

# Package ‘eegc’

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**Type** Package

**Title** Engineering Evaluation by Gene Categorization (eegc)

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**Description** This package has been developed to evaluate cellular engineering processes for direct differentiation of stem cells or conversion (transdifferentiation) of somatic cells to primary cells based on high throughput gene expression data screened either by DNA microarray or RNA sequencing. The package takes gene expression profiles as inputs from three types of samples: (i) somatic or stem cells to be (trans)differentiated (input of the engineering process), (ii) induced cells to be evaluated (output of the engineering process) and (iii) target primary cells (reference for the output). The package performs differential gene expression analysis for each pair-wise sample comparison to identify and evaluate the transcriptional differences among the 3 types of samples (input, output, reference). The ideal goal is to have induced and primary reference cell showing overlapping profiles, both very different from the original cells.

**VignetteBuilder** knitr

**Depends** R (>= 3.4.0)

**Imports** R.utils, gplots, sna, wordcloud, igraph, pheatmap, edgeR, DESeq2, clusterProfiler, S4Vectors, ggplot2, org.Hs.eg.db, org.Mm.eg.db, limma, DOSE, AnnotationDbi

**Suggests** knitr

**biocViews** ImmunoOncology, Microarray, Sequencing, RNASeq, DifferentialExpression, GeneRegulation, GeneSetEnrichment, GeneExpression, GeneTarget

**License** GPL-2

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barplotEnrich	<i>Barplot the enrichResult</i>
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---

### Description

This function is revised from the [barplot.enrichResult](#) function DOSE package, and used to perform a barplot of the enrichResult object.

**Usage**

```
barplotEnrich(height, x = "Count", colorBy = "p.adjust", top = 5,
font.size = 12, title = "", color = NULL,...)
```

**Arguments**

height            enrichResult object, alternatively output from [functionEnrich](#) function.

x                 one of "Count" and "GeneRatio" to specify the x axis.

colorBy          one of 'pvalue', 'p.adjust', 'qvalue'.

top               number of top categories to show.

font.size, title       font size and title.

color             the color of the bar.

...               see parameters in [fortify](#) function.

**Value**

bar plot of enrichment results

**Examples**

```
## Not run:
# plot the "enrichResult" of Inactive category
inactive = goenrichraw[[2]]
barplotEnrich(inactive, top =5, color ="#2c7bb6", title = "Inactive")

## End(Not run)
```

---

cate.gene

*Categorized genes*

---

**Description**

A list with five gene categories.

**Usage**

```
data(cate.gene)
```

**Format**

A list

**Value**

A list with five gene categories.

---

cate.ratio	<i>Expression Difference ratios of categorized genes</i>
------------	--

---

**Description**

A list with five data frames of gene ED ratios

**Usage**

```
data(cate.ratio)
```

**Format**

A list

**Value**

A list with ED ratios for five gene categories.

---

categorizeGene	<i>Gene Categorization</i>
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---

**Description**

This function categorizes differential genes of each pair-wise comparison among e.g. initiating A, derived B and primary C samples during a cellular engineering, into five categories named from *Reversed, Inactive, Insufficient, Successful* and *Over* representing the gene reprogrammed states, and calculates the ratio of expression difference (ED) between B and A to the ED between C and A.

**Usage**

```
categorizeGene(expr, diffGene, from.sample, to.sample, target.sample)
```

**Arguments**

expr	a data frame with expression for all genes in <code>diffGene</code> , alternatively output from <a href="#">diffGene</a> function.
diffGene	a list of differential genes in three comparisons, alternatively output by <a href="#">diffGene</a> function.
from.sample, to.sample, target.sample	character to specify the name of initiating sample, derived sample and primary sample during a cellular engineering, must be consistent with sample names in the <code>expr</code> data frame.

