

# Package ‘debrowser’

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**Type** Package

**Title** Interactive Differential Expression Analysis Browser

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**Description** Bioinformatics platform containing interactive plots and tables for differential gene and region expression studies. Allows visualizing expression data much more deeply in an interactive and faster way. By changing the parameters, users can easily discover different parts of the data that like never have been done before. Manually creating and looking these plots takes time. With DEBrowser users can prepare plots without writing any code. Differential expression, PCA and clustering analysis are made on site and the results are shown in various plots such as scatter, bar, box, volcano, ma plots and Heatmaps.

**Depends** R (>= 3.5.0),

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**LazyData** true

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---

actionButtonDE	<i>Buttons including Action Buttons and Event Buttons</i>
----------------	---

---

## Description

Creates an action button whose value is initially zero, and increments by one each time it is pressed.

## Usage

```
actionButtonDE(
  inputId,
  label,
  styleclass = "",
  size = "",
  block = FALSE,
  icon = NULL,
  css.class = "",
  ...
)
```

## Arguments

inputId	Specifies the input slot that will be used to access the value.
label	The contents of the button—usually a text label, but you could also use any other HTML, like an image.
styleclass	The Bootstrap styling class of the button—options are primary, info, success, warning, danger, inverse, link or blank
size	The size of the button—options are large, small, mini
block	Whether the button should fill the block

icon	Display an icon for the button
css.class	Any additional CSS class one wishes to add to the action button
...	Other argument to feed into shiny::actionButton

### Examples

```
actionButtonDE("goDE", "Go to DE Analysis")
```

---

addDataCols	<i>addDataCols</i>
-------------	--------------------

---

### Description

add additional data columns to de results

### Usage

```
addDataCols(data = NULL, de_res = NULL, cols = NULL, conds = NULL)
```

### Arguments

data	loaded dataset
de_res	de results
cols	columns
conds	inputconds

### Value

data

### Examples

```
x <- addDataCols()
```

addID                      *addID*

---

**Description**

Adds an id to the data frame being used.

**Usage**

```
addID(data = NULL)
```

**Arguments**

data                      loaded dataset

**Value**

data

**Examples**

```
x <- addID()
```

---

all2all                      *all2all*

---

**Description**

Prepares all2all scatter plots for given datasets.

**Usage**

```
all2all(data, cex = 2)
```

**Arguments**

data                      data that have the sample names in the header.  
cex                        text size

**Value**

all2all scatter plots

**Examples**

```
plot<-all2all(mtcars)
```

---

all2allControlsUI	<i>all2allControlsUI</i>
-------------------	--------------------------

---

**Description**

Generates the controls in the left menu for an all2all plot

**Usage**

```
all2allControlsUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

returns the controls for left menu

**Note**

all2allControlsUI

**Examples**

```
x <- all2allControlsUI("bar")
```

---

applyFilters	<i>applyFilters</i>
--------------	---------------------

---

**Description**

Applies filters based on user selected parameters to be displayed within the DEBrowser.

**Usage**

```
applyFilters(filt_data = NULL, cols = NULL, conds = NULL, input = NULL)
```

**Arguments**

filt_data	loaded dataset
cols	selected samples
conds	seleced conditions
input	input parameters

**Value**

data

**Examples**

```
x <- applyFilters()
```

---

<code>applyFiltersNew</code>	<i>applyFiltersNew</i>
------------------------------	------------------------

---

**Description**

Apply filters based on foldChange cutoff and padj value. This function adds a "Legend" column with "Up", "Down" or "NS" values for visualization.

**Usage**

```
applyFiltersNew(data = NULL, input = NULL)
```

**Arguments**

<code>data</code>	loaded dataset
<code>input</code>	input parameters

**Value**

data

**Examples**

```
x <- applyFiltersNew()
```

---

<code>applyFiltersToMergedComparison</code>	<i>applyFiltersToMergedComparison</i>
---	---------------------------------------

---

**Description**

Gathers the merged comparison data to be used within the DEBrowser.

**Usage**

```
applyFiltersToMergedComparison(dc = NULL, nc = NULL, input = NULL)
```

**Arguments**

dc	all data
nc	the number of comparisons
input	input params

**Value**

data

**Examples**

```
x <- applyFiltersToMergedComparison()
```

---

barMainPlotControlsUI *barMainPlotControlsUI*

---

**Description**

Generates the controls in the left menu for a bar main plot

**Usage**

```
barMainPlotControlsUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

returns the controls for left menu

**Note**

```
barMainPlotControlsUI
```

**Examples**

```
x <- barMainPlotControlsUI("bar")
```

---

batchEffectUI	<i>batchEffectUI</i> Creates a panel to correct batch effect
---------------	--

---

**Description**

batchEffectUI Creates a panel to correct batch effect

**Usage**

```
batchEffectUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

panel

**Examples**

```
x <- batchEffectUI("batcheffect")
```

---

batchMethod	<i>batchMethod</i>
-------------	--------------------

---

**Description**

select batch effect method

**Usage**

```
batchMethod(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

radio control

**Note**

batchMethod

**Examples**

```
x <- batchMethod("batch")
```

---

BoxMainPlotControlsUI *BoxMainPlotControlsUI*

---

**Description**

Generates the controls in the left menu for a Box main plot

**Usage**

```
BoxMainPlotControlsUI(id)
```

**Arguments**

id                    namespace id

**Value**

returns the controls for left menu

**Note**

BoxMainPlotControlsUI

**Examples**

```
x <- BoxMainPlotControlsUI("box")
```

---

changeClusterOrder    *changeClusterOrder*

---

**Description**

change order of K-means clusters

**Usage**

```
changeClusterOrder(order = NULL, cld = NULL)
```

**Arguments**

order                order  
cld                   data

**Value**

heatmap plot area

**Note**

`changeClusterOrder`

**Examples**

```
x <- changeClusterOrder()
```

---

`checkCountData`

*checkCountData*

---

**Description**

Returns if there is a problem in the count data.

**Usage**

```
checkCountData(input = NULL)
```

**Arguments**

`input`            `inputs`

**Value**

error if there is a problem about the loaded data

**Note**

`checkCountData`

**Examples**

```
x <- checkCountData()
```

---

checkMetaData	<i>checkMetaData</i>
---------------	----------------------

---

**Description**

Returns if there is a problem in the count data.

**Usage**

```
checkMetaData(input = NULL, counttable = NULL)
```

**Arguments**

input	input
counttable	counttable

**Value**

error if there is a problem about the loaded data

**Note**

checkMetaData

**Examples**

```
x <- checkMetaData()
```

---

clusterData	<i>clusterData</i>
-------------	--------------------

---

**Description**

Gathers the Cluster analysis data to be used within the GO Term plots.

**Usage**

```
clusterData(dat = NULL)
```

**Arguments**

dat	the data to cluster
-----	---------------------

**Value**

clustered data

**Note**

```
clusterData
```

**Examples**

```
mycluster <- clusterData()
```

---

```
clustFunParamsUI      clustFunParamsUI
```

---

**Description**

get cluster function parameter control

**Usage**

```
clustFunParamsUI()
```

**Value**

cluster params

**Note**

```
clustFunParamsUI
```

**Examples**

```
x <- clustFunParamsUI()
```

---

```
compareClust      compareClust
```

---

**Description**

Compares the clustered data to be displayed within the GO Term plots.

**Usage**

```
compareClust(  
  dat = NULL,  
  ont = "CC",  
  org = "org.Hs.eg.db",  
  fun = "enrichGO",  
  title = "Ontology Distribution Comparison",  
  pvalueCutoff = 0.01  
)
```

**Arguments**

dat            data to compare clusters  
ont            the ontology to use  
org            the organism used  
fun            fun  
title          title of the comparison  
pvalueCutoff   pvalueCutoff

**Value**

compared cluster

**Note**

compareClust

**Examples**

```
x <- compareClust()
```

---

condSelectUI

*condSelectUI Creates a panel to select samples for each condition*

---

**Description**

condSelectUI Creates a panel to select samples for each condition

**Usage**

```
condSelectUI()
```

**Value**

panel

**Examples**

```
x <- condSelectUI()
```

---

correctCombat	<i>Correct Batch Effect using Combat in sva package</i>
---------------	---

---

**Description**

Batch effect correction

**Usage**

```
correctCombat(input = NULL, idata = NULL, metadata = NULL, method = NULL)
```

**Arguments**

input	input values
idata	data
metadata	metadata
method	method: either Combat or CombatSeq

**Value**

data

**Examples**

```
x<-correctCombat ()
```

---

correctHarman	<i>Correct Batch Effect using Harman</i>
---------------	--

---

**Description**

Batch effect correction

**Usage**

```
correctHarman(input = NULL, idata = NULL, metadata = NULL)
```

**Arguments**

input	input values
idata	data
metadata	metadata

**Value**

data

**Examples**

```
x<-correctHarman ()
```

---

customColorsUI	<i>customColorsUI</i>
----------------	-----------------------

---

**Description**

get Custom Color controls

**Usage**

```
customColorsUI(id)
```

**Arguments**

id                    namespace ID

**Value**

color range

**Note**

getColRng

**Examples**

```
x <- customColorsUI("heatmap")
```

---

cutOffSelectionUI	<i>cutOffSelectionUI</i>
-------------------	--------------------------

---

**Description**

Gathers the cut off selection for DE analysis

**Usage**

```
cutOffSelectionUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

returns the left menu according to the selected tab;

**Note**

cutOffSelectionUI

**Examples**

```
x <- cutOffSelectionUI("cutoff")
```

---

dataLCFUI	<i>dataLCFUI Creates a panel to filter low count genes and regions</i>
-----------	--

---

**Description**

dataLCFUI Creates a panel to filter low count genes and regions

**Usage**

