Gene expression

Mixture-model based estimation of gene expression variance from public database improves identification of differentially expressed genes in small sized microarray data

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ABSTRACT

Motivation: The small number of samples in many microarray experiments is a challenge for the correct identification of differentially expressed genes (DEGs) by conventional statistical means. Information from public microarray databases can help more efficient identification of DEGs. To model various experimental conditions of a public microarray database, we applied Gaussian mixture model and extracted bi- or tri-modal distributions of gene expression. Prior variance of Baldi’s Bayesian framework was estimate for the analysis of the small sample-sized datasets.

Results: First, we estimated the prior variance of a gene expression by pooling variances obtained from mixture modeling of large samples in the public microarray database. Then, using the prior variance, we identified DEGs in small sample-sized test datasets using the Baldi’s framework. For benchmark study, we generated test datasets having several samples from relatively large datasets. Our proposed method outperformed other benchmark methods in terms of detecting gold-standard DEGs from the test datasets. The results may be a challenging evidence for usage of public microarray databases in microarray data analysis.

Availability: Supplementary data are available at http://www.snubi.org/publication/MixBayes

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1 INTRODUCTION

Differential expression analysis of large-scale microarray studies requires more than five replicates in each comparison group for stable results (Hwang et al., 2002; Pavlidis et al., 2003). Many microarray studies, however, are performed with fewer than five samples in each group due to high-cost limitation or scarcity of biological source materials. In the analysis of the small sample-sized microarray data, it is difficult to correctly identify differentially expressed genes using standard group-comparison statistics because estimation of gene-specific variances, with which to determine the statistical significance of observed changes in gene expression, becomes unstable with a small number of replicates.

Many methods have been introduced to address this variance estimation problem. A popular approach has been certain type of regularization of t-test. In the significance analysis of microarrays (SAM) (Tusher et al., 2001), a non-specific small constant is added to all variance estimates so that they are not too small. In Cyber-T (Baldi and Long, 2001), a posterior variance in Bayesian framework is used for the variance estimation of a gene combining a prior variance from neighboring genes and a data variance of the gene. Empirical Bayes methods compensate for the small number of replicates by combining information across arrays (Efron and Raftery, 2001; Kendziorski et al., 2003; Maureen et al., 2006). The Bayesian approaches have tried to improve the identification of differentially expressed genes by using information across other genes having similar expression.

On the other hand, a very different approach was suggested by Kim and Park (2004) to estimate the ‘natural’ variance of individual genes using a large number of experiments performed previously. This became possible with large public databases of microarray experiments such as the Gene Expression Omnibus (GEO) (Edgar et al., 2002) and ArrayExpress (Brazma et al., 2003). This approach has a natural strength over the Bayesian methods in that gene-specific variance is estimated not from the expression of other genes but from the prior values of expression of the same gene.

However, the GEO-adjusted method used the information in GEO database without considering any information in experimental data for estimating gene-specific variances. Moreover, the variance estimate is non-specific to the experimental dataset. Expression variance is not only gene-specific but also condition-specific. While one may want to obtain an estimation of gene-specific variance under certain condition that is comparable to that of the experimental dataset, direct computation over the whole GEO database returns the global variance rather than the variance within the desired condition.

Because GEO database is an aggregate of many experiments across many different conditions, we cannot assume that a gene has a single distribution across the whole GEO database. As demonstrated in Figure 1, the distribution of expression of a gene in GEO database may be composed of multiple distributions. Therefore, it makes more sense to assume that a gene expression has a multi-distributional structure in GEO database, instead of single compositional structure.

In the present study, we performed comparative study about estimating the gene-specific and condition-adjusted variances of...
The Gaussian mixture model improves the prior variance estimation

Without application of the Gaussian mixture model, the density

While the probe 1799_at seems to show uni-modal distribution, the probes 1737_s_at and 195_s_at seem to show bi- and tri-modal distributions, respectively.

We used two kinds of datasets, i.e. test and reference datasets. Test datasets

distributions of 1737_s_at and 195_s_at into two and three Gaussian distributions, respectively. In the Affymetrix U95A platform, using Gaussian mixture

gene-specific variance assuming that a gene has a single expression distribution across GEO database. Using Gaussian mixture model, we decomposed the

distributional structure in GEO database.

