Microarray meta-analysis database (M²DB): a uniformly pre-processed, quality controlled, and manually curated human clinical microarray database

Wei-Chung Cheng†, Min-Lung Tsai‡, Cheng-Wei Chang¹, Ching-Lung Huang¹, Chaang-Ray Chen¹, Wun-Yi Shu§, Yun-Shien Lee⁴,⁵, Tzu-Hao Wang⁵,⁶, Ji-Hong Hong⁷,⁸, Chia-Yang Li¹, Ian C Hsu* *

Abstract
Background: Over the past decade, gene expression microarray studies have greatly expanded our knowledge of genetic mechanisms of human diseases. Meta-analysis of substantial amounts of accumulated data, by integrating valuable information from multiple studies, is becoming more important in microarray research. However, collecting data of special interest from public microarray repositories often present major practical problems. Moreover, including low-quality data may significantly reduce meta-analysis efficiency.

Results: M²DB is a human curated microarray database designed for easy querying, based on clinical information and for interactive retrieval of either raw or uniformly pre-processed data, along with a set of quality-control metrics. The database contains more than 10,000 previously published Affymetrix GeneChip arrays, performed using human clinical specimens. M²DB allows online querying according to a flexible combination of five clinical annotations describing disease state and sampling location. These annotations were manually curated by controlled vocabularies, based on information obtained from GEO, ArrayExpress, and published papers. For array-based assessment control, the online query provides sets of QC metrics, generated using three available QC algorithms. Arrays with poor data quality can easily be excluded from the query interface. The query provides values from two algorithms for gene-based filtering, and raw data and three kinds of pre-processed data for downloading.

Conclusion: M²DB utilizes a user-friendly interface for QC parameters, sample clinical annotations, and data formats to help users obtain clinical metadata. This database provides a lower entry threshold and an integrated process of meta-analysis. We hope that this research will promote further evolution of microarray meta-analysis.

Background
Rapid accumulation of vast amounts of microarray data in public databases like Gene Expression Omnibus (GEO) [1] and ArrayExpress [2] over the past few years has now made it possible to retrieve, integrate, and compare microarray results from many datasets [3,4]. Research has used meta-analysis of microarray results by integrating data from multiple independent studies to successfully identify novel prognosis and diagnosis signatures for cancer and other diseases [5-8]. Microarray meta-analysis involves a systematic search for suitable datasets in retrieval, filtering, re-processing, integration, and analysis. The entire process is complex, laborious, and time-consuming [4]. In an effort to disentangle the complexity of microarray meta-analysis studies, Ramasamy et al. addressed several key issues [4]. However, as noted by these authors, obstacles and challenges remain.

First, identifying suitable studies for meta-analysis is a time-consuming process because experimental information is often stored in a free-text format in a data
warehouse. Although most microarray repositories have adopted the Minimum Information about a Microarray Experiment (MIAME) [9] standard, consistent formats and terminologies for annotating experiments and samples are not specified. The completeness and accuracy of information largely depend on the meticulousness of authors, and this issue constitutes a major challenge for microarray meta-analysis.

Second, re-processing raw data is of great importance for integrating data from multiple datasets [4,10,11], but raw data are not always available. As cautioned by Ochsner et al., fewer than 50% of all microarray studies published in the twenty top-ranked journals during 2007 resulted in depositing datasets into microarray data repositories [12]. Only some of the deposited datasets provide raw intensity data. Taking the Affymetrix HG-U133A platform as an example, only 44% of the samples submitted to the GEO contain raw data files [10].

Third, using pre-processed data by different algorithms will introduce variations into the results of meta-analysis [4,13]. Different datasets typically use different normalization methods, and therefore data downloaded from different sets of experiments are unlikely to be directly comparable. These data are unsuitable for meta-analysis and may produce non-combinable results [4,14]. As suggested by Ramasamy et al., even for studies conducted using the same microarray platform, the raw data should be uniformly pre-processed and normalized using the same algorithm to remove systematic biases for all tested datasets [4].

Fourth, several investigators have suggested considering data quality within the context of microarray meta-analysis [4,11,13]. Recent studies conducted by the MicroArray Quality Control (MAQC) consortium and others have demonstrated that good laboratory proficiency and the resulting improved data quality significantly enhance inter-laboratory and inter-platform reproducibility [15-17]. Moreover, including potential outliers in meta-analysis reduces normalization efficiency, especially when using small datasets for pre-processing [11]. Therefore, it is important to identify and eliminate poor-quality data before the pre-processing step [4,10]. However, quality assessment does not accompany microarray data retrieved from public repositories. Therefore, extra efforts are needed to determine the quality of retrieved microarray data.

