

# Package ‘DEsubs’

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**Title** DEsubs: an R package for flexible identification of differentially expressed subpathways using RNA-seq expression experiments

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**Description** DEsubs is a network-based systems biology package that extracts disease-perturbed subpathways within a pathway network as recorded by RNA-seq experiments. It contains an extensive and customizable framework covering a broad range of operation modes at all stages of the subpathway analysis, enabling a case-specific approach. The operation modes refer to the pathway network construction and processing, the subpathway extraction, visualization and enrichment analysis with regard to various biological and pharmacological features. Its capabilities render it a tool-guide for both the modeler and experimentalist for the identification of more robust systems-level biomarkers for complex diseases.

**Depends** R (>= 3.3), locfit

**SystemRequirements**

**License** GPL-3

**NeedsCompilation** no

**LazyLoad** yes

**Imports** graph, igraph, RBGL, circlize, limma, edgeR, EBSeq, NBPSeq, stats, grDevices, graphics, pheatmap, utils, ggplot2, Matrix, jsonlite, tools, DESeq2, methods

**Suggests** RUnit, BiocGenerics, knitr, rmarkdown

**VignetteBuilder** knitr

**biocViews** SystemsBiology, GraphAndNetwork, Pathways, KEGG, GeneExpression, NetworkEnrichment, Network, RNASeq, DifferentialExpression, Normalization, ImmunoOncology

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## R topics documented:

DEsubs	2
geneVisualization	3
organismVisualization	5
subpathwayToGraph	7
subpathwayTypes	8
subpathwayVisualization	11

<b>Index</b>	<b>13</b>
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DEsubs	<i>Default run of DEsubs</i>
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## Description

Default run of DEsubs

## Usage

```
DEsubs(org, mRNAexpr, mRNAomenclature, pathways, DETool, DEpar,
        CORTool, CORpar, subpathwayType, rankedList, verbose)
```

## Arguments

org	Organism identifier ('hsa', 'mmu', 'rno', 'sce', 'ath', 'dme', 'dre')
mRNAexpr	RNA-seq expression data in the form of either a matrix or a filename of a text file stored in the 'User' directory.
mRNAomenclature	mRNAomenclature ('entrezgene', 'ensembl_gene_id', 'ensembl_transcript_id', 'ensembl_peptide_id', 'hgnc_id', 'hgnc_symbol', 'hgnc_transcript_name', 'refseq_mrna', 'refseq_peptide')
pathways	Pathway type ('All', 'Non-Metabolic', 'Metabolic')
DETool	DEG analysis tool selection for NodeRule ('edgeR', 'DESeq2', 'EBSeq', 'NBPSeq', 'voom+limma', 'vst2+limma', 'TSPM')

DEpar	DE analysis tools Q-value threshold of NodeRule (default: DEGpar = 0.05)
CORtool	Correlation measure selection for EdgeRule ('pearson', 'kendall', 'spearman')
CORpar	Correlation measure threshold of EdgeRule (default: CORpar = 0.6)
subpathwayType	Subpathway extraction type selection (get all available options from <a href="#">subpathwayTypes</a> )
rankedList	A named vector of genes and their corresponding significance of differential expression in the form of a Q-value. If the argument is not null, no DEtool is used for differential expression analysis.
verbose	TRUE to display informative messages, FALSE to hide.

### Details

- Class vector needed values 1 and 2 for each class (eg. control and disease samples).
- DEpar should be less than 0.05 in order to return statistically significant DEGs.
- Higher CORpar values result in stricter correlation criteria, i.e. less acceptable interactions.

### Value

A list used as input in [geneVisualization](#), [subpathwayVisualization](#), [subpathwayToGraph](#), [organismVisualization](#)

### Examples

```
load(system.file('extdata', 'data.RData', package='DEsubs'))
```

```
DEsubs.run <- DEsubs(  org='hsa',
                       mRNAexpr=mRNAexpr,
                       mRNAomenclature='entrezgene',
                       pathways='All',
                       DEtool=NULL, DEpar=0.05,
                       CORtool='pearson', CORpar=0.6,
                       subpathwayType=NULL,
                       rankedList=rankedList)
```

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geneVisualization      *Gene level visualization*

---

### Description

Visualizes topologically and functionally significant genes using graph theory measures as well as their correlation to pathway, disease, drug, ontology, microRNA and Transcription Factor terms based on external references.

