Package ‘metaArray’

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Title Integration of Microarray Data for Meta-analysis

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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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biocViews Microarray, DifferentialExpression

NeedsCompilation yes

R topics documented:

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mdata  metaArray sample dataset

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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