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► **To cite this version:**

Mélanie Lubrano, Yaëlle Bellahsen-Harrar, Sylvain Berlemont, Sarah Atallah, Emmanuelle Vaz, et al..
Diagnosis with confidence: deep learning for reliable classification of laryngeal dysplasia. *Histopathology*, 2023, 84 (2), pp.343-355. 10.1111/his.15067 . hal-04396387

HAL Id: hal-04396387

<https://minesparis-psl.hal.science/hal-04396387v1>

Submitted on 15 Jan 2024

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Diagnosis with confidence: deep learning for reliable classification of laryngeal dysplasia

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Date of submission 4 July 2023

Accepted for publication 24 September 2023

Lubrano M, Bellahsen-Harrar Y, Berlemont S, Atallah S, Vaz E, Walter T & Badoual C

(2023) *Histopathology*. <https://doi.org/10.1111/his.15067>

Diagnosis with confidence: deep learning for reliable classification of laryngeal dysplasia

Background: Diagnosis of head and neck (HN) squamous dysplasias and carcinomas is critical for patient care, cure, and follow-up. It can be challenging, especially for grading intraepithelial lesions. Despite recent simplification in the last WHO grading system, the inter- and intraobserver variability remains substantial, particularly for nonspecialized pathologists, exhibiting the need for new tools to support pathologists.

Methods: In this study we investigated the potential of deep learning to assist the pathologist with automatic and reliable classification of HN lesions following the 2022 WHO classification system. We created, for the first time, a large-scale database of histological samples (>2000 slides) intended for developing an automatic diagnostic tool. We developed and trained a weakly supervised model performing classification from whole-slide images (WSI). We evaluated our

model on both internal and external test sets and we defined and validated a new confidence score to assess the predictions that can be used to identify difficult cases.

Results: Our model demonstrated high classification accuracy across all lesion types on both internal and external test sets (respectively average area under the curve [AUC]: 0.878 (95% confidence interval [CI]: [0.834–0.918]) and 0.886 (95% CI: [0.813–0.947])) and the confidence score allowed for accurate differentiation between reliable and uncertain predictions.

Conclusion: Our results demonstrate that the model, associated with confidence measurements, can help in the difficult task of classifying HN squamous lesions by limiting variability and detecting ambiguous cases, taking us one step closer to a wider adoption of AI-based assistive tools.

Keywords: AI assistance, AI confidence, computational pathology, deep learning, diagnosis, dysplasia, grading, head and neck

Introduction

Head and neck squamous cell carcinomas (HNSCC) stand as a substantial global public health threat, occupying the sixth position among the most prevalent

forms of cancer.¹ The distressing morbidity and mortality statistics associated with HNSCC are primarily due to late-stage diagnoses and challenging treatment protocols.^{2–4} Early diagnosis of head and neck (HN) lesions is therefore essential to prevent the progression to invasive carcinoma.⁵ Yet the categorization of HN dysplasias remains a contentious issue^{6,7} due to the varying terminologies, grading methodologies, and low to moderate reproducibility among pathologists^{6,8,9,10,11,12} (Table 1).

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In order to improve inter- and intra-rater reliability, the World Health Organization (WHO) recommended in 2017 to grade laryngeal squamous dysplasias with only two categories: low grade and high grade.^{13,14} This approach indicated that high-grade dysplasias carried a 10-fold higher risk of developing into invasive carcinoma compared to low-grade lesions.¹⁵ Despite this, reproducibility remains moderate,⁸ due to the multiple elements to take into account both at the cytological and architectural levels, variations in epithelial thickness depending on the anatomical location, and inflammatory and dystrophic changes that often pose challenges in distinguishing true dysplasia.¹³ Moreover, imposing classification categories on a continuous spectrum of lesions without clear boundaries further exacerbates subjectivity. Given these complexities, the field is in need of new tools to help pathologists make robust and consistent classifications of squamous HN lesions. This would offer physicians better guidance for patients' monitoring and treatment modalities.

Numerous artificial intelligence (AI) algorithms have been created to support pathologists' accuracy and consistency.¹⁶⁻²⁵ The classification of HN squamous lesions could significantly benefit from computer-assisted analysis, facilitating standardization and bias reduction in grading. However, research focusing on dysplasia grading, particularly in HN pathology, remains limited. Most studies to date have

primarily employed classical machine-learning methods rather than deep learning,^{4,26} concentrating mostly on the oral cavity and not addressing laryngeal lesions.²⁶ The lack of studies in this field could be explained by the absence of public databases including dysplastic lesion annotations, and by the difficulty to achieve grading consensus.