```
dataLCFUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

panel

**Examples**

```
x <- dataLCFUI("lcf")
```

---

dataLoadUI	<i>dataLoadUI</i>
------------	-------------------

---

**Description**

Creates a panel to upload the data

**Usage**

```
dataLoadUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

panel

**Examples**

```
x <- dataLoadUI("load")
```

---

debrowserall2all	<i>debrowserall2all</i>
------------------	-------------------------

---

**Description**

Module for a bar plot that can be used in data prep, main plots low count removal modules or any desired module

**Usage**

```
debrowserall2all(input, output, session, data = NULL, cex = 2)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values
cex	the size of the dots

**Value**

all2all plot

**Examples**

```
x <- debrowserall2all()
```

---

debrowserbarmainplot *debrowserbarmainplot*

---

**Description**

Module for a bar plot that can be used in data prep, main plots low count removal modules or any desired module

**Usage**

```
debrowserbarmainplot(  
  input,  
  output,  
  session,  
  data = NULL,  
  cols = NULL,  
  conds = NULL,  
  cond_names = NULL,  
  key = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values
cols	columns
conds	conditions
cond_names	condition names
key	the gene or region name

**Value**

density plot

**Examples**

```
x <- debrowserbarmainplot()
```

---

debrowserbatcheffect *debrowserbatcheffect*

---

**Description**

Module to correct batch effect

**Usage**

```
debrowserbatcheffect(input, output, session, ldata = NULL)
```

**Arguments**

input	input variables
output	output objects
session	session
ldata	loaded data

**Value**

main plot  
panel

**Examples**

```
x <- debrowserbatcheffect()
```

---

debrowserboxmainplot *debrowserboxmainplot*

---

**Description**

Module for a box plot that can be used in DEanalysis main part and used heatmaps

**Usage**

```
debrowserboxmainplot(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  data = NULL,  
  cols = NULL,  
  conds = NULL,  
  cond_names = NULL,  
  key = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values
cols	columns
conds	conditions
cond_names	condition names
key	the gene or region name

**Value**

density plot

**Examples**

```
x <- debrowserboxmainplot()
```

---

debrowsercondselect    *debrowsercondselect*

---

**Description**

Condition selection This is not a module. Module construction didn't used here, just use it as functions not in a module.

**Usage**

```
debrowsercondselect(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  data = NULL,  
  metadata = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
data	count data
metadata	metadata

**Value**

main plot  
panel

**Examples**

```
x <- debrowsercondselect()
```

---

debrowserdataload      *debrowserdataload*

---

**Description**

Module to load count data and metadata

**Usage**

```
debrowserdataload(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  nextpagebutton = NULL  
)
```

**Arguments**

input            input variables  
output           output objects  
session          session  
nextpagebutton   the name of the next page button after loading the data

**Value**

main plot  
panel

**Examples**

```
x <- debrowserdataload()
```

---

debrowserdeanalysis    *debrowserdeanalysis*

---

**Description**

Module to perform and visualize DE results.

**Usage**

```
debrowserdeanalysis(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  data = NULL,  
  metadata = NULL,  
  columns = NULL,  
  conds = NULL,  
  params = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values
metadata	metadata
columns	columns
conds	conditions
params	de parameters

**Value**

DE panel

**Examples**

```
x <- debrowserdeanalysis()
```

---

debrowserdensityplot *debrowserdensityplot*

---

**Description**

Module for a density plot that can be used in data prep and low count removal modules

**Usage**

```
debrowserdensityplot(input = NULL, output = NULL, session = NULL, data = NULL)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values

**Value**

density plot

**Examples**

```
x <- debrowserdensityplot()
```

---

debrowserheatmap *debrowserheatmap*

---

**Description**

Heatmap module to create interactive heatmaps and get selected list from a heatmap

**Usage**

```
debrowserheatmap(input, output, session, expdata = NULL)
```

**Arguments**

input	input variables
output	output objects
session	session
expdata	a matrix that includes expression values

**Value**

heatmaply plot

**Examples**

```
x <- debrowserheatmap()
```

---

debrowserhistogram    *debrowserhistogram*

---

**Description**

Module for a histogram that can be used in data prep and low count removal modules

**Usage**

```
debrowserhistogram(input = NULL, output = NULL, session = NULL, data = NULL)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values

**Value**

histogram

**Examples**

```
x <- debrowserhistogram()
```

---

debrowserIQRplot      *debrowserIQRplot*

---

**Description**

Module for an IQR plot that can be used in data prep and low count removal modules

**Usage**

```
debrowserIQRplot(input = NULL, output = NULL, session = NULL, data = NULL)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values

**Value**

IQR

**Examples**

```
x <- debrowserIQRplot()
```

---

debrowserlowcountfilter  
*debrowserlowcountfilter*

---

**Description**

Module to filter low count genes/regions

**Usage**

```
debrowserlowcountfilter(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  ldata = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
ldata	loaded data

**Value**

main plot  
panel

**Examples**

```
x <- debrowserlowcountfilter()
```

---

debrowsermainplot      *debrowsermainplot*

---

**Description**

Module for a scatter, volcano and ma plots that are going to be used as a mainplot in debrowser

**Usage**

```
debrowsermainplot(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  data = NULL,  
  cond_names = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
data	a matrix that includes expression values
cond_names	condition names

**Value**

main plot  
panel

**Examples**

```
x <- debrowsermainplot()
```

---

debrowserpcaplot	<i>debrowserpcaplot</i>
------------------	-------------------------

---

**Description**

Module for a pca plot with its loadings as a mainplot in debrowser

**Usage**

```
debrowserpcaplot(  
  input = NULL,  
  output = NULL,  
  session = NULL,  
  pccadata = NULL,  
  metadata = NULL  
)
```

**Arguments**

input	input variables
output	output objects
session	session
pccadata	a matrix that includes expression values
metadata	metadata to color the plots

**Value**

main plot  
panel

**Examples**

```
x <- debrowserpcaplot()
```

dendControlsUI      *dendControlsUI*

---

**Description**

get distance metric parameters

**Usage**

```
dendControlsUI(id, dendtype = "Row")
```

**Arguments**

id	module ID
dendtype	Row or Col

**Value**

controls

**Note**

dendControlsUI

**Examples**

```
x <- dendControlsUI("heatmap")
```

---

densityPlotControlsUI      *densityPlotControlsUI*

---

**Description**

Generates the controls in the left menu for a densityPlot

**Usage**

```
densityPlotControlsUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

returns the left menu

**Note**

```
densityPlotControlsUI
```

**Examples**

```
x <- densityPlotControlsUI("density")
```

---

deServer

*deServer*

---

**Description**

Sets up shinyServer to be able to run DEBrowser interactively.

**Usage**

```
deServer(input, output, session)
```

**Arguments**

input	input params from UI
output	output params to UI
session	session variable

**Value**

the panel for main plots;

**Note**

deServer

**Examples**

```
deServer
```

---

deUI	<i>deUI</i>
------	-------------

---

**Description**

Creates a shinyUI to be able to run DEBrowser interactively.

**Usage**

```
deUI()
```

**Value**

the panel for main plots;

**Note**

deUI

**Examples**

```
x<-deUI()
```

---

distFunParamsUI	<i>distFunParamsUI</i>
-----------------	------------------------

---

**Description**

get distance metric parameters

**Usage**

```
distFunParamsUI()
```

**Value**

funParams

**Note**

distFunParamsUI

**Examples**

```
x <- distFunParamsUI()
```

---

drawKEGG	<i>drawKEGG</i>
----------	-----------------

---

**Description**

draw KEGG pathway with expression values

**Usage**

```
drawKEGG(input = NULL, dat = NULL, pid = NULL)
```

**Arguments**

input	input
dat	expression matrix
pid	pathway id

**Value**

enriched DO

**Note**

drawKEGG

**Examples**

```
x <- drawKEGG()
```

---

drawPCAExplained	<i>Creates a more detailed plot using the PCA results from the selected dataset.</i>
------------------	--

---

**Description**

Creates a more detailed plot using the PCA results from the selected dataset.

**Usage**

```
drawPCAExplained(explainedData = NULL)
```

**Arguments**

explainedData	selected data
---------------	---------------

**Value**

explained plot

**Examples**

```
x <- drawPCAExplained()
```

---

fileTypes

*fileTypes*

---

**Description**

Returns fileTypes that are going to be used in creating fileUpload UI

**Usage**

```
fileTypes()
```

**Value**

file types

**Note**

fileTypes

**Examples**

```
x <- fileTypes()
```

---

fileUploadBox

*fileUploadBox*

---

**Description**

File upload module

**Usage**

```
fileUploadBox(id = NULL, inputId = NULL, label = NULL)
```

**Arguments**

id	namespace id
inputId	input file ID
label	label

**Value**

radio control

**Note**

fileUploadBox

**Examples**

```
x <- fileUploadBox("meta", "metadata", "Metadata")
```

---

generateTestData      *generateTestData*

---

**Description**

This generates a test data that is suitable to main plots in debrowser

**Usage**

```
generateTestData(dat = NULL)
```

**Arguments**

dat	DESeq results will be generated for loaded data
-----	---

**Value**

testData

**Examples**

```
x <- generateTestData()
```

---

<code>getAfterLoadMsg</code>	<code><i>getAfterLoadMsg</i></code>
------------------------------	-------------------------------------

---

**Description**

Generates and displays the message to be shown after loading data within the DEBrowser.

**Usage**

```
getAfterLoadMsg()
```

**Value**

return After Load Msg

**Note**

```
getAfterLoadMsg
```

**Examples**

```
x <- getAfterLoadMsg()
```

---

<code>getAll2AllPlotUI</code>	<code><i>getAll2AllPlotUI</i></code>
-------------------------------	--------------------------------------

---

**Description**

all2all plots UI.