A number of databases or web servers have recently been developed to tackle these problems. For example, Celsius [18] is a data warehouse that collects Affymetrix CEL files and seven kinds of pre-processed metadata. CleanEX [19] re-annotates microarray datasets with MeSH terms to facilitate the data-retrieval process. MaRe [20] and GEOmetadb [21] provide tools to facilitate the search and retrieval of data from GEO or ArrayExpress. The M³DB [14] has collected Affymetrix microarray data and provides manually curated experimental conditions, and uniformly normalized microarray data on three microbial species for download. Oncomine [22] has extensively collected, annotated, and standardized human cancer arrays for various platforms. GeneSapiens [23] re-annotates the samples, applies quantile normalization, and offers gene-based scatterplot/correlations between pairs of genes across tissues in its website. However, depending on the aim and scope of these studies, the problems listed above have only been partially resolved.

This study develops M²DB, an expert curated database, to solve microarray data retrieval, annotation, pre-processing, and quality-assessment problems. M²DB contains more than 10,000 previously published Affymetrix array data, re-annotated with controlled vocabularies from ontologies (most from NCI Thesaurus), according to available clinical information. Samples of interest can be easily queried, based on five clinical annotations: “Disease State,” “Disease State Suppl.,” “Disease Location,” “Organism Part,” and “Organism Part Subtype.” Raw data were retrieved from HG-U133A and HG-U133 plus 2.0 and were uniformly pre-processed using Affymetrix Microarray Suite 5 (MAS5) [24], robust multi-chip average (RMA) [25], and GC-robust multi-chip average (GCRMA) [26]. Quality-control assessment reports, for array-base filtering, generated using SimpleAffy [27], Mahalanobis Distance Quality Control (MDQC) [28], and Parametric MultiVariate Outlier labeling (PMVO) [29], packages of Bioconductor [30], were provided for all samples. Arrays with low-quality measurements can be easily excluded from the M²DB web query interface. MAS5call and labeling efficiency values (LEV) [31] are supplied for gene-based filtering for further analysis. The many features offered by M²DB efficiently facilitate the search and retrieval process, as well as ensuring the reliability of human clinical microarray metadata. In summary, M²DB provides human curated annotations, raw data, uniformly pre-processed data, and sets of QC metrics, and significantly improves the quality and comparability of microarray metadata generated by different laboratories.

Construction and content
As illustrated in Figure 1, datasets for human studies were collected from public repositories. After the completion of sample annotation, quality assessment, and data pre-processing, the data were stored in the M²DB server.

Dataset collection and pre-processing
Raw intensity data (CEL files) generated using Affymetrix HG-U133A and HG-U133 plus 2.0 platforms were
retrieved from GEO and ArrayExpress. Arrays performed using samples other than human clinical specimens, such as cell lines, primary cells, and transformed cells, were excluded. In addition, datasets without links to publications were also excluded except Expression Project for Oncology (expO) (GSE2109). A total of 69% of published arrays which contain raw data were performed by human clinical samples. The other 31% of arrays were hybridized to cell lines, primary culture cells, transformed cells, etc. About 8% of clinical arrays were uploaded to repositories more than once. We removed the redundant arrays according to the generation date of CEL files. Eventually, M²DB contains more than 10,000 Affymetrix GeneChip arrays from 192 experiments in ArrayExpress (158 out of 192 experiments also belong to GEO). All microarray raw data were pre-processed using three different algorithms: MAS5, RMA, and GCRMA as implemented in the Bioconductor packages. RMA and GCRMA processed data on a multi-array basis; therefore all arrays of the same platform were uniformly pre-processed to reduce variance.

The Affymetrix microarray system is recognized as naturally suited for meta-analysis [32] and was used as the only microarray system in M²DB, based on several factors. First, the Affymetrix platform provides a consistent and reliable system with a high level of reproducibility [10,14,33]. Second, mapping probes to genes using datasets on different platforms is a complex process [4]. Using datasets originating from the same platform...
circumvents this problem. Third, the single-channel design enables between-chip comparison without a common reference for all arrays [14]. Fourth, many pre-processing, normalization, and QC algorithms are readily available for the Affymetrix platform. Fifth, Affymetrix is the most popular commercial microarray platform, and a very large number of Affymetrix microarray datasets have been deposited into public microarray repositories [34]. On the other hand, there are several obstacles in integrating data from different platforms (including Affymetrix and non-Affymetrix), such as various data processing methods, complex probe-to-gene relationships, and difficulty in comparing results [17]. Moreover, the strategy of M2DB is providing relative “pure” data to reduce the variance of data processing in meta-analysis. For these reasons, we excluded non-Affymetrix platforms from M2DB.