## Details

Gene (g) categorization is achieved by considering the pair-wise comparisons (Expression Difference, ED eq. 1) among the three types of samples and the ratio of such differences (EDg ratio, eq. 2).  $EDg(B, A) = \text{average expression of } g \text{ in } B \text{ minus average expression of } g \text{ in } A$  (1)  
 $EDg \text{ ratio} = EDg(B, A) / EDg(C, A)$  (2)

*Reversed*, EDg(B,A) and EDg(B,C) are significantly differential, while EDg(C,A) is not limited by differential or not, EDg ratio is smaller than 0; *Inactive*, EDg(C,A) and EDg(B,C) are significantly differential, while EDg(B,A) is not differential; *Insufficient*, EDg(B,A), EDg(C,A) and EDg(B,C) are all significantly differential, EDg ratio is between 0 and 1; *Successful*, EDg(B,A) and EDg(C,A) are significantly differential, while EDg(B,C) is not differential; *Over*, EDg(B,A) and EDg(B,C) are significantly differential, while EDg(C,A) is not limited by differential or not, EDg ratio is greater than 1. For the *Inactive* and *Successful* categories, genes with bottom and top 5 percentage ED ratios are removed to avoid the ambiguous categorization with *Reversed*, *Insufficient* or *Over* categories.

## Value

A list with components: a list of the five gene categories a list of the ED ratios for the five gene categories.

## Examples

```
data(expr.filer)
data(diffgene.genes)

category = categorizeGene(expr = expr.filter, diffGene = diffgene.genes,
                          from.sample="DMEC", to.sample="rEChMPP", target.sample="CB")
cate.gene = category[[1]]
cate.ratio = category[[2]]
```

---

densityPlot

*Quantify Genes and Corresponding ED ratios in Each Category*

---

## Description

Quantify genes in each gene category and their expression difference (ED) ratios in a density plot.

## Usage

```
densityPlot(ratio, color = NULL, main = NA, xlab = NA, ylab = "Density",
            legend.labels = NULL, shade = TRUE, transparency = TRUE, proportion = TRUE,
            out.file = NULL, ...)
```

## Arguments

**ratio** a list of ED ratios for five gene categories, alternatively output by [categorizeGene](#).  
**color** vector of colors for the five gene categories.

main, xlab, ylab	the overall title, title for x axis, and title for y axis, see <a href="#">title</a> .
legend.labels	vector of labels for the legend.
shade	logical to determine if the five categories are filled with shades.
transparency	logical to determine if the density plot is transparent.
proportion	logical to determine whether the proportion of each category genes over the all genes is drawn on the density plot.
out.file	a character string naming the output file with density plot.
...	parameters in <a href="#">plot</a> .

**Value**

a density plot

**Examples**

```
data(cate.ratio)
names(cate.ratio)
# make the extreme ED ratios in Reversed and Over categories to the median values
reverse = cate.ratio[[1]]
over = cate.ratio[[5]]
reverse[reverse[,1] <= median(reverse[,1]), 1] = median(reverse[,1])
over[over[,1] >= median(over[,1]), 1] = median(over[,1])
cate.ratio[[1]] = reverse
cate.ratio[[5]] = over

# densityPlot(cate.ratio, xlab = "ED ratio", ylab = "Density", proportion = TRUE)
```

---

diffGene

*Gene Expression Differential Analysis*

---

**Description**

Identify the differentially expressed genes for each pair-wise comparison of given three types of samples.

**Usage**

```
diffGene(expr, array = TRUE, fpkm = FALSE, counts = FALSE, method = c("limma", "DESeq2"),
from.sample, to.sample, target.sample, filter = FALSE, filter.perc = 0.4,
padjust = "fdr", signif = TRUE, pvalue = 0.05)
```

