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CENTRO DE CIÊNCIAS, TECNOLOGIAS E SAÚDE DO CAMPUS ARARANGUÁ
CURSO DE GRADUAÇÃO EM ENGENHARIA DE COMPUTAÇÃO

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Classification of Breast Cancer Patterns in Immunohistochemistry (IHC) Images based on Multi-Class Targets

Araranguá, Santa Catarina
24 de junho
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Trabalho de Conclusão de Curso do Curso de Graduação em Engenharia de Computação submetido ao Centro de Ciências, Tecnologias e Saúde do Campus Araranguá da Universidade Federal de Santa Catarina para a obtenção do título de Bacharel em Engenharia de Computação.
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Este Trabalho de Conclusão de Curso foi julgado adequado para obtenção do Título de Bacharel em Engenharia de Computação e aprovado em sua forma final pelo Curso de Graduação em Engenharia de Computação.

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***Abstract*—Microscopic analysis of biopsy slides, particularly immunohistochemistry (IHC), plays a critical role in cancer diagnosis. This process still largely relies on the visual assessment and cell counting, which are time-consuming and subject to error and variability. Recent advances in *Deep Learning*, especially convolutional neural networks (CNNs), have enabled the development of interesting architectures for cell detection, counting, and classification, providing robustness and standardization for histopathological analysis. In this paper we present a comparative study of CNN architectures applied to the analysis of microscopic biopsy images in breast cancer pathology. The proposed approach considers object detection (OB) and object classification (OC) paradigms. For OB, a *Faster R-CNN* framework with a ResNet-50 backbone and a *Feature Pyramid Network* (FPN) was considered. For OC, architectures such as DenseNet-121 were evaluated due to their dense connectivity, which promotes efficient feature reuse and improved representation of fine-grained textural patterns. The experimental results were applied in a prepared environment, where dataset partitioning, data augmentation, normalization, and evaluation were considered, as well as the objective evaluation metrics mean Average Precision (mAP), precision, recall, F1-score, and cell counting error. The obtained experimental results indicate the RESNET as the most suitable approach for multi-class classification with 82.89% precision, suggesting it as a promising solution for diagnosis in microscopic biopsy analysis.**

***Index Terms*—Breast cancer image classification, immunohistochemistry, convolutional neural networks, object detection, computer-aided diagnosis**

I. Introduction

The analysis of microscopic biopsy slides is a fundamental task for diagnosing several diseases, especially neoplasms [1]. In histology and immunohistochemistry (IHC), pathologists evaluate morphological patterns, staining intensity, and the proportion of positive and negative cells based on the degree of a biomarker. These analyses directly influence numerous tumor classifications, prognoses, as well as the decision-making to conduct treatments [2]. However, slide interpretation may be imprecise and may lead to considerable subjectivity and variability, particularly for assessing staining intensity and cell proportion [3], [4]. In addition, the process is largely manual and time-consuming, especially in complex cases.

Over the years, many studies have explored automated cell detection and counting using classical image processing techniques, such as segmentation and handcrafted feature extraction [5]. Although these approaches provide some level of interpretability, they are usually not robust to noise, illumination variations, and acquisition conditions, which limits their generalization to different histological patterns [6].

Advances in the *Deep Learning* area, particularly the Convolutional Neural Networks (CNNs), have significantly impacted digital pathology and histopathology [7]. CNN-based models can automatically learn relevant features from data, providing robust detection, counting, and classification of cells and target patterns. In several histopathological applications, especially in IHC analysis and nuclei detection, these models have shown interesting accuracy and reproducibility compared to traditional classical methods [8], [9]. Architectures such as ResNet and DenseNet, as well as models incorporating hierarchical features, have demonstrated strong performance in dealing with variations in texture, color, and scale that are common in microscopic images. However, the amount of CNN models and new architectures imposes difficulties when choosing a suitable CNN method for IHC identification.

For this purpose, in this paper we present a comparative evaluation of CNN architectures for microscopic biopsy image analysis in the IHC context. Both detection and classification paradigms are investigated for real-world histopathological