Sample annotation

To ensure annotation consistency and make the retrieval process more efficient, clinical information for each sample was manually curated, based on data obtained from GEO, ArrayExpress, and published papers. As shown in Figure 1, each sample was re-annotated with five clinical characteristics: Disease State, Disease State Suppl., Disease Location, Organism Part, and Organism Part Subtype. Organism Part and Organism Part Subtype describe the sample location. Disease State, Disease State Suppl., and Disease Location describe the physiological state and disease information of individuals. “Organism Part” describes the anatomical location of a sample, such as tissue, organ, blood, or body part. “Organism Part Subtype” is an additional annotation for “Organism Part,” containing information such as cell types or specified regions in an organ (for example, Organism Part: heart; Organism Part Subtype: left ventricular). “Disease State” simply classifies samples into four categories: Normal, Cancer or Tumor, Disease, and Abnormality. “Normal” means specimens were collected from apparently healthy individuals without signs of disease. “Cancer or Tumor” specifies that the sample was collected from a cancerous tissue. “Disease” describes that the sample was collected from a diseased site or one under the influence of disease. “Abnormality” means the specimen was collected from an apparently healthy individual who was under the influence of chemical agents, such as alcohol, or was classified as having a metabolic syndrome, such as abnormal glucose tolerance. These annotations are designed to help users find the required samples quickly and easily. “Disease State Suppl.” contains supplementary information for “Disease State,” for example, the disease name for a “Disease” specimen or the reasons why a sample is annotated as “Abnormality.” “Disease Location” specifies the anatomical location of a disease or the primary site of a cancer. In most cases, clinical samples were obtained from the diseased organ, and therefore the organism part is the same as the disease location. However, when samples were obtained from a tissue other than the diseased organ, the organism part is different from the disease location.

These five characteristics were derived from MGED ontology, but some were modified for easier querying. In order to obtain an accurate clinical annotation from the free-text description in GEO, ArrayExpress, and related papers, terms used in annotations are controlled vocabularies from existing ontologies (besides the terms of Disease State Suppl. in Abnormality of Disease State). This research manually extracted relative information from the free-text description of each sample, then identified accurate terms and unified the synonyms via the Biportal [35], Ontology Lookup Service (OLS) [36] and NCI Enterprise Vocabulary Services (EVS). To fit in with the authors’ original intention of the adopted papers and provide an accurate clinical annotation from the free-text description, this work adopted several ontologies instead of a single ontology. About 90% of terms are from NCI thesaurus, and 10% from other ontologies such as the Foundation Model of Anatomy (FMA) and the Systematized Nomenclature of Medicine-Clinical Terms (SNOMED-CT). [See Additional file 1 and 2 for each term and its source]. Terms for each sample were identified by a team of six biologists and medical doctors. Therefore, we annotate all samples with these five characteristics. Approximately 5% of clinical arrays were excluded due to incomplete information for sample annotation. Other clinical information, such as sex, age, or ethnicity, was not included in M2DB for query because it is frequently not available.

Data quality control

For array-based quality control, Affymetrix recommends using a set of QC factors to describe hybridization performance and array quality. M2DB provides QC metrics generated by three R packages, SimpleAffy, MDQC, and PMVO. SimpleAffy provides a set of QC factors developed based on the Affymetrix QC report. PMVO and MDQC are multivariate approaches that used to evaluate the quality of an array. MDQC examines the “Mahalanobis distance” of its quality attributes from those of other arrays, while PMVO uses parametric multivariate outlier testing using a multivariate Gaussian model.

Five QC factors are included on the query interface for custom definition: scale factor, average background, the 3'5' intensity ratio of GAPDH, the 3'5' intensity ratio of beta-actin, and the proportion of probes called present (percentpresent) as provided by SimpleAffy. The default cutoff values were selected according to the
recommendations of Affymetrix, SimpleAffy, and Larson et al. [10]: scale factor < 3 fold differences; the 3’/5’ intensity ratio of GAPDH < 1.25; the 3’/5’ intensity ratio of beta-actin < 3; percent present > 10%. These factors are also used for multivariate testing in MDQC and PMVO. Three percentiles, 90, 95, and 99, are provided as selection criteria for respective distributions on the query interface for these two methods.

For gene-based filtering, the database provides MASScall and LEVs. The MAS5 algorithm supplies the MAS5call, which annotates whether the gene is expressed in specimen. LEV accesses the effect of RNA-labeling efficiency and RNA quality. Research has proven that filtering out genes with highly variable LEV improves the comparability between different laboratories and the homogeneity of gene expression profiles within the same class of specimens [31].

**Utility**  
**Query interface**

As shown in Figure 2, the M^2^DB web query interface consists of two parts. Part I provides “sample type,” “platform,” and “quality control” criteria for selection. “Sample type” indicates whether the RNA samples for hybridization are “individual,” from a single individual, or “pooled,” from multiple individuals. Only two platforms, HU133A and HU133 plus 2.0, are supported in M^2^DB, and users can choose either one or both. The “quality control” option provides SimpleAffy, PMVO, and MDQC QC factors. For SimpleAffy, users can choose the default value or define a customized value for each QC factor. For PMVO and MDQC, three distribution percentiles are offered in their respective algorithms as QC thresholds.

Part II provides a “flexible combination selection” of five clinical annotations for samples which passed the criteria in Part I. Users can define from one to five annotations for query. The types of annotation and their quantities can be visualized in real time according to users’ combined selections. This combination selection helps users quickly reduce the number of items submitted for quality. For example, there are more than 250 items in “Disease State Suppl.” By applying the combination of “Cancer or Tumor” in “Disease State” and “uterine cervix” in “Disease Location”, the number of items submitted for selection in “Disease State Suppl.” reduces to less than five. On the other hand, users can define different combinations according to their demand. For example, users can select 222 tumors collected from the lung by applying the combination of “Cancer or Tumor” in “Disease State” and “lung” in “Organism Part”. When adding the criterion: “lung” in “Disease Location”, there are only 215/222 samples classified into lung cancer. In this case, 7/222 samples are classified into lung metastasis.