**Arguments**

<code>expr</code>	a data frame with gene expression data.
<code>array, fpkm, counts</code>	logical, specifying the type of input gene expression data.
<code>method</code>	differential analysis method, alternatively to "limma" and "DESeq2", default to "limma". "DESeq2" can be chosen only when counts is TRUE.
<code>from.sample, to.sample, target.sample</code>	character to specify the name of initiating sample, derived sample and primary sample during a cellular engineering.
<code>filter</code>	logical to indicate whether the genes need to be filtered when match the parameter <code>filter.perc</code> , only applied to fpkm and counts data.
<code>filter.perc</code>	a 0 to 1 number to specify the gene filter criteria by the percentage of samples with non-zero expression. Only used to fpkm and counts data when <code>filter</code> is TRUE, and filter the genes with non-zero expression in less than <code>filter.perc</code> samples.
<code>p.adjust</code>	indicate the method to do p.value correction, default to "fdr". See <a href="#">p.adjust</a> .
<code>signif</code>	logical to indicate whether only the significantly differential genes are output, default to FALSE.
<code>pvalue</code>	a cutoff p.value for the significant genes, default to 0.05, only used when <code>signif</code> is TRUE.

**Details**

This function can be applied on both microarray and RNA-seq data for differential analysis when one of the "array", "fpkm", or "counts" is specified. It does differential analysis to each pair-wise sample comparison among the `from.sample`, `to.sample` and `target.sample`.

**Value**

A list with components : a list with differential analysis result for each pair-wise comparison; a list with differential gene names for each pair-wise comparison; a data frame with filtered/unfiltered gene expression.

**Examples**

```
data(SandlerFPKM)

# differential expression analysis:
diffgene = diffGene(expr = SandlerFPKM, array=FALSE, fpkm=TRUE, counts=FALSE,
                    from.sample="DMEC", to.sample="rEChMPP", target.sample="CB",
                    filter=TRUE, filter.perc =0.4, pvalue = 0.05 )

# differential analysis results
diffgene.result = diffgene[[1]]
# differential genes
diffgene.genes = diffgene[[2]]
# filtered expression data
expr.filter = diffgene[[3]]
```

---

diffgene.genes      *Differential genes for three comparisons*

---

### Description

A list of three vectors with significantly differential genes among three comparisons.

### Usage

```
data(diffgene.genes)
```

### Format

A list

### Value

A list with differential genes in three comparisons

---

dotPercentage      *Percentage Calculation and Visualization*

---

### Description

This function calculate the percentage of genes in each category over given annotated gene sets and plot the percentages.

### Usage

```
dotPercentage(cate.gene, annotated.gene, order.by = NULL, type = "l", lty = 1,
pch = NULL, col = NULL, srt = 50, font = 1, adj = c(1,1), cex = 1, add.line = TRUE,
legend = TRUE, legend.label = NULL, ...)
```

### Arguments

cate.gene      a list of the five gene categories, alternatively output by [categorizeGene](#).

annotated.gene      a list of the annotated gene sets which the cate.gene are proportioned in.

order.by      one character out of of "Reversed","Inactive","Insufficient","Successful" and "Over" to specify a gene category the percentage is ordered by.

type, lty, pch, col      parameters for the plotting, specifying the type of plotting; the line type when type is "l"; the symbol of points on the line; and the color of lines, see graphic parameters in [par\(\)](#).



srt, font, cex, adj  
 parameters for the text labeled on x-axis, specifying the string rotation in degrees; the font of text; the text size, see graphic parameters in [par\(\)](#).

add.line  
 logical to determine if to add lines on the dots, logical to TRUE.

legend  
 logical to determine whether the legend is added on the figure, default to TRUE.

legend.label  
 labels of the legend, applied only when legend is TRUE.

...  
 other parameters see [plot](#).

### Value

a data frame with the percentage of cate.gene in the annotated.gene.

### Examples

```
# load the C/T-specific genes in 16 cells/tissues
data(human.gene)
data(cate.gene)
# perc = dotPercentage(cate.gene = cate.gene, annotated.gene = human.gene,
#                       order.by = "Successful")
```

---

eegc	<i>eegc</i>
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---

### Description

eegc

---

enrichment	<i>Enrichment Analysis by Hypergeometric Distribution Test</i>
------------	--

---

### Description

Enrichment Analysis by Hypergeometric Distribution Test

### Usage

```
enrichment(cate.gene, annotated.gene, background.gene, padjust.method = "fdr" )
```

### Arguments

cate.gene  
 a list of the five gene categories, alternatively output by [categorizeGene](#).

annotated.gene  
 a list of annotated gene sets which the cate.gene are enriched in.

background.gene  
 vector of background genes, e.g. all genes screened by microarray or RNA-sequencing.

padjust.method  
 correction method for enrichment p-values, one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none", default to "fdr", see details in [p.adjust](#).

