChange)) +
  geom_point(color='black', alpha=0.5)

outplot <- reactive({ p })

# app with a single button to download a plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      downloadButtonUI('p')
    ),
    server = function(input, output, session){
      downloadButtonServer('p', outplot, 'maplot')
    }
  )
}
```

---

dummy\_genetonic

*Make dummy GeneTonic object*

---

**Description**

Make dummy GeneTonic object

**Usage**

```
dummy_genetonic(eres)
```

**Arguments**

eres            enrichResult object

**Value**

GeneTonic object

---

emapmod

*Enrichment map plot module*

---

## Description

UI & module to generate enrichment map plots.

## Usage

```
enrichmapUI(id, panel)
```

```
enrichmapServer(id, obj, res_obj, config)
```

## Arguments

|         |   |
|---------|---|
| id      | Module id   |
| panel   | string, can be 'sidebar' or 'main'                |
| obj     | reactiveValues object containing GeneTonic object |
| res_obj | reactive, dataframe containing enrichment results |
| config  | reactive list with config settings                |

## Value

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

## Examples

```
library(shiny)

# get DESeqResults object
data(res_dex, package='carnation')

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

obj <- reactive({
  list(l_gs = gt$l_gs,
       anno_df = gt$anno_df,
       label = 'comp1')
})

res_obj <- reactive({ res })

config <- reactiveVal(get_config())
```

```
# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(enrichmapUI('p', 'sidebar')),
      mainPanel(enrichmapUI('p', 'main'))
    ),
    server = function(input, output, session){
      enrichmapServer('p', obj, res_obj, config)
    }
  )
}
```

---

enrich\_to\_genetonic    *Convert enrichResult to GeneTonic object*

---

## Description

This function takes an enrichResult object and DE analysis results and creates a GeneTonic object.

## Usage

```
enrich_to_genetonic(enrich, res)
```

## Arguments

|        |                                     |
|--------|-------------------------------------|
| enrich | enrichResult object                 |
| res    | data frame with DE analysis results |

## Value

GeneTonic object

## Examples

```
# get enrich & res objects
data(res_dex, package="carnation")
data(eres_dex, package="carnation")

# convert to GeneTonic object
gt <- enrich_to_genetonic(eres_dex, res_dex)
```

---

|           |   |
|-----------|---|
| eres_cell | <i>An enrichResult object for differentially expressed genes in the cell line comparison.</i> |
|-----------|---|

---

**Description**

An `enrichResult` object for differentially expressed genes in the cell line comparison.

**Format**

An `enrichResult` object, generated with the `enrichGO` function from the `clusterProfiler` package.

**Details**

This `enrichResult` object was created to test for functional enrichment using the GO Biological Process (BP) ontology on the top 100 differentially expressed genes from the cell line comparison.

Details on how this object has been created are included in the `create_carnation_data.R` script, included in the `scripts` folder of the `Carnation` package.

**References**

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderma B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." *PLoS One*. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778

---

|          |   |
|----------|---|
| eres_dex | <i>An enrichResult object for differentially expressed genes in the dexamethasone treatment comparison.</i> |
|----------|---|

---

**Description**

An `enrichResult` object for differentially expressed genes in the dexamethasone treatment comparison.

**Format**

An `enrichResult` object, generated with the `enrichGO` function from the `clusterProfiler` package.

**Details**

This enrichResult object was created to test for functional enrichment using the GO Biological Process (BP) ontology on the top 100 differentially expressed genes from the dexamethasone treatment comparison.

Details on how this object has been created are included in the create\_carnation\_data.R script, included in the scripts folder of the Carnation package.

**References**

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderma B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778

---

|              |   |
|--------------|---|
| format_genes | <i>format gene names to look pretty in table output</i> |
|--------------|---|

---

**Description**

This function works by grouping long lists of genes into groups of a specified size. Each group is collapsed using commas, while groups are separated by spaces so that datatable formatting is tricked into separating space-separated groups and not comma-separated groups

**Usage**

```
format_genes(g, sep = "\\/", genes.per.line = 6)
```

**Arguments**

|                |                                   |
|----------------|-----------------------------------|
| g              | vector of gene names              |
| sep            | gene name separator               |
| genes.per.line | number of genes to show in a line |

**Value**

vector of gene names prettified for data.table output

**Examples**

```
# string with genes separated by '/'
g <- "gene1/gene2/gene3/gene4/gene5/gene6/gene7"

gg <- format_genes(g, genes.per.line=3)
```

---

fromList.with.names     *Prepare list for UpSet plots, but include rownames*

---

**Description**

Prepare list for UpSet plots, but include rownames

**Usage**

```
fromList.with.names(lst)
```

**Arguments**

lst                    List of sets to compare (same input as to UpSetR::fromList)

**Value**

data.frame of 1 and 0 showing which genes are in which sets

**Examples**

```
# list of genes
lst <- list(group1 = c(a = "gene1", b = "gene2", c = "gene3", d = "gene4"),
            group2 = c(c = "gene3", d = "gene4"))

# binarized matrix with group membership
df <- fromList.with.names(lst)
```

---

funenrichmod             *Functional enrichment module*

---

**Description**

UI & module to show functional enrichment tables & plots.

**Usage**

```
enrichUI(id, panel, tab = "none")
```

```
enrichServer(id, obj, upset_table, gene_scratchpad, reset_genes, config)
```

**Arguments**

|                 |  |
|-----------------|--|
| id              | ID string used to match the ID used to call the module UI function   |
| panel           | string, can be 'sidebar' or 'main'   |
| tab             | string, if 'table' show table settings, if 'plots' show plot settings; if 'compare_results', show comparison settings. |
| obj             | reactiveValues object containing carnation object  |
| upset_table     | reactive, data from upset plot module  |
| gene_scratchpad |  |
|                 | reactive, genes selected in gene scratchpad  |
| reset_genes     | reactive to reset genes in scratchpad  |
| config          | reactive list with config settings   |

**Value**

UI returns tagList with plot UI server returns reactive with gene selected from functional enrichment tables.

**Examples**

```
library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

upset_table <- reactiveValues(tbl=NULL, intersections=NULL, set_labels=NULL)

gene_scratchpad <- reactive({ c('gene1', 'gene2') })

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(
      conditionalPanel(condition = "input.func == 'Table'",
        enrichUI('p', 'sidebar', 'table')
      ),
      conditionalPanel(condition = "input.func == 'Plot'",
        enrichUI('p', 'sidebar', 'plot')
      ),
    ),

```

```

        conditionalPanel(condition = "input.func == 'Compare results'",
          enrichUI('p', 'sidebar', 'compare_results')
        )
      ),
      mainPanel(
        tabsetPanel(id='func',
          tabPanel('Table',
            enrichUI('p', 'main', 'table')
          ), # tabPanel table

          tabPanel('Plot',
            enrichUI('p', 'main', 'plot')
          ), # tabPanel plot

          tabPanel('Compare results',
            enrichUI('p', 'main', 'compare_results')
          ) # tabPanel compare_results

        ) # tabsetPanel func
      ) # tabPanel
    ),
    server = function(input, output, session){
      enrich_data <- enrichServer('p', obj,
        upset_table,
        gene_scratchpad,
        reactive({ FALSE }),
        config)
    }
  )
)

```

---

 fuzzymod

*Fuzzy enrichment map module*


---

### Description

UI & module to generate fuzzy enrichment map plots.

### Usage