**Usage**

```
geneVisualization(DEsubs.out, measures.topological, measures.functional,
  measures.barplot, topGenes, colors.topological, colors.functional,
  colors.barplot, size.topological, size.functional, size.barplot,
  outfile.topological, outfile.functional, outfile.barplot,
  export, verbose)
```

**Arguments**

DEsubs.out      Return value from [DEsubs](#)

measures.topological      Functional visualization type(s).

measures.functional      Topological visualization type(s).

measures.barplot      Gene level Visualization type

topGenes      Number of genes with greater Q-values. Default value is 10.

colors.topological      A custom color mode which overrides the default settings.

colors.functional      A custom color mode which overrides the default settings.

colors.barplot      A custom color mode which overrides the default settings.

size.topological      A vector storing width and height of the topological measures visualization

size.functional      A vector storing width and height of the functional measures visualization

size.barplot      A vector storing width and height of the barplot visualization

outfile.topological      Output file name of the topological measures visualization.

outfile.functional      Output file name of the functional measures visualization.

outfile.barplot      Output file name of the barplot visualization.

export      Export type of visualizations ('plot', 'pdf')

verbose      TRUE to display informative messages, FALSE to hide.

**Details**

- Topological visualization type contains six topological graph theory measures, namely degree, betweenness centrality, closeness centrality, hub\_score, eccentricity and page\_rank. The available options are 'degree', 'betweenness', 'closeness', 'hub\_score', 'eccentricity' and 'page\_rank'. If no argument is supplied, all available options are selected by default. If the argument is NULL, no visualization is exported.

- Functional visualization type contains associations with (i) KEGG's pathway terms, (ii) Gene Ontologies of Molecular function, biological processes and cellular components (iii) Disease terms from OMIM and GAD databases), (iv) Drug substances from DrugBank) and the influence of (v) microRNA targets from miRecords and (vi) Transcription Factor targets from Transfac and Jaspar. The available options are 'KEGG', 'GO\_bp', 'GO\_cc', 'GO\_mf', 'Disease\_OMIM', 'Disease\_GAD', 'Drug\_DrugBank', 'miRNA' and 'TF'. If no argument is supplied, all available options are selected by default. If the argument is NULL, no visualization is exported. Using option 'all' results in the selection of all aforementioned options, along with any other custom gene sets within the 'DEsubs/Data' user specified-directory.

## Value

Individual measure results in matrix form.

## Examples

```
load(system.file('extdata', 'data.RData', package='DEsubs'))

outfile.topological <- tempfile(fileext='.pdf')
outfile.functional <- tempfile(fileext='.pdf')
outfile.barplot <- tempfile(fileext='.pdf')

res <- geneVisualization(
  DEsubs.out=DEsubs.out, top=10,
  measures.topological=c( 'degree', 'betweenness', 'closeness',
                        'eccentricity', 'page_rank'),
  measures.functional=c( 'KEGG',
                        'Disease_OMIM', 'Disease_GAD',
                        'Drug_DrugBank', 'miRNA', 'TF'),
  size.topological=c(5,4),
  size.functional=c(7,4),
  size.barplot=c(5,6),
  export='pdf',
  outfile.topological=outfile.topological,
  outfile.functional=outfile.functional,
  outfile.barplot=outfile.barplot,
  verbose=FALSE)
```

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organismVisualization *Organism level visualization*

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## Description

Organism level measures

## Usage

```
organismVisualization( DEsubs.out, references, topSubs, topTerms, colors,
                      export, width, height, outfiles, verbose )
```

**Arguments**

DEsubs.out	Return value from <a href="#">DEsubs</a>
references	Functional associations with (i) KEGG's pathway terms, (ii) Gene Ontologies of Molecular function, biological processes and cellular components (iii) Disease terms from OMIM and GAD databases), (iv) Drug substances from DrugBank) and the influence of (v) microRNA targets from miRecords and (vi) Transcription Factor targets from Transfac and Jaspar. The corresponding options are 'KEGG', 'GO_bp', 'GO_cc', 'GO_mf', 'Disease_OMIM', 'Disease_GAD', 'Drug_DrugBank', 'miRNA' and 'TF'. If no argument is supplied, no option is selected. Using option 'all' results in the selection of all aforementioned options, along with any other custom gene sets within the 'DEsubs/Data' user specified-directory.
topSubs	Default value is 10
topTerms	Default value is 20
colors	A custom color mode which overrides the default settings.
export	Export type of visualizations ('plot', 'pdf')
width	The width of the printable area (pdf)
height	The height of the printable area (pdf)
outfiles	Output filenames of the visualizations. If the argument is not specified, default filenames are used ('DEsubs/Output').
verbose	TRUE to display informative messages, FALSE to hide.

