

Deep learning approach for breast cancer prediction with Biglycan as a potential biomarker

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Breast cancer is the most common cancer among women in Sri Lanka, with significant mortality rates. Over the years, there has been a significant focus on developing more efficient, convenient screening methods and identifying diagnostically sensitive, noninvasive and minimally invasive biomarkers. DNA and microRNAs are some of the most promising biomarkers currently being implemented, with Biglycan emerging as a potential biomarker. Biglycan is a small leucine-rich extracellular proteoglycan identified to be associated with the aggressiveness of cancers. This study presents a novel approach combining Convolutional Neural Networks and the exploration of Biglycan as a potential biomarker for breast cancer prediction using the Biglycan breast cancer dataset. The dataset consists of histological images of cancerous (n = 203) and non-cancerous (n = 203)133) breast tissue, with the expression of the Biglycan biomarker. The class imbalance of the dataset was handled using several data augmentation techniques. The study utilized a CNN model architecture with two fully connected layers to reduce the risk of overfitting of the model due to the relatively small dataset size. The model training process employed a 70:30 train:validation split and RMSprop optimizer with 40 epochs and achieved a training and validation accuracy of 61% and 60%, respectively. The cancerous and non-cancerous images were classified with a precision of 0.70 and 0.65 and a recall of 0.80 and 0.70, respectively. Hence, additional model fine-tuning techniques and further validation using data representing diverse populations are required to assess the potential of using Biglycan as a biomarker for breast cancer prediction.

Key words: Breast cancer, diagnosis, Biglycan, machine learning, biomarker

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