Early prediction of breast cancer based on the classification of HER-2 and ER Biomarkers using Deep Neural Network

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Abstract

Background: Due to the highly coarse chromatin, multi-dimensionality of the histo image, irregularity of shape and size, texture, and appearance, nuclei extraction is challenging. To address these complexities, a deep learning algorithm called a stacked sparse autoencoder had been considered a research factor in this paper. *Methods and Material*: This paper focuses on detecting the epithelial regions and extracting high-level features to segment the patches based on the nuclei and classify the biomarkers concerning the nuclei patches. We used 6,53,400 microscopic image patches of 363 patients sourced from the BreakHis database, of which 4,90,050 prominent image patches containing only nuclei were utilized for Biomarker classification (Basically eliminating the non-nuclei patches from 363 Whole slide Images (WSI)). The non-nuclei patches were eliminated due to imbalanced class distribution. *Results:* The classifier finally classifies if the nuclei detected based on the features are benign or malignant, or normal with an accuracy of 99.73%, using which the early prediction is performed by extracting and classifying the biomarkers HER2 and ER. The overall classification rate of classifying HER-2 and ER is 97.52%. *Conclusion:* The HER2 +ve was classified with intensity above 23%, and Total nuclei in the range 150-1000 are termed ER positive. Based on these 40 patients with HER2 +ve and 25 patients with ER +ve were detected out of 363 patients. From the observation, it is concluded that 25-40 patients are risked of breast cancer in the next 5 years due to the cell proliferation rate of 7000.

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