```
fuzzyPlotUI(id, panel)
```

```
fuzzyPlotServer(id, obj, args, config)
```

### Arguments

|       |  |
|-------|--|
| id    | Module id  |
| panel | string, can be 'sidebar' or 'main'                 |
| obj   | reactive containing 'distilled' enrichment results |

args                reactive, list with plot arguments, 'numcat' (number of categories to plot)  
 config             reactive list with config settings

### Value

UI returns tagList with plot UI server returns reactive with number of plotted terms

### Examples

```
library(shiny)

# get enrichResult object
data(eres_dex, package='carnation')

# preprocess & convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

# get distilled results
df <- GeneTonic::gs_fuzzyclustering(gt[seq_len(10)],,
  similarity_threshold = 0.35,
  fuzzy_seeding_initial_neighbors = 3,
  fuzzy_multilinkage_rule = 0.5)

# number of plotted terms
args <- reactive({ list(numcat=10) })

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(fuzzyPlotUI('p', 'sidebar')),
      mainPanel(fuzzyPlotUI('p', 'main'))
    ),
    server = function(input, output, session){
      numcat <- observe({
        fuzzyPlotServer('p',
          reactive({ df }),
          args,
          config)
      })
    }
  )
}
```

**Description**

UI & server for module to create gene plot

**Usage**

```
genePlotUI(id, panel)
```

```
genePlotServer(id, obj, coldata, plot_args, config)
```

**Arguments**

|           |   |
|-----------|---|
| id        | Module id   |
| panel     | string, can be 'sidebar' or 'main'  |
| obj       | reactiveValues object containing carnation object   |
| coldata   | reactiveValues object containing object metadata  |
| plot_args | reactive list with 3 elements: 'gene.id' (all gene IDs) & 'gene_scratchpad' (genes selected in scratchpad) & 'comp_all' (selected comparison) |
| config    | reactive list with config settings  |

**Value**

UI returns tagList with gene plot UI. Server invisibly returns NULL (used for side effects).

**Examples**

```
library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

# Set up coldata structure that the module expects
coldata <- reactiveValues(
  curr = list(
    all_samples = colData(oobj$dds$main),
    main = colData(oobj$dds$main)
  )
)

plot_args <- reactive({
```

```
list(
  gene.to.plot = c("gene1", "gene2"),
  gene.id = rownames(obj$dds$main),
  comp_all = "comp1"
)
})

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(genePlotUI('p', 'sidebar')),
    mainPanel(genePlotUI('p', 'main'))
  ),
  server = function(input, output, session){
    genePlotServer('p', obj, coldata, plot_args, config)
  }
)
```

---

getcountplot

*Create gene plot*

---

## Description

This function creates the gene plot.

## Usage

```
getcountplot(
  df,
  intgroup = "group",
  factor.levels,
  title = NULL,
  ylab = "Normalized counts",
  color = "gene",
  nrow = 2,
  ymin = NULL,
  ymax = NULL,
  log = TRUE,
  freey = FALSE,
  trendline = "smooth",
  facet = NULL,
  legend = TRUE,
  boxes = TRUE,
  rotate_x_labels = 30
)
```

**Arguments**

|                              |   |
|------------------------------|---|
| <code>df</code>              | data.frame with gene counts                             |
| <code>intgroup</code>        | metadata variable to plot on x-axis                     |
| <code>factor.levels</code>   | levels of intgroup to show on x-axis                    |
| <code>title</code>           | title of plot   |
| <code>ylab</code>            | y-axis label  |
| <code>color</code>           | metadata variable to color by                           |
| <code>nrow</code>            | number of rows to plot if faceting                      |
| <code>ymin</code>            | y-axis lower limit                                      |
| <code>ymax</code>            | y-axis upper limit                                      |
| <code>log</code>             | should y-axis be log10-transformed?                     |
| <code>freey</code>           | should y-axes of faceted plots have independent scales? |
| <code>trendline</code>       | type of trendline to draw                               |
| <code>facet</code>           | metadata variable to facet by                           |
| <code>legend</code>          | show legend?  |
| <code>boxes</code>           | show boxes?   |
| <code>rotate_x_labels</code> | angle to rotate x-axis labels (default=30)              |

**Value**

ggplot handle

**Examples**

```
# make example DESeq dataset
dds <- DESeq2::makeExampleDESeqDataSet()

# get gene counts
df <- get_gene_counts(dds, gene = c('gene1', 'gene2'))

# standard gene plot
p <- getcountplot(df, intgroup = "condition", factor.levels = c("A", "B"))

# with genes faceted
p1 <- getcountplot(df, intgroup = "condition", factor.levels = c("A", "B"), facet = "gene")
```

---

|                 |                                     |
|-----------------|-------------------------------------|
| get_access_path | <i>Get path to access yaml file</i> |
|-----------------|-------------------------------------|

---

**Description**

This function checks for an environment variable 'CARNATION\_ACCESS\_YAML' to specify directory to save access yaml. If env variable does not exist uses home directory as save location.

**Usage**

```
get_access_path()
```

**Value**

path to access yaml

**Examples**

```
p <- get_access_path()
```

---

|            |                   |
|------------|-------------------|
| get_config | <i>Get config</i> |
|------------|-------------------|

---

**Description**

This function reads the config.yaml and returns the list

**Usage**

```
get_config()
```

**Value**

list containing config items

**Examples**

```
cfg <- get_config()
```

---

get\_degplot

*Plot a degPatterns object*


---

### Description

This function plots a degPatterns object.

### Usage

```
get_degplot(
  obj,
  time,
  color = NULL,
  cluster_column = "cluster",
  cluster_to_show,
  x_order,
  points = TRUE,
  boxes = TRUE,
  smooth = "smooth",
  lines = TRUE,
  facet = TRUE,
  prefix_title = "Cluster ",
  genes_to_label = NULL
)
```

### Arguments

|                 |   |
|-----------------|---|
| obj             | degPatterns object  |
| time            | metadata variable to plot on x-axis                                 |
| color           | variable to color plot  |
| cluster_column  | column to use for grouping genes                                    |
| cluster_to_show | which clusters to show in plot                                      |
| x_order         | order of x-axis values  |
| points          | boolean, show samples on plot? Default: TRUE                        |
| boxes           | boolean, show boxes on plot? Default: TRUE                          |
| smooth          | what type of trendline to use? can be 'smooth' (default) or 'line'. |
| lines           | show lines joining samples? Default: TRUE                           |
| facet           | boolean, should plot be faceted? Default: TRUE                      |
| prefix_title    | string, prefix for facet titles                                     |
| genes_to_label  | genes to label on plot  |

**Value**

ggplot handle

**Examples**

```
# get degpatterns object
data(degpatterns_dex, package = 'carnation')

# get pattern plot
all_clusters <- unique(degpatterns_dex$normalized$cluster)

dp <- get_degplot(degpatterns_dex, time='dex',
                  cluster_to_show=all_clusters,
                  x_order=c('untrt','trt'))
```

---

|                              |                                 |
|------------------------------|---------------------------------|
| <code>get_gene_counts</code> | <i>Get read counts for gene</i> |
|------------------------------|---------------------------------|

---

**Description**

This is a simple function to obtain read counts for a specified gene, based on the DESeq2::plotCounts function.

**Usage**

```
get_gene_counts(dds, gene, intgroup = "condition", norm_method = "libsize")
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>dds</code>         | DESeqDataSet object                                       |
| <code>gene</code>        | gene name vector  |
| <code>intgroup</code>    | metadata variable to attach to counts                     |
| <code>norm_method</code> | normalization method, can be 'libsize' (default) or 'vst' |