**Experiment/Sample information**

The experiment information table contains simple descriptions of experiments and hyperlinks to the GEO, ArrayExpress, and PubMed websites to obtain more complete information. The sample information table contains complete clinical annotations and QC factors from SimpleAffy, PMVO, and MDQC for each sample. Moreover, the database provides an “additional selection box” for each sample to enable making further selections. Users have an additional option to decide whether a sample is suitable for further analysis according to the complete information in the table.

**Data format and submission**

After confirming the selected samples, users can define which type of data to download. M^2^DB offers four data types: one is raw data (CEL files), and the other three are normalized data (RMA, GCRMA, and MAS5). The database also provides MAS5call and LEVs as gene-base filtering. After entering an email address, the user submits the job to the server. The user receives two email alerts. One is a confirmation email informing the user that the job has been successfully submitted and is being processed. The other email with a download link is sent when the job is completed.

**Discussion**

To quickly and easily query samples, annotation categories adopt a flat list instead of a tree structure. For example, only two annotations, the Organism Part and the Organism Part Subtype, are used to describe the sample location in anatomic position. This choice is motivated by the increased complexity of the ontological tree structure in our web design. Additionally, the Organism Part is only used to describe the sample location in MGED ontology. In M^2^DB, we created the Organism Part Subtype to assist users to define the sample location. For example, T lymphocyte samples can be derived from blood, bone marrow, or umbilical cord blood in the database. The two annotations, Organism Part and Organism Part Subtype, can be more accurate, efficient, and less complicated to define the sample location. According to our annotation categories, users can easily and quickly find samples defined in the selection via our web query interface. It provides instantaneous visualization and selective combination (up to five criteria) of the various quantities and types of items selected.

Detailed descriptions of experimental parameters and sample clinical information are necessary to make the metadata fully interpretable. However, complete descriptions are frequently not available or only partially available in either microarray repositories or published papers. Accordingly, in M^2^DB, the authors supplied
elementary annotations that were manually curated according to free-text descriptions of the collected experiments. If researchers require further clinical information for advanced analysis, support from the authors of original published papers will be necessary. The authors therefore urge public microarray repositories to request microarray researchers for more detailed information, such as sex, age, disease-free survival...etc. This would greatly encourage microarray meta-analysis across different experiments.

The uniform pre-processing eliminates the technical variance of data transformation, such as background...
correction, probe-set summarization, and normalization. Gaggin et al. demonstrated that two different summarizations of the same data may produce differential expression gene (DEG) lists that are only 30% concordant [37]. However, laboratory-to-laboratory variation is hard to eliminate, even if adopting the same data transformation process. Yang et al. carried out a study in which a common set of RNA sample was performed five times in four different laboratories using Affymetrix GeneChip arrays. Significant discrepancies exist in intensity profiles and DEG lists across laboratories [38], resulting in intrinsic variance for meta-analysis studies. There are several statistical algorithms developed to relieve this problem [39-42]. Microarray analysis websites, for example ArrayMining [43], also provide cross studies/platforms normalization. Another way to alleviate laboratory-to-laboratory variance is by removing poor quality arrays. Several studies have emphasized the importance of QC for integrative microarray studies [4,10,11,13]. Owzar et al. proved that removing the outlier arrays could relieve batch effect [11]. Ramasamy et al. suggested array quality control as one of the key issues of microarray meta-analysis studies [4].

Housekeeping genes have been used for normalization in gene expression analysis, such as quantitative RT-PCR, northern blots, and gene expression microarray [44-47]. Furthermore, the expression variation of housekeeping genes between arrays has been used to evaluate the effectiveness of normalization methods [48]. We had used the expression variation of housekeeping genes to examine the effect of array quality control. HU133A arrays performed by normal skeleton muscle in M2DB were selected for the analysis. After submitting these clinical annotations for query, forty-nine samples from seven different datasets were identified by M2DB. The expression variation of each housekeeping gene is presented as C.V. of intensity as shown in the Additional file 3. In general, the expression variation of the housekeeping genes was reduced when one of the array-based QC methods was applied. These results indicate that applying any of the array-based QC methods effectively excludes arrays with poor quality and reduces laboratory-to-laboratory variance in the microarray meta-analysis.

M2DB can be used by researchers to collect metadata for the following purposes: 1) Searching for biomarkers of prognosis or disease [49-51]. 2) Using metadata to validate their own results. For example, according to gene expression pattern derived from 28 patients, Vachani et al. identified a panel of ten genes to accurately distinguish two tumor types; this set of marker genes was validated by 134 individuals collected from four independent previously published Affymetrix datasets [52]. 3) Integrating with their own datasets to increase sample size. For example, Lu et al. applied a meta-analysis of datasets including their own samples and five experimental data collected from other microarray studies [53]. Furthermore, for clinical studies, collecting normal samples is a major difficulty. M2DB includes more than 1,800 normal samples from healthy individuals without diseases, abnormalities, or treatments according to the descriptions of the experiments. These data from normal samples can help researchers discover and address the differences between normal and diseased (abnormal) specimens by cross-comparing different datasets.