**Value**

A list of enrichment results for the five gene categories.

**Examples**

```
# load the cell/tissue-specific genes
data(tissueGenes)
# load the mapping file of cells/tissues to grouped cells/tissues
data(tissueGroup)

# get the background genes
data(expr.filter)
genes = rownames(expr.filter)
# enrichment analysis for the five gene categories
data(cate.gene)
tissueenrich = enrichment(cate.gene = cate.gene, annotated.gene = tissueGenes,
                        background.gene = genes, padjust.method = "fdr")
# select a group of cells/tissues
tissueGroup.selec = c("stem cells", "B cells", "T cells", "Myeloid", "Endothelial CD105+")
tissues.selec = tissueGroup[tissueGroup[, "Group"] %in% tissueGroup.selec, c(2,3)]
# tissuetable = heatmapPlot(tissueenrich, terms = tissues.selec, GO=FALSE,
#                           annotated_row = TRUE, annotation_legend = TRUE,
#                           main = "Tissue-specific enrichment")
```

---

expr.filter

*Filtered expression data*

---

**Description**

A data frame with filtered RNASeq FPKM data.

**Usage**

```
data(expr.filter)
```

**Format**

A data frame

**Value**

A data frame with filtered gene expression

---

functionEnrich	<i>Functional Enrichment Analysis</i>
----------------	---------------------------------------

---

### Description

This function performs Gene Ontology (GO) and KEGG pathways functional enrichment for the five gene categories by calling **clusterProfiler** package.

### Usage

```
functionEnrich(cate.gene, organism = "human", convert = TRUE, from = "SYMBOL", ont = "BP",
pAdjustMethod = "bonferroni", GO = TRUE, KEGG = FALSE, enrichResult = FALSE)
```

### Arguments

cate.gene	a list of the five gene categories, alternatively output by <a href="#">categorizeGene</a> .
organism	a character of organism "human" or "mouse" to indicate the species of background genes.
convert	logical to determine whether the gene ID should be converted to "ENTREZID", default to TRUE.
from	the gene id type of input data, see the key types of <a href="#">org.Hs.eg.db</a> .
ont	One of "MF", "BP", and "CC" subontologies, see <a href="#">enrichGO</a> .
pAdjustMethod	correction method for p-value, one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none", default to "fdr", see details in <a href="#">p.adjust</a> .
GO	logical to determine whether the functional enrichment is performed on Gene Ontology, default to TRUE.
KEGG	logical to determine whether the functional enrichment is performed on KEGG pathways, default to FALSE.
enrichResult	logical to determine if the "enrichResult" is output, default to FALSE to output a summary of the "enrichResult".

### Value

Function enrichment analysis results.

### Examples

```
data(cate.gene)
# result in "enrichResult" class by specifying TRUE to enrichResult parameter
goenrichraw = functionEnrich(cate.gene, organism = "human", pAdjustMethod = "fdr",
                             GO = TRUE, KEGG = FALSE, enrichResult = TRUE)

# result of the summary of "enrichResult" by specifying FALSE to enrichResult parameter
# GO enrichment
goenrich = functionEnrich(cate.gene, organism = "human", pAdjustMethod = "fdr",
                           GO = TRUE, KEGG = FALSE, enrichResult = FALSE)
```

```
# KEGG enrichment
keggenrich = functionEnrich(cate.gene, organism = "human", pAdjustMethod = "fdr",
                           GO = FALSE, KEGG = TRUE, enrichResult = FALSE)
```

---

goenrich

*GO enrichment results*

---

### Description

A list of 5 data frames with the Gene ontology enrichment results for the five gene categories.