**Value**

data.frame with gene counts

**Examples**

```
# make example DESeq data set
dds <- DESeq2::makeExampleDESeqDataSet()

# get counts for gene1
gg <- get_gene_counts(dds, 'gene1')
```

---

```
get_project_name_from_path  
    Get project name from path
```

---

### Description

This function takes in a path to an RDS file and returns a string to be used as project name

### Usage

```
get_project_name_from_path(  
  x,  
  depth = 2,  
  end_offset = 0,  
  staging_dir = "dev",  
  fsep = .Platform$file.sep  
)
```

### Arguments

|             |  |
|-------------|--|
| x           | character path to RDS file                   |
| depth       | integer how many levels below path to look?  |
| end_offset  | integer how far from the end of path to end? |
| staging_dir | name of staging directory                    |
| fsep        | file separator to split path with            |

### Value

project name parsed from path to object

### Examples

```
# path to carnation object  
obj_path <- "/path/to/project/test/main.rnaseq.rds"  
  
# parsed project name  
get_project_name_from_path(obj_path, depth = 2, end_offset = 0)
```

---

|                 |                                  |
|-----------------|----------------------------------|
| get_upset_table | <i>Generate upset plot table</i> |
|-----------------|----------------------------------|

---

**Description**

Generate upset plot table

**Usage**

```
get_upset_table(gene.lists, comp_split_pattern = ";")
```

**Arguments**

|                    |   |
|--------------------|---|
| gene.lists         | list with character vectors of gene names |
| comp_split_pattern | character used to separate gene set names |

**Value**

list with upset table elements

**Examples**

```
lst <- list(group1 = c(a = "gene1", b = "gene2", c = "gene3", d = "gene4"),
            group2 = c(b = "gene2", d = "gene4", e = "gene5"),
            group3 = c(d = "gene4", e = "gene5", f = "gene6"))

df <- get_upset_table(lst)
str(df)
```

---

|            |                                  |
|------------|----------------------------------|
| get_y_init | <i>Get initial y-axis limits</i> |
|------------|----------------------------------|

---

**Description**

Get initial y-axis limits

**Usage**

```
get_y_init(df, y_delta, pseudocount)
```

**Arguments**

|             |   |
|-------------|---|
| df          | data.frame with counts. Must have column 'count'          |
| y_delta     | y-axis padding for visualization, must be between 0 and 1 |
| pseudocount | pseudo-count to add to the data.frame                     |

**Value**

min and max limits for count column, padded for visualization

**Examples**

```
# make example DESeq dataset
dds <- DESeq2::makeExampleDESeqDataSet()

# get gene counts
df <- get_gene_counts(dds, gene = c('gene1', 'gene2'))

# get y axis limits
get_y_init(df, y_delta = 0.01, pseudocount = 1)
```

---

gs\_radar

*Radar plot*

---

**Description**

This is a copy of gs\_radar from GeneTonic where the labels of gene sets are converted to parameters

**Usage**

```
gs_radar(
  res_enrich,
  res_enrich2 = NULL,
  label1 = "scenario 1",
  label2 = "scenario 2",
  n_gs = 20,
  p_value_column = "gs_pvalue"
)
```

**Arguments**

|                |  |
|----------------|--|
| res_enrich     | GeneTonic object for comparison 1                  |
| res_enrich2    | GeneTonic object for comparison 2 (default = NULL) |
| label1         | label for comparison 1                             |
| label2         | label for comparison 2                             |
| n_gs           | number of gene sets (default = 20)                 |
| p_value_column | column to use as p-value (default = 'gs_pvalue')   |

**Value**

ggplot handle

**Examples**

```

library(GeneTonic)

# get DESeqResults object
data(res_dex, package='carnation')

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- shake_enrichResult(eres_dex)

# get annotation df
idx <- match(c('gene','symbol'), tolower(colnames(res_dex)))
anno_df <- res_dex[,idx]
colnames(anno_df) <- c('gene_id', 'gene_name')

# add aggregate score columns
gt <- get_aggrscores(gt, res_dex, anno_df)

# make radar plot
p <- gs_radar(gt)

```

heatmapmod

*Heatmap module***Description**

Module UI & server to generate heatmap.

**Usage**

```
heatmapUI(id, panel)
```

```
heatmapServer(id, obj, coldata, plot_args, gene_scratchpad, config)
```

**Arguments**

|                 |  |
|-----------------|--|
| id              | Module id  |
| panel           | string, can be 'sidebar' or 'main'   |
| obj             | reactiveValues object containing carnation object  |
| coldata         | reactiveValues object containing object metadata   |
| plot_args       | reactive containing 'fdr.thres' (padj threshold), 'fc.thres' (log2FC) & 'upset_data' (list containing data from upset plot module) |
| gene_scratchpad | reactiveValues object containing genes selected in scratchpad which will be labeled  |
| config          | reactive list with config settings   |

**Value**

UI returns tagList with heatmap UI. Server invisibly returns NULL (used for side effects).

**Examples**

```

library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

cdata <- lapply(oobj$rld, function(x) colData(x))

coldata <- reactiveValues( all=cdata, curr=cdata )

plot_args <- reactive({
  list(
    fdr.thres=0.1,
    fc.thres=0,
    upset_data=list(genes=NULL, labels=NULL)
  )
})

gene_scratchpad <- reactive({ c('gene1', 'gene2') })

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(heatmapUI('p', 'sidebar')),
    mainPanel(heatmapUI('p', 'sidebar'))
  ),
  server = function(input, output, session){
    heatmapServer('p', obj, coldata,
                  plot_args, gene_scratchpad, config)
  }
)

```

**Description**

Module UI & server for help buttons.

**Usage**

```
helpButtonUI(id)
```

```
helpButtonServer(id, ...)
```

**Arguments**

|     |   |
|-----|---|
| id  | Module id. This also doubles as prefixes for help text files. |
| ... | other params passed to helpModal()                            |

**Value**

UI returns tagList with help button UI. Server invisibly returns NULL (used for side effects).

**Examples**

```
library(shiny)

# app with a single help button to show DE summary table details
if(interactive()){
  shinyApp(
    ui = fluidPage(
      helpButtonUI('de_summary_help')
    ),
    server = function(input, output, session){
      helpButtonServer('de_summary_help')
    }
  )
}
```

---

helpModal

*Help modal*

---

**Description**

This generates a modal dialog that includes text from a markdown file.

**Usage**

```
helpModal(mdfile, title = NULL, ...)
```

**Arguments**

mdfile            path to markdown file  
title            Title of modal dialog  
...            other params passed to modalDialog()

**Value**

Modal dialog with help documentation.

---

|            |                            |
|------------|----------------------------|
| horizonmod | <i>Horizon plot module</i> |
|------------|----------------------------|

---

**Description**

UI & module to generate horizon plots.

**Usage**

```
horizonUI(id, panel)

horizonServer(id, obj, config)
```

**Arguments**

id            Module id  
panel        string, can be 'sidebar' or 'main'  
obj        reactiveValues object containing two GeneTonic objects  
config      reactive list with config settings

**Value**

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

**Examples**

```
library(shiny)

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

# get second enrichResult object
data(eres_cell, package='carnation')

# convert to GeneTonic object
```

```

gt1 <- GeneTonic::shake_enrichResult(eres_cell)

obj <- reactive({
  list(
    obj1 = list(l_gs = gt$l_gs,
               anno_df = gt$anno_df,
               label = 'comp1'),
    obj2 = list(l_gs = gt1$l_gs,
               anno_df = gt1$anno_df,
               label = 'comp2')
  )
})

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(horizonUI('p', 'sidebar')),
      mainPanel(horizonUI('p', 'main'))
    ),
    server = function(input, output, session){
      horizonServer('p', obj, config)
    }
  )
}

```

---

|                   |  |
|-------------------|--|
| install_carnation | <i>Create carnation python environment</i> |
|-------------------|--|

---

## Description

This function installs 'plotly' and 'kaleido' python packages in an environment to allow PDF downloads from plotly plots.

