A Dual-Network Approach with Contrastive Noisy Label Learning for Immune Cell Infiltration Detection in Mouse Model

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***Abstract*—Metabolic dysfunction-associated steatotic liver disease (MASLD) can lead to severe liver conditions such as metabolic dysfunction-associated steatohepatitis (MASH) and hepatocellular carcinoma (HCC). MASH is characterized by immune cell infiltration in histopathological images. Although deep learning can help detect immune cell infiltration, it requires a large volume of precise labels, which is impractical in real-life applications. Through dual-network training, the present study mitigates the effects of noisy labels caused by misjudgments of non-immune and non-infiltrating immune cells in the histopathological image. The results show that the proposed approach enhances the robustness and accuracy of deep-learning-based detection methods in the challenging context of noisy histopathology images.**

Keywords: Infiltrating immune cells, MASH, noisy label, contrastive learning

I. Introduction

MASLD is a common cause of chronic liver disease that may progress to severe conditions such as MASH, cirrhosis, and HCC. No officially approved MASLD drugs exist. Thus, researchers generally rely on mouse models for drug testing. However, identifying immune cell infiltration in liver tissue histopathological images is challenging. Although deep learning models are helpful in this regard, they require large quantities of accurately labeled data, which is often impractical in real-world scenarios.

The present study addresses this problem by using a dual-network approach. It aims to handle the issue of noisy labels, which arise from the misclassification of non-immune cells and non-infiltrating immune cells as infiltrated immune cells in annotated pathological images. The proposed method additionally leverages contrastive learning to enhance feature extraction in the presence of noisy labels.

II. Proposed Methods

In dealing with noisy labels during training, the proposed method first selects accurate labels to prevent the model from overfitting to noisy data and then differentiates the feature representations of accurate and noisy labels.

The first task is performed by employing collaborative training and a progressive selection module. During early training, two networks with distinct learning capacities are used collaboratively to filter out erroneous information from the noisy labels. The progressive selection module then selects appropriate labels for immune cell segmentation. By matching the histological features of the immune cells, the module selects labels that accurately define the cell boundaries and hence enhance their segmentation.

The second task is accomplished using a contrastive module in which a contrastive learning approach is used to encourage a clear distinction between the feature representations of the accurate and noisy labels selected by the progressive selection module. The contrastive learning process reinforces the difference between the two feature representations, thereby enhancing the ability of the model to effectively handle noisy labels.

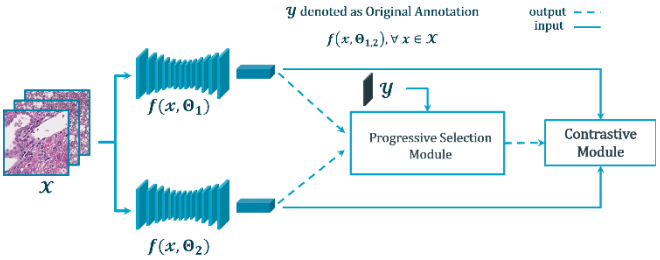

Figure 1. Proposed Method Architecture.

III. Experimental Results

The experimental results confirm that the proposed method outperforms existing noisy label methods. Furthermore, the use of prior knowledge enhances the robustness of the model toward noisy data, thereby improving its potential for the advancement of liver disease analysis and diagnostic tools.

Conclusion

This study has addressed the challenge of detecting immune cells in MASH mouse model histopathology images with noisy labels. The proposed approach provides a useful tool for MASH diagnosis and research.

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