**Usage**

```
getAll2AllPlotUI(id)
```

**Arguments**

<code>id</code>	namespace id
-----------------	--------------

**Value**

the panel for all2all plots;

**Note**

```
getAll2AllPlotUI
```

**Examples**

```
x <- getA112A11PlotUI("bar")
```

---

`getBarMainPlot`      *getBarMainPlot*

---

**Description**

Makes Density plots

**Usage**

```
getBarMainPlot(  
  data = NULL,  
  cols = NULL,  
  conds = NULL,  
  cond_names = NULL,  
  key = NULL,  
  title = "",  
  input = NULL  
)
```

**Arguments**

<code>data</code>	count or normalized data
<code>cols</code>	cols
<code>conds</code>	conds
<code>cond_names</code>	condition names
<code>key</code>	key
<code>title</code>	title
<code>input</code>	input

**Examples**

```
getBarMainPlot()
```

---

<code>getBarMainPlotUI</code>	<i>getBarMainPlotUI</i>
-------------------------------	-------------------------

---

**Description**

main bar plots UI.

**Usage**

```
getBarMainPlotUI(id)
```

**Arguments**

`id` namespace id

**Value**

the panel for Density plots;

**Note**

```
getBarMainPlotUI
```

**Examples**

```
x <- getBarMainPlotUI("bar")
```

---

<code>getBoxMainPlot</code>	<i>getBoxMainPlot</i>
-----------------------------	-----------------------

---

**Description**

Makes Density plots

**Usage**

```
getBoxMainPlot(  
  data = NULL,  
  cols = NULL,  
  conds = NULL,  
  cond_names = NULL,  
  key = NULL,  
  title = "",  
  input = NULL  
)
```

**Arguments**

<code>data</code>	count or normalized data
<code>cols</code>	cols
<code>conds</code>	conds
<code>cond_names</code>	condition names
<code>key</code>	key
<code>title</code>	title
<code>input</code>	input

**Examples**

```
getBoxMainPlot()
```

---

<code>getBoxMainPlotUI</code>	<i>getBoxMainPlotUI</i>
-------------------------------	-------------------------

---

**Description**

main Box plots UI.

**Usage**

```
getBoxMainPlotUI(id)
```

**Arguments**

<code>id</code>	namespace id
-----------------	--------------

**Value**

the panel for Density plots;

**Note**

```
getBoxMainPlotUI
```

**Examples**

```
x <- getBoxMainPlotUI("box")
```

getBSTableUI                    *getBSTableUI prepares a Modal to put a table*

---

**Description**

getBSTableUI prepares a Modal to put a table

**Usage**

```
getBSTableUI(  
  name = NULL,  
  label = NULL,  
  trigger = NULL,  
  size = "large",  
  modal = NULL  
)
```

**Arguments**

name	name
label	label
trigger	trigger button for the modal
size	size of the modal
modal	modal yes/no

**Value**

the modal

**Examples**

```
x<- getBSTableUI()
```

---

getColors                    *getColors*

---

**Description**

get colors for the domains

**Usage**

```
getColors(domains = NULL)
```

**Arguments**

domains            domains to be colored

**Value**

colors

**Examples**

```
x<-getColor()
```

---

`getColorShapeSelection`  
*getColorShapeSelection*

---

**Description**

Generates the fill and shape selection boxes for PCA plots. metadata file has to be loaded in this case

**Usage**

```
getColorShapeSelection(metadata = NULL, input = NULL, session = NULL)
```

**Arguments**

metadata            metadata table  
input                input  
session              session

**Value**

Color and shape selection boxes

**Examples**

```
x <- getColorShapeSelection()
```

---

`getCompSelection`      *getCompSelection*

---

**Description**

Gathers the user selected comparison set to be used within the DEBrowser.

**Usage**

```
getCompSelection(name = NULL, count = NULL)
```

**Arguments**

<code>name</code>	the name of the selectInput
<code>count</code>	comparison count

**Note**

```
getCompSelection
```

**Examples**

```
x <- getCompSelection(name="comp", count = 2)
```

---

`getConditionSelector`      *getConditionSelector*

---

**Description**

Selects user input conditions to run in DESeq.

**Usage**

```
getConditionSelector(num = NULL, choices = NULL, selected = NULL)
```

**Arguments**

<code>num</code>	panel that is going to be shown
<code>choices</code>	sample list
<code>selected</code>	selected sample list

**Examples**

```
x <- getConditionSelector()
```

---

```
getConditionSelectorFromMeta
      getConditionSelectorFromMeta
```

---

**Description**

Selects user input conditions to run in DESeq from metadata

**Usage**

```
getConditionSelectorFromMeta(
  metadata = NULL,
  input = NULL,
  index = 1,
  num = 0,
  choices = NULL,
  selected = NULL
)
```

**Arguments**

metadata	meta data table
input	input
index	index
num	num
choices	choices
selected	selected

**Examples**

```
x <- getConditionSelectorFromMeta()
```

---

```
getCondMsg      getCondMsg
```

---

**Description**

Generates and displays the current conditions and their samples within the DEBrowser.

**Usage**

```
getCondMsg(dc = NULL, input = NULL, cols = NULL, conds = NULL)
```

**Arguments**

dc	columns
input	selected comparison
cols	columns
conds	selected conditions

**Value**

return conditions

**Note**

getCondMsg

**Examples**

```
x <- getCondMsg()
```

---

getCovariateDetails    *getCovariateDetails*

---

**Description**

get the covariate detail box after DE method selected

**Usage**

```
getCovariateDetails(num = NULL, input = NULL, metadata = NULL)
```

**Arguments**

num	panel that is going to be shown
input	user input
metadata	metadata

**Examples**

```
x <- getCovariateDetails()
```

---

`getCutOffSelection`     *getCutOffSelection*

---

**Description**

Gathers the cut off selection for DE analysis

**Usage**

```
getCutOffSelection(nc = 1)
```

**Arguments**

`nc`                    total number of comparisons

**Value**

returns the left menu according to the selected tab;

**Note**

`getCutOffSelection`

**Examples**

```
x <- getCutOffSelection()
```

---

`getDataAssesmentText`     *getDataAssesmentText DataAssesment text*

---

**Description**

`getDataAssesmentText` *DataAssesment text*

**Usage**

```
getDataAssesmentText()
```

**Value**

help text for data assesment

**Examples**

```
x<- getDataAssesmentText()
```

---

getDataForTables	<i>getDataForTables</i> get data to fill up tables tab
------------------	--

---

### Description

getDataForTables get data to fill up tables tab

### Usage

```
getDataForTables(  
  input = NULL,  
  init_data = NULL,  
  filt_data = NULL,  
  selected = NULL,  
  getMostVaried = NULL,  
  mergedComp = NULL,  
  explainedData = NULL  
)
```

### Arguments

input	input parameters
init_data	initial dataset
filt_data	filt_data
selected	selected genes
getMostVaried	most varied genes
mergedComp	merged comparison set
explainedData	pca gene set

### Value

data

### Examples

```
x <- getDataForTables()
```

---

`getDataPreparationText`      *getDataPreparationText DataPreparation text*

---

**Description**

`getDataPreparationText` DataPreparation text

**Usage**

`getDataPreparationText()`

**Value**

help text for data preparation

**Examples**

```
x<- getDataPreparationText()
```

---

`getDEAnalysisText`      *getDEAnalysisText DEAnalysis text*

---

**Description**

`getDEAnalysisText` DEAnalysis text

**Usage**

`getDEAnalysisText()`

**Value**

help text for DE Analysis

**Examples**

```
x<- getDEAnalysisText()
```

---

<code>getDensityPlot</code>	<i>getDensityPlot</i>
-----------------------------	-----------------------

---

**Description**

Makes Density plots

**Usage**

```
getDensityPlot(data = NULL, input = NULL, title = "")
```

**Arguments**

<code>data</code>	count or normalized data
<code>input</code>	input
<code>title</code>	title

**Examples**

```
getDensityPlot()
```

---

<code>getDensityPlotUI</code>	<i>getDensityPlotUI</i>
-------------------------------	-------------------------

---

**Description**

Density plot UI.

**Usage**

```
getDensityPlotUI(id)
```

**Arguments**

<code>id</code>	namespace id
-----------------	--------------

**Value**

the panel for Density plots;

**Note**

```
getDensityPlotUI
```

**Examples**

```
x <- getDensityPlotUI("density")
```

---

<code>getDEResultsUI</code>	<i>getDEResultsUI</i> Creates a panel to visualize DE results
-----------------------------	---

---

**Description**

`getDEResultsUI` Creates a panel to visualize DE results

**Usage**

```
getDEResultsUI(id)
```

**Arguments**

`id` namespace id

**Value**

panel

**Examples**

```
x <- getDEResultsUI("batcheffect")
```

---

<code>getDomains</code>	<i>getDomains</i>
-------------------------	-------------------

---

**Description**

Get domains for the main plots.

**Usage**

```
getDomains(filt_data = NULL)
```

**Arguments**

`filt_data` data to get the domains

**Value**

domains

**Examples**

```
x<-getDomains()
```

---

getDown	<i>getDown get down regulated data</i>
---------	--

---

**Description**

getDown get down regulated data

**Usage**

```
getDown(filt_data = NULL)
```

**Arguments**

filt\_data      filt\_data

**Value**

data

**Examples**

```
x <- getDown()
```

---

getDownloadSection	<i>getDownloadSection</i>
--------------------	---------------------------

---

**Description**

download section button and dataset selection box in the menu for user to download selected data.

**Usage**

```
getDownloadSection(choices = NULL)
```

**Arguments**

choices      main vs. QC section

**Value**

the panel for download section in the menu;

**Note**

`getDownloadSection`

**Examples**

```
x<- getDownloadSection()
```

---

`getEnrichDO`

*getEnrichDO*

---

**Description**

Gathers the Enriched DO Term analysis data to be used within the GO Term plots.

