

Package ‘metaArray’

October 17, 2020

Title Integration of Microarray Data for Meta-analysis

Version 1.66.0

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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

git_url <https://git.bioconductor.org/packages/metaArray>

git_branch RELEASE_3_11

git_last_commit 81724ce

git_last_commit_date 2020-04-27

Date/Publication 2020-10-16

R topics documented:

mdata 1

Index 2

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)
```

Index

*** methods**

 mdata, 1

chen (mdata), 1

garber (mdata), 1

lapointe (mdata), 1

mdata, 1

mergedata (mdata), 1