

Package ‘metaArray’

April 14, 2017

Title Integration of Microarray Data for Meta-analysis

Version 1.52.0

Author Debashis Ghosh <ghoshd@psu.edu> Hyungwon Choi
<hyung_won_choi@nuhs.edu.sg>

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

Maintainer Hyungwon Choi <hyung_won_choi@nuhs.edu.sg>

License LGPL-2

biocViews Microarray, DifferentialExpression

NeedsCompilation yes

R topics documented:

mdata 1

Index 2

mdata	<i>metaArray sample dataset</i>
-------	---------------------------------

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](#)