Many public microarray web servers have provided analysis tools such as differential expression, clustering, and supervised classification. Thus, M2DB does not put extra effort into constructing online analysis tools. Users can directly upload the M2DB's results to those analysis web servers, for example Expression Profiler [54], GEPAS [55], EzArray [56], or ArrayMining [43]. Users with advanced knowledge and skills in data analysis may find it is more feasible to download raw data files (CEL files) and QC metrics to local computers or to transfer them to public analysis web servers, such as WebArrayDB [57], CARMAweb [58], Expression Profiler [54], GEPAS [55], and EzArray [56], which allow user upload CEL files, for more advanced meta-analysis.

MIAME 2.0 now requests authors to deposit their raw data files in public microarray depositories. This policy will greatly help in data integration and meta-analysis. M2DB is updated periodically to incorporate new experiments which provide raw intensity data. Newly incorporated microarray data will be re-annotated. It took six researchers about one month to curate ~20,000 arrays (including clinical and non-clinical arrays) and to annotate clinical arrays into five clinical characteristics. Finally, we selected 10,202 arrays into M2DB. In the future, when expending the dataset, the needed time will be proportional to the amount of new arrays. In addition, the entire set of raw data will be uniformly reprocessed using normalization as well as QC algorithms when adding new chips into M2DB.

Conclusions

This research develops M2DB to facilitate the search and retrieval process, as well as to ensure the reliability of human clinical microarray metadata. Providing raw data, uniformly pre-processed data, and several sets of QC metrics, M2DB can be used to significantly improve the quality and comparability of microarray metadata generated by different laboratories. The manually curated annotations with the "flexible combination selection" relieve time-consuming searching and help researchers easily find the clinical expression data they need. M2DB provides a lower entry threshold and an
integrated process of meta-analysis. We hope that this database will promote further evolution of microarray meta-analysis.

Availability and requirements

The web-application is freely accessible at http://metadb.m2db.

Additional material

Additional file 1: Summary list of sample location. The excel file containing the summary list of sample location for 10202 samples of M2DB.

Additional file 2: Summary list of disease information. The excel file containing the summary list of disease information for 10202 samples of M2DB.

Additional file 3: The intensity C.V. of 14 housekeeping genes in normal skeleton muscles. The expression variation of 14 housekeeping genes in normal skeleton muscles.

Acknowledgements

We are grateful to the National Center for High-performance Computing for computer time and facilities.

Author details

1Department of Biomedical Engineering and Environmental Sciences, National Tsing Hua University, No. 101, Section 2, Kuang-Fu Road, Hsinchu, 300, Taiwan. 2Institute of Athletics, National Taiwan Sport University, No. 16, Section 1, Shuan-Shih Road, Taichung, 404, Taiwan. 3Institute of Statistics, National Tsing Hua University, No. 101, Section 2, Kuang-Fu Road, Hsinchu, 300, Taiwan. 4Department of Biotechnology, Ming Chuan University, No.5, Ming Rd, Gui Shan District, Taoyuan, 333, Taiwan. 5Genomic Medicine Research Core Laboratory, Chang Gung Memorial Hospital, No.5, Fuxing St., Taoyuan, 333, Taiwan. 6Department of Obstetrics and Gynecology, Lin-Kou Medical Center, Chang Gung Memorial Hospital and Chang Gung University, No.5, Fuxing St., Taoyuan, 333, Taiwan. 7Department of Radiation Oncology, Chang Gung Memorial Hospital, No.5, Fuxing St., Taoyuan, 333, Taiwan. 8Department of Medical Imaging and Radiological Science, Chang Gung University, No.259 Wen-Hwa 1st Road, Kwe-Shan, Taoyuan, 333, Taiwan.

Authors’ contributions

WC, MT, and IH wrote the manuscript. WC, CH, and CWC collected the datasets. WC, MT, TW, JH, CL, and CWC carried out sample annotation. YL and WS performed QC and statistical analysis. OCR and CWC carried out the data pre-process and database server construction. IH, WS, and CH contributed to the discussion and commented the manuscript. IH financially supported this study. All authors read and approved the final manuscript.