For effective integration into pathologists' workflows, AI models should provide a confidence estimate for each prediction. While the concept of AI model uncertainty has been studied extensively in the past years,²⁷⁻²⁹ its application to computational pathology has been sparse.^{30,31} Tempering the AI model's predictions with a measure of its confidence could help pathologists to better blend them into their routine grading, thereby fostering model acceptance.

In this study we developed a fully automated, weakly supervised model for accurate diagnosis of dysplasias and squamous cell carcinomas of the HN following the current WHO grading system. Figure 1 summarizes the pipeline. The proposed model aims to assist pathologists in achieving automatic and reliable classification of these lesions, with the added benefit of a confidence evaluation of the model's predictions. We evaluated its performance on a reviewed internal test set as well as an external dataset and proposed a competitive solution to assess the model's confidence, making it a true tool of peer-review, and thus helping pathologists in their clinical routine.

Table 1. History of dysplasia classification: Overview of the different grading systems for intraepithelial head and neck lesions proposed over the years in the literature

Level of abnormal maturation	Ljubljana (2000)	SIN (2001)	WHO (2005)	LIN (2012)	Ljubljana (2014)	WHO (2017)
	Squamous hyperplasia	Squamous hyperplasia	Squamous hyperplasia		Low-grade SIL	Low-grade dysplasia
Lower 1/3	Basal/parabasal hyperplasia	SIN 1	Mild dysplasia	LIN 1		
Lower 1/3–1/2	Atypical hyperplasia	SIN 1 or SIN 2	Moderate dysplasia		High-grade SIL	
Lower 2/3				LIN 2		
1/2–3/4		SIN 2				High-grade dysplasia
More than 2/3				LIN 3		
All thickness	Carcinoma <i>in situ</i>		Severe dysplasia			
			Carcinoma <i>in situ</i>		Carcinoma <i>in situ</i>	

Table inspired from WHO Blue Book. LIN, Laryngeal intraepithelial neoplasia; SIL, Squamous Intraepithelial Lesions; SIN, Squamous Intraepithelial Neoplasia.