The Bayesian framework improves the previous GEO-adjusted

mixture model, and then integrates the priors with the data variances

from GEO database in terms of performance exploiting the multi-
dimensional structure in GEO database.

2 METHODS

2.1 Datasets

We used two kinds of datasets, i.e. test and reference datasets. Test datasets are used to compare various benchmark methods. The test datasets should have two groups for comparison and enough number of replicates for each group such that we can reliably make a 'gold-standard' DEG list and have enough number of repeats for repeated microarray sampling.

Reference datasets are used to estimate gene-specific prior variances. They are expected to have large quantity across various conditions such that we can stably estimate the condition-adjusted variability of each gene.

In the present study, we used four test (Table 1) and 33 reference datasets (see Supplementary Table 1). The test datasets includes the prostate and Duchenne muscular dystrophy datasets (Haslett et al., 2002; Singh et al., 2002) used in the study of Kim and Park (2004), and two more datasets (Sturniuko et al., 2005; Stearman et al., 2005) having large number of replicates for both comparison groups and with CEL files available. We chose to analyze Affymetrix HG-U95A chip datasets such that we can make more stable comparison and avoid the complexity of between-platform comparisions. We chose four well known microarray datasets which have been conventionally used in microarray study and do not consider reference datasets. This testing on sampled microarrays and comparison to gold-

standard list. We measured the performance of various methods as the number of top K genes from the gold-standard list that were correctly returned by

the methods. This testing on sampled microarrays and comparison to gold-

standard list was repeated. For reliable conclusion, the performances are averaged over 500 repeats. In the present study, the sampling number ranged from two to five.

2.2 Benchmark outline

For the purpose of comparison, we used ‘repeated sampling procedure’ which was used both by Pavlidis et al. (2003) and Kim and Park (2004). First, a gold-standard DEG list was determined for each dataset by standard t-test comparing all samples in the dataset and sorted the resultant DEGs in a descending order by the absolute value of T-statistic. Second, a small number of microarrays (n = 2–5) were sampled from each comparison group to obtain DEGs by applying benchmark methods. For brevity, we use the same notation ‘NvN’ to denote a two-group comparison with N arrays versus N arrays following Kim and Park (2004). The list of DEGs was compared to the gold-

standard list. We measured the performance of various methods as the number of top K genes from the gold-standard list that were correctly returned by

the methods. This testing on sampled microarrays and comparison to gold-

standard list was repeated. For reliable conclusion, the performances are averaged over 500 repeats. In the present study, the sampling number ranged from two to five.

2.3 Test statistics for differential expression

Test statistics appear in this study can be categorized into four groups. The first group consists of standard methods which have been conventionally used in microarray study and do not consider reference datasets. This group contains mean-fold, standard t-test and regularized t-test. The second group consists of GEO-adjusted methods which replace the data variance with the gene-specific variance estimated from GEO database. This group contains previously proposed GEO-global test and pooled test, and the

Fig. 1. Examples about distributions of GEO-wide gene expression. Expression density plots were obtained from ~1400 microarrays present in GEO database. Without application of the Gaussian mixture model, the density function generated these bi- and tri-modal distribution plots. It may not be sensible to estimate gene-specific variance assuming that a gene has a single expression distribution across GEO database. Using Gaussian mixture model, we decomposed the distributions of 1737_s_at and 195_s_at into two and three Gaussian distributions, respectively. In the Affymetrix U95A platform, using Gaussian mixture model, 6173 (48.9%) and 4384 (34.7%) among the 12 625 probes are modeled to have bi- and tri-modal distributions, respectively.

Table 1. Summary of test datasets

| Dataset | GEO ID | Replicates |
|---------|--------|------------|
| Duchenne muscular dystrophy | GSE1004, GDS563 | 21 (10/11) |
| Macular degeneration and dental fibroblast response to sublethal oxidative stress | GSE1719, GDS963 | 36 (18/18) |
| Pulmonary adenocarcinoma | GSE2514, GDS1650 | 39 (19/20) |
| Prostate cancer | GSE1004 | 102 (50/52) |

*Numbers of total (normal/disease) samples.