Received: 23 April 2010 Accepted: 10 August 2010
Published: 10 August 2010

References

1. Edgar R, Domrachev M, Lash AE. Gene Expression Omnibus: NCBI gene expression and hybridization array data repository. Nucleic Acids Res 2002, 30:207-210.
2. Brazma A, Parkinson H, Sarkans U, Shojaotabab M, Vilo J, Abeygunawardena N, Holloway E, Kapushesky M, Kemmeren P, Lara GC, Oezcimen A, Rocca-Serra P, Sarisone SA. ArrayExpress—a public repository for microarray gene expression data at the EBI. Nucleic Acids Res 2003, 31:68-71.
3. Moreau Y, Aerts S, De Moor B, De Strooper B, Dabrowski M. Comparison and meta-analysis of microarray data: from the bench to the computer desk. Trends Genet 2003, 19:570-577.
4. Ramasamy A, Mondry A, Holmes CC, Altman DG. Key Issues in Conducting a Meta-Analysis of Gene Expression Microarray Datasets. PloS Med 2008, 5:e184.
5. Rhodes DR, Yu J, Shanker K, Deshpande N, Varambally R, Ghosh D, Barrette T, Pandey A, Chinnaian AM. Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. Proc Natl Acad Sci USA 2004, 101:9309-9314.
6. Rhodes DR, Barrette TR, Rubin MA, Ghosh D, Chinnaian AM. Meta-analysis of microarrays: interstudy validation of gene expression profiles reveals pathway dysregulation in prostate cancer. Cancer Res 2002, 62:4437-4433.
7. Xu L, Geman D, Winslow RL. Large-scale integration of cancer microarray data identifies a robust common cancer signature. BMC Bioinformatics 2007, 8:275.
8. Rasche A, Al-Hasani H, Henwig R. Meta-analysis approach identifies candidate genes and associated molecular networks for type-2 diabetes mellitus. BMC Genomics 2008, 9:110.
9. Brazma A, Hingamp P, Quackenbush J, Sherlock G, Spellman P, Stoeckert C, Aach J, Ansorge W, Ball CA, Causton HC, Gaasterland T, Gephen P, Holstege FC, Kim IF, Markowitz V, Matese JC, Parkinson H, Robinson A, Sarkans U, Schulze-Kremer S, Stewart J, Taylor R, Vilo J, Vingron M. Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. Nat Genet 2001, 29:95-96.
10. Larson O, Sandberg R. Lack of correct data format and comparability limits future integrative microarray research. Nat Biotechnol 2006, 24:1322-1323.
11. Osvari K, Barry WT, Jung SH, Sohn I, George SL. Statistical challenges in preprocessing in microarray experiments in cancer. Clin Cancer Res 2008, 14:5959-5966.
12. Ochsner SA, Steffen DL, Stoeckert CJ Jr, McKenna NJ. Much room for improvement in deposition rates of expression microarray datasets. Nat Methods 2008, 5:991.
13. Cahan P, Roweigo F, Mooney D, Newman JC, St Laurent G, McCaffrey TA. Meta-analysis of microarray results: challenges, opportunities, and recommendations for standardization. Gene 2007, 401:12-18.
14. Faith JJ, Driscoll ME, Fusaro VA, Cosgrove EJ, Hayete B, Juhn FS, Kerns AS, Jr, Li KL, Ihmels J, Yeger L, Butte AJ. Large-scale meta-analysis of gene expression in diabetic complications. Genome Biology 2006, 7(Suppl 2):S2.
15. Shi L, Tong W, Fang H, Scheur F, Han J, Puri RK, Freue FW, Goodsaaid FM, Guo L, Su Z, Han T, Fuscoe JC, Xu ZA, Patterson TA, Hong H, Xie Q, Perkins RG, Chen JJ, Ciscano DA. Cross-platform comparability of microarray technology: intra-platform consistency and appropriate data analysis procedures are essential. BMC Bioinformatics 2005, 6(Suppl 2):S12.
16. Han T, Melvin CD, Shi L, Branham WS, Moland CL, Pine PS, Thompson KL, Fuscoe J. Improvement in the Reproducibility and Accuracy of DNA Microarray Quantification by Optimizing Hybridization Conditions. BMC Bioinformatics 2006, 7(Suppl 2):S17.
17. Irizarry RA, Warren D, Spencer F, Kim F, Biswal S, Frank BC, Gabrielon E, Garcia JG, Geoghegan J, Germino G, Griffin C, Hilmer SC, Hoffman E, Jedlicka AE, Kawasaki E, Martinez-Murillo F, Moriberger L, Lee H, Petersen D, Quackenbush J, Scott A, Wilson M, Yang Y, Ye SQ, Yu W. Multiple-laboratory comparison of microarray platforms. Nat Methods 2005, 2:455-456.
18. Day A, Carlson MR, Dong J, O’Connor BD, Nelson SF. Celcius: a community resource for Affymetrix microarray data. Genome Biol 2007, 8:R112.
19. Praz V, Bucher P. CleanEx: new data extraction and merging tools based on MeSH term annotation. Nucleic Acids Res 2009, 37:D860-884.
20. Iliev AE, t Hoen PA, Vilegas MP, den Dunnen JT, Brands BD. Cross-platform comparability of microarray platforms. Nucleic Acids Res 2008, 36:W273-331.
21. Shen KD, Jiang X, Dhillon IS, Kulis B, Sra S. Consensus clustering by spectral partitioning. Machine Learning 2008, 71:161-187.
22. Zhao J, Altman RB, Denkhaus D. Meta-analysis of microarray data: a new approach to hypergeometric analysis of gene expression data. Bioinformatics 2004, 20:206-214.
23. Monteiro AJ, Quackenbush J, Sherlock G. Meta-analysis of microarray data: a new approach to hypergeometric analysis of gene expression data. Bioinformatics 2004, 20:206-214.
24. Monteiro AJ, Quackenbush J, Sherlock G. Meta-analysis of microarray data: a new approach to hypergeometric analysis of gene expression data. Bioinformatics 2004, 20:206-214.
25. Monteiro AJ, Quackenbush J, Sherlock G. Meta-analysis of microarray data: a new approach to hypergeometric analysis of gene expression data. Bioinformatics 2004, 20:206-214.
bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. Genome Biol 2008, 9:R139.

