Package 'metaArray'

March 26, 2013

Title Integration of Microarray Data for Meta-analysis

Version 1.36.0

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

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

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

License LGPL-2

R topics documented:

---

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