### Usage

```
data(goenrich)
```

### Format

A list with 5 data frames

### Value

A list of GO enrichment results

---

grnPlot

*Gene Regulatory Network Plot*

---

### Description

This function plot the a cell/tissue-specific gene regulatory network with genes in the five categories, alternatively reducing the network size by plotting given specific genes as nodes.

### Usage

```
grnPlot(grn.data, cate.gene, filter = TRUE, nodes = NULL, centrality.score,
        col = NULL, main= NULL, vertex.label =NULL, vertex.label.dist = 0, vertex.label.font = 1,
        vertex.label.cex = 0.5, vertex.label.color="black", edge.arrow.size = 0.4,
        edge.color = "grey", layout ="layout_with_lgl", legend.labels = NULL, ...)
```

**Arguments**

grn.data	a data frame with two columns named "TF" and "TG" to specify the genes as transcription regulators (TF) and target genes being regulated (TG).
cate.gene	a list of the five gene categories as nodes in the network, alternatively output by <a href="#">categorizeGene</a> .
filter	logical to specify if the network is reduced to less nodes by a filter, logical to TRUE for a clear visualization.
nodes	a character vector of genes to kept in the network, only applied when filter is TRUE.
centrality.score	a vector or data frame of centrality scores for genes in the network, alternatively calculated by <a href="#">networkAnalyze</a> function.
col	colors of gene vertex in each cate.gene.
main	title of the plot.
vertex.label, vertex.label.dist, vertex.label.font, vertex.label.cex, vertex.label.color	parameters for vertex labels, to specify the labels of vertex, the position of labels on the vertex, font size, cex and color for label, see details in <a href="#">igraph.plotting</a> .
edge.arrow.size, edge.color	parameters for edge to specify the arrow size and color of edge, see details in <a href="#">igraph.plotting</a> .
layout	the layout of network plot, see details in <a href="#">layout</a> .
legend.labels	vector of label names for each cate.gene.
...	other parameters used in <a href="#">igraph.plotting</a> .

**Value**

a igraph plot for gene regulatory network.

**Examples**

```
## Not run:
# select genes to shown their regulation with others
node.genes = c("ZNF641", "BCL6")
# enlarge the centrality
centrality.score = degree$centrality*100
names(centrality.score) = degree$Gene
par(mar = c(2,2,3,2))
grnPlot(grn.data = human.grn[[tissue]], cate.gene = cate.gene, filter = TRUE,
        nodes = node.genes, centrality.score = centrality.score,
        main = "Gene regulatory network")

## End(Not run)
```

---

heatmapPlot	<i>Heatmap Plot of Enriched Terms</i>
-------------	---------------------------------------

---

### Description

This function plot the significantly enriched terms in a heatmap by calling **pheatmap** package.

### Usage

```
heatmapPlot(enrichresult, GO = FALSE, terms = NULL, padjust = TRUE, pvalue = 0.05,
top= NA, filter = FALSE, main = NA, annotation = NULL, annotation_col = NULL,
annotated_row = FALSE, annotation_row = NULL, annotation_colors = NA,
display_numbers = FALSE, annotation_legend = FALSE,...)
```

### Arguments

enrichresult	a list of data frames with enrichment results, alternatively output by <a href="#">functionEnrich</a> or <a href="#">enrichment</a> .
GO	logical to determine whether the terms are Gene Ontology(GO) terms enriched by <a href="#">functionEnrich</a> .
terms	a character vector to specify the terms chosen to be listed in the heatmap, selected from the enrichment result, or a data frame with terms and corresponding term annotations used for annotation_row.
padjust	logical to determine whether the significantly enriched terms were selected by adjusted p.value rather than the p.value, default to TRUE.
pvalue	a cutoff value to select the significantly enriched terms.
top	a number to specify the most significantly enriched terms to be drawn in each category, default to NA without specifying.
filter	logical to specify whether the enriched terms need to be filtered with the ones which are significant among the first four categories.
main	a character of main title on the heatmap plot.
annotation, annotation_row, annotation_col, annotation_colors, annotation_legend, ...	see details in <a href="#">pheatmap</a> .
annotated_row	logical to determine whether the the rows are annotated by annotation_row, default to FALSE. When it's TRUE, annotation_row should be specified or using annotations in a data frame of terms.
display_numbers	logical to determine whether the gene counts number is shown on the heatmap.