**Usage**

```
getEnrichDO(genelist = NULL, pvalueCutoff = 0.01)
```

**Arguments**

<code>genelist</code>	gene list
<code>pvalueCutoff</code>	the p value cutoff

**Value**

enriched DO

**Note**

`getEnrichDO`

**Examples**

```
x <- getEnrichDO()
```

---

<code>getEnrichGO</code>	<i>getEnrichGO</i>
--------------------------	--------------------

---

**Description**

Gathers the Enriched GO Term analysis data to be used within the GO Term plots.

**Usage**

```
getEnrichGO(  
  genelist = NULL,  
  pvalueCutoff = 0.01,  
  org = "org.Hs.eg.db",  
  ont = "CC"  
)
```

**Arguments**

<code>genelist</code>	gene list
<code>pvalueCutoff</code>	p value cutoff
<code>org</code>	the organism used
<code>ont</code>	the ontology used

**Value**

Enriched GO

**Note**

`getEnrichGO`

**Examples**

```
x <- getEnrichGO()
```

---

getEnrichKEGG	<i>getEnrichKEGG</i>
---------------	----------------------

---

**Description**

Gathers the Enriched KEGG analysis data to be used within the GO Term plots.

**Usage**

```
getEnrichKEGG(genelist = NULL, pvalueCutoff = 0.01, org = "org.Hs.eg.db")
```

**Arguments**

genelist	gene list
pvalueCutoff	the p value cutoff
org	the organism used

**Value**

Enriched KEGG

**Note**

getEnrichKEGG

**Examples**

```
x <- getEnrichKEGG()
```

---

getEntrezIds	<i>getEntrezIds</i>
--------------	---------------------

---

**Description**

Gathers the gene list to use for GOTerm analysis.

**Usage**

```
getEntrezIds(genes = NULL, org = "org.Hs.eg.db")
```

**Arguments**

genes	gene list with fold changes
org	organism for gene symbol entrez ID conversion

**Value**

ENTREZ ID list

**Note**

GOTerm  
getEntrezIds symbol to ENTREZ ID conversion

**Examples**

```
x <- getEntrezIds()
```

---

getEntrezTable	<i>getEntrezTable</i>
----------------	-----------------------

---

**Description**

Gathers the entrezIds of the genes in given list and their data

**Usage**

```
getEntrezTable(genes = NULL, dat = NULL, org = "org.Hs.eg.db")
```

**Arguments**

genes	gene list
dat	data matrix
org	organism for gene symbol entrez ID conversion

**Value**

table with the entrez IDs in the rownames

**Note**

GOTerm  
getEntrezTable symbol to ENTREZ ID conversion

**Examples**

```
x <- getEntrezTable()
```

---

getGeneList	<i>getGeneList</i>
-------------	--------------------

---

**Description**

Gathers the gene list to use for GOTerm analysis.

**Usage**

```
getGeneList(  
  genes = NULL,  
  org = "org.Hs.eg.db",  
  fromType = "SYMBOL",  
  toType = c("ENTREZID")  
)
```

**Arguments**

genes	gene list
org	organism for gene symbol entrez ID conversion
fromType	from Type
toType	to Type

**Value**

ENTREZ ID list

**Note**

GOTerm  
getGeneList symbol to ENTREZ ID conversion

**Examples**

```
x <- getGeneList(c('OCLN', 'ABCC2'))
```

getGeneSetData            *getGeneSetData*

---

**Description**

Gathers the specified gene set list to be used within the DEBrowser.

**Usage**

```
getGeneSetData(data = NULL, geneset = NULL)
```

**Arguments**

data	loaded dataset
geneset	given gene set

**Value**

data

**Examples**

```
x <- getGeneSetData()
```

---

getGOLeftMenu            *getGOLeftMenu*

---

**Description**

Generates the GO Left menu to be displayed within the DEBrowser.

**Usage**

```
getGOLeftMenu()
```

**Value**

returns the left menu according to the selected tab;

**Note**

```
getGOLeftMenu
```

**Examples**

```
x <- getGOLeftMenu()
```

---

`getGoPanel`*getGoPanel*

---

**Description**

Creates go term analysis panel within the shiny display.

**Usage**

```
getGoPanel()
```

**Value**

the panel for go term analysis;

**Note**

```
getGoPanel
```

**Examples**

```
x <- getGoPanel()
```

---

`getGOPlots`*getGOPlots*

---

**Description**

Go term analysis panel. Generates appropriate GO plot based on user selection.

**Usage**

```
getGOPlots(dataset = NULL, GSEARes = NULL, input = NULL)
```

**Arguments**

dataset	the dataset used
GSEARes	GSEA results
input	input params

**Value**

the panel for go plots;

**Note**

getGOPlots

**Examples**

```
x<- getGOPlots()
```

---

getGroupSelector	<i>getGroupSelector Return the groups</i>
------------------	---

---

**Description**

getGroupSelector Return the groups

**Usage**

```
getGroupSelector(metadata = NULL, input = NULL, index = 1, num = 0)
```

**Arguments**

metadata	meta data table
input	input params
index	index
num	num

**Value**

meta select box

**Examples**

```
x<-getGroupSelector()
```

---

getGSEA	<i>getGSEA</i>
---------	----------------

---

**Description**

Gathers the Enriched KEGG analysis data to be used within the GO Term plots.

**Usage**

```
getGSEA(  
  dataset = NULL,  
  pvalueCutoff = 0.01,  
  org = "org.Hs.eg.db",  
  sortfield = "log2FoldChange"  
)
```

**Arguments**

dataset	dataset
pvalueCutoff	the p value cutoff
org	the organism used
sortfield	sort field for GSEA

**Value**

GSEA

**Note**

getGSEA

**Examples**

```
x <- getGSEA()
```

---

getHeatmapUI	<i>getHeatmapUI</i>
--------------	---------------------

---

**Description**

Generates the left menu to be used for heatmap plots

**Usage**

```
getHeatmapUI(id)
```

**Arguments**

id                    module ID

**Value**

heatmap plot area

**Note**

getHeatmapUI

**Examples**

```
x <- getHeatmapUI("heatmap")
```

---

getHelpButton	<i>getHelpButton prepares a helpbutton for to go to a specific site in the documentation</i>
---------------	--

---

**Description**

getHelpButton prepares a helpbutton for to go to a specific site in the documentation

**Usage**

```
getHelpButton(name = NULL, link = NULL)
```

**Arguments**

name                    name that are going to come after info  
link                    link of the help

**Value**

the info button

**Examples**

```
x<- getHelpButton()
```

---

`getHideLegendOnOff`      *getHideLegendOnOff*

---

**Description**

hide legend

**Usage**

```
getHideLegendOnOff(id = "pca")
```

**Arguments**

id                    namespace id

**Examples**

```
x <- getHideLegendOnOff("pca")
```

---

`getHistogramUI`              *getHistogramUI*

---

**Description**

Histogram plots UI.

**Usage**

```
getHistogramUI(id)
```

**Arguments**

id                    namespace id

**Value**

the panel for PCA plots;

**Note**

```
getHistogramUI
```

**Examples**

```
x <- getHistogramUI("histogram")
```

---

getIntroText	<i>getIntroText Intro text</i>
--------------	--------------------------------

---

**Description**

getIntroText Intro text

**Usage**

```
getIntroText()
```

**Value**

the JS for tab updates

**Examples**

```
x<- getIntroText()
```

---

getIQRPlot	<i>getIQRPlot</i>
------------	-------------------

---

**Description**

Makes IQR boxplot plot

**Usage**

```
getIQRPlot(data = NULL, input = NULL, title = "")
```

**Arguments**

data	count or normalized data
input	input
title	title

**Examples**

```
getIQRPlot()
```

---

`getIQRPlotUI`                      *getIQRPlotUI*

---

**Description**

IQR plot UI.

**Usage**

```
getIQRPlotUI(id)
```

**Arguments**

`id`                      namespace id

**Value**

the panel for IQR plots;

**Note**

```
getIQRPlotUI
```

**Examples**

```
x <- getIQRPlotUI("IQR")
```

---

`getJSLine`                      *getJSLine*

---

**Description**

heatmap JS code for selection functionality

**Usage**

```
getJSLine()
```

**Value**

JS Code

**Examples**

```
x <- getJSLine()
```

---

getKEGGModal	<i>getKEGGModal prepares a modal for KEGG plots</i>
--------------	---

---

**Description**

getKEGGModal prepares a modal for KEGG plots

getKEGGModal prepares a helpbutton for to go to a specific site in the documentation

**Usage**

```
getKEGGModal()
```

```
getKEGGModal()
```

**Value**

the info button

the info button

**Examples**

```
x<- getKEGGModal()
```

```
x<- getKEGGModal()
```

---

getLeftMenu	<i>getLeftMenu</i>
-------------	--------------------

---

**Description**

Generates the left menu for for plots within the DEBrowser.

**Usage**

```
getLeftMenu(input = NULL)
```

**Arguments**

input            input values

**Value**

returns the left menu according to the selected tab;

**Note**

`getLeftMenu`

**Examples**

```
x <- getLeftMenu()
```

---

<code>getLegendColors</code>	<i>getLegendColors</i>
------------------------------	------------------------

---

**Description**

Generates colors according to the data

**Usage**

```
getLegendColors(Legend = c("up", "down", "NS"))
```

**Arguments**

Legend            unique Legends

**Value**

`mainPlotControls`

**Note**

`getLegendColors`

**Examples**

```
x <- getLegendColors(c("up", "down", "GS", "NS"))
```

---

<code>getLegendRadio</code>	<i>getLegendRadio</i>
-----------------------------	-----------------------

---

**Description**

Radio buttons for the types in the legend

**Usage**

```
getLegendRadio(id)
```

**Arguments**

<code>id</code>	<code>namespace id</code>
-----------------	---------------------------

**Value**

radio control

**Note**

```
getLegendRadio
```

**Examples**

```
x <- getLegendRadio("deprog")
```

---

<code>getLegendSelect</code>	<i>getLegendSelect</i>
------------------------------	------------------------

---

**Description**

select legend

**Usage**

```
getLegendSelect(id = "pca")
```

**Arguments**

<code>id</code>	<code>namespace id</code>
-----------------	---------------------------

**Note**

```
getLegendSelect
```

**Examples**

```
x <- getLegendSelect("pca")
```

---

*getLevelOrder*                      *getLevelOrder*

---

**Description**

Generates the order of the overlapping points

**Usage**

```
getLevelOrder(Level = c("up", "down", "NS"))
```

**Arguments**

Level                      factor levels shown in the legend

**Value**

order

**Note**

*getLevelOrder*

**Examples**

```
x <- getLevelOrder(c("up", "down", "GS", "NS"))
```

---

*getLoadingMsg*                      *getLoadingMsg*

---

**Description**

Creates and displays the loading message/gif to be displayed within the DEBrowser.