24. Hubbell E, Liu WM, Mei R: Robust estimators for expression analysis. Bioinformatics 2002, 18:1585-1592.

25. Irizarry RA, Hobbs B, Collins F, Beazer-Barclay YD, Antonellis KJ, Scherf U, Speed TP: Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Bioinformatics 2003, 19:249-264.

26. Wu ZJ, Irizarry RA, Gentleman R, Martinez-Murillo F, Spencer F: A model-based background adjustment for oligonucleotide expression arrays. J Am Stat Assoc 2004, 99:909-917.

27. Wilson CL, Miller CJ: Simpleaffy: a BioConductor package for Affymetrix Quality Control and data analysis. Bioinformatics 2005, 21:3683-3685.

28. Cohen Freue GV, Hollandier L, Shen E, Zamar RH, Balshaw R, Scherer A, McManus B, Keewon P, McMaster WR, Ng RT: MDQC: a new quality assessment method for microarrays based on quality control reports. Bioinformatics 2007, 23:3162-3169.

29. Asare AL, Gao Z, Carey VJ, Wang R, Seyfert-Margolis V: Power enhancement via multivariate outlier testing with gene expression arrays. Bioinformatics 2009, 25:48-53.

30. Gentleman RC, Carey VJ, Bates DM, Bolstad B, Dettling M, Dudoit S, Ellis B, Gautier L, Ge Y, Gentry J, Hornik K, Hothorn T, Huber W, Iacus S, Irizarry R, Leisch F, Li C, Maechler M, Rossini A, Sawitzki G, Smith C, Smyth G, Tierney L, Yang Y, Zhang J: Bioconductor: open software development for computational and biological biology. Genome Biol 2004, 5:R80.

31. Lee YS, Chen CH, Tsai CN, Tsai CL, Chao A, Wang TH: Microarray labeling extension values: laboratory signatures for Affymetrix GeneChips. Nucleic Acids Res 2008, 36:e63.

32. Stevens JR, Doerge RW: Combining Affymetrix microarray results. BMC Bioinformatics 2005, 6:57.

33. Shi L, Reid LH, Jones WD, Shipp MA, Ber�ó-Kaesler EK, Puri RK, Schuijf U, T, Wang CH, Yang W, Zhang L, Zhong S, Zong Y, Su Z, Sun H, Szallasi Z, Tezak Z, Thierry-Mieg D, Thompson KL, Tikhonova I, Budczies J, Cheng J, Chudin E, Corson J, Corton JC, Croner LJ, Davies C, Davison TS, Brunner A, Canales R, Cao XM, Cebula TA, Chen JJ, Cheng J, Chudin E, Corson J, Corton JC, Croner LJ, Davies C, Davison TS, Delenstar G, Deng X, Dorris D, Eklund AC, Fan XH, Fang H, Fuller LM, Gentles AK, Gentles JS, Gerhard DS, Golub TR, et al: A 10-gene classifier for distinguishing head and neck squamous cell carcinoma and lung squamous cell carcinoma. Clin Cancer Res 2008, 14:5158-5165.

34. Griffith OL, Melck A, Jones SJM: Meta-analysis and meta-review of thyroid cancer gene expression profiling studies identifies important diagnostic biomarkers. J Clin Oncol 2006, 24:5043-5051.

35. Vachani A, Nebozhyn M, Singhal S, Allia L, Wakedan E, Muschel R, Powell CA, Gaffney P, Singh B, Brose MS, Litzky LA, Kucharczuk J, Kaiser LR, Marshall JS, Albera SM, Shek L: A 10-gene classifier for distinguishing head and neck squamous cell carcinoma and lung squamous cell carcinoma. Clin Cancer Res 2007, 13:2905-2915.

36. Lu Y, Lemoir W, Liu Y, Yi Y, Morrison C, Yang P, Sun Z, Szabo J, Gerald WL, Mathew M, Goyardon R, You M: A gene expression signature predicts survival of patients with stage I non-small cell lung cancer. PLoS Med 2006, 3:2229-2243.

37. Kapushesky M, Kermeneen P, Cullene AC, Dunnick S, Ihmels J, Komer C, Kull M, Torante A, Sarkans U, Vilo J, Braza A: Expression Profiler: next generation—an online platform for expression analysis of microarray data. Nucleic Acids Res 2004, 32:W465-470.

