

Image Preprocessing for cDNA Microarray Using Deconvolution Method

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1 Introduction

The image of cDNA microarray does not print actual intensity value because cDNA microarray methods are one of the methods using fluorescence dye. In scanning process for detecting emission of fluorescence light, the intensity of Cy3 (RED) and Cy5 (GREEN) are not identical in same conditions. We know that experiment for detecting emission of fluorescence light have several faults in itself. All of experiment using fluorescence detection have same problem. In actually, the function which calculates intensity for fluorescence light is not linear function but sigmoid function. Sigmoid function is mistaken in high or low level intensity. In this phenomenon is occurred by the character of PMT tube. If we take a detail information about above sigmoid function, we can do reverse trace step for recalculation original intensity. It is called 'Deconvolution'. Then, Deconvolution method can apply several image processing step, recalculation original intensity step and dye-swap problem.

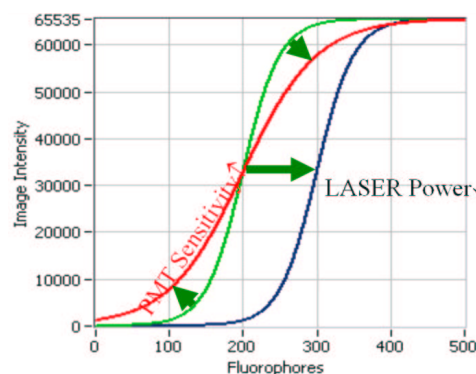


Figure 1: The image intensities of distorted by the nonlinear ranges.

2 Implementation

As a result of dye-swap in cDNA microarray experiment, we got 24 chip image file (TIFF format) which is processed on 4 step condition and multiple by the three times in developmental stage of mouse brain tissue

First, we calculate to find relative position in three dimensional space of 24 chip image using Principle component analysis (PCA), and then we found that the most important principle component is dye swap efficient

Second, we perform Deconvolution methods for finding original intensity of spot on the image and remake the converted to image, we perform same first method by converted methods

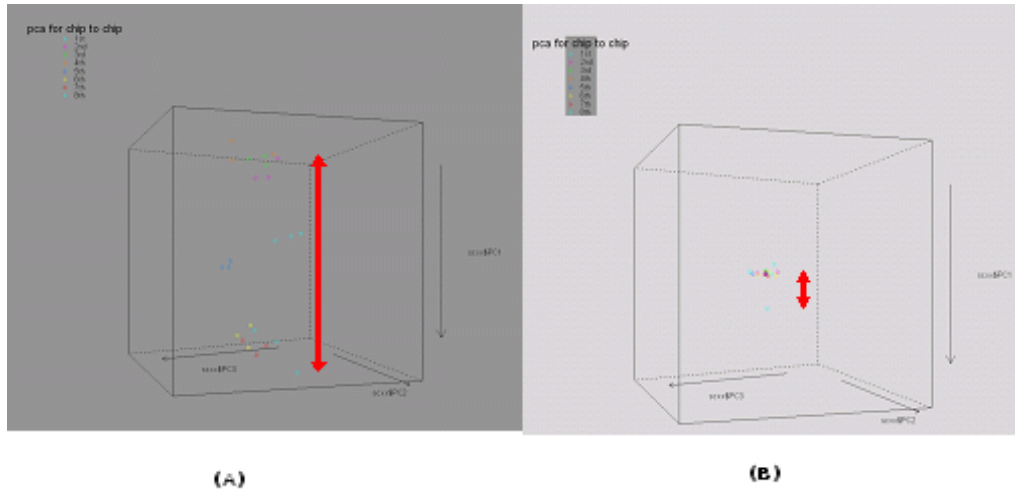


Figure 2: Before(A) and after(B) PCA result in 3D scatter plot using Deconvolution method.

3 Discussion

We solve the problem which raises dye-swap condition in cDNA microarray experiment, the change of intensity make different three dimensional scatter plot which is more available. However Deconvolution methods are too slow to access high throughput data processing. We will make a challenge to upgrade performance.

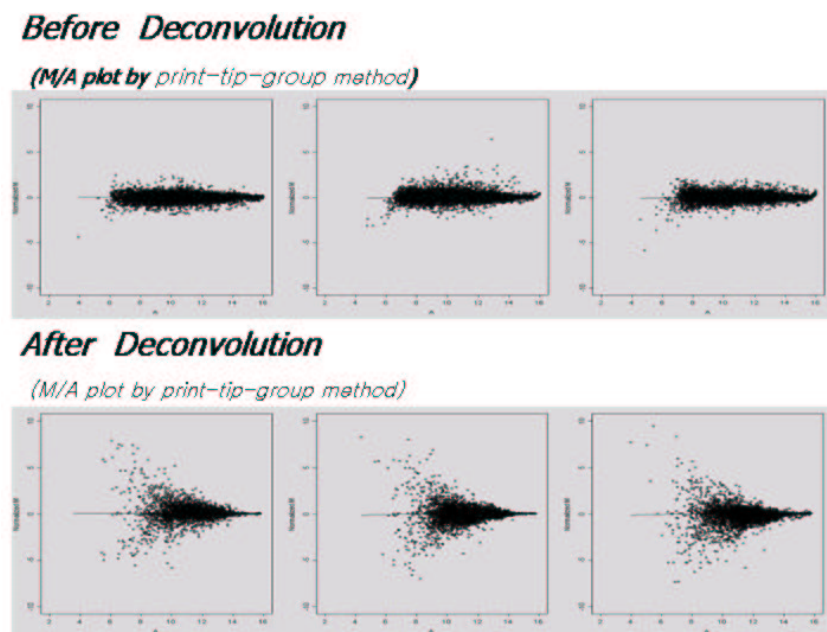


Figure 3: Result of the change intensity.

References

- [1] JinHyuk, K., Compensation of scanner before robust m regression normalization in cDNA microarray, *Proc. 11th ISMB 2003*, 108, 2003.