**Usage**

```
getLoadingMsg(output = NULL)
```

**Arguments**

output                      output message

**Value**

loading msg

**Note**

getLoadingMsg

**Examples**

```
x <- getLoadingMsg()
```

---

getLogo

*getLogo*

---

**Description**

Generates and displays the logo to be shown within DEBbrowser.

**Usage**

```
getLogo()
```

**Value**

return logo

**Note**

getLogo

**Examples**

```
x <- getLogo()
```

---

<code>getMainPanel</code>	<i><code>getMainPanel</code></i>
---------------------------	----------------------------------

---

**Description**

main panel for volcano, scatter and maplot. Barplot and box plots are in this page as well.

**Usage**

```
getMainPanel()
```

**Value**

the panel for main plots;

**Note**

```
getMainPanel
```

**Examples**

```
x <- getMainPanel()
```

---

<code>getMainPlotsLeftMenu</code>	<i><code>getMainPlotsLeftMenu</code></i>
-----------------------------------	--

---

**Description**

Generates the Main Plots Left menu to be displayed within the DEBrowser.

**Usage**

```
getMainPlotsLeftMenu()
```

**Value**

returns the left menu according to the selected tab;

**Note**

```
getMainPlotsLeftMenu
```

**Examples**

```
x <- getMainPlotsLeftMenu()
```

---

getMainPlotUI	<i>getMainPlotUI</i>
---------------	----------------------

---

**Description**

main plot for volcano, scatter and maplot.

**Usage**

```
getMainPlotUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

the panel for main plots;

**Note**

```
getMainPlotUI
```

**Examples**

```
x <- getMainPlotUI("main")
```

---

getMean	<i>getMean</i>
---------	----------------

---

**Description**

Gathers the mean for selected condition.

**Usage**

```
getMean(data = NULL, selcols = NULL)
```

**Arguments**

data	dataset
selcols	input cols

**Value**

data

**Examples**

```
x <- getMean()
```

---

`getMergedComparison`     *getMergedComparison*

---

**Description**

Gathers the merged comparison data to be used within the DEBrowser.

**Usage**

```
getMergedComparison(dc = NULL, nc = NULL, input = NULL)
```

**Arguments**

dc	data container
nc	the number of comparisons
input	input params

**Value**

data

**Examples**

```
x <- getMergedComparison()
```

---

`getMetaSelector`     *getMetaSelector*

---

**Description**

Return the sample selection box using meta data table

**Usage**

```
getMetaSelector(metadata = NULL, input = NULL, n = 0)
```

**Arguments**

metadata	meta data table
input	input params
n	the box number

**Value**

meta select box

**Examples**

```
x<-getMetaSelector()
```

---

getMethodDetails	<i>get the detail boxes after DE method selected</i>
------------------	--

---

**Description**

get the detail boxes after DE method selected

**Usage**

```
getMethodDetails(num = NULL, input = NULL)
```

**Arguments**

num	panel that is going to be shown
input	user input

**Examples**

```
x <- getMethodDetails()
```

---

getMostVariedList	<i>getMostVariedList</i>
-------------------	--------------------------

---

**Description**

Calculates the most varied genes to be used for specific plots within the DEBrowser.

**Usage**

```
getMostVariedList(datavar = NULL, cols = NULL, input = NULL)
```

**Arguments**

datavar	loaded dataset
cols	selected columns
input	input

**Value**

data

**Examples**

```
x <- getMostVariedList()
```

---

`getNormalizedMatrix`    *getNormalizedMatrix*

---

**Description**

Normalizes the matrix passed to be used within various methods within DEBrowser. Requires edgeR package

**Usage**

```
getNormalizedMatrix(M = NULL, method = "TMM")
```

**Arguments**

M	numeric matrix
method	normalization method for edgeR. default is TMM

**Value**

normalized matrix

**Note**

`getNormalizedMatrix`

**Examples**

```
x <- getNormalizedMatrix(mtcars)
```

---

<code>getOrganism</code>	<i>getOrganism</i>
--------------------------	--------------------

---

**Description**

`getOrganism`

**Usage**

```
getOrganism(org)
```

**Arguments**

`org`                    `organism`

**Value**

organism name for keg

**Note**

`getOrganism`

**Examples**

```
x <- getOrganism()
```

---

<code>getOrganismBox</code>	<i>getOrganismBox</i>
-----------------------------	-----------------------

---

**Description**

Get the organism Box.

**Usage**

```
getOrganismBox()
```

**Value**

`selectInput`

**Note**

`getOrganismBox`  
`getOrganismBox` makes the organism box

**Examples**

```
x <- getOrganismBox()
```

---

getOrganismPathway     *getOrganismPathway*

---

**Description**

getOrganismPathway

**Usage**

```
getOrganismPathway(org)
```

**Arguments**

org                    organism

**Value**

organism name for pathway

**Note**

getOrganismPathway

**Examples**

```
x <- getOrganismPathway()
```

---

getPCAcontolUpdatesJS     *getPCAcontolUpdatesJS in the prep menu we have two PCA plots to show how batch effect correction worked. One set of PCA input controls updates two PCA plots with this JS.*

---

**Description**

getPCAcontolUpdatesJS in the prep menu we have two PCA plots to show how batch effect correction worked. One set of PCA input controls updates two PCA plots with this JS.

**Usage**

```
getPCAcontolUpdatesJS()
```

**Value**

the JS for tab updates

**Examples**

```
x<- getTabUpdateJS()
```

---

getPCAexplained	<i>getPCAexplained</i>
-----------------	------------------------

---

**Description**

Creates a more detailed plot using the PCA results from the selected dataset.

**Usage**

```
getPCAexplained(datasetInput = NULL, pca_data = NULL, input = NULL)
```

**Arguments**

datasetInput	selected data
pca_data	from user
input	input params

**Value**

explained plot

**Examples**

```
load(system.file("extdata", "demo", "demodata.Rda", package="debrowser"))
input<-c()
input$qcplot<-"pca"
input$col_list<-colnames(demodata[,1:6])
dat <- getNormalizedMatrix(demodata[,1:6])
pca_data <- run_pca(dat)
x <- getPCAexplained(dat, pca_data, input)
```

---

getPCAPlotUI	<i>getPCAPlotUI</i>
--------------	---------------------

---

**Description**

PCA plots UI.

**Usage**

```
getPCAPlotUI(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

the panel for PCA plots;

**Note**

```
getPCAPlotUI
```

**Examples**

```
x <- getPCAPlotUI("pca")
```

---

getPCselection	<i>getPCselection</i>
----------------	-----------------------

---

**Description**

Generates the PC selection number to be used within DEBrowser.

**Usage**

```
getPCselection(id, num = 1, xy = "x")
```

**Arguments**

id	namespace id
num	PC selection number
xy	x or y coordinate

**Value**

PC selection for PCA analysis

**Note**

`getPCselection`

**Examples**

```
x <- getPCselection("pca")
```

---

`getPlotArea`

*getPlotArea*

---

**Description**

returns plot area either for `heatmaply` or `heatmap.2`

**Usage**

```
getPlotArea(input = NULL, session = NULL)
```

**Arguments**

<code>input</code>	input variables
<code>session</code>	session

**Value**

`heatmaply/heatmap.2` plot area

**Examples**

```
x <- getPlotArea()
```

---

`getProgramTitle`      *getProgramTitle*

---

**Description**

Generates the title of the program to be displayed within DEBbrowser. If it is called in a program, the program title will be hidden

**Usage**

```
getProgramTitle(session = NULL)
```

**Arguments**

`session`      session var

**Value**

program title

**Note**

```
getProgramTitle
```

**Examples**

```
title<-getProgramTitle()
```

---

`getQAText`      *getQAText Some questions and answers*

---

**Description**

`getQAText` Some questions and answers

**Usage**

```
getQAText()
```

**Value**

help text for QA

**Examples**

```
x<- getQAText()
```

getQCLeftMenu            *getQCLeftMenu*

---

**Description**

Generates the left menu to be used for QC plots within the DEBrowser.

**Usage**

```
getQCLeftMenu(input = NULL)
```

**Arguments**

input            input values

**Value**

QC left menu

**Note**

getQCLeftMenu

**Examples**

```
x <- getQCLeftMenu()
```

---

getQCPanel            *getQCPanel*

---

**Description**

Gathers the conditional panel for QC plots

**Usage**

```
getQCPanel(input = NULL)
```

**Arguments**

input            user input

**Value**

the panel for QC plots

**Note**

getQCSection

**Examples**

```
x <- getQCPanel()
```

---

getSampleDetails      *getSampleDetails*

---

**Description**

get sample details

**Usage**

```
getSampleDetails(output = NULL, summary = NULL, details = NULL, data = NULL)
```

**Arguments**

output	output
summary	summary output name
details	details ouput name
data	data

**Value**

panel

**Examples**

```
x <- getSampleDetails()
```

---

<code>getSampleNames</code>	<i>getSampleNames</i>
-----------------------------	-----------------------

---

**Description**

Prepares initial samples to fill condition boxes. it reads the sample names from the data and splits into two.

