Analysis of Dataset 2

Preliminary Report

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Microarray Data Cleaning

Microarray dataset needs to be preprocessed before mining.

- Remove the “Gene Description” and change the “Gene Accession Number” to “ID”.
- Normalize all data values to the range [20, 16,000]. (i.e. the value less than 20 or over 16,000 was considered as unreliable by biologists.)
- Add a “Class” row to indicate the type of leukemia. (note for the test dataset all values for “Class” are “?”.)
- Transpose the dataset making each column to be an attribute, and each row to be a testing sample.

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Data Clean Dataset

After cleaning the microarray data, our dataset is ready for mining.

- 7070 genes(attributes) for each sample.
- Class Variable: $Class \in ALL,\ AML$.
- “Class” is treated as nominal here.
- “ID” should be further removed.

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- Attribute's Discrimination Ability.
- The Signal-to-Noise (*S2N*) ratio and T-value:

$$S2N = \frac{\mu_1 - \mu_2}{\delta_1 + \delta_2}$$

$$T - value = \frac{\mu_1 - \mu_2}{\sqrt{\frac{\delta_1^2}{N_1} + \frac{\delta_2^2}{N_2}}}$$

where μ is the average, δ is the standard derivation, and N is the number of samples.

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- Join the two measures to hope a better set.

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Selected Attributes

Three attribute sets have been selected by the following approaches.

- Rank the genes by the absolute value of *S2N* ratio and get top 50 genes.
- Rank the genes by the absolute value of *T-value* and get top 50 genes.
- Combine the previous two sets with the *common* genes.

Detail information of the selected genes can be found on my page: *http://www.cs.queensu.ca/home/xiao/dm.html*.

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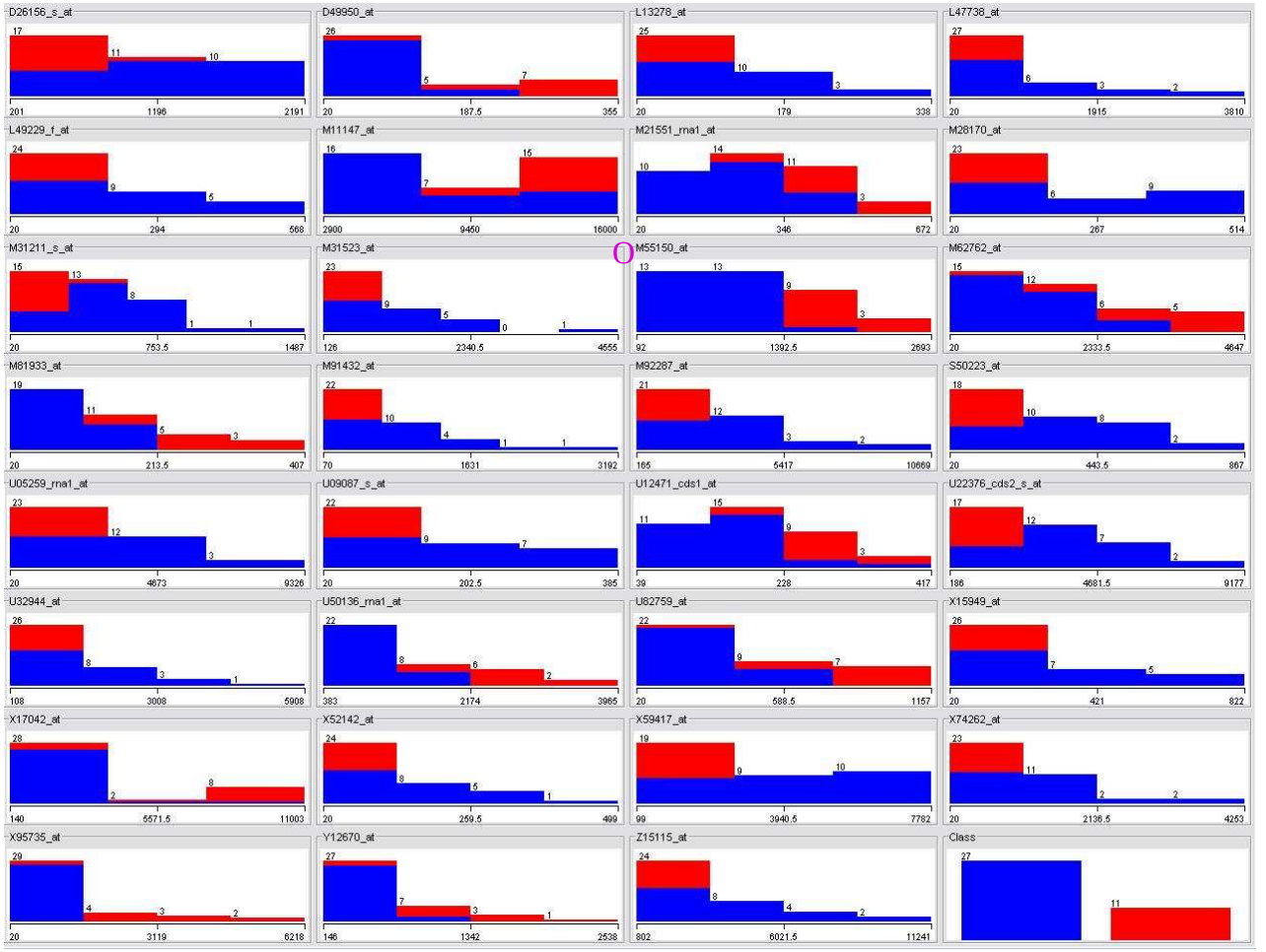
Attribute Visualization



Preliminary Experiment

Naïve Bayes and Bayes Net have been applied.

- Load training dataset and provide testing dataset.
- Testing dataset attributes are mirrored from the training dataset's.
- Save the "error distribution" to see the classification result of the testing dataset.
- Compare the classification results (i.e. *ALL* or *AML* for each testing sample with different gene sets and different mining techniques.

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Some Preliminary Result

The results of applying two techniques with different gene sets are showed in below table.

Class	*NB(S2N)*	*BN(S2N)*	*NB(T)*	*BN(T)*	*NB(C)*	*BN(C)*
ALL	20	23	27	25	24	24
AML	14	11	7	9	10	10

- NB: Naïve Bayes; BN: Bayes Net.
- T: *T-value*; C: Common gene set.
- Disagree sample ID's: $\{51, 54, 60, 61, 62, 63, 64, 67\}$.

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Some Preliminary Results

Some knowledge from the experiments.

- The most different two classifications comes from applying Naïve Bayes between *S2N* set and *T-value* set.
- The most likely two classifications come from applying Naïve Bayes and Bayes Net on Common set.
- Common set may have a better discrimination power.
- Sample 61 is the most confused case with 3 *ALL* votes and 3 *AML* votes.

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Discussion

Some related questions and further mining plan.

- *S2N* and *T-value* measures, or others?
- Validate the results.
- Improvement from Biology point of view.
- Possibility of other types of leukemia.

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Ending

Questions regarding Analysis results?

Information Site: http://www.cs.queensu.ca/home/xiao/dm.html

E-mail: xiao@cs.queens.ca

Thank you

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