# Package 'MIND'

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**Type** Package

**Title** Using Multiple Measurements of Tissue to Estimate Individual-
And Cell-Type-Specific Gene Expression via Deconvolution

**Version** 0.1.0

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**Description** A method to glean more insights from bulk gene expression. It borrows information across multiple measurements of the same tissue per individual, such as multiple regions of the brain, using an empirical Bayes approach to estimate individual- and cell-type-specific gene expression via deconvolution.

**Depends** igraph, edgebundleR

**License** GPL

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**URL** https://github.com/randel/MIND

**BugReports** https://github.com/randel/MIND/issues

## R topics documented:

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example | *A data example*

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## Description

A data list for demonstration.

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**Value**

A list containing

| | |
|---|---|
| X | bulk gene expression (gene x individual x measure). |
| W | subject-specific cell type fraction (individual x measure x cell type). |

**Examples**

```
data(example)
```

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get_network                    *Making a network plot for co-expressed genes*

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**Description**

It makes a circle network plot for co-expressed genes based on the weighted correlation of the deconvolved cell-type-specific expression. The correlation is weighted by the average cell type fraction per person.

**Usage**

```
get_network(alpha, W, cell_type, cor_cutoff = 0.9, gene_color = "#CD2836")
```

**Arguments**

| | |
|---|---|
| alpha | the deconvolved cell-type-specific gene expression (gene x cell type x individual). |
| W | subject-specific cell type fraction (individual x measure x cell type). |
| cell_type | a numeric index indicating which cell type to be plotted. |
| cor_cutoff | the threshold of weighted correlation for linkages to be plotted. |
| gene_color | the color to depict genes in the network. When a single value is provided, all genes are plotted in the same color. If a vector of length of genes is provided, each gene will be plotted with the provided color. |

**Value**

An interactive circle network plot made by edgebundleR to visualize the weighted co-expression of genes based on deconvolved expression.

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mind *The Multi-measure INdividual Deconvolution (MIND) algorithm*

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## Description

It calculates the empirical Bayes estimates of cell-type-specific gene expression, per individual, via a computationally efficient EM algorithm.

## Usage

```
mind(X, W, maxIter = 100, tol = 0.001, verbose = F)
```

## Arguments

X               bulk gene expression (gene x individual x measure).

W               subject-specific cell type fraction (individual x measure x cell type).

maxIter         maximum number of iterations for the EM algorithm.

tol             tolerance level of absolute relative change of the log-likelihood to stop the EM algorithm.

verbose         logical, to print the detailed information for each iteration: iter (the iteration number), logLike_change, sigma2_e, Sigma_c.

## Value

A list containing the output of the EM deconvolution algorithm

alpha           the deconvolved cell-type-specific gene expression (gene x cell type x individual).

iter            the number of iterations used in the EM algorithm.

Sigma_c         the covariance matrix for the deconvolved cell-type-specific expression (cell type x cell type).

sigma2_e        the error variance.

loglikelihood   the log-likelihood for each EM iterations.

## References

Wang, Jiebiao, Bernie Devlin, Kathryn Roeder. Using multiple measurements of tissue to estimate individual- and cell-type-specific gene expression via deconvolution. Submitted.

## Examples

```
data(example)

deconv = mind(X = example$X, W = example$W)

get_network(alpha = deconv$alpha, W = example$W, cell_type = 3, cor_cutoff = 0.7)
```

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