

# Package ‘metaArray’

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**Title** Integration of Microarray Data for Meta-analysis

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**Author** Debashis Ghosh <ghoshd@psu.edu> Hyungwon Choi <hyung\_won\_choi@nuhs.edu.sg>

**Imports** Biobase, MergeMaid, graphics, stats

**biocViews** Microarray, Bioinformatics, DifferentialExpression

**Description** 1) Data transformation for meta-analysis of microarray Data:  
Transformation of gene expression data to signed probability scale (MCMC/EM methods)  
2) Combined differential expression on raw scale:  
Weighted Z-score after stabilizing mean-variance relation within platform

**Maintainer** Hyungwon Choi <hyung\_won\_choi@nuhs.edu.sg>

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## R topics documented:

mdata . . . . . 1

**Index** 2

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mdata	<i>metaArray sample dataset</i>
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## Description

Three datasets from liver, lung, and prostate cancer microarrays. Please refer to the bibliography in the vignette. Chen (30 primary, 9 metastatic), Garber (30 primary, 6 metastatic), Lapointe (30 primary, 9 metastatic)

## Usage

data(mdata)

# Index

## \*Topic **methods**

mdata, [1](#)

chen (mdata), [1](#)

garber (mdata), [1](#)

lapointe (mdata), [1](#)

mdata, [1](#)

mergedata (mdata), [1](#)