*Data is not available in GEO and downloaded from author’s website.
2.4 Estimation of prior variances from reference datasets

\[ \sigma_{\text{Prior}}^2 = \frac{1}{n} \sum_{i=1}^{n} (y_i - \bar{y})^2 \]

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where \( \sigma_{\text{Prior}}^2 \) is the posterior variance for the i-th gene, calculated from the prior variance \( \sigma_{\text{Global}}^2 \) and the data variance \( \sigma_i^2 \) in the Bayesian framework. Please notice that while \( \sigma_{\text{Global}}^2 \) can adjust to different data, \( \sigma_{\text{Prior}}^2 \) and \( \sigma_{\text{Pooled}}^2 \) are specific to experimental data (see Section 2.4 for the prior estimation and Section 2.5 for the Bayesian integration).

2.5 Bayesian framework for variance integration

Bayesian framework has been used for differential expression analysis of microarray study (Baldi and Long, 2001; Gottardo et al., 2003). Previously, the prior variance was estimated from the neighboring genes or fixed to a non-specific value. The GEO database, however, can provide natural estimates of prior. We can estimate the prior of a gene using the prior GEO expression values of the same gene instead of the expression values of other genes. For Bayesian integration of the prior variance and the data variance, we use the formula by Baldi and Long (2001) that models log-expression values by normal distributions, parameterized by corresponding means and variances with hierarchical prior distributions.

\[ \sigma_{\text{Pooled}}^2 = \frac{1}{n} \left[ \sum_{i=1}^{n} (y_i - \bar{y})^2 \right] \]

In essence, the posterior variance is represented as a weighted average of prior variance and data variance. The parameter, \( \kappa = \sigma_{\text{Prior}}^2 + n \), determines the degree of confidence in the prior variance \( \sigma_{\text{Prior}}^2 \) versus the data variance \( \sigma_{\text{Data}}^2 \). Different posterior variances are derived from the same data variance depending on the prior variances. In case of \( \sigma_{\text{GEO Mixed}} \), \( \sigma_{\text{Pooled}}^2 \) is derived when \( \sigma_{\text{Global}}^2 \) is used for prior.

3 RESULTS

3.1 Performance comparison

For the four test datasets, our proposed method, \( \text{GEO Mixed} \), is compared to the standard methods, \( \text{F-Mean}, \text{T-Stan} \) and \( \text{T-Reg} \), and the previous GEO-adjusted methods, \( \text{G_Pooled} \). Sample sizes were chosen from two to five, under which standard methods were known to be ineffective (Pavlidis et al., 2003). This range was also used by Kim and Park (2004).
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3.1.1 Comparison of each dataset

Figure 2 demonstrates the performance of the six test statistics for the four datasets. The methods show relatively high performance for the Haslett’s dataset and relatively low performance for the Singh’s dataset. This variation is an expected one since the dependence not only on the test statistics but also on the characteristics of the dataset such as the number of samples and the degrees of within-group homogeneity and between-group separation. Despite the variations, common tendencies in the performance curves are well demonstrated with the different datasets. First, G_MixBayes shows the best performance in most of the comparisons (13 out of 16 comparisons). Second, regularized t-test shows improved performance than standard t-test. This confirms the previous studies of variance regularization. Third, the performance of the statistics estimating variances from test datasets, T_Stan, T_Reg and G_MixBayes increases as the number of samples is increased. But the performance of the statistics ignoring test dataset variances, T_Mean, G_Global and G_Pooled do not increase as much as the increment of sample size. Note that G_MixBayes is the only method that uses both test and reference datasets for gene-specific variance estimation, while G_Global and G_Pooled utilizes reference datasets only.