**Value**

A list of matrices, containing Subpathway/Term/P-Value results for each reference.

**Examples**

```
load(system.file('extdata', 'data.RData', package='DEsubs'))

outfile <- tempfile(fileext='.pdf')

res <- organismVisualization(
  DEsubs.out=DEsubs.out, references='KEGG',
  topSubs=10, topTerms=20,
  width=7, height=6,
  export='pdf',
  outfile=outfile,
  verbose=FALSE)
```

---

subpathwayToGraph      *Subpathway To Graph*

---

## Description

Subpathway plotting as a graph.

## Usage

```
subpathwayToGraph( DEsubs.out, submethod, subname, colors, size, export,
                  width, height, outfile, verbose )
```

## Arguments

DEsubs.out	Return value from <a href="#">DEsubs</a>
submethod	Subpathway extraction type selection (get all available options from <a href="#">subpathwayTypes</a> )
subname	Subpathway name as contained in <a href="#">DEsubs</a> return value, i.e. 'sub1'.
colors	A custom color mode which overrides the default settings.
size	A vector storing width and height of the barplot visualization.
export	A set of options for exporting subpathway data. Possible options are 'plot', 'pdf', 'edgelist', 'json', 'gml', 'ncol', 'lgl', 'graphml', 'dot'.
width	The width of the printable area (pdf)
height	The height of the printable area (pdf)
outfile	Output file name of the visualization. If multiple export types have been selected, the outfile should have an extension '.*'
verbose	TRUE to display informative messages, FALSE to hide.

## Value

No value is returned.

## Examples

```
load(system.file('extdata', 'data.RData', package='DEsubs'))

outfile <- tempfile(fileext='.pdf')

res <- subpathwayToGraph(
  DEsubs.out=DEsubs.out,
  submethod='community.walktrap',
  subname=paste0('sub', 6),
  size=c(10,10),
  export='pdf',
  outfile=outfile )
```

---

subpathwayTypes      *All subpathway types*

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### Description

All subpathway types.

### Usage

subpathwayTypes(grouping)

### Arguments

grouping      By supplying one of the available groupings, specific subsets of available subpathway types can be extracted.

### Details

Apart from the 124 distinct subpathway types, several groupings are available:

**'all'** All subpathway options.

**'all.bwd'** Forward propagation.

**'all.fwd'** Backward propagation.

**'all.stream'** All possible genes targeting or are targeted via a path starting from a gene of interest.

**'all.neighbourhood'** All adjacent genes of a gene of interest with incoming or outgoing links.

**'all.cascade'** A finite sequence of interactions connecting a sequence of genes starting or ending from a gene of interest.

**'all.community'** Group of genes sharing common properties.

**'all.component'** Subgraphs on which any two vertices are (strongly) connected to each other by paths.

**'all.functional'** Forward and backward streams starting from genes/nodes with crucial functional role within the network. Individual options include GO\_bp, GO\_cc, GO\_mf, KEGG, Disease\_OMIM, Disease\_GAD, Drug\_DrugBank, miRNA, TF, DEG, which are defined below.

**'all.GO\_bp'** Genes acting as a bridge among Gene Ontology (GO) Biological Process terms.

**'all.GO\_cc'** Genes acting as a bridge among Gene Ontology (GO) Cellular Component terms.

**'all.GO\_mf'** Genes acting as a bridge among Gene Ontology (GO) Molecular Function terms.

**'all.KEGG'** Genes acting as a bridge among KEGG pathway maps.

**'all.Disease\_OMIM'** Genes acting as a bridge among OMIM Disease targets.

**'all.Disease\_GAD'** Genes acting as a bridge among GAD Disease targets.

**'all.Drug\_DrugBank'** Genes acting as a bridge among DrugBank Drug targets.

**'all.miRNA'** Genes acting as a bridge among microRNA-gene targets.



- 'all.TF' Genes acting as a bridge among TF-gene targets.
- 'all.DEG' Genes with highly Differentially expressed by each experimental data.
- 'all.topological' Forward and backward streams starting from genes/nodes with crucial topological role within the network. Individual options include degree, betweenness, closeness, hub\_score, eccentricity, page\_rank, start\_nodes which are defined below.
- 'all.degree' Number of gene's adjacent interactions.
- 'all.betweenness' Number of shortest paths from all vertices to others passing through a node.
- 'all.closeness' Inverse of farness, which is the sum of distances to all other nodes.
- 'all.hub\_score' Kleinberg's hub centrality score.
- 'all.eccentricity' Shortest path distance from the farthest other node in the graph.
- 'all.page\_rank' Google Page Rank.
- 'all.start\_nodes' Gene nodes without incoming links.