**Usage**

```
getSampleNames(cnames = NULL, part = 1)
```

**Arguments**

<code>cnames</code>	sample names in the header of a dataset
<code>part</code>	c(1,2). 1=first half and 2= second half

**Value**

sample names.

**Examples**

```
x<-getSampleNames()
```

---

<code>getSearchData</code>	<i>getSearchData</i>
----------------------------	----------------------

---

**Description**

search the geneset in the tables and return it

**Usage**

```
getSearchData(dat = NULL, input = NULL)
```

**Arguments**

<code>dat</code>	table data
<code>input</code>	input params

**Value**

data

**Examples**

```
x <- getSearchData()
```

---

`getSelectedCols`      *getSelectedCols*

---

**Description**

gets selected columns

**Usage**

```
getSelectedCols(data = NULL, datasetInput = NULL, input = NULL)
```

**Arguments**

<code>data</code>	all loaded data
<code>datasetInput</code>	selected dataset
<code>input</code>	user input params

**Examples**

```
getSelectedCols()
```

---

`getSelectedDatasetInput`  
*getSelectedDatasetInput*

---

**Description**

Gathers the user selected dataset output to be displayed.

**Usage**

```
getSelectedDatasetInput(  
  rdata = NULL,  
  getSelected = NULL,  
  getMostVaried = NULL,  
  mergedComparison = NULL,  
  input = NULL  
)
```

**Arguments**

rdata	filtered dataset
getSelected	selected data
getMostVaried	most varied data
mergedComparison	merged comparison data
input	input parameters

**Value**

data

**Examples**

```
x <- getSelectedDatasetInput()
```

---

getSelectInputBox	<i>getSelectInputBox</i>
-------------------	--------------------------

---

**Description**

Selects user input conditions to run in DESeq.

**Usage**

```
getSelectInputBox(
  id = NULL,
  name = NULL,
  num = 0,
  choices = NULL,
  selected = NULL,
  cw = 2,
  multiple = FALSE
)
```

**Arguments**

id	input id
name	label of the box
num	panel that is going to be shown
choices	sample list
selected	selected sample list
cw	column width
multiple	if multiple choices are available

**Examples**

```
x <- getSelectInputBox()
```

---

getSelHeat                      *getSelHeat*

---

**Description**

heatmap selection functionality

**Usage**

```
getSelHeat(expdata = NULL, input = NULL)
```

**Arguments**

expdata	selected genes
input	input params

**Value**

plot

**Examples**

```
x <- getSelHeat()
```

---

getShapeColor                      *getShapeColor*

---

**Description**

Generates the fill and shape selection boxes for PCA plots. metadata file has to be loaded in this case

**Usage**

```
getShapeColor(input = NULL)
```

**Arguments**

input	input values
-------	--------------

**Value**

Color and shape from selection boxes or defaults

**Examples**

```
x <- getShapeColor()
```

---

`getStartPlotsMsg`      *getStartPlotsMsg*

---

**Description**

Generates and displays the starting message to be shown once the user has first seen the main plots page within DEBrowser.

**Usage**

```
getStartPlotsMsg()
```

**Value**

return start plot msg

**Note**

```
getStartPlotsMsg
```

**Examples**

```
x <- getStartPlotsMsg()
```

---

`getStartupMsg`      *getStartupMsg*

---

**Description**

Generates and displays the starting message within DEBrowser.

**Usage**

```
getStartupMsg()
```

**Value**

return startup msg

**Note**

```
getStartupMsg
```

**Examples**

```
x <- getStartupMsg()
```

---

<code>getTableDetails</code>	<i>getTableDetails</i>
------------------------------	------------------------

---

**Description**

get table details To be able to put a table into two lines are necessary; into the server part; `getTableDetails(output, session, "dataname", data, modal=TRUE)` into the ui part; `uiOutput(ns("dataname"))`

**Usage**

```
getTableDetails(  
  output = NULL,  
  session = NULL,  
  tablename = NULL,  
  data = NULL,  
  modal = NULL  
)
```

**Arguments**

<code>output</code>	output
<code>session</code>	session
<code>tablename</code>	table name
<code>data</code>	matrix data
<code>modal</code>	if it is true, the matrix is going to be in a modal

**Value**

panel

**Examples**

```
x <- getTableDetails()
```

---

getTableModal	<i>getTableModal prepares table modal for KEGG</i>
---------------	--

---

**Description**

getTableModal prepares table modal for KEGG

**Usage**

```
getTableModal()
```

**Value**

the info button

**Examples**

```
x<- getTableModal()
```

---

getTableStyle	<i>getTableStyle</i>
---------------	----------------------

---

**Description**

User defined selection that selects the style of table to display within the DEBrowser.

**Usage**

```
getTableStyle(  
  dat = NULL,  
  input = NULL,  
  padj = c("padj"),  
  foldChange = c("foldChange"),  
  DEsection = TRUE  
)
```

**Arguments**

dat	dataset
input	input params
padj	the name of the padj value column in the dataset
foldChange	the name of the foldChange column in the dataset
DEsection	if it is in DESection or not

**Note**

getTableStyle

**Examples**

```
x <- getTableStyle()
```

---

getTabUpdateJS	<i>getTabUpdateJS premenu tab and discovery menu tab updates</i>
----------------	--

---

**Description**

getTabUpdateJS premenu tab and discovery menu tab updates

**Usage**

```
getTabUpdateJS()
```

**Value**

the JS for tab updates

**Examples**

```
x<- getTabUpdateJS()
```

---

getUp	<i>getUp get up regulated data</i>
-------	------------------------------------

---

**Description**

getUp get up regulated data

**Usage**

```
getUp(filt_data = NULL)
```

**Arguments**

filt\_data      filt\_data

**Value**

data

**Examples**

```
x <- getUp()
```

---

getUpDown	<i>getUpDown get up+down regulated data</i>
-----------	---

---

**Description**

getUpDown get up+down regulated data

**Usage**

```
getUpDown(filt_data = NULL)
```

**Arguments**

filt_data	filt_data
-----------	-----------

**Value**

data

**Examples**

```
x <- getUpDown()
```

---

getVariationData	<i>getVariationData</i>
------------------	-------------------------

---

**Description**

Adds an id to the data frame being used.

**Usage**

```
getVariationData(inputdata = NULL, cols = NULL, conds = NULL, key = NULL)
```

**Arguments**

inputdata	dataset
cols	columns
conds	conditions
key	gene or region name

**Value**

plotdata

**Examples**

```
x <- getVariationData()
```

---

```
get_conditions_given_selection  
  get_conditions_given_selection
```

---

**Description**

Return the two set of conditions given the selection of meta select box

**Usage**

```
get_conditions_given_selection(metadata = NULL, selection = NULL)
```

**Arguments**

metadata	meta data table
selection	selection

**Value**

meta select box

**Examples**

```
x<-get_conditions_given_selection()
```

---

```
heatmapControlsUI  heatmapControlsUI
```

---

**Description**

Generates the left menu to be used for heatmap plots

**Usage**

```
heatmapControlsUI(id)
```

**Arguments**

id                    module ID

**Value**

HeatmapControls

**Note**

heatmapControlsUI

**Examples**

```
x <- heatmapControlsUI("heatmap")
```

---

heatmapJScore

*heatmapJScore*

---

**Description**

heatmap JS code for selection functionality

**Usage**

```
heatmapJScore()
```

**Value**

JS Code

**Examples**

```
x <- heatmapJScore()
```

---

heatmapServer	<i>heatmapServer</i>
---------------	----------------------

---

**Description**

Sets up shinyServer to be able to run heatmapServer interactively.

**Usage**

```
heatmapServer(input, output, session)
```

**Arguments**

input	input params from UI
output	output params to UI
session	session variable

**Value**

the panel for main plots;

**Note**

heatmapServer

**Examples**

```
heatmapServer
```

---

heatmapUI	<i>heatmapUI</i>
-----------	------------------

---

**Description**

Creates a shinyUI to be able to run DEBrowser interactively.

**Usage**

```
heatmapUI(input, output, session)
```

**Arguments**

input	input variables
output	output objects
session	session

**Value**

the panel for heatmapUI;

**Note**

heatmapUI

**Examples**

```
x<-heatmapUI()
```

---

hideObj

*hideObj*

---

**Description**

Hides a shiny object.

**Usage**

```
hideObj(btns = NULL)
```

**Arguments**

btns           hide group of objects with shinyjs

**Examples**

```
x <- hideObj()
```

---

histogramControlsUI

*histogramControlsUI*

---

**Description**

Generates the controls in the left menu for a histogram

**Usage**

```
histogramControlsUI(id)
```

**Arguments**

id               namespace id

**Value**

returns the left menu

**Note**

histogramControlsUI

**Examples**

```
x <- histogramControlsUI("histogram")
```

---

<i>installpack</i>	<i>installpack</i>
--------------------	--------------------

---

**Description**

install packages if they don't exist display.