## Usage

```
install_carnation(envname, ...)
```

## Arguments

|         |   |
|---------|---|
| envname | name of the python environment              |
| ...     | parameters passed to reticulate::py_install |

## Value

NULL, invisibly. The function is called for its side effects.

**Examples**

```
if(interactive()){
  install_carnation()
}
```

---

|                |                                   |
|----------------|-----------------------------------|
| in_admin_group | <i>is user is in admin group?</i> |
|----------------|-----------------------------------|

---

**Description**

is user is in admin group?

**Usage**

```
in_admin_group(u)
```

**Arguments**

|   |          |
|---|----------|
| u | username |
|---|----------|

**Value**

TRUE/FALSE to indicate if the user is part of the admin group

**Examples**

```
# save access details to file
home <- Sys.getenv('HOME')

# create carnation data area if it doesn't exist
carnation_home <- file.path(home, 'carnation/data')
if(!dir.exists(carnation_home)) dir.create(carnation_home)

create_access_yaml(user = 'admin',
                  user_group = 'admin',
                  data_area = carnation_home)

check <- in_admin_group('user')
```

---

|               |                          |
|---------------|--------------------------|
| is_site_admin | <i>is user an admin?</i> |
|---------------|--------------------------|

---

**Description**

is user an admin?

**Usage**

```
is_site_admin(u)
```

**Arguments**

|   |          |
|---|----------|
| u | username |
|---|----------|

**Value**

boolean to indicate is user is in admin group

**Examples**

```
# check if default user is admin
yy <- is_site_admin(u='admin')
```

---

|         |                         |
|---------|-------------------------|
| loadmod | <i>Load data module</i> |
|---------|-------------------------|

---

**Description**

Module UI & server to load new data

**Usage**

```
loadDataUI(id)
```

```
loadDataServer(id, username, config, rds = NULL)
```

**Arguments**

|          |                                    |
|----------|------------------------------------|
| id       | Module id                          |
| username | user name                          |
| config   | reactive list with config settings |
| rds      | Object to be edited                |

**Value**

UI returns tagList with module UI Server returns reactive with app reload trigger

**Examples**

```
library(shiny)

username <- 'admin'

config <- reactiveVal(get_config())

obj <- make_example_carnation_object()

rds <- reactive({ obj=obj })

shinyApp(
  ui = fluidPage(
    loadDataUI('p')
  ),
  server = function(input, output, session){
    loadDataServer('p', username=username, config, rds)
  }
)
```

---

|                  |   |
|------------------|---|
| makeEnrichResult | <i>Make an enrichResult obj from a data frame</i> |
|------------------|---|

---

**Description**

Most of the parameters are just placeholders and the dataframe must contain the columns 'ID' and 'geneID'

**Usage**

```
makeEnrichResult(
  df,
  split = "/",
  keytype = "UNKNOWN",
  ontology = "UNKNOWN",
  type = "enrichResult"
)
```

**Arguments**

|       |   |
|-------|---|
| df    | data frame with functional enrichment results |
| split | string, character used to split gene IDs      |

|          |   |
|----------|---|
| keytype  | type of gene ID                               |
| ontology | ontology database being used                  |
| type     | string, can be 'enrichResult' or 'gseaResult' |

**Value**

enrichResult object

**Examples**

```
# get enrichResult object
data(eres_dex, package='carnation')

# extract the results
df <- as.data.frame(eres_dex)

# convert to a stripped down enrichResult object
eres2 <- makeEnrichResult(df)
```

---

make\_example\_carnation\_object  
*Make example carnation object*

---

**Description**

Returns example carnation object used in examples & testing

**Usage**

```
make_example_carnation_object()
```

**Value**

reactiveValues object containing carnation object

**Examples**

```
obj <- make_example_carnation_object()
```

---

|                   |  |
|-------------------|--|
| make_final_object | <i>Make final object for internal use by the app</i> |
|-------------------|--|

---

### Description

This function takes an uploaded object and sanitizes it to make sure it is suitable for internal use along with other additions:

- adds a 'dds\_mapping' element that maps dds\_list keys to res\_list objects.
- if there are multiple dds\_list objects, it adds a 'all\_dds' element combining all samples.

### Usage

```
make_final_object(obj)
```

### Arguments

obj                    list object containing lists of DE analysis results, functional enrichment objects, pattern analysis objects & raw and normalized counts objects.

### Value

final carnation object with additional pre-processing

### Examples

```
library(DESeq2)

# make example DESeq dataset
dds <- makeExampleDESeqDataSet()

# run DE analysis
dds <- DESeq(dds)

# extract comparison of interest
res <- results(dds, contrast = c("condition", "A", "B"))

# perform VST normalization
rld <- varianceStabilizingTransformation(dds, blind = TRUE)

# build minimal object
obj <- list(
  res_list = list(
    comp = list(
      res = res,
      dds = "main",
      label = "A vs B"
    )
  ),
)
```

```

        dds_list = list(main = dds),
        rld_list = list(main = rld)
    )

# final object
final_obj <- make_final_object(obj)

```

---

maplotmod

*MA plot module*


---

## Description

UI & server for module to create MA plot

## Usage

```
maPlotUI(id, panel)
```

```
maPlotServer(id, obj, plot_args, config)
```

## Arguments

|           |  |
|-----------|--|
| id        | Module id  |
| panel     | string, can be 'sidebar' or 'main'   |
| obj       | reactiveValues object containing carnation object  |
| plot_args | reactive containing 'fdr.thres' (p <sub>adj</sub> threshold), 'fc.thres' (log <sub>2</sub> FC threshold) & 'gene.to.plot' (genes selected in scratchpad) |
| config    | reactive list with config settings   |

## Value

UI returns tagList with MA plot UI. Server invisibly returns NULL (used for side effects).

## Examples

```

library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,

```

```

    dds_mapping = oobj$dds_mapping
  )

# Set up coldata structure that the module expects
coldata <- reactiveValues(
  curr = list(
    all_samples = colData(obj$dds$main),
    main = colData(obj$dds$main)
  )
)

plot_args <- reactive({
  list(
    fdr.thres=0.1,
    fc.thres=0,
    gene.to.plot=c('gene1', 'gene2')
  )
})

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(maPlotUI('p', 'sidebar')),
    mainPanel(maPlotUI('p', 'main'))
  ),
  server = function(input, output, session){
    maPlotServer('p', obj, plot_args, config)
  }
)

```

---

metamod

*Metadata module*


---

## Description

This module generates the metadata tab that allows users to view the metadata associated with the loaded carnation object.

## Usage

```
metadataUI(id, panel)
```

```
metadataServer(id, obj, cols.to.drop)
```

## Arguments

|       |  |
|-------|--|
| id    | Module id  |
| panel | context for generating ui elements ('sidebar' or 'main') |

obj                    reactiveValues object containing carnation object  
 cols.to.drop        columns to hide from table

### Value

UI returns tagList with metadata UI. Server returns reactive object with metadata.