An exhaustive list of all 124 subpathway types follows:

#### STREAM-TOPOLOGICAL

'bwd.stream.topological.degree'	'fwd.stream.topological.degree'
'bwd.stream.topological.betweenness'	'fwd.stream.topological.betweenness'
'bwd.stream.topological.closeness'	'fwd.stream.topological.closeness'
'bwd.stream.topological.hub_score'	'fwd.stream.topological.hub_score'
'bwd.stream.topological.eccentricity'	'fwd.stream.topological.eccentricity'
'bwd.stream.topological.page_rank'	'fwd.stream.topological.page_rank'
'bwd.stream.topological.start_nodes'	'fwd.stream.topological.start_nodes'

#### STREAM-FUNCTIONAL

'bwd.stream.functional.GO_bp'	'fwd.stream.functional.GO_bp'
'bwd.stream.functional.GO_cc'	'fwd.stream.functional.GO_cc'
'bwd.stream.functional.GO_mf'	'fwd.stream.functional.GO_mf'
'bwd.stream.functional.KEGG'	'fwd.stream.functional.KEGG'
'bwd.stream.functional.Disease_OMIM'	'fwd.stream.functional.Disease_OMIM'
'bwd.stream.functional.Disease_GAD'	'fwd.stream.functional.Disease_GAD'
'bwd.stream.functional.Drug_DrugBank'	'fwd.stream.functional.Drug_DrugBank'
'bwd.stream.functional.miRNA'	'fwd.stream.functional.miRNA'
'bwd.stream.functional.TF'	'fwd.stream.functional.TF'
'bwd.stream.functional.DEG'	'fwd.stream.functional.DEG'

#### NEIGHBOURHOOD-TOPOLOGICAL

'bwd.neighbourhood.topological.degree'	'fwd.neighbourhood.topological.degree'
'bwd.neighbourhood.topological.betweenness'	'fwd.neighbourhood.topological.betweenness'
'bwd.neighbourhood.topological.closeness'	'fwd.neighbourhood.topological.closeness'
'bwd.neighbourhood.topological.hub_score'	'fwd.neighbourhood.topological.hub_score'
'bwd.neighbourhood.topological.eccentricity'	'fwd.neighbourhood.topological.eccentricity'

'bwd.neighbourhood.topological.page_rank'	'fwd.neighbourhood.topological.page_rank'
'bwd.neighbourhood.topological.start_nodes'	'fwd.neighbourhood.topological.start_nodes'
NEIGHBOURHOOD-FUNCTIONAL	
'bwd.neighbourhood.functional.GO_bp'	'fwd.neighbourhood.functional.GO_bp'
'bwd.neighbourhood.functional.GO_cc'	'fwd.neighbourhood.functional.GO_cc'
'bwd.neighbourhood.functional.GO_mf'	'fwd.neighbourhood.functional.GO_mf'
'bwd.neighbourhood.functional.KEGG'	'fwd.neighbourhood.functional.KEGG'
'bwd.neighbourhood.functional.Disease_OMIM'	'fwd.neighbourhood.functional.Disease_OMIM'
'bwd.neighbourhood.functional.Disease_GAD'	'fwd.neighbourhood.functional.Disease_GAD'
'bwd.neighbourhood.functional.Drug_DrugBank'	'fwd.neighbourhood.functional.Drug_DrugBank'
'bwd.neighbourhood.functional.miRNA'	'fwd.neighbourhood.functional.miRNA'
'bwd.neighbourhood.functional.TF'	'fwd.neighbourhood.functional.DEG'
CASCADE-TOPOLOGICAL	
'bwd.cascade.topological.degree'	'fwd.cascade.topological.degree'
'bwd.cascade.topological.betweenness'	'fwd.cascade.topological.betweenness'
'bwd.cascade.topological.closeness'	'fwd.cascade.topological.closeness'
'bwd.cascade.topological.hub_score'	'fwd.cascade.topological.hub_score'
'bwd.cascade.topological.eccentricity'	'fwd.cascade.topological.eccentricity'
'bwd.cascade.topological.page_rank'	'fwd.cascade.topological.page_rank'
'bwd.cascade.topological.start_nodes'	'fwd.cascade.topological.start_nodes'
CASCADE-FUNCTIONAL	
'bwd.cascade.functional.GO_bp'	'fwd.cascade.functional.GO_bp'
'bwd.cascade.functional.GO_cc'	'fwd.cascade.functional.GO_cc'
'bwd.cascade.functional.GO_mf'	'fwd.cascade.functional.GO_mf'
'bwd.cascade.functional.KEGG'	'fwd.cascade.functional.KEGG'
'bwd.cascade.functional.Disease_OMIM'	'fwd.cascade.functional.Disease_OMIM'
'bwd.cascade.functional.Disease_GAD'	'fwd.cascade.functional.Disease_GAD'
'bwd.cascade.functional.Drug_DrugBank'	'fwd.cascade.functional.Drug_DrugBank'
'bwd.cascade.functional.miRNA'	'fwd.cascade.functional.miRNA'
'bwd.cascade.functional.TF'	'fwd.cascade.functional.TF'
'bwd.cascade.functional.DEG'	'fwd.cascade.functional.DEG'
COMMUNITY	
'community.walktrap'	'community.edge_betweenness'
'community.fast_greedy'	'community.leading_eigen'
'community.infomap'	'community.louvain'
COMPONENT-CLIQUEs	
'component.max_cliques'	'component.decompose'
'component.3-cliques'	...
...	'component.9-cliques'
COMPONENT-CORENESS	
'component.3-coreness'	...

