

# Package ‘levi’

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**Type** Package

**Title** Landscape Expression Visualization Interface

**Version** 1.25.0

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**Description** The tool integrates data from biological networks with transcriptomes, displaying a heatmap with surface curves to evidence the altered regions.

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.1

**Suggests** rmarkdown, BiocStyle

**Imports** DT(>= 0.4), RColorBrewer(>= 1.1-2), colorspace(>= 1.3-2), dplyr(>= 0.7.4), ggplot2(>= 2.2.1), httr(>= 1.3.1), igraph(>= 1.2.1), reshape2(>= 1.4.3), shiny(>= 1.0.5), shinydashboard(>= 0.7.0), shinyjs(>= 1.0), xml2(>= 1.2.0), knitr, Rcpp (>= 0.12.18), grid, grDevices, stats, utils, testthat, methods, rmarkdown

**LinkingTo** Rcpp

**License** GPL (>= 2)

**biocViews** GeneExpression, Sequencing, Network, Software

**VignetteBuilder** knitr

**LazyLoad** yes

**NeedsCompilation** yes

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|      |             |
|------|-------------|
| levi | <i>levi</i> |
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## Description

This is the Levi script mode. It allows you to create the integration of networks and gene expression levels as batch processing

## Usage

```
levi(expressionInput, fileTypeInput, networkCoordinatesInput,
networkInteractionsInput, geneSymbolInput, readExpColumn,
contrastValueInput, zoomValueInput, resolutionValueInput,
smoothValueInput, expressionLog, contourLevi, setcolor)
```

## Arguments

|                          |   |
|--------------------------|---|
| expressionInput          | Filename of gene expression data, which is a numeric data.frame or matrix. The rows represent genes/proteins and the columns represent the experiment (RNA-seq, microarray, etc). |
| fileTypeInput            | Filename of biological network. Levi can read files written in the following formats: Medusa (DAT), RedeR (DYN), Pajek (NET) and STRING/STITCH                                    |
| networkCoordinatesInput  | It allows the user to load the coordinate of the nodes the network.   |
| networkInteractionsInput | Parameter available only to STRING/STITCH data format. It allows the user to load the interaction data file of the network.   |
| geneSymbolInput          | Column name from gene expression data containing the identifier (gene Symbol, Entrez ID, EMSEMBL, etc).   |
| readExpColumn            | Variable from readExpColumn function containing the comparisons of the experiments  |

|                      |  |
|----------------------|--|
| contrastValueInput   | Numeric value for image contrast. The variable range is 0 to 100. The default value is 50  |
| zoomValueInput       | Numeric value for image zoom. The variable range is 0 to 100. The default value is 50.   |
| resolutionValueInput | Numeric value for image resolution. The variable range is 0 to 100. The default value is 50.   |
| smoothValueInput     | Numeric value for image smoothness. The variable range is 0 to 100. The default is 50.   |
| expressionLog        | Logical variable to indicate Log2 normalization in the expression levels. The default is FALSE   |
| contourLevi          | Logical variable to allow contour lines. The default is TRUE.  |
| setcolor             | Select the color palette to build the heatmap. There is two options the <b>Multicolor</b> has 20 color levels combined. The <b>Two colors</b> has two types of color and the options available are: <i>purple_pink</i> , <i>green_blue</i> , <i>blue_yellow</i> , <i>pink_green</i> , <i>orange_purple</i> , <i>green_marine</i> . |

### Details

Integrates the biological network and gene expression levels (or other type of data)

### Value

Return a ggplot object and print a image (heatmap).

### Author(s)

Isabelle Mira da Silva (isabelle.silva@unesp.br), José Rafael Pilan (rafael.pilan@unesp.br)

### Examples

```
template_network <- file.path(system.file(package="levi"), "extdata",
  "medusa.dat", fsep = .Platform$file.sep)

template_expression <- file.path(system.file(package="levi"),
  "extdata", "expression.dat", fsep = .Platform$file.sep)

multicolor <- levi(networkCoordinatesInput = template_network,
  expressionInput = template_expression, fileTypeInput = "dat",
  geneSymbolInput = "ID",
  readExpColumn=readExpColumn("TumorCurrentSmoker-NormalNeverSmoker"),
  contrastValueInput = 50, resolutionValueInput = 50, zoomValueInput = 50,
  smoothValueInput = 50, expressionLog = FALSE, contourLevi = TRUE)

twocolors <- levi(networkCoordinatesInput = template_network,
  expressionInput = template_expression, fileTypeInput = "dat",
  geneSymbolInput = "ID",
  readExpColumn = readExpColumn("TumorCurrentSmoker-NormalNeverSmoker"),
  setcolor = "pink_green", contourLevi = FALSE)
```

LEVIui

*LEVIui*

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**Description**

Launch the Levi Graphical User Interface (GUI) in local machine.

**Usage**

```
LEVIui(browser)
```

**Arguments**

|         |  |
|---------|--|
| browser | This argument is necessary to launch Levi GUI. To launch Levi in the web browser the argument required "TRUE". To launch Levi in the R environment the argument required "FALSE". The default is "FALSE" |
|---------|--|

**Details**

This function launch the LEVI Graphical User Interface. The interface provides the same tools available in the script mode. There are two tools only available in the user interface: 1) Selection of area from heatmap to calculate the gene expression levels in the area selected; 2) Selection of the genes in some specific area from the image.

**Value**

return a GUI

**Author(s)**

José Rafael Pilan <rafael.pilan@unesp.br> & Isabelle Mira da Silva (isabelle.silva@unesp.br)

**Examples**

```
LEVIui(browser)
#LEVIui(browser=TRUE) #Launch Levi to Browser.
#LEVIui(browser=FALSE) #Launch Levi to R environment.
```

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|               |                      |
|---------------|----------------------|
| readExpColumn | <i>readExpColumn</i> |
|---------------|----------------------|

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**Description**

This function helps to prepare the data in the script mode. It also allows the obtention of dataset plot as a batch processing.

**Usage**

```
readExpColumn(x,...)
```

**Arguments**

|     |   |
|-----|---|
| x   | Names of two expression datasets to be compared. They should be separated by hyphen (-) |
| ... | To add more comparisons, each combination must be separated by comma (,).               |

**Details**

List the names of the expression datasets that will be used for comparison

**Value**

Returns the names of comparisons to be used by Levi

**Note**

To generate a plot from a single dataset, the name of the sample must be informed twice (Ex. "CaseA-CaseA")

**Author(s)**

José Rafael Pílan (rafael.pilan@unesp.br)

**Examples**

```
base <- readExpColumn(a="NormalNeverSmoker-NormalNeverSmoker")
```

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