### Examples

```
library(shiny)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

config <- get_config()
cols.to.drop <- config$server$cols.to.drop

shinyApp(
  ui = fluidPage(
    sidebarPanel(metadataUI('p', 'sidebar')),
    mainPanel(metadataUI('p', 'main'))
  ),
  server = function(input, output, session){
    # reactiveVal to save updates
    saved_data <- reactiveVal()

    cdata <- metadataServer('p', obj, cols.to.drop)

    observeEvent(cdata(), {
      saved_data(cdata())
    })
  }
)
```

### Description

summary(res) prints out info; this function captures it into a dataframe

**Usage**

```
my.summary(res, dds, alpha, lfc.thresh = 0)
```

**Arguments**

|            |   |
|------------|---|
| res        | DESeq2 results object                                     |
| dds        | DESeq2 object   |
| alpha      | Alpha level at which to call significantly changing genes |
| lfc.thresh | log2FoldChange threshold                                  |

**Value**

Dataframe of summarized results

**Examples**

```
n_genes <- 100

# make mock dds list
dds <- DESeq2::makeExampleDESeqDataSet(n=n_genes)

# make mock results df
res <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),
  stat = rnorm(n_genes, 0, 3),
  pvalue = runif(n_genes, 0, 1),
  padj = runif(n_genes, 0, 1),
  symbol = paste0("GENE", 1:n_genes),
  row.names = paste0("gene", 1:n_genes)
)

# get summary
df <- my.summary(res, dds, alpha=0.1)
```

---

pcamod

*PCA plot module*

---

**Description**

Module UI + server to generate a pca plot.

**Usage**

```
pcaPlotUI(id, panel)
```

```
pcaPlotServer(id, obj, coldata, config)
```

**Arguments**

|         |   |
|---------|---|
| id      | Module id   |
| panel   | string, can be 'sidebar' or 'main'                |
| obj     | reactiveValues object containing carnation object |
| coldata | reactiveValues object containing object metadata  |
| config  | reactive list with config settings                |

**Value**

UI returns tagList with PCA plot UI. Server invisibly returns NULL (used for side effects).

**Examples**

```
library(shiny)
library(DESeq2)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)

# Set up coldata structure that the module expects
coldata <- reactiveValues(
  curr = list(
    all_samples = colData(oobj$dds$main),
    main = colData(oobj$dds$main)
  )
)

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(pcaPlotUI('p', 'sidebar')),
    mainPanel(pcaPlotUI('p', 'main'))
  ),
  server = function(input, output, session){
    pcaPlotServer('p', obj, coldata, config)
  }
)
```

---

|              |                                 |
|--------------|---------------------------------|
| plotMA.label | <i>Create a labeled MA plot</i> |
|--------------|---------------------------------|

---

## Description

This function creates an MA plot from a data.frame containing DE analysis results.

## Usage

```
plotMA.label(  
  res,  
  fdr.thres = 0.01,  
  fc.thres = 0,  
  fc.lim = NULL,  
  lab.genes = NULL,  
  tolower.cols = c("SYMBOL", "ALIAS")  
)
```

## Arguments

|              |   |
|--------------|---|
| res          | data.frame with DE analysis results. Must contain "padj" & "log2FoldChange" columns |
| fdr.thres    | False discovery rate (FDR) threshold  |
| fc.thres     | log2FoldChange threshold  |
| fc.lim       | y-axis limits   |
| lab.genes    | genes to label on MA plot   |
| tolower.cols | column names that will be converted to lower case                                   |

## Value

ggplot handle

## Examples

```
# make mock results df  
n_genes <- 100  
res <- data.frame(  
  baseMean = runif(n_genes, 10, 1000),  
  log2FoldChange = rnorm(n_genes, 0, 2),  
  lfcSE = runif(n_genes, 0.1, 0.5),  
  stat = rnorm(n_genes, 0, 3),  
  pvalue = runif(n_genes, 0, 1),  
  padj = runif(n_genes, 0, 1),  
  symbol = paste0("GENE", 1:n_genes),  
  row.names = paste0("gene", 1:n_genes)  
)
```

```
plotMA.label(res, lab.genes = c("gene1", "gene2"))
```

---

plotMA.label\_ly      *Create an interactive labeled MA plot*

---

## Description

This function creates an MA plot from a data.frame containing DE analysis results using plot\_ly

## Usage

```
plotMA.label_ly(  
  res,  
  fdr.thres = 0.01,  
  fc.thres = 0,  
  fc.lim = NULL,  
  lab.genes = NULL,  
  tolower.cols = c("SYMBOL", "ALIAS")  
)
```

## Arguments

|              |   |
|--------------|---|
| res          | data.frame with DE analysis results. Must contain "padj" & "log2FoldChange" columns |
| fdr.thres    | False discovery rate (FDR) threshold  |
| fc.thres     | log2FoldChange threshold  |
| fc.lim       | y-axis limits   |
| lab.genes    | genes to label on MA plot   |
| tolower.cols | column names that will be converted to lower case                                   |

## Value

plotly handle

## Examples

```
# make mock results df  
n_genes <- 100  
res <- data.frame(  
  baseMean = runif(n_genes, 10, 1000),  
  log2FoldChange = rnorm(n_genes, 0, 2),  
  lfcSE = runif(n_genes, 0.1, 0.5),  
  stat = rnorm(n_genes, 0, 3),  
  pvalue = runif(n_genes, 0, 1),  
  padj = runif(n_genes, 0, 1),  
  symbol = paste0("GENE", 1:n_genes),
```

```
        row.names = paste0("gene", 1:n_genes)
      )
plotMA.label_ly(res, lab.genes = c("gene1", "gene2"))
```

---

plotPCA.ly

*Plot an interactive PCA plot*

---

### Description

Plot an interactive PCA plot

### Usage

```
plotPCA.ly(rld, intgroup)
```

### Arguments

|          |   |
|----------|---|
| rld      | DESeqTransform object output by <code>varianceStabilizingTransformation()</code> or <code>rlog()</code> |
| intgroup | character vector of names in <code>colData(x)</code> to use for grouping                                |

### Value

Handle to ggplot with added label field in `aes_string()` for plotting with `ggplotly()`

### Examples

```
# make example dds object
dds <- DESeq2::makeExampleDESeqDataSet()

# normalize
rld <- DESeq2::varianceStabilizingTransformation(dds, blind=TRUE)

# make pca plot
p <- plotPCA.ly(rld, intgroup='condition')
```

---

`plotPCA.san`*Adjustable PCA plot*

---

**Description**

Create a PCA plot with specified PCs on x- and y-axis

**Usage**

```
plotPCA.san(  
  object,  
  intgroup = "group",  
  pcx,  
  pcy,  
  pcz = NULL,  
  ntop = 500,  
  samples = NULL,  
  loadings = FALSE,  
  loadings_ngenes = 10  
)
```

**Arguments**

|                              |  |
|------------------------------|--|
| <code>object</code>          | normalized DESeqDataSet object   |
| <code>intgroup</code>        | metadata variable to use for grouping samples  |
| <code>pcx</code>             | principal component to plot on x-axis  |
| <code>pcy</code>             | principal component to plot on y-axis  |
| <code>pcz</code>             | principal component to plot on z-axis. If not NULL, function returns a 3-D PCA plot. |
| <code>ntop</code>            | number of most-variable genes to use   |
| <code>samples</code>         | vector of sample names to show on plot   |
| <code>loadings</code>        | boolean, show gene loadings? Default is FALSE.                                       |
| <code>loadings_ngenes</code> | integer, # genes to show loadings for (default=10)                                   |