### Value

heatmap plot and the terms with p.values for the heatmap

**Examples**

```
# plot the enrichment results by the five gene categories
data(goenrich)
heatmactable = heatmapPlot(goenrich, GO = TRUE, top = 5, filter = FALSE,
                           main = "Gene ontology enrichment",
                           display_numbers = FALSE)
```

---

human.gene	<i>Gene regulatory network based human cell/tissue-specific gene sets</i>
------------	---

---

**Description**

A list of 16 human cells/tissues-specific gene sets summarized from the gene regulatory network downloaded from the CellNet website.

**Usage**

```
data(human.gene)
```

**Format**

A list

**Value**

A list with 16 human cells/tissues-specific gene sets from CellNet.

---

human.grn	<i>Human cell/tissue-specific gene-gene regulation</i>
-----------	--

---

**Description**

A list of 16 data frames (cells/tissues) with transcription factors (TF) to target genes (TG) regulation information.

**Usage**

```
data(human.grn)
```

**Format**

A list with 16 data frames

**Value**

A list of human gene regulatory information.

---

human.tf	<i>Gene regulatory network based human cell/tissue-specific transcription factor (TF) regulated gene sets</i>
----------	---

---

**Description**

A list of 1455 human cells/tissues-specific TF regulated gene sets summarized from the gene regulatory network downloaded from the CellNet website.

**Usage**

```
data(human.tf)
```

**Format**

A list

**Value**

A list with 1455 human cells/tissues-specific TF regulated gene sets

---

markers	<i>Marker genes</i>
---------	---------------------

---

**Description**

A vector containing 65 genes specific in endothelial and haematopoietic cells as listed in Sandler's paper.

**Usage**

```
data(markers)
```

**Format**

A vector

**Value**

A vector of marker genes



---

 markerScatter                      *Scatter Plot for Gene Expression*


---

**Description**

Generates an expression profile of each gene category in one sample against another, alternatively plot the regression line from linear modeling fitting.

**Usage**

```
markerScatter(expr, log = FALSE, samples, cate.gene, markers = NULL, pch = 19, cex = 0.5,
  col = NULL, xlab = NULL, ylab = NULL, main = NULL, add.line = TRUE, text.cex = 1, legend.labels = NULL,
  ... )
```

**Arguments**

expr	a data frame with gene expression.
log	logical to determine if the gene expression data is log converted (add a small constant 2), default to FALSE.
samples	a vector of samples to compare on the x axis and y axis.
cate.gene	a list of the gene categories, alternatively output by <a href="#">categorizeGene</a> .
markers	vector of marker genes to be highlighted in the plot. No gene is highlighted when it's NULL.
pch, cex, col, xlab, ylab, main	plot parameters, see details in <a href="#">par</a> .
add.line	logical to determine if the linear model fitting line is added on the figure.
text.cex	font size for the text on markers, see details in <a href="#">text</a> .
legend.labels	vector of labels for the marker legend.
...	other parameters in <a href="#">plot</a> .

**Details**

Visualization of gene expression in the five categories under each pair-wised comparison.

**Value**

plot with gene expression profile.

**Examples**

```
#load the marker genes of somatic and primary cells
data(markers)
data(expr.filter)
#scatterplot
col = c("#abd9e9", "#2c7bb6", "#fee090", "#d7191c", "#fdae61")
markerScatter(expr = expr.filter, log = TRUE, samples = c("CB", "DMEC"),
```

```
cate.gene = cate.gene[2:4], markers = markers, col = col[2:4],
xlab = expression('log'[2]*' expression in CB (target)'),
ylab = expression('log'[2]*' expression in DMEC (input)'),main = "")
```

---

mouse.gene

*Gene regulatory network based mouse cell/tissue-specific gene sets*


---

### Description

A list of 20 mouse cells/tissues-specific gene sets summarized from the gene regulatory network downloaded from the CellNet website.

