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Abstract

Normal Lung and carcinoid are high relative classes in our "Detection and Prediction of Lung Cancer using the zNose with the Support Vector Machine Classifier" project. The mRNA expression level of these two classes was analyzed by using oligonucleotide microarrays. The correlation coefficient measurement results referred to the 20 subclasses (mRNA expression) of normal lung and carcinoid, which were collected from a total of 203 specimens (186 snap-frozen lung tumors and 17 normal lungs). The distinct subclasses (mRNA expressions) are 31687_f_at hemoglobin (?), 31525_s_at hemoglobin (?2), and 31481_s_at thymosin (?10). The Correlation Coefficient reflected the results at 0. 8702, 0. 8935 and 0. 9105 respectively (SMOreg PolyKernel -E 1. 0). This study also showed the best prediction class was the first level class which was reflected from the correlation coefficient, recorded at 0. 9409. This result was further verified by the prediction capacity of our proposed system.

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Index Terms

Computer Science

Artificial Intelligence

Keywords

Correlation Coefficient Gene Expression Prediction Accuracy Case-Based Reasoning and Support Vector Machine (SVM)