**Value**

ggplot handle

**Examples**

```
# make example dds object  
dds <- DESeq2::makeExampleDESeqDataSet()  
  
# normalize
```

```
rld <- DESeq2::varianceStabilizingTransformation(dds, blind=TRUE)

# make pca plot
p <- plotPCA.san(rld, intgroup='condition', pcx='PC1', pcy='PC2')
```

---

plotScatter.label      *Plot a scatterplot to compare two contrasts*

---

### Description

Plot a scatterplot to compare two contrasts

### Usage

```
plotScatter.label(
  compare,
  df,
  label_x,
  label_y,
  lim.x,
  lim.y,
  color.palette,
  lab.genes = NULL,
  plot_all = "no",
  name.col = "geneid",
  lines = c("yes", "yes", "yes"),
  alpha = 1,
  size = 4,
  show.grid = "yes"
)
```

### Arguments

|               |  |
|---------------|--|
| compare       | string, what values to plot? can be 'log2FoldChange' or 'P-adj'  |
| df            | data frame with log2FoldChange & padj values to plot from 2 contrasts  |
| label_x       | string, label for x-axis   |
| label_y       | string, label for y-axis   |
| lim.x         | x-axis limits  |
| lim.y         | y-axis limits  |
| color.palette | character vector of colors to use for significance categories 'Both - same LFC sign', 'Both - opposite LFC sign', 'None', label_x, label_y |
| lab.genes     | genes to label (default=NULL)  |
| plot_all      | string, can be 'yes' or 'no'. if 'yes', points outside axis limits are plotted along x/y axis lines (default='no').                        |

|           |   |
|-----------|---|
| name.col  | gene name column to merge the 2 results, also used for labeling points  |
| lines     | 3-element character vector to plot gridlines in the order (x=0, y=0, x=y), with 'yes' or 'no' values. E.g. ('yes', 'yes', 'no') will plot dotted lines for x = 0 & y = 0, but not the x = y diagonal. |
| alpha     | float, marker opacity (default=1).  |
| size      | float, marker size (default=4).   |
| show.grid | string, can be 'yes' (default) or 'no'.   |

**Value**

ggplot handle

**Examples**

```
# make mock results df
n_genes <- 100
res1 <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),
  stat = rnorm(n_genes, 0, 3),
  pvalue = runif(n_genes, 0, 1),
  padj = runif(n_genes, 0, 1),
  symbol = paste0("GENE", 1:n_genes),
  row.names = paste0("gene", 1:n_genes)
)

res2 <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),
  stat = rnorm(n_genes, 0, 3),
  pvalue = runif(n_genes, 0, 1),
  padj = runif(n_genes, 0, 1),
  symbol = paste0("GENE", 1:n_genes),
  row.names = paste0("gene", 1:n_genes)
)

# add geneid column
res1 <- cbind(geneid=row.names(res1), res1)
res2 <- cbind(geneid=row.names(res2), res2)

# make merged df from the two comparisons
cols.sub <- c('log2FoldChange', 'padj', 'geneid')
df_full <- dplyr::inner_join(
  dplyr::select(as.data.frame(res1), all_of(cols.sub)),
  dplyr::select(as.data.frame(res2), all_of(cols.sub)),
  by = 'geneid',
  suffix = c('.x', '.y')
)
```

```

# calculate x & y limits for log2FoldChange
xlim <- range(df_full[[ 'log2FoldChange.x' ]])
ylim <- range(df_full[[ 'log2FoldChange.y' ]])

# get color palette
color.palette <- RColorBrewer::brewer.pal(n=5, name='Set2')

# add significance column
sig.x <- df_full$padj.x < 0.1 & !is.na(df_full$padj.x)
sig.y <- df_full$padj.y < 0.1 & !is.na(df_full$padj.y)
up.x <- df_full$log2FoldChange.x >= 0
up.y <- df_full$log2FoldChange.y >= 0
significance <- rep('None', nrow(df_full))
significance[ sig.x & sig.y & ((up.x & up.y) | (!up.x & !up.y)) ] <- 'Both - same LFC sign'
significance[ sig.x & sig.y & ((up.x & !up.y) | (!up.x & up.y)) ] <- 'Both - opposite LFC sign'
significance[ sig.x & !sig.y ] <- 'A vs B'
significance[ !sig.x & sig.y ] <- 'B vs A'
df_full$significance <- significance

# generate scatter plot
p <- plotScatter.label(compare = 'log2FoldChange',
                      df = df_full,
                      label_x = 'A vs B',
                      label_y = 'B vs A',
                      lim.x = xlim,
                      lim.y = ylim,
                      color.palette = color.palette)

```

---

plotScatter.label\_ly *Plot an interactive scatterplot to compare two contrasts*

---

## Description

Plot an interactive scatterplot to compare two contrasts

## Usage

```

plotScatter.label_ly(
  compare,
  df,
  label_x,
  label_y,
  lim.x,
  lim.y,
  color.palette,
  lab.genes = NULL,
  name.col = "geneid",
  lines = c("yes", "yes", "yes"),

```

```

    alpha = 1,
    size = 4,
    show.grid = "yes"
  )

```

### Arguments

|               |   |
|---------------|---|
| compare       | string, what values to plot? can be 'log2FoldChange' or 'P-adj'   |
| df            | data frame with log2FoldChange & padj values to plot from 2 contrasts   |
| label_x       | string, label for x-axis  |
| label_y       | string, label for y-axis  |
| lim.x         | x-axis limits   |
| lim.y         | y-axis limits   |
| color.palette | character vector of colors to use for significance categories 'Both - same LFC sign', 'Both - opposite LFC sign', 'None', label_x, label_y  |
| lab.genes     | genes to label (default=NULL)   |
| name.col      | gene name column to merge the 2 results, also used for labeling points  |
| lines         | 3-element character vector to plot gridlines in the order (x=0, y=0, x=y), with 'yes' or 'no' values. E.g. ('yes', 'yes', 'no') will plot dotted lines for x = 0 & y = 0, but not the x = y diagonal. |
| alpha         | float, marker opacity (default=1).  |
| size          | float, marker size (default=4).   |
| show.grid     | string, can be 'yes' (default) or 'no'.   |

### Value

plotly handle

### Examples

```

# make mock results df
n_genes <- 100
res1 <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),
  stat = rnorm(n_genes, 0, 3),
  pvalue = runif(n_genes, 0, 1),
  padj = runif(n_genes, 0, 1),
  symbol = paste0("GENE", 1:n_genes),
  row.names = paste0("gene", 1:n_genes)
)

res2 <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),

