

# Package ‘metaArray’

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

**Version** 1.56.0

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

**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

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**License** LGPL-2

**biocViews** Microarray, DifferentialExpression

**NeedsCompilation** yes

## R topics documented:

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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)
```

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