3.1.2 Comparison summary

Figure 3 exhibits the summary of the performances in Figure 2. G_MixBayes was the best performer across all sample range, returning 17 and 37% more of top genes than the second best F_Stan in 2v2 and 3v5 tests, respectively, and 13 and 5% more of top genes than the second best T_Reg in 4v4 and 5v5 tests, respectively. G_Global and G_Pooled were better than T_Stan and T_Reg in 2v2 test but their improvement in 2v2 was not as large as to be comparable to T_Stan in 5v5 and T_Reg in 3v3, as claimed in the Kim and Park’s study. In each dataset, the Kim and Park’s GEO methods outperformed only in Stearman’s dataset where the performances of G_Global and G_Pooled in 2v2 were comparable to T_Stan in 5v5 and T_Reg in 4v4. The detailed information about the magnitude of improvement of G_MixBayes is available in the supplementary web site.

3.1.3 Reproducibility of the results

There can be many possible reasons why some of the performance improvements of Kim and Park are not observed in our study. First of all, the results of Kim and Park are only based on single test dataset, Singh’s dataset. As can be seen in Figure 2, there are variations in performance among test datasets. Thus it is probable that the result of Kim and Park are dependent on the specific dataset. Second, the configuration of reference datasets, GEO database specifically, has changed. Although T_Reg outperforms the Kim and Park’s GEO methods in general, the opposite results were observed in 2v2 comparison. In 3v3 comparison, T_Reg was not superior to the Kim and Park’s GEO methods with the Haslett dataset. We observed similar results with increasing number of DEGs in the test datasets (see Supplementary Material). These results indicated that the Kim and Park’s method may outperform with small number of samples (n < 4).
3.1.4 Comparison in hybrid method with regularized t-test
Another advantage of previous GEO-adjusted methods, $G_{\text{Pooled}}$ and $G_{\text{Global}}$, is that they perform well when combined with $T_{\text{Reg}}$ at gene rank level. The hybrid method averaged 75% of the value of the lower rank and 25% of the value of the higher rank to merge ranks in $T_{\text{Reg}}$ and the corresponding GEO-adjusted methods. This 75%/25% ratio was highly tuned empirically for better results in the previous study (Kim and Park, 2004). In the present study using the proposed 75%/25% ratio, $G_{\text{Pooled}}$ and $G_{\text{Global}}$ could find 52 and 75% more of the top genes, respectively, in hybrid use with $T_{\text{Reg}}$ than in single use (the percentages are averages over the four datasets). The performance of $G_{\text{MixBayes}}$, however, is little improved with hybrid use with $T_{\text{Reg}}$. Specifically, its performance was improved by 13% in Hasletete’s, 1% in Strunskova’s, 2% in Stearns’s and 1% in Singh’s test datasets. This limited improvement in the hybrid scheme with $G_{\text{MixBayes}}$ is possibly because $G_{\text{MixBayes}}$ already incorporates the benefit of $T_{\text{Reg}}$ in the level of statistical calculation through the Bayesian integration of test- and reference-dataset variances. There might have been less room for improvement by adding information from $T_{\text{Reg}}$ at the level of gene ranks. Although their substantial improvements by hybrid method, $G_{\text{Global}}$ and $G_{\text{Pooled}}$ outperform $G_{\text{MixBayes}}$ only in Stearns’s test dataset (t-test, $P < 0.05$). In the rest, $G_{\text{MixBayes}}$ outperformed significantly (t-test, $P < 0.05$).

3.2 Sources of improvement
Here, higher performance of $G_{\text{MixBayes}}$ over $G_{\text{Pooled}}$ and $G_{\text{Global}}$ was well demonstrated in the four test datasets. $G_{\text{MixBayes}}$ is modified from earlier GEO-adjusted methods in two aspects: estimation of prior variance using Gaussian mixture model and Bayesian integration of both testing and reference dataset variances. To assess the individual contributions of the two modifications for the performance improvement, we performed two additional comparisons:

1. Comparing $G_{\text{Pooled}}$ and $G_{\text{Global}}$ to $G_{\text{Mixture}}$: an un-integrated version of $G_{\text{MixBayes}}$
2. Comparing $G_{\text{MixBayes}}$ to the Bayesian version of $G_{\text{Pooled}}$ and $G_{\text{Global}}$

In the above comparison, $G_{\text{Mixture}}$ used the pooled variance of mixture distributions of the reference datasets without using the experimental dataset. The Bayesian version $G_{\text{Pooled}}$ and $G_{\text{Global}}$ was computed by substituting prior variance of equation (10) with the $\sigma^2_{\text{Pooled}}$ and $\sigma^2_{\text{Global}}$.