```

```

    stat = rnorm(n_genes, 0, 3),
    pvalue = runif(n_genes, 0, 1),
    padj = runif(n_genes, 0, 1),
    symbol = paste0("GENE", 1:n_genes),
    row.names = paste0("gene", 1:n_genes)
  )

# add geneid column
res1 <- cbind(geneid=row.names(res1), res1)
res2 <- cbind(geneid=row.names(res2), res2)

# make merged df from the two comparisons
cols.sub <- c('log2FoldChange', 'padj', 'geneid')
df_full <- dplyr::inner_join(
  dplyr::select(as.data.frame(res1), all_of(cols.sub)),
  dplyr::select(as.data.frame(res2), all_of(cols.sub)),
  by = 'geneid',
  suffix = c('.x', '.y')
)

# calculate x & y limits for log2FoldChange
xlim <- range(df_full[[ 'log2FoldChange.x' ]])
ylim <- range(df_full[[ 'log2FoldChange.y' ]])

# get color palette
color.palette <- RColorBrewer::brewer.pal(n=5, name='Set2')

# add significance column
sig.x <- df_full$padj.x < 0.1 & !is.na(df_full$padj.x)
sig.y <- df_full$padj.y < 0.1 & !is.na(df_full$padj.y)
up.x <- df_full$log2FoldChange.x >= 0
up.y <- df_full$log2FoldChange.y >= 0
significance <- rep('None', nrow(df_full))
significance[ sig.x & sig.y & ((up.x & up.y) | (!up.x & !up.y)) ] <- 'Both - same LFC sign'
significance[ sig.x & sig.y & ((up.x & !up.y) | (!up.x & up.y)) ] <- 'Both - opposite LFC sign'
significance[ sig.x & !sig.y ] <- 'A vs B'
significance[ !sig.x & sig.y ] <- 'B vs A'
df_full$significance <- significance

# generate scatter plot
p <- plotScatter.label_ly(compare = 'log2FoldChange',
  df = df_full,
  label_x = 'A vs B',
  label_y = 'B vs A',
  lim.x = xlim,
  lim.y = ylim,
  color.palette = color.palette)

```

**Description**

UI & module to generate radar plots.

**Usage**

```
radarUI(id, panel, type = "")
radarServer(id, obj, config, type = "")
```

**Arguments**

|        |   |
|--------|---|
| id     | Module id   |
| panel  | string, can be 'sidebar' or 'main'                |
| type   | string, if 'comp' then show the comparison view   |
| obj    | reactiveValues object containing GeneTonic object |
| config | reactive list with config settings                |

**Value**

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

**Examples**

```
library(shiny)

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

obj <- reactive({
  list(l_gs = gt$l_gs,
       anno_df = gt$anno_df,
       label = 'comp1')
})

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(radarUI('p', 'sidebar')),
      mainPanel(radarUI('p', 'main'))
    ),
    server = function(input, output, session){
      radarServer('p', obj, config)
    }
  )
}
```

```
}
```

---

|                  |   |
|------------------|---|
| read_access_yaml | <i>Read access yaml with user groups and data areas</i> |
|------------------|---|

---

### Description

This function reads the access yaml file and returns user groups and data areas as a list of data frames.

### Usage

```
read_access_yaml()
```

### Value

return carnation access settings from yaml file

### Examples

```
# save access details to file
home <- Sys.getenv('HOME')

# create carnation data area if it doesn't exist
carnation_home <- file.path(home, 'carnation/data')
if(!dir.exists(carnation_home)) dir.create(carnation_home)

create_access_yaml(user = 'admin',
                   user_group = 'admin',
                   data_area = carnation_home)

al <- read_access_yaml()
```

---

|          |   |
|----------|---|
| res_cell | <i>A DESeqResults object testing the difference between two cell lines of smooth muscle cells</i> |
|----------|---|

---

### Description

A DESeqResults object testing the difference between two cell lines of smooth muscle cells

### Format

A DESeqResults object, generated in the DESeq2 framework

**Details**

This DESeqResults object on the data from the airway package has been created comparing two smooth muscle cell lines, accounting for the effect of dexamethasone treatment.

Details on how this object has been created are included in the create\_carnation\_data.R script, included in the scripts folder of the Carnation package.

**References**

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderma n B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778

---

|         |   |
|---------|---|
| res_dex | <i>A DESeqResults object testing the effect of dexamethasone on smooth muscle cells</i> |
|---------|---|

---

**Description**

A DESeqResults object testing the effect of dexamethasone on smooth muscle cells

**Format**

A DESeqResults object, generated in the DESeq2 framework

**Details**

This DESeqResults object on the data from the airway package has been created comparing dexamethasone treated vs untreated samples, accounting for the different cell lines included.

Details on how this object has been created are included in the create\_carnation\_data.R script, included in the scripts folder of the Carnation package.

**References**

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderma n B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778

---

|               |                  |
|---------------|------------------|
| run_carnation | <i>Carnation</i> |
|---------------|------------------|

---

**Description**

Interactive shiny dashboard for exploring RNA-Seq analysis.

**Usage**

```
run_carnation(credentials = NULL, passphrase = NULL, enable_admin = TRUE, ...)
```

**Arguments**

|              |  |
|--------------|--|
| credentials  | path to encrypted sqlite db with user credentials.   |
| passphrase   | passphrase for credentials db.   |
| enable_admin | if TRUE, admin view is shown. Note, this is only available if credentials have sqlite backend. |
| ...          | parameters passed to shinyApp() call   |

**Value**

shinyApp object

**Examples**

```
if(interactive()){
  shiny::runApp(
    run_carnation()
  )
}
```

---

|         |                              |
|---------|------------------------------|
| savemod | <i>Save object module UI</i> |
|---------|------------------------------|

---

**Description**

Module UI & server to save carnation object.

**Usage**

```
saveUI(id)
```

```
saveServer(id, original, current, coldata, pattern, username, config)
```

**Arguments**

|          |  |
|----------|--|
| id       | Module id  |
| original | original carnation object                        |
| current  | current carnation object                         |
| coldata  | reactiveValues object containing object metadata |
| pattern  | regex pattern for finding carnation data         |
| username | user name  |
| config   | reactive list with config settings               |

**Value**

UI returns actionButton Server returns reactive with trigger to refresh the app

**Examples**

```

library(shiny)
library(DESeq2)

# default username
username <- reactive({ NULL })

# internal carnation config
config <- reactiveVal(get_config())

# regex to find carnation files
pattern <- reactive({ config()$server$pattern })

# get example object
obj <- make_example_carnation_object()

# make reactive with obj & path
original <- reactiveValues( obj = obj, path = "/path/to/carnation/obj.rds" )

# extract metadata
coldata <- reactive({ lapply(obj$dds, colData) })

# edit metadata
coldata_edit <- lapply(coldata, function(x){
  x$type <- 'new'; x
})

# add to object
edit_obj <- obj
for(name in names(edit_obj$dds)){
  colData(edit_obj$dds[[ name ]]) <- coldata_edit[[ name ]]
}

# run simple shiny app with plot
shinyApp(

```

```

    ui = fluidPage(
      saveUI('p')
    ),
    server = function(input, output, session){
      save_event <- saveServer('save_object',
                              original=original,
                              current=reactive({ edit_obj }),
                              coldata=coldata,
                              pattern=pattern(),
                              username=username,
                              config)
    }
  )

```

---

|                  |                                 |
|------------------|---------------------------------|
| save_access_yaml | <i>Save access yaml to file</i> |
|------------------|---------------------------------|

---

### Description

This function saves access details (user groups and data areas) to the designated access yaml file.

### Usage

```
save_access_yaml(lst)
```

### Arguments

lst                    list of data frames with user\_groups and data\_areas

### Value

save access settings to yaml file

### Examples

```

# save access details to file
home <- Sys.getenv('HOME')

# create carnation data area if it doesn't exist
carnation_home <- file.path(home, 'carnation/data')
if(!dir.exists(carnation_home)) dir.create(carnation_home)

create_access_yaml(user = 'admin',
                  user_group = 'admin',
                  data_area = carnation_home)

# read access yaml
lst <- read_access_yaml()

```

```
# add new user
lst$user_group$admin <- c(lst$user_group$admin, 'user1')

# save to access settings
save_access_yaml(lst)
```

---

scattermod

*Scatterplot module*


---

### Description

Module UI + server for generating scatter plots.

