

to the target set while surpassing the other methods in terms of structure preservation, showing minimal loss. Additionally, on average, StainGAN takes 129 seconds to preprocess a whole slide image (WSI) on an NVIDIA RTX 4090. In contrast, this method completes the same task in 3.8 seconds, allowing ample time for subsequent AI analysis.

Conclusion: The proposed method effectively balances the need for detailed structure preservation with the efficiency required for practical use in digital pathology. By significantly reducing preprocessing time without compromising on quality, it offers a viable solution for integrating into routine AI supported diagnostic workflows.

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MammaPrint prediction from haematoxylin-eosin whole-slide images: preliminary interpretability analysis

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Background & Objectives: Artificial intelligence (AI) models from H&E-stained whole-slide images (WSIs) often lack interpretability. We have implemented an attention-based AI algorithm that achieves strong performance (n=380 WSI, AUC=0.86), but its decision-making process remains unclear. This study evaluates attention heatmaps in a subset of correctly classified cases to identify histologic features influencing predictions.

Methods: Using an attention-based multiple instance-learning model (CLAM), we predicted MammaPrint risk (high vs. low risk) in early-stage breast cancer WSIs. Attention heatmaps were generated by colour-coding patches (red: high attention, blue: low attention). We assessed attention distribution across tumour epithelium, stroma, tumour-infiltrating lymphocytes (TILs), normal epithelium, and in situ carcinoma. Differences between MammaPrint risk groups were analysed using Chi-squared/Fisher's exact tests.

Results: We assessed 60 cases (20 high-risk, 40 low-risk) that were correctly classified by the model. Normal epithelium showed significantly higher attention in low-risk cases (p<0.005), while in situ carcinoma trended toward significance (p=0.066). Tumour epithelium and TILs consistently received high attention, irrespective of risk category. Stroma showed no differential attention.

Conclusion: The model's attention primarily focused on tumour epithelium and TILs in all cases, suggesting that these features drive predictions universally. Normal epithelium, however, was more attended to in low-risk cases, hinting at a potential discriminator. These preliminary findings reveal limited interpretability for MammaPrint prediction, warranting further analysis in additional cases to elucidate underlying patterns.

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Automated nuclear grading of breast cancer based on the analysis of selected areas of histological slides (ROI) using AI

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Background & Objectives: Breast cancer is the leading oncological pathology among the female population worldwide and in Russia. A key factor in treatment strategy is the histological NGS grade, that includes tubular, nuclear, and mitotic grades. In routine analysis assessment is time-consuming, often subjective, leading to potential errors. The degree of nuclear atypia is scored (1, 2, 3) based on a combination of factors. As per WHO guidelines, the nuclear grade is determined by the highest score within the analysed tumour sections. Tumour heterogeneity may cause discrepancies in grading by pathologists.

The implementation of digital pathology into routine practice opens up the possibility of using AI in morphological diagnostics.

Methods: The research aimed to develop and validate machine learning algorithms to support medical decision-making in routine breast cancer diagnosis. The main task was to create methods for automated determination of nuclear grade based on AI analysis of extracted regions from histological slides (ROI).

The model is tested on regions annotated by two annotating doctors and a validating doctor, then sent for model inference. The results from the machine learning algorithm are compared with those of the doctors and analysed.

For the "Nuclear Grade" algorithm, the target metrics were: kappa score = 0.4 and mean accuracy = 0.6. Internal evaluation on the test dataset yielded kappa = 0.445 and mean accuracy = 0.67.

Results: The algorithm highlights tumour areas with different levels of nuclear atypia, showing the proportion of each class and calculating the weighted average score (with 1-2 decimal places). This helps the pathologist make more informed decisions and improves the reproducibility of grade assessments within and across studies.

Conclusion: The obtained metrics exceed the target values, that allows to make a preliminary conclusion about the successful implementation of the "Nuclear Grade" machine learning algorithm and the readiness of the ML model for clinical validation.

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Deep learning-based diagnostic model for papillary thyroid cancer

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Background & Objectives: Diagnosing PTC remains a significant clinical challenge, significantly when differentiating malignant lesions with borderline nuclear features. Manual histopathological examination, although a standard practice, is time-consuming and limited by subjective variability and the increasing volume of cases. The need for more accurate, efficient, and scalable diagnostic tools is growing, particularly in regions with a high incidence of PTC, such as Oman. Artificial intelligence (AI), intense learning, offers a promising avenue for improving diagnostic workflows in pathology. This study aims to develop and evaluate a novel deep learning-based neural network model to assist in the classification of malignant and benign thyroid pathology images. The goal is to support pathologists with an automated system that reduces workload, increases