### Usage

```
data(mouse.gene)
```

### Format

A list

### Value

A list of 20 mouse cells/tissues-specific gene sets

---

mouse.grn

*Mouse cell/tissue-specific gene-gene regulation*


---

### Description

A list of 20 data frames (cells/tissues) with transcription factors (TF) to target genes (TG) regulation information.

### Usage

```
data(mouse.grn)
```

### Format

A list with 20 data frames

### Value

A list of mouse gene regulatory information.

---

mouse.tf	<i>Gene regulatory network based mouse cell/tissue-specific transcription factor (TF) regulated gene sets</i>
----------	---

---

**Description**

A list of 1744 mouse cells/tissues-specific TF regulated gene sets summarized from the gene regulatory network downloaded from the CellNet website.

**Usage**

```
data(mouse.tf)
```

**Format**

A list

**Value**

A list of 1744 mouse cells/tissues-specific TF regulated gene sets.

---

networkAnalyze	<i>Network Topological Analysis</i>
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**Description**

This function analyzes the topological structure of gene regulation network (GRN) by calculating the "degree", "betweenness", "closeness" and "stress" parameters, and output the centrality values for given genes in each gene categories.

**Usage**

```
networkAnalyze(grn.data, cate.gene, centrality = c("degree", "betweenness",
"stress", "closeness"), mode = c("all", "in", "out", "total"))
```

**Arguments**

grn.data	a data frame with two columns named "TF" and "TG" to specify the genes as transcription regulators (TF) and target genes (TG) being regulated.
cate.gene	a list of the five gene categories as nodes in the network, alternatively output by <a href="#">categorizeGene</a> .
centrality	character string of "degree", "betweenness", "closeness" and "stress" to calculate the centrality of network built from input grn.data, see <a href="#">degree</a> , <a href="#">betweenness</a> , <a href="#">closeness</a> , and <a href="#">stresscent</a> for details.
mode	character string of "all", "in", "out" and "total", only used when centrality is "degree" or "closeness", see <a href="#">degree</a> , <a href="#">closeness</a> for details.

**Value**

data frame with genes and centrality scores.

**Examples**

```
# load the CellNet GRN and gene categories
data(human.grn)
data(cate.gene)

# specify a tissue-specific network
tissue = "Hspc"
degree = networkAnalyze(human.grn[[tissue]], cate.gene = cate.gene,
                        centrality = "degree", mode = "all")
```

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SandlerFPKM

*RNA-seq data in FPKM A data frame containing 16692 gene in 7 samples from paper published by Sandler et.al. in 2014., samples are named from somatic dermal microvascular endothelial cell (DMEC) to induced multipotent haematopoietic progenitor (rEChMPP) cells and primary cord blood (CB) cells.*

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**Description**

RNA-seq data in FPKM A data frame containing 16692 gene in 7 samples from paper published by Sandler et.al. in 2014., samples are named from somatic dermal microvascular endothelial cell (DMEC) to induced multipotent haematopoietic progenitor (rEChMPP) cells and primary cord blood (CB) cells.

**Usage**

```
data(SandlerFPKM)
```

**Format**

A data frame with 16692 rows and 7 columns specifying for genes and samples.

**Value**

A data frame with gene expression data.

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tissueGenes	<i>Cell/Tissue specific gene sets</i>
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**Description**

A list of 126 cells/tissues-specific gene sets identified by SpeCond algorithm from 126 cells/tissues in Gene Enrichment Profiler database.

**Usage**

```
data(tissueGenes)
```

**Format**

A list

**Value**

A list with 126 cells/tissues-specific gene sets

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tissueGroup	<i>Tissue mapping to groups</i>
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**Description**

A data frame with 126 cells/tissues and 30 C/T groups they belong to.

**Usage**

```
data(tissueGroup)
```

**Format**

A data frame with 126 rows (tissues) and 3 columns (Tissue, Tissue\_abbr, Group)

**Value**

A data frame with 126 cells/tissues and 30 C/T groups they mapped to

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