### Usage

```
scatterPlotUI(id, panel)

scatterPlotServer(id, obj, plot_args, config)
```

### Arguments

|           |   |
|-----------|---|
| id        | Module id   |
| panel     | string, can be 'sidebar' or 'main' passed to UI   |
| obj       | reactiveValues object containing carnation object passed to server  |
| plot_args | reactive containing 'fdr.thres' (padj threshold), 'fc.thres' (log2FC) & 'gene.to.plot' (genes to be labeled) passed to server |
| config    | reactive list with config settings passed to server   |

### Value

UI returns tagList with scatter plot UI. Server invisibly returns NULL (used for side effects).

### Examples

```
library(shiny)

# Create reactive values to simulate app state
oobj <- make_example_carnation_object()

obj <- reactiveValues(
  dds = oobj$dds,
  rld = oobj$rld,
  res = oobj$res,
  all_dds = oobj$all_dds,
  all_rld = oobj$all_rld,
  dds_mapping = oobj$dds_mapping
)
```

```

plot_args <- reactive({
  list(
    fdr.thres=0.1,
    fc.thres=0,
    gene.to.plot=c('gene1', 'gene2')
  )
})

config <- reactiveVal(get_config())

shinyApp(
  ui = fluidPage(
    sidebarPanel(scatterPlotUI('p', 'sidebar')),
    mainPanel(scatterPlotUI('p', 'main'))
  ),
  server = function(input, output, session){
    scatterPlotServer('p', obj, plot_args, config)
  }
)

```

---

 settingsmod

*Settings module*


---

## Description

Module UI & server for user access details interface.

Server code for settings module

## Usage

```
settingsUI(id, panel, username)
```

```
settingsServer(id, details, depth, end_offset, assay_fun, config)
```

## Arguments

|            |  |
|------------|--|
| id         | Module id  |
| panel      | context for generating ui elements ('sidebar' or 'main') |
| username   | user name  |
| details    | reactive list with user name & app location details      |
| depth      | project name depth                                       |
| end_offset | project name end offset                                  |
| assay_fun  | function to parse assay names from file path             |
| config     | reactive list with config settings                       |



---

summarize.res.list      *Combine everything in the results list into a single table*

---

## Description

Combine everything in the results list into a single table

## Usage

```
summarize.res.list(  
  res.list,  
  dds.list,  
  dds_mapping,  
  alpha,  
  lfc.thresh,  
  labels = NULL  
)
```

## Arguments

|             |   |
|-------------|---|
| res.list    | Named list of lists, where each sublist contains the following names: c('res', 'dds', 'label'). "res" is a DESeqResults object, "dds" is either the indexing label for the dds.list object or the DESeq object, and "label" is a nicer-looking label to use. NOTE: backwards compatibility with older versions of lcdb-wf depends on no dds.list object being passed. |
| dds.list    | List of DESeqDataSet objects whose names are expected to match 'dds' slots in the 'res.list' object   |
| dds_mapping | List mapping names of dds.list to res.list elements   |
| alpha       | false-discovery rate threshold  |
| lfc.thresh  | log2FoldChange threshold  |
| labels      | list of descriptions for res.list elements  |

## Value

Dataframe

## Examples

```
n_genes <- 100  
  
# make mock dds list  
dds_list <- list(main=DESeq2::makeExampleDESeqDataSet(n=n_genes))  
  
# make mock results df  
res1 <- data.frame(  
  baseMean = runif(n_genes, 10, 1000),
```

```

        log2FoldChange = rnorm(n_genes, 0, 2),
        lfcSE = runif(n_genes, 0.1, 0.5),
        stat = rnorm(n_genes, 0, 3),
        pvalue = runif(n_genes, 0, 1),
        padj = runif(n_genes, 0, 1),
        symbol = paste0("GENE", 1:n_genes),
        row.names = paste0("gene", 1:n_genes)
    )

res2 <- data.frame(
  baseMean = runif(n_genes, 10, 1000),
  log2FoldChange = rnorm(n_genes, 0, 2),
  lfcSE = runif(n_genes, 0.1, 0.5),
  stat = rnorm(n_genes, 0, 3),
  pvalue = runif(n_genes, 0, 1),
  padj = runif(n_genes, 0, 1),
  symbol = paste0("GENE", 1:n_genes),
  row.names = paste0("gene", 1:n_genes)
)

# make list of results
res_list <- list(
  comp1=res1,
  comp2=res2
)

# make dds mapping
dds_mapping <- list(comp1='main', comp2='main')

# get summary
df <- summarize.res.list(res_list, dds_list, dds_mapping, alpha=0.1, lfc.thresh=0)

```

---

sumovmod

*Summary overview plot module*


---

## Description

UI & module to generate summary overview plots.

## Usage

```

sumovPlotUI(id, panel, type = "")

sumovPlotServer(id, obj, config, type = "")

```

## Arguments

|       |                                    |
|-------|------------------------------------|
| id    | Module id                          |
| panel | string, can be 'sidebar' or 'main' |

type            string, if 'comp' then show the comparison view  
 obj             reactiveValues object containing GeneTonic object  
 config          reactive list with config settings

### Value

UI returns tagList with plot UI server invisibly returns NULL (used for side effects)

### Examples

```

library(shiny)

# get enrichResult object
data(eres_dex, package='carnation')

# convert to GeneTonic object
gt <- GeneTonic::shake_enrichResult(eres_dex)

obj <- reactive({
  list(l_gs = gt$l_gs,
       anno_df = gt$anno_df,
       label = 'comp1')
})

config <- reactiveVal(get_config())

# run simple shiny app with plot
if(interactive()){
  shinyApp(
    ui = fluidPage(
      sidebarPanel(sumovPlotUI('p', 'sidebar')),
      mainPanel(sumovPlotUI('p', 'main'))
    ),
    server = function(input, output, session){
      sumovPlotServer('p', obj, config)
    }
  )
}

```

---

top.genes

*Get top DE genes by log2FoldChange or adjusted p-value*


---

### Description

Get top DE genes by log2FoldChange or adjusted p-value

### Usage

```
top.genes(res, fdr.thres = 0.01, fc.thres = 0, n = 10, by = "log2FoldChange")
```

**Arguments**

|           |  |
|-----------|--|
| res       | data.frame with DE analysis results                        |
| fdr.thres | FDR threshold  |
| fc.thres  | log2FoldChange threshold                                   |
| n         | number of genes to return                                  |
| by        | metric to determine top genes ('log2FoldChange' or 'padj') |

**Value**

vector of gene symbols

**Examples**

```
# get DE results
data(res_dex, package='carnation')

g <- top.genes(res_dex)
```

---

upsetmod

*Upset plot module*


---

**Description**

Module UI & server to generate upset plots.

**Usage**

```
upsetPlotUI(id, panel)

upsetPlotServer(id, obj, plot_args, gene_scratchpad, reset_genes, config)
```

**Arguments**

|                 |  |
|-----------------|--|
| id              | Module id  |
| panel           | string, can be 'sidebar' or 'main'                                     |
| obj             | reactiveValues object containing carnation object                      |
| plot_args       | reactive containing 'fdr.thres' (padj threshold) & 'fc.thres' (log2FC) |
| gene_scratchpad | reactiveValues object containing genes selected in scratchpad          |
| reset_genes     | reactive to reset gene scratchpad selection                            |
| config          | reactive list with config settings                                     |

**Value**

UI returns tagList with upset plot UI. Server returns reactive with list containing upset table, intersections & selected genes.



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