38. Herrejero J, Al-Shahryor F, Diaz-Urriarte R, Mateos A, Vaquerizas JM, Santoyo J, Dopoza J: GEPA: A web-based resource for microarray gene expression data analysis. Nucleic Acids Res 2003, 31:3461-3467.

39. Zheng H, Xiu W: EzArray: a web-based highly automated Affymetrix expression array data management and analysis system. Bioinformatics 2008, 24:421-425.

40. Xia XQ, McClelland M, Parnovik S, Song W, Cong X, Wang Y: WebArrayDB: cross-platform microarray data analysis and public data repository. Bioinformatics 2009, 25:2425-2429.

41. Rainer J, Sanchez-Cabo F, Stocker G, Stum A, Trajanoski Z: CARMAweb: comprehensive R- and bioconductor-based web service for microarray data analysis. Nucleic Acids Res 2006, 34:W498-503.

42. Schabalin AA, Tjelmeland H, Fan C, Peraud CM, Nobel AB: Merging two gene-expression studies via cross-platform normalization. Bioinformatics 2008, 24:1154-1160.

43. Johnson WE, Li C, Rabinovic A: Adjusting batch effects in microarray expression data using empirical Bayes methods. Biostatistics 2007, 8:118-127.

44. Warnat P, Eils R, Bros C: Cross-platform analysis of cancer microarray data improves gene expression classification of phenotypes. BMC Bioinformatics 2005, 6:265.

45. Glaab E, Ganzbaldi JM, Krasnogor N: ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. Bioinformatics 2009, 10:358.

46. Zeni A, Zimmer R, Lengauer T: Centralization: a new method for the normalization of gene expression data. Bioinformatics 2001, 17(suppl 1):S23-S31.

47. Lu B, Yu J, Xu J, Chen J, Lai M: A novel approach to detect differentially expressed genes from count-based digital databases by normalizing with housekeeping genes. Genomics 2009, 94:211-216.

48. Xiong H, Zhang D, Martyniuk CJ, Trudeau WL, Xia A: Using generalized procrustes analysis (GPA) for normalization of cDNA microarray data. BMC Bioinformatics 2008, 9:25.

49. Wilson DI, Buckley MJ, Hellwell CA, Wilson IW: New normalization methods for cDNA microarray data. Bioinformatics 2003, 19:1325-1332.

50. Auto R, Kiplinen S, Saarela M, Kallionemi O, Hautaniemi S, Astola J: Comparison of Affymetrix data normalization methods using 6,926 experiments across five array generations. BMC Bioinformatics 2009, 10(Suppl 1):S24.

51. Vachani A, Nebozhyn M, Singhal S, Allia L, Wakeham E, Muschel R, Powell CA, Gaffney P, Singh B, Brose MS, Litzky LA, Kucharczuk J, Kaiser LR, Marshall JS, Albera SM, Shek L: A 10-gene classifier for distinguishing head and neck squamous cell carcinoma and lung squamous cell carcinoma. Clin Cancer Res 2008, 14:5158-5165.

52. Griffith OL, Melck A, Jones SJM: Meta-analysis and meta-review of thyroid cancer gene expression profiling studies identifies important diagnostic biomarkers. J Clin Oncol 2006, 24:5043-5051.

53. Vachani A, Nebozhyn M, Singhal S, Allia L, Wakeham E, Muschel R, Powell CA, Gaffney P, Singh B, Brose MS, Litzky LA, Kucharczuk J, Kaiser LR, Marshall JS, Albera SM, Shek L: A 10-gene classifier for distinguishing head and neck squamous cell carcinoma and lung squamous cell carcinoma. Clin Cancer Res 2007, 13:2905-2915.

54. Lu Y, Lemoir W, Liu Y, Yi Y, Morrison C, Yang P, Sun Z, Szabo J, Gerald WL, Mathew M, Goyardon R, You M: A gene expression signature predicts survival of patients with stage I non-small cell lung cancer. PLoS Med 2006, 3:2229-2243.

55. Kapushesky M, Kermeneen P, Cullene AC, Dunnick S, Ihmels J, Komer C, Kull M, Torante A, Sarkans U, Vilo J, Braza A: Expression Profiler: next generation—an online platform for expression analysis of microarray data. Nucleic Acids Res 2004, 32:W465-470.

56. Herrejero J, Al-Shahryor F, Diaz-Urriarte R, Mateos A, Vaquerizas JM, Santoyo J, Dopoza J: GEPA: A web-based resource for microarray gene expression data analysis. Nucleic Acids Res 2003, 31:3461-3467.

57. Zhong H, Xiu W: EzArray: a web-based highly automated Affymetrix expression array data management and analysis system. BMC Bioinformatics 2008, 9:46.

58. Xia XQ, McClelland M, Parnovik S, Song W, Cong X, Wang Y: WebArrayDB: cross-platform microarray data analysis and public data repository. Bioinformatics 2009, 25:2425-2429.

59. Rainer J, Sanchez-Cabo F, Stocker G, Stum A, Trajanoski Z: CARMAweb: comprehensive R- and bioconductor-based web service for microarray data analysis. Nucleic Acids Res 2006, 34:W498-503.