Package ‘metaArray’

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Title Integration of Microarray Data for Meta-analysis
Version 1.52.0
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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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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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