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:

mdata .......................................................... 1

Index 2

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)
Index

*Topic methods*
  mdata, 1
chen (mdata), 1
garber (mdata), 1
lapointe (mdata), 1
mdata, 1
mergedata (mdata), 1