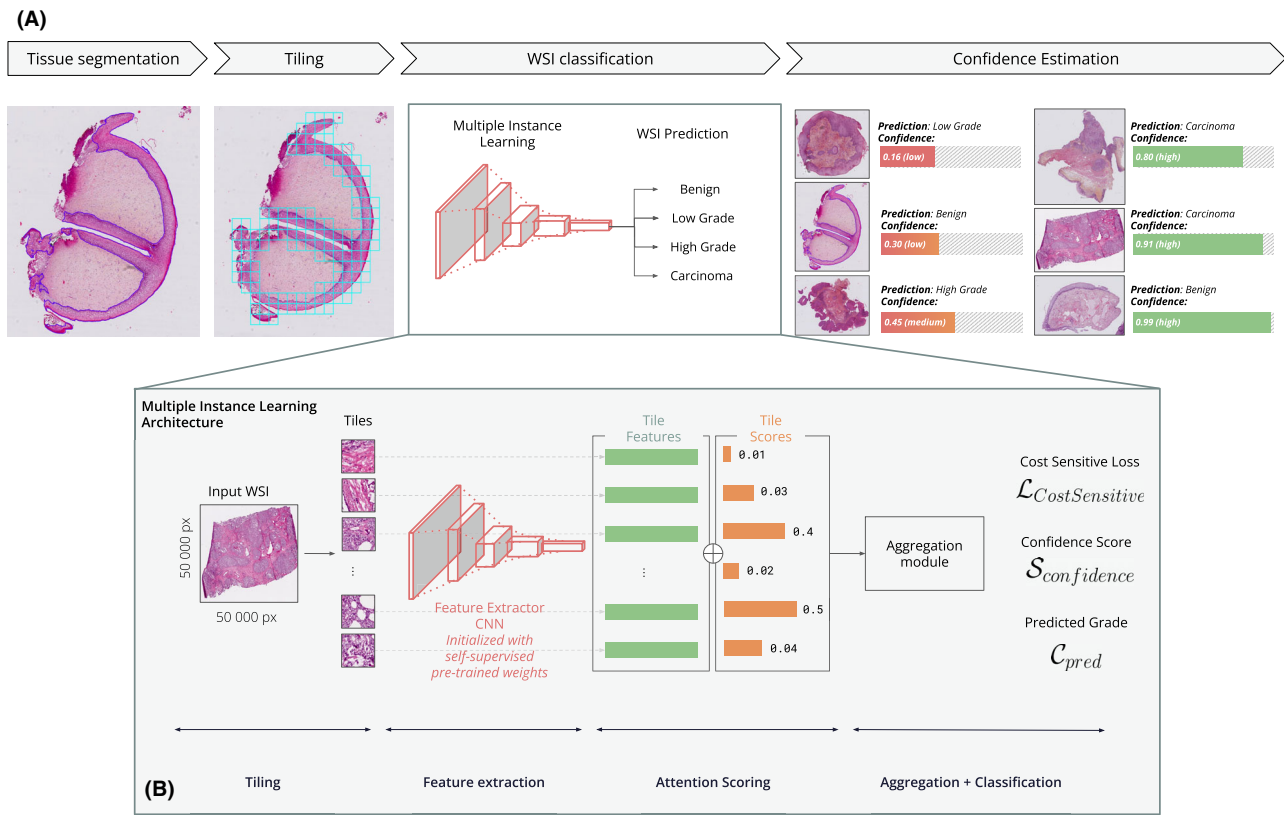


Figure 1. (A) Description of the AI-assistive tool pipeline. The AI-assistive tool relies on several steps: (1) The tissue of interest (epithelial tissue) is selected with a segmentation model. (2) Small tiles of 224×224 pixels are extracted from the selected areas. (3) Multiple Instance Learning architecture is used to perform WSI classification, choosing between four grades: nondysplastic, low-grade dysplasia, high-grade dysplasia, or invasive carcinoma. (4) Confidence of the prediction is evaluated thanks to a relevant confidence score. (B) Description of the deep learning model: (1) Small tiles are extracted from the WSI. (2) The tiles are fed to a frozen feature extractor initialized with pretrained weights. Relevant features are thus extracted from each tile, resulting in a list of feature vectors of dimension $[1, 1024]$ (the tile's features). (3) The feature vectors are scored with an attention-based scoring module according to their importance for the downstream classification. (4) An aggregation module performs the weighted sum between the features vectors and the attention scores, and use the resulting vector to perform the final classification. A cost-sensitive loss is used to take into account the ordinal nature of the classes. A confidence score is computed from the outputted risks from the network.

Materials and methods

DATASET COLLECTION

A total of 557 patients were selected retrospectively from 2000 to 2013 from the Hôpital Européen Georges Pompidou (HEGP, Paris, France) clinical database. Patients were at least 18 years old and diagnosed with HN squamous cell dysplasia or carcinoma in the larynx or the pharynx (oropharynx and nasopharynx excluded). Both biopsies and surgical samples were included. In cases of multiple slides per sample, we selected the most representative for the lesion. Pathology reports indicating an inability to discern high-grade dysplasia from invasive carcinoma due to tangent inclusion were excluded. The samples were stained using haematoxylin, eosin, and saffron (HES) at the time of collection.

Slides were digitized at a $20\times$ magnification (Hamamatsu NanoZoomer s360, Japan), resulting in a pixel resolution of $0.45 \mu\text{m}$. We excluded slides with either no surface epithelium or significant artefacts, but retained slides with artefacts that did not compromise clear diagnosis.

Each slide was assigned a global label reflecting the most severe lesion in the sample, adhering to the WHO classification and the clinical report. These initial labels were designated by multiple ENT pathologists from 2000 to 2013. Lesions previously labelled as “mild to moderate” dysplasia were collectively reevaluated by the pathologist investigators and reclassified according to the latest grading system. The total number of slides was 2064. Table 2 presents patient characteristics and a summary of the cohort.

Table 2. Cohort description

Characteristics	Training and validation sets	Gold standard sets (after consensus)	External set
Number of patients	456	101	67
Male	376 (82.5%)	79 (78.2%)	14 (20.9%)
Female	80 (17.5%)	22 (21.8%)	53 (79.1%)
Number of samples	677	115	72
Biopsies	460 (67.9%)	115 (100%)	71 (98.6%)
Surgical resections	217 (32.1%)	0 (0%)	1 (1.4%)
Anatomical localization			
Larynx	562	68	77
Hypopharynx	142	21	10
Number of slides	1949	115	87
Biopsies	1370 (70.3%)	115 (100%)	86 (98.9%)
Surgical resections	579 (29.7%)	0 (0%)	1 (1.1%)
Diagnosis (worst lesions on the slide)			
Benign (negative for dysplasia or carcinoma)	527 (27.0%)	28 (24.3%)	21 (24.1%)
Low-grade dysplasia	205 (10.5%)	21 (18.3%)	26 (29.9%)
High-grade dysplasia	602 (30.9%)	30 (26.1%)	17 (19.5%)
Invasive carcinoma	615 (31.6%)	36 (31.3%)	23 (26.4%)
Including micro-invasive carcinoma	149 (24.2%)	7 (19.4%)	0
Vital status			
Alive	87 (19.1%)	19 (18.8%)	–
Dead	140 (30.7%)	33 (32.7%)	–
Lost	229 (50.2%)	49 (48.5%)	–