**Usage**

```
installpack(package_name = NULL)
```

**Arguments**

package\_name    package name to be installed

**Note**

installpack

**Examples**

```
x <- installpack()
```

IQRPlotControlsUI      *IQRPlotControlsUI*

---

**Description**

Generates the controls in the left menu for an IQR plot#'

**Usage**

```
IQRPlotControlsUI(id)
```

**Arguments**

id                    namespace id

**Value**

returns the left menu

**Note**

IQRPlotControlsUI

**Examples**

```
x <- IQRPlotControlsUI("IQR")
```

---

kmeansControlsUI      *kmeansControlsUI*

---

**Description**

get kmeans controls

**Usage**

```
kmeansControlsUI(id)
```

**Arguments**

id                    module ID

**Value**

controls

**Note**

kmeansControlsUI

**Examples**

```
x <- kmeansControlsUI("heatmap")
```

---

lcfMetRadio

*lcfMetRadio*

---

**Description**

Radio buttons for low count removal methods

**Usage**

```
lcfMetRadio(id)
```

**Arguments**

id                    namespace id

**Value**

radio control

**Note**

lcfMetRadio

**Examples**

```
x <- lcfMetRadio("lcf")
```

loadpack                    *loadpack*

---

**Description**

load packages

**Usage**

```
loadpack(package_name = NULL)
```

**Arguments**

package\_name    package name to be loaded

**Note**

loadpack

**Examples**

```
x <- loadpack()
```

---

mainPlotControlsUI    *mainPlotControlsUI*

---

**Description**

Generates the left menu to be used for main plots

**Usage**

```
mainPlotControlsUI(id)
```

**Arguments**

id                    module ID

**Value**

mainPlotControls

**Note**

mainPlotControlsUI

**Examples**

```
x <- mainPlotControlsUI("main")
```

---

mainScatterNew	<i>mainScatterNew</i>
----------------	-----------------------

---

**Description**

Creates the main scatter, volcano or MA plot to be displayed within the main panel.

**Usage**

```
mainScatterNew(input = NULL, data = NULL, cond_names = NULL, source = NULL)
```

**Arguments**

input	input params
data	dataframe that has log2FoldChange and log10padj values
cond_names	condition names
source	for event triggering to select genes

**Value**

scatter, volcano or MA plot

**Examples**

```
x <- mainScatterNew()
```

---

niceKmeans	<i>niceKmeans</i>
------------	-------------------

---

**Description**

Generates hierarchially clustered K-means clusters

**Usage**

```
niceKmeans(df = NULL, input = NULL, iter.max = 1000, nstart = 100)
```

**Arguments**

df	data
input	user inputs
iter.max	max iteration for kmeans clustering
nstart	n for kmeans clustering

**Value**

heatmap plot area

**Note**

niceKmeans

**Examples**

```
x <- niceKmeans()
```

---

normalizationMethods *normalizationMethods*

---

**Description**

Select box to select normalization method prior to batch effect correction

**Usage**

```
normalizationMethods(id)
```

**Arguments**

id	namespace id
----	--------------

**Value**

radio control

**Note**

normalizationMethods

**Examples**

```
x <- normalizationMethods("batch")
```

---

palUI	<i>palUI</i>
-------	--------------

---

**Description**

get pallete

**Usage**

```
palUI(id)
```

**Arguments**

id                    namespace ID

**Value**

pals

**Note**

palUI

**Examples**

```
x <- palUI("heatmap")
```

---

panel.cor	<i>panel.cor</i>
-----------	------------------

---

**Description**

Prepares the correlations for the all2all plot.

**Usage**

```
panel.cor(x, y, prefix = "rho=", cex.cor = 2, ...)
```

**Arguments**

x                    numeric vector x  
y                    numeric vector y  
prefix                prefix for the text  
cex.cor               correlation font size  
...                    additional parameters

**Value**

all2all correlation plots

**Examples**

```
panel.cor(c(1,2,3), c(4,5,6))
```

---

panel.hist

*panel.hist*

---

**Description**

Prepares the histogram for the all2all plot.

**Usage**

```
panel.hist(x, ...)
```

**Arguments**

x                    a vector of values for which the histogram is desired  
 ...                  any additional params

**Value**

all2all histogram plots

**Examples**

```
panel.hist(1)
```

---

pcaPlotControlsUI

*pcaPlotControlsUI*

---

**Description**

Generates the PCA PLOTS Left menu to be displayed within the DEBrowser.

**Usage**

```
pcaPlotControlsUI(id = "pca")
```

**Arguments**

id                    namespace id

**Value**

returns the left menu according to the selected tab;

**Note**

pcaPlotControlsUI

**Examples**

```
x <- pcaPlotControlsUI("pca")
```

---

plotData

*plotData*

---

**Description**

prepare plot data for mainplots

**Usage**

```
plotData(pdata = NULL, input = NULL)
```

**Arguments**

pdata	data
input	input

**Value**

prepdata

**Note**

plotData

**Examples**

```
x <- plotData()
```

plotMarginsUI

*plotMarginsUI*

---

**Description**

Margins module for plotly plots

**Usage**

```
plotMarginsUI(id, t = 20, b = 100, l = 100, r = 20)
```

**Arguments**

id	id
t	top margin
b	bottom margin
l	left margin
r	right margin

**Value**

size and margins controls

**Note**

plotMarginsUI

**Examples**

```
x <- plotMarginsUI("heatmap")
```

---

plotSizeMarginsUI*plotSizeMarginsUI*

---

**Description**

Size and margins module for plotly plots

**Usage**

```
plotSizeMarginsUI(id, w = 800, h = 640, t = 20, b = 100, l = 100, r = 20)
```

**Arguments**

id	id
w	width
h	height
t	top margin
b	bottom margin
l	left margin
r	right margin

**Value**

size and margins controls

**Note**

plotSizeMarginsUI

**Examples**

```
x <- plotSizeMarginsUI("heatmap")
```

---

plotSizeUI

*plotSizeUI*

---

**Description**

Size module for plotly plots

**Usage**

```
plotSizeUI(id, w = 800, h = 600)
```

**Arguments**

id	id
w	width
h	height

**Value**

size and margins controls

**Note**

plotSizeUI

**Examples**

```
x <- plotSizeUI("heatmap")
```

---

plotTypeUI

*plotTypeUI*

---

**Description**

Plot download type

**Usage**

```
plotTypeUI(id)
```

**Arguments**

id id

**Value**

size and margins controls

**Note**

plotTypeUI

**Examples**

```
x <- plotTypeUI("heatmap")
```

---

plot\_pca

*plot\_pca*

---

**Description**

Plots the PCA results for the selected dataset.

**Usage**

```
plot_pca(
  dat = NULL,
  pcx = 1,
  pcy = 2,
  metadata = NULL,
  color = NULL,
  shape = NULL,
  size = NULL,
  textonoff = "On",
  legendSelect = "samples",
  input = NULL
)
```

**Arguments**

dat	data
pcx	x axis label
pcy	y axis label
metadata	additional data
color	color for plot
shape	shape for plot
size	size of the plot
textonoff	text on off
legendSelect	select legend
input	input param

**Value**

pca list

**Examples**

```
load(system.file("extdata", "demo", "demodata.Rda",
  package="debrowser"))
metadata<-cbind(colnames(demodata[,1:6]),
  colnames(demodata[,1:6]),
  c(rep("Cond1",3), rep("Cond2",3)))
colnames(metadata)<-c("samples", "color", "shape")

a <- plot_pca(getNormalizedMatrix(
  demodata[rowSums(demodata[,1:6])>10,1:6]),
  metadata = metadata, color = "samples",
  size = 5, shape = "shape")
```

---

```
prepDataContainer      prepDataContainer
```

---

**Description**

Prepares the data container that stores values used within DESeq.

**Usage**

```
prepDataContainer(data = NULL, counter = NULL, input = NULL, meta = NULL)
```

**Arguments**

data	loaded dataset
counter	the number of comparisons
input	input parameters
meta	loaded metadata

**Value**

data

**Examples**

```
x <- prepDataContainer()
```

---

```
prepGroup              prepGroup
```

---

**Description**

prepare group table

**Usage**

```
prepGroup(conds = NULL, cols = NULL, metadata = NULL, covariates = NULL)
```

**Arguments**

conds	inputconds
cols	columns
metadata	metadata
covariates	covariates

**Value**

data

**Examples**

```
x <- prepGroup()
```

---

prepHeatData	<i>prepHeatData</i>
--------------	---------------------

---

**Description**

scales the data

**Usage**

```
prepHeatData(expdata = NULL, input = NULL)
```

**Arguments**

expdata            a matrixthat includes expression values  
input              input variables

**Value**

heatdata

**Examples**

```
x <- prepHeatData()
```

---

prepPCADat	<i>prepPCADat</i>
------------	-------------------

---

**Description**

prepares pca data with metadata. If metadata doesn't exists it puts all the sampels into a signlge group; "Conds".

**Usage**

```
prepPCADat(pca_data = NULL, metadata = NULL, input = NULL, pcx = 1, pcy = 2)
```

**Arguments**

<code>pca_data</code>	pca run results
<code>metadata</code>	additional meta data
<code>input</code>	input
<code>pcx</code>	x axis label
<code>pcy</code>	y axis label

**Value**

Color and shape from selection boxes or defaults

**Examples**

```
x <- prepPCADat()
```

---

`push`

*push*

---

**Description**

Push an object to the list.

**Usage**

```
push(l, ...)
```

**Arguments**

<code>l</code>	that are going to push to the list
<code>...</code>	list object

**Value**

combined list

**Examples**

```
mylist <- list()  
newlist <- push ( 1, mylist )
```

---

removeCols	<i>removeCols</i>
------------	-------------------

---

**Description**

remove unnecessary columns

**Usage**

```
removeCols(cols = NULL, dat = NULL)
```

**Arguments**

cols	columns that are going to be removed from data frame
dat	data

**Value**

data

**Examples**

```
x <- removeCols()
```

---

removeExtraCols	<i>removeExtraCols</i>
-----------------	------------------------

---

**Description**

remove extra columns for QC plots

**Usage**

```
removeExtraCols(dat = NULL)
```

**Arguments**

dat	selected data
-----	---------------

**Examples**

```
removeExtraCols()
```

---

round_vals	<i>round_vals</i>
------------	-------------------

---

**Description**

Plot PCA results.

**Usage**

```
round_vals(1)
```

**Arguments**

1            the value

**Value**

round value

**Examples**

```
x<-round_vals(5.1323223)
```

---

runDE	<i>runDE</i>
-------	--------------

---

**Description**

Run DE algorithms on the selected parameters. Output is to be used for the interactive display.