As demonstrated in Figure 4, both of our modifications improved the performance. Bayesian integration improved the performance of all methods in all test datasets. It improved more as increasing number of samples were in test datasets, resulting steep performance curves. This is because the more stable variance estimation of test datasets was used for Bayesian integration. We also found performance improvements when the mixture prior estimation is used alone. In the three methods using the prior variance only, $G_{\text{MixBayes}}$ outperforms $G_{\text{Pooled}}$ and $G_{\text{Global}}$ in three out of four test datasets. The improvements were constant across all sample sizes because the sample size only affected the variance estimates of test datasets which were not used for these prior-only methods. The improving effects were additive when Bayesian integration and mixture prior estimation were used together. This may be because they incorporated different information in the steps of variance calculation. The maximum performance was achieved when both Bayesian integration and mixture prior were used.

3.3 The effect of other parameters
There are a number of parameters that may affect the results of the present analysis. We evaluated the performance of the benchmark statistics with the following different parameter set.

3.3.1 GEO change
The change of reference datasets in GEO database may affect the estimation. This may be in part the reason why $G_{\text{Global}}$ and $G_{\text{Pooled}}$ did not perform as well in the present study as claimed in the previous one. To test whether our findings are only specific to current state of GEO, we compared the performance of $G_{\text{MixBayes}}, G_{\text{Global}}$ and $G_{\text{Pooled}}$ across various states of GEO database (Fig. 5). By means of random-sampling from GEO, we compared the methods using reference datasets with 500–1200 arrays. For reliability, we repeated the computation 100 times for each sample size. Five hundred is the same size to the study of Kim and Park, though the composition is not identical. The maximum size that we could produce enough replications from the total of 1400 microarrays was 1200. Across all conditions, we found that $G_{\text{MixBayes}}$ consistently outperformed both $G_{\text{Global}}$ and $G_{\text{Pooled}}$. Therefore, we believe that the findings are not limited to the specific state of reference datasets that $G_{\text{MixBayes}}$ may outperform in the future composition of GEO.
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3.3.2 Top K genes In this study, the performance of test method is measured as the number of genes common between top 50 in gold-standard DEG list and the test DEG list. Depending on the number of top K genes, the performance can change. We reproduced the results under other top K genes and found that our results are not significantly affected by K (see Supplementary Material).

3.3.3 Prior confidence In Bayesian integration, the prior confidence parameter should be determined by user. We used $\kappa=6$ in this study. Similar results were obtained in other $\kappa$ values ranging from 6 to 15 (see Supplementary Material).

4 DISCUSSION AND CONCLUSIONS

In this analysis, we improved identification of differentially expressed genes in datasets having a small number of samples by obtaining prior variance from mixture modeling of microarray data in the public database.

The success of our methods seemed to come from estimation of prior variances using mixture modeling. The Baldi’s Bayesian framework performs well in the microarray data having small samples. This is re-validated in our analysis (Fig. 4). Instead of estimating prior variance based on uni-modal distribution, we selected prior variance from the multi-modal mixture model. As shown in Figure 1, a large number of genes had bi- or tri-modal distributions in their expression values. Simple pooled variances of such genes are likely to be larger than that of a single density of the mixture model because the pooled variance is equivalent to the sum of the variances from each component of the mixture model. This is especially the case with the Kim and Park’s method. Therefore, the prior variances were tended to be small and it influenced the posterior variances to be small in the Bayesian estimation. This might contribute to the better performance of our approach because test statistics will increase as the variance decreases with a same mean difference obtained from the experimental data. This may be the same reason for outperforming the regularized t-test.

The number of data is still increasing in public microarray data repositories. With the success of the microarray application in genomic research, more investigators are willing to use microarray experiment. However, the number of samples and cost are the main obstacles to the application of microarray. This research provided a candidate solution for the analysis of small sample-sized data using public repositories.

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