

2-4-2010

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Wang, Xiaosheng and Gotoh, Osamu, "A robust gene selection method for microarray-based cancer classification." (2010). *Journal Articles: Genetics, Cell Biology & Anatomy*. Paper 11.

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A Robust Gene Selection Method for Microarray-based Cancer Classification

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Abstract: Gene selection is of vital importance in molecular classification of cancer using high-dimensional gene expression data. Because of the distinct characteristics inherent to specific cancerous gene expression profiles, developing flexible and robust feature selection methods is extremely crucial. We investigated the properties of one feature selection approach proposed in our previous work, which was the generalization of the feature selection method based on the depended degree of attribute in rough sets. We compared the feature selection method with the established methods: the depended degree, chi-square, information gain, Relief-F and symmetric uncertainty, and analyzed its properties through a series of classification experiments. The results revealed that our method was superior to the canonical depended degree of attribute based method in robustness and applicability. Moreover, the method was comparable to the other four commonly used methods. More importantly, the method can exhibit the inherent classification difficulty with respect to different gene expression datasets, indicating the inherent biology of specific cancers.

Keywords: microarrays, cancer classification, feature selection, dependent degree, rough sets, machine learning

Cancer Informatics 2010:9 15–30

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Background

One major problem in applying gene expression profiles to cancer classification and prediction is that the number of features (genes) greatly surpasses the number of samples. Some studies have shown that a small collection of genes selected correctly can lead to good classification results.¹⁻⁴ Therefore gene selection is crucial in molecular classification of cancer. Numerous methods of selecting informative gene groups to conduct cancer classification have been proposed. Most of the methods first ranked the genes based on certain criteria, and then selected a small set of informative genes for classification from the top-ranked genes. The most used gene ranking approaches include t-score, chi-square, information entropy-based, Relief-F, symmetric uncertainty etc.

In,² we used a new feature selection method for gene selection. The feature selection method was based on the

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