**Usage**

```
runDE(  
  data = NULL,  
  metadata = NULL,  
  columns = NULL,  
  conds = NULL,  
  params = NULL  
)
```

**Arguments**

data	A matrix that includes all the expression raw counts, rownames has to be the gene, isoform or region names/IDs
metadata	metadata of the matrix of expression raw counts
columns	is a vector that includes the columns that are going to be analyzed. These columns has to match with the given data.
conds	experimental conditions. The order has to match with the column order
params	all params for the DE methods

**Value**

de results

**Examples**

```
x <- runDE()
```

---

runDESeq2

*runDESeq2*

---

**Description**

Run DESeq2 algorithm on the selected conditions. Output is to be used for the interactive display.

**Usage**

```
runDESeq2(
  data = NULL,
  metadata = NULL,
  columns = NULL,
  conds = NULL,
  params = NULL
)
```

**Arguments**

data	A matrix that includes all the expression raw counts, rownames has to be the gene, isoform or region names/IDs
metadata	metadata of the matrix of expression raw counts
columns	is a vector that includes the columns that are going to be analyzed. These columns has to match with the given data.
conds	experimental conditions. The order has to match with the column order

params            fitType: either "parametric", "local", or "mean" for the type of fitting of dispersions to the mean intensity. See estimateDispersions for description. betaPrior: whether or not to put a zero-mean normal prior on the non-intercept coefficients See nbinomWaldTest for description of the calculation of the beta prior. By default, the beta prior is used only for the Wald test, but can also be specified for the likelihood ratio test. testType: either "Wald" or "LRT", which will then use either Wald significance tests (defined by nbinomWaldTest), or the likelihood ratio test on the difference in deviance between a full and reduced model formula (defined by nbinomLRT) shrinkage: Adds shrunken log2 fold changes (LFC) and SE to a results table from DESeq run without LFC shrinkage. For consistency with results, the column name lfcSE is used here although what is returned is a posterior SD. Three shrinkage estimators for LFC are available via type (see the vignette for more details on the estimators). The apeglm publication demonstrates that 'apeglm' and 'ashr' outperform the original 'normal' shrinkage estimator.

### Value

deseq2 results

### Examples

```
x <- runDESeq2()
```

---

runEdgeR

*runEdgeR*

---

### Description

Run EdgeR algorithm on the selected conditions. Output is to be used for the interactive display.

### Usage

```
runEdgeR(
  data = NULL,
  metadata = NULL,
  columns = NULL,
  conds = NULL,
  params = NULL
)
```

### Arguments

data            A matrix that includes all the expression raw counts, rownames has to be the gene, isoform or region names/IDs

metadata        metadata of the matrix of expression raw counts

columns	is a vector that includes the columns that are going to be analyzed. These columns has to match with the given data.
conds	experimental conditions. The order has to match with the column order
params	normfact: Calculate normalization factors to scale the raw library sizes. Values can be "TMM", "RLE", "upperquartile", "none". dispersion: either a numeric vector of dispersions or a character string indicating that dispersions should be taken from the data object. If a numeric vector, then can be either of length one or of length equal to the number of genes. Allowable character values are "common", "trended", "tagwise" or "auto". Default behavior ("auto" is to use most complex dispersions found in data object. testType: exactTest or glmLRT. exactTest: Computes p-values for differential abundance for each gene between two digital libraries, conditioning on the total count for each gene. The counts in each group as a proportion of the whole are assumed to follow a binomial distribution. glmLRT: Fit a negative binomial generalized log-linear model to the read counts for each gene. Conduct genewise statistical tests for a given coefficient or coefficient contrast.

**Value**

edgeR results

**Examples**

```
x <- runEdgeR()
```

---

runHeatmap

*runHeatmap*

---

**Description**

Creates a heatmap based on the user selected parameters within shiny

**Usage**

```
runHeatmap(input = NULL, session = NULL, expdata = NULL)
```

**Arguments**

input	input variables
session	session
expdata	a matrix that includes expression values

**Value**

heatmapply plot

**Examples**

```
x <- runHeatmap()
```

---

runHeatmap2	<i>runHeatmap2</i>
-------------	--------------------

---

**Description**

Creates a heatmap based on the user selected parameters within shiny

**Usage**

```
runHeatmap2(input = NULL, session = NULL, expdata = NULL)
```

**Arguments**

input	input variables
session	session
expdata	a matrix that includes expression values

**Value**

heatmap.2

**Examples**

```
x <- runHeatmap2()
```

---

runLimma	<i>runLimma</i>
----------	-----------------

---

**Description**

Run Limma algorithm on the selected conditions. Output is to be used for the interactive display.

**Usage**

```
runLimma(  
  data = NULL,  
  metadata = NULL,  
  columns = NULL,  
  conds = NULL,  
  params = NULL  
)
```

**Arguments**

data	A matrix that includes all the expression raw counts, rownames has to be the gene, isoform or region names/IDs
metadata	metadata of the matrix of expression raw counts
columns	is a vector that includes the columns that are going to be analyzed. These columns has to match with the given data.
conds	experimental conditions. The order has to match with the column order
params	normfact: Calculate normalization factors to scale the raw library sizes. Values can be "TMM", "RLE", "upperquartile", "none". fitType, fitting method; "ls" for least squares or "robust" for robust regression normBet: Normalizes expression intensities so that the intensities or log-ratios have similar distributions across a set of arrays.

**Value**

Limma results

**Examples**

```
x <- runLimma()
```

---

run\_pca

*run\_pca*

---

**Description**

Runs PCA on the selected dataset.

**Usage**

```
run_pca(x = NULL, retx = TRUE, center = TRUE, scale = TRUE)
```

**Arguments**

x	dataframe with experiment data
retx	specifies if the data should be returned
center	center the PCA (Boolean)
scale	scale the PCA (Boolean)

**Value**

pca list

**Examples**

```
load(system.file("extdata", "demo", "demodata.Rda",
  package="debrowser"))
pca_data<-run_pca(getNormalizedMatrix(
  demodata[rowSums(demodata[,1:6])>10,1:6]))
```

---

selectConditions	<i>selectConditions</i>
------------------	-------------------------

---

**Description**

Selects user input conditions, multiple if present, to be used in DESeq.

**Usage**

```
selectConditions(
  Dataset = NULL,
  metadata = NULL,
  choicecounter = NULL,
  session = NULL,
  input = NULL
)
```

**Arguments**

Dataset	used dataset
metadata	metadatatable to select from metadata
choicecounter	choicecounter to add multiple comparisons
session	session
input	input params

**Value**

the panel for go plots;

**Note**

selectConditions

**Examples**

```
x<- selectConditions()
```

---

selectedInput	<i>selectedInput</i>
---------------	----------------------

---

**Description**

Selects user input conditions to run in DESeq.

**Usage**

```
selectedInput(id = NULL, num = 0, default = NULL, input = NULL)
```

**Arguments**

id	input id
num	panel that is going to be shown
default	default text
input	input params

**Examples**

```
x <- selectedInput()
```

---

selectGroupInfo	<i>selectGroupInfo</i>
-----------------	------------------------

---

**Description**

Group info column selection. This can be used in batch effect or coloring the groups in the plots.

**Usage**

```
selectGroupInfo(
  metadata = NULL,
  input = NULL,
  selectname = "groupselect",
  label = "Group info"
)
```

**Arguments**

metadata	metadata
input	input values
selectname	name of the select box
label	label of the select box

**Note**

```
selectGroupInfo
```

**Examples**

```
x <- selectGroupInfo()
```

---

sepRadio	<i>sepRadio</i>
----------	-----------------

---

**Description**

Radio button for separators

**Usage**

```
sepRadio(id, name)
```

**Arguments**

id	module id
name	name

**Value**

radio control

**Note**

```
sepRadio
```

**Examples**

```
x <- sepRadio("meta", "metadata")
```

---

setBatch	<i>setBatch to skip batch effect correction batch variable set with the filter results</i>
----------	--

---

**Description**

setBatch to skip batch effect correction batch variable set with the filter results

**Usage**

```
setBatch(fd = NULL)
```

**Arguments**

fd                    filtered data

**Value**

fd data

**Examples**

```
x <- setBatch()
```

---

showObj	<i>showObj</i>
---------	----------------

---

**Description**

Displays a shiny object.

**Usage**

```
showObj(btns = NULL)
```

**Arguments**

btns                    show group of objects with shinyjs

**Examples**

```
x <- showObj()
```

---

startDEBrowser	<i>startDEBrowser</i>
----------------	-----------------------

---

**Description**

Starts the DEBrowser to be able to run interactively.

**Usage**

```
startDEBrowser()
```

**Value**

the app

**Note**

```
startDEBrowser
```

**Examples**

```
startDEBrowser()
```

---

startHeatmap	<i>startHeatmap</i>
--------------	---------------------

---

**Description**

Starts the DEBrowser heatmap

**Usage**

```
startHeatmap()
```

**Value**

the app

**Note**

```
startHeatmap
```

**Examples**

```
startHeatmap()
```

textareaInput                      *textareaInput*

**Description**

Generates a text area input to be used for gene selection within the DEBrowser.

**Usage**

```
textareaInput(id, label, value, rows = 20, cols = 35, class = "form-control")
```

**Arguments**

id	id of the control
label	label of the control
value	initial value
rows	the # of rows
cols	the # of cols
class	css class

**Examples**

```
x <- textareaInput("genesetarea", "Gene Set",
  "Fgf21", rows = 5, cols = 35)
```

togglePanels                      *togglePanels*

**Description**

User defined toggle to display which panels are to be shown within DEBrowser.

**Usage**

```
togglePanels(num = NULL, nums = NULL, session = NULL)
```

**Arguments**

num	selected panel
nums	all panels
session	session info

**Note**

togglePanels

**Examples**

```
x <- togglePanels()
```

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