

Package ‘metaArray’

April 5, 2014

Title Integration of Microarray Data for Meta-analysis

Version 1.40.0

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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

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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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