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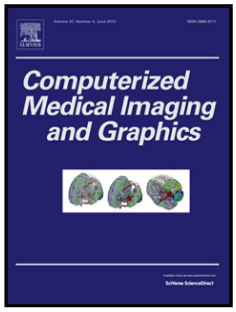

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Efficient Deep Learning Model for Mitosis Detection using Breast Histopathology Images

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Abstract

Mitosis detection is one of the critical factors of cancer prognosis, carrying significant diagnostic information required for breast cancer grading. It provides vital clues to estimate the aggressiveness and the proliferation rate of the tumour. The manual mitosis quantification from whole slide images is a very labor-intensive and challenging task. The aim of this study is to propose a supervised model to detect mitosis signature from breast histopathology WSI images. The model has been designed using deep learning architecture with handcrafted features. We used handcrafted features issued from previous medical challenges MITOS @ ICPR 2012, AMIDA-13 and projects (MICO ANR TecSan) expertise. The deep learning architecture mainly consists of five convolution layers, four max-pooling layers, four rectified linear units (ReLU), and two fully connected layers. ReLU has been used after each convolution layer as an activation function. Dropout layer has been included after first fully connected layer to avoid overfitting. Handcrafted features mainly consist of morphological, textural and intensity features. The proposed architecture has shown to have an improved 92% precision, 88% recall and 90% F-score. Prospectively, the proposed model will be very beneficial in routine exam, providing pathologists with efficient and - as we will prove - effective second opinion for breast cancer grading from whole slide images. Last but not the least, this model could lead junior and senior pathologists, as medical researchers, to a superior understanding and evaluation of breast cancer stage and genesis.

Keywords: Breast cancer, mitosis, deep neural network, handcrafted features, convolution, hematoxylin and eosin.

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