Analysis of DNA Microarray Data by Using Self-Organizing Maps

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Keywords: Self-Organizing Maps, DNA microarray, genes

1 Introduction

Self-Organizing Maps (SOM) is a kind of an artificial neural network. SOM is an unsupervised learning. By that, various, multi-dimensional data can be made visible and then clustered. Moreover, by making the component maps, it will be known what kind of influence any arbitrary dimensional component can give for clustering.

Then, an attractively new analytical technique which uses SOM is proposed and used for DNA microarray data in this article. MATLAB was used for the analysis.

2 Method and Results

We used datas which analyzed rat RNA samples with DNA microarray of rat 3824 genes. The kinds of genes of data used at this time is 3824 kinds, and the number of samples is 35.

Moreover, the gene name of this sample data was assigned as ID from A1 to A3824. The samples can be clustered according to the following procedures.

1. Each item of 3824 which corresponds to the kind of the gene is assumed to be each dimension of the data vector.

2. The 35 teacher labels according to the samples are located.
   - Thus, the number of data is 35, and each data has a multi-dimensional vector of 3824 dimensions.

3. The result by SOM learning is shown in Fig. 1.

A more accurate phase relation is examined by using spherical SOM in adding to an ordinary plane SOM. The results by a spherical SOM are not presented here. Using this, it was possible to classify 35 conditions results into six classes. These classes are arranged Class A to Class F, as shown in the Table 1, using the result of Fig. 1.
Table 1: Clustering results.

<table>
<thead>
<tr>
<th>ClassA</th>
<th>ClassB</th>
<th>ClassC</th>
<th>ClassD</th>
<th>ClassE</th>
<th>ClassF</th>
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<td>L10C03</td>
<td>L14824</td>
<td>IN4820</td>
<td>IN0C20</td>
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<td>SP0C10</td>
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</table>

To exclude needless genes for clustering, the following procedures are carried out for the preprocessing.

1. The 35 samples are used as variate, and the variance of each gene is examined.

2. Genes which have small standard deviations are excluded. 424 genes which have large standard deviations are chosen for experiment.

3. 424 kinds of component maps are made for these chosen genes.

Finally, by the SOM method, the genes are clustered according to the following procedures.

(a) The data vector is made based on dark and bright informations on each unit on the component map. In the case, we use the vector of 100 dimensions because the map size was 10×10.

(b) ID of the chosen gene is assumed to be a teacher label of each item.
   • The number of data is 424, and each data has a multi-dimensional vector of 100 dimensions.

(c) The result by SOM learning is shown in the Fig. 2.

![Figure 2: Clustering of genes.](image_url)

Here, a plane SOM and a spherical SOM were used for the DNA microarray analysis. And, the result was equivalent with a usual clustering method. However, the result was obtained in a reasonable shorter time.

References
