Fusion of Quantitative Image and Genomic Biomarkers to Improve Prognosis Assessment of Early Stage Lung Cancer Patients

This study aims to develop a new quantitative image feature analysis scheme and investigate its role along with 2 genomic biomarkers namely, protein expression of the excision repair cross-complementing 1 (ERCC1) genes and a regulatory subunit of ribonucleotide reductase (RRM1), in predicting cancer recurrence risk of Stage I non-small-cell lung cancer (NSCLC) patients after surgery. Methods: By using chest computed tomography images, we developed a computer-aided detection scheme to segment lung tumors and computed tumor-related image features. After feature selection, we trained a Naïve Bayesian network based classifier using 8 image features and a Multilayer Perceptron classifier using 2 genomic biomarkers to predict cancer recurrence risk, respectively. Two classifiers were trained and tested using a dataset with 79 Stage I NSCLC cases, a synthetic minority oversampling technique and a leave-one-case-out validation method. A fusion method was also applied to combine prediction scores of two classifiers. Results: AUC (areas under ROC curves) values are 0.78±0.06 and 0.68±0.07 when using the image feature and genomic biomarker based classifiers, respectively. AUC value significantly increased to 0.84±0.05 (p<0.05) when fusion of two classifier-generated prediction scores using an equal weighting factor. Conclusion: A quantitative image feature based classifier yielded significantly higher discriminatory power than a genomic biomarker based classifier in predicting cancer recurrence risk. Fusion of prediction scores generated by the two classifiers further improved prediction performance. Significance: We demonstrated a new approach that has potential to assist clinicians in more effectively managing Stage I NSCLC patients to reduce cancer recurrence risk.