... 'component.9-coreness'

## Value

A vector of all 124 basic subpathway types. See Details section for handy groupings.

## Examples

```
basic.types <- subpathwayTypes()
stream.types <- subpathwayTypes(grouping='all.stream')
```

---

subpathwayVisualization

*Subpathway level visualization*

---

## Description

Circular diagrams containing subpathways enrichment in potential key regulators (miRNAs, TFs) and biological, biomedical and pharmacological issues.

## Usage

```
subpathwayVisualization( DEsubs.out, references, submethod, subname, colors,
                        scale, shuffleColors, outfiles, export, verbose )
```

## Arguments

DEsubs.out	Return value from <a href="#">DEsubs</a> .
references	Topological references include degree, betweenness centrality, closeness centrality, hub_score, eccentricity and page_rank. The corresponding options are 'degree', 'betweenness', 'closeness', 'hub_score', 'eccentricity' and 'page_rank'. Functional references include (i) KEGG's pathway terms, (ii) Gene Ontologies of Molecular function, biological processes and cellular components (iii) Disease terms from OMIM and GAD databases), (iv) Drug substances from DrugBank) and the influence of (v) microRNA targets from miRecords and (vi) Transcription Factor targets from Transfac and Jaspar. The corresponding options are 'KEGG', 'GO_bp', 'GO_cc', 'GO_mf', 'Disease_OMIM' , 'Disease_GAD', 'Drug_DrugBank', 'miRNA' and 'TF'. Using option 'all' results in the selection of all aforementioned options, along with any other custom gene sets within the 'DEsubs/Data' user specified-directory.
submethod	Subpathway extraction type selection (see all 124 options along with their R commands in supplementary document)
subname	Subpathway name as contained in <a href="#">DEsubs</a> return value, i.e. 'sub1'
colors	A custom color mode which overrides the default settings.

scale	A value in (0,1] used to scale the visualization. Useful in the case of long labels which are trimmed by default.
shuffleColors	TRUE to shuffle user defined or default colors. Defaults to FALSE.
outfiles	Output filenames of the visualizations. If the argument is not specified, default filenames are used ('DEsubs/Output').
export	Export type of visualizations ('plot', 'pdf')
verbose	TRUE to display informative messages, FALSE to hide.

### Details

The associations of subpathways with various biological and pharmacological features are estimated through a hypergeometric test. The enriched associations of a subpathway to each feature are illustrated through circular diagrams.

### Value

A list of matrices, each containing the P-Value of enrichment between the terms for a specific reference (rows) and each of the subpathway genes (columns). If there is no enrichment, the value is NA.

### Examples

```
load(system.file('extdata', 'data.RData', package='DEsubs'))

outfile <- tempfile(fileext='.pdf')

res <- subpathwayVisualization(
  DEsubs.out=DEsubs.out,
  references=c('TF'),
  submethod='community.walktrap',
  subname='sub1',
  scale=c(1.0),
  export='pdf',
  outfile=outfile )
```

# Index

DEsubs, [2](#), [4](#), [6](#), [7](#), [11](#)

geneVisualization, [3](#), [3](#)

organismVisualization, [3](#), [5](#)

subpathwayToGraph, [3](#), [7](#)

subpathwayTypes, [3](#), [7](#), [8](#)

subpathwayVisualization, [3](#), [11](#)