Package ‘metaArray’

March 22, 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 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