

# 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

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

**Examples**

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

---

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

---

**Description**

add additional data columns to de results

**Usage**

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

**Arguments**

<code>data,</code>	loaded dataset
<code>de_res,</code>	de results
<code>cols,</code>	columns
<code>conds,</code>	inputconds

**Value**

data

**Examples**

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

---

addID	<i>addID</i>
-------	--------------

---

**Description**

Adds an id to the data frame being used.

**Usage**

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

**Arguments**

data,                   loaded dataset

**Value**

data

**Examples**

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

---

all2all	<i>all2all</i>
---------	----------------

---

**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, selected 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      *cutOffSelectionUI*

---

**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                    *dataLCFUI Creates a panel to filter low count genes and regions*

---

**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	<i>debrowsermainplot</i>
-------------------	--------------------------

---

**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,  
  pcadata = NULL,  
  metadata = NULL  
)
```

**Arguments**

input,	input variables
output,	output objects
session,	session
pcadata,	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

*deUI*

---

**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

*distFunParamsUI*

---

**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	<i>generateTestData</i>
------------------	-------------------------

---

**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>getAfterLoadMsg</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>getA112A11PlotUI</code>	<code>getA112A11PlotUI</code>
-------------------------------	-------------------------------

---

**Description**

all2all plots UI.

**Usage**

```
getA112A11PlotUI(id)
```

**Arguments**

`id`, `namespace id`

**Value**

the panel for all2all plots;

**Note**

```
getA112A11PlotUI
```

**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()
```

---

`getBarMainPlotUI`      *getBarMainPlotUI*

---

**Description**

main bar plots UI.

**Usage**

```
getBarMainPlotUI(id)
```

**Arguments**

`id`,                  namespace `id`

**Value**

the panel for Density plots;

**Note**

```
getBarMainPlotUI
```

**Examples**

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

---

`getBoxMainPlot`      *getBoxMainPlot*

---

**Description**

Makes Density plots

**Usage**

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



**Arguments**

data,	count or normalized data
cols,	cols
conds,	conds
cond_names,	condition names
key,	key
title,	title
input,	input

**Examples**

```
getBoxMainPlot()
```

---

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

---

**Description**

main Box plots UI.

**Usage**

```
getBoxMainPlotUI(id)
```

**Arguments**

id,	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<-getColorColors()
```

---

`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      *getDataForTables* 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**

`genelist`,      gene list  
`pvalueCutoff`,   the p value cutoff

**Value**

enriched DO

**Note**

`getEnrichDO`

**Examples**

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

---

getEnrichGO	<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**

genelist,	gene list
pvalueCutoff,	p value cutoff
org,	the organism used
ont,	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'))
```

---

<code>getGeneSetData</code>	<i>getGeneSetData</i>
-----------------------------	-----------------------

---

**Description**

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

**Usage**

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

**Arguments**

<code>data</code> ,	loaded dataset
<code>geneset</code> ,	given gene set

**Value**

data

**Examples**

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

---

<code>getGOLeftMenu</code>	<i>getGOLeftMenu</i>
----------------------------	----------------------

---

**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      *getGroupSelector Return the groups*

---

**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	<i>getIQRPlotUI</i>
--------------	---------------------

---

**Description**

IQR plot UI.

**Usage**

```
getIQRPlotUI(id)
```

**Arguments**

id, namespace id

**Value**

the panel for IQR plots;

**Note**

```
getIQRPlotUI
```

**Examples**

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

---

getJSLine	<i>getJSLine</i>
-----------	------------------

---

**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**

`id`, `namespace id`

**Value**

radio control

**Note**

```
getLegendRadio
```

**Examples**

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

---

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

---

**Description**

select legend

**Usage**

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

**Arguments**

`id`, `namespace id`

**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      *getPCAexplained*

---

**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**

`input`,           input variables  
`session`,         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> ,	<code>c(1,2)</code> . 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**

`data`,            all loaded data  
`datasetInput`,   selected dataset  
`input`,            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**

<code>rdata,</code>	filtered dataset
<code>getSelected,</code>	selected data
<code>getMostVaried,</code>	
	most varied data
<code>mergedComparison,</code>	
	merged comparison data
<code>input,</code>	input parameters

**Value**

data

**Examples**

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

---

<code>getSelectInputBox</code>	<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**

<code>id,</code>	input id
<code>name,</code>	label of the box
<code>num,</code>	panel that is going to be shown
<code>choices,</code>	sample list
<code>selected,</code>	selected sample list
<code>cw,</code>	column width
<code>multiple,</code>	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</i> prepares table modal for KEGG
---------------	--

---

**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")
```

---

<code>installpack</code>	<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()
```

---

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

---

**Description**

scales the data

**Usage**

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

**Arguments**

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

**Value**

heatdata

**Examples**

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

---

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

---

**Description**

prepares pca data with metadata. If metadata doesn't exist it puts all the samples into a single 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

*runHeatmap2*

---

**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

*runLimma*

---

**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

*sepRadio*

---

**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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