Interpretable Deep Learning in Computational Histopathology for refined identification of Alzheimer's Disease biomarkers

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Abstract

Background: In this research, an explainable deep-learning based framework is proposed for the segmentation of tau protein biomarkers like plaques, and tangles in histopathological whole slide images (WSI). The concept is to integrate an explainable deep learning model with collaborative human feedback to improve the model precision of identifying tau biomarkers as well as making the results interpretable to human experts. The final goal of this project is to refine AD patients' stratification.

Method: A pilot study has been done on 6 WSIs stained with ALZ50 monoclonal antibody. The preliminary models have been extended to a larger database of 15 WSIs stained with an AT8 monoclonal antibody. All WSIs are post-mortem brain samples corresponding to the frontal cortex. In the proposed system, firstly, for automatic segmentation of Tau aggregates, deep learning (DL) models are trained and tested using the initial database (6 WSIs). Secondly, we train deep learning models with interpretability features, such as Attention U-Net, CA-net and graph neural networks. With these models, two operational loops (Figure 1) are implemented. In the first loop, a technical expert looks at the predictions of the trained model and provides corrections. The corrected predictions are fed back to the training dataset to improve the model performance. In the second loop, a clinical expert looks at the explainability results from the model and provides further corrective feedback.

Result: A preliminary version of our DL models achieved promising F1 scores for tangles and neuritic plaques as reported in [1]. Currently, a second larger dataset of 15 WSIs (AT8) is studied and used for training an evolved version of the DL model, by including explainable visual features. These new overall results will be presented and discussed during the conference.

Conclusion: The proposed interactive and interpretable tau protein segmentation framework is envisioned to be impactful towards Alzheimer's patient stratification problems which requires high accuracy identification of AD biomarkers.

[1] K Maňoušková, V Abadie, M Ounissi, G Jimenez, L Stimmer, B. Delatour, S. Durrleman, D. Racoceanu. Tau Protein Discrete Aggregates in Alzheimer's Disease: Neuritic Plaques and Tangles Detection and Segmentation using Computational Histopathology. SPIE Medical Imaging 2022, Feb 2022, San Diego, United States.
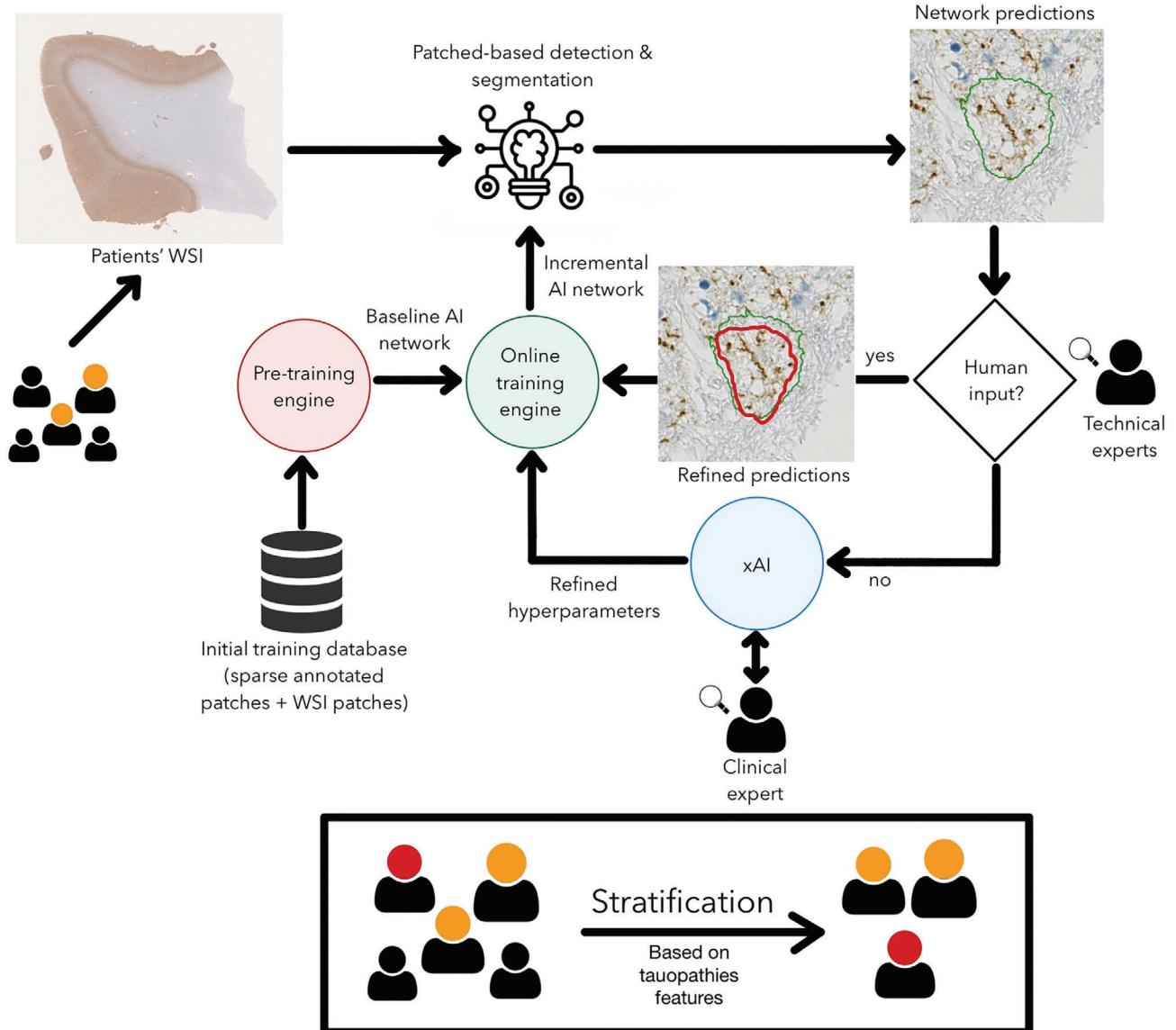
Figure 1. Alzheimer disease stratification using explainable artificial intelligence in computational pathology