DEEPLARNING MODEL

Our model builds upon the Attention-based Multiple Instance Learning (MIL) architecture by Ilse *et al.*³² The WSI is decomposed into small images (called tiles), each of which is mapped to a vector by a Neural Network (NN1). These vectors are then weighted by attention scores (NN2) and summed to build the slide representation, from which the grade is predicted (NN3). NN1 is trained by self-supervised learning (SSL), a powerful technique to learn generic vector representations of images. Of note, SSL allows representation learning independently from the grade prediction task (SimCLR³³). NN2 and NN3 are trained with a cost-aware classification loss³⁴ to take advantage of the ordinal nature of the classes. The

model was trained to estimate class-specific risk, as opposed to posterior probability, with risks determined by a cost matrix (Table S2) that penalizes large errors. For further details, please refer to Appendix S1. All model implementations utilized Python 3.8.0 and Tensorflow 2.5.0.

TRAINING AND VALIDATION

A subset of the dataset was kept aside to create a reference standard test set (115 slides). The remaining slides (1949 slides from 456 patients) were divided into five subsets, four of which were used for training and one for validation (cross-validation [CV] scheme). The subsets were sampled randomly but stratified by patient and grade. Hyperparameters were set to

minimize the error measured on the validation folds. Consequently, there were five training rounds, with different training (4-fold) and validation sets (1-fold), resulting in five unique models. The outputs of these five models were then averaged to build the final output of the system.

Following best practices, we ensured that there was no patient overlap between training, validation, and reference standard test sets.

For performance evaluation, we calculated class-wise classification metrics in a one-vs-all manner. Class-wise scores were averaged to compute overall performance. We evaluated performances by comparing model predictions and labels, with metrics reported alongside 95% confidence intervals (CIs) via a bootstrapping method. We further examined predictions through heatmaps of attention scores overlaid on WSIs.

REFERENCE STANDARD TEST SET

Evaluation of AI algorithms can be problematic if the ground truth is likely to contain errors as well. For this, we defined a reference set to evaluate our model on the best possible ground truth. To fit with the diagnosis use case, only biopsies were included. The data scientist investigators, not taking part in the grading, were tasked with slide selection, ensuring initial class balance and sample independence. Each slide was selected from either independent patients or from patient slides collected several years apart, with a maximum of two per patient. Slides from the same patient within the same year were excluded, resulting in 115 slides selected from 101 patients (Table 2). The reference standard label was determined in two rounds. Two experts independently reviewed the selected slides using the (EyeDo, TRIBUN HEALTH, Paris, France) platform, without access to clinical information, initial diagnosis, or the other reviewer's rating. Afterwards, the two raters met during a consensus meeting to thoroughly discuss the slides on which they disagreed. If the disagreement persisted, the slides were excluded. The initial diagnosis extracted from the patient's records were used as an additional independent review to measure model performance.

EXTERNAL TEST SET

After the validation of the model on the reference test set, we performed an external validation on slides sourced from another hospital (Hôpital Tenon, APHP, Paris). This external test set included 87 slides from

67 patients (Table 2). The selection criteria were consistent with those of the primary dataset, despite a much more recent timeframe of inclusion (samples from 2016 to 2023). The labelling of the slides followed the most severe lesion directly sourced in the pathology report.

CONFIDENCE SCORE AND ANALYSIS OF MISCLASSIFIED SLIDES

We calculated a confidence score for each model prediction following the methods described previously,³⁵ and in Appendix S1. This score was defined as the difference between the two highest risk outputs from the network, with smaller differences indicating diagnostic uncertainty, and larger differences showing greater confidence. To evaluate the relevance of the confidence score in routine practice, such as screening, we established a threshold to exclude uncertain predictions, optimizing this threshold on the validation set to achieve an overall area under the curve (AUC) > 0.9. We assessed the model's performance on the reference standard test set both before and after the exclusion of uncertain predictions. To understand the model's limitations, we analysed attention score heatmaps of slides that were incorrectly, yet confidently, classified.

Results

REFERENCE STANDARD TEST SET

The dual blind review yielded independent agreement on 71 slides in the initial round. The remaining 47 slides were subjected to a consensus meeting, resulting in the exclusion of three slides and a consensus decision on the 44 others. Consequently, we used 115 slides from 101 patients as the reference standard test set. Table S3 contains additional review details.

CLASSIFICATION PERFORMANCE OF THE DEEP-LEARNING MODEL ON THE REFERENCE STANDARD TEST SET

On the reference standard test set, the model delivered an average AUC of 0.878 (95% CI: [0.801–0.937]) across the four classes and achieved an AUC > 0.8 for all classes and an AUC > 0.9 for carcinoma detection (ROC AUC displayed in Figure 2). Comparatively, when using initial labels as a reference for comparison, the average AUC significantly dropped (AUC = 0.817 [0.734–0.888]), confirming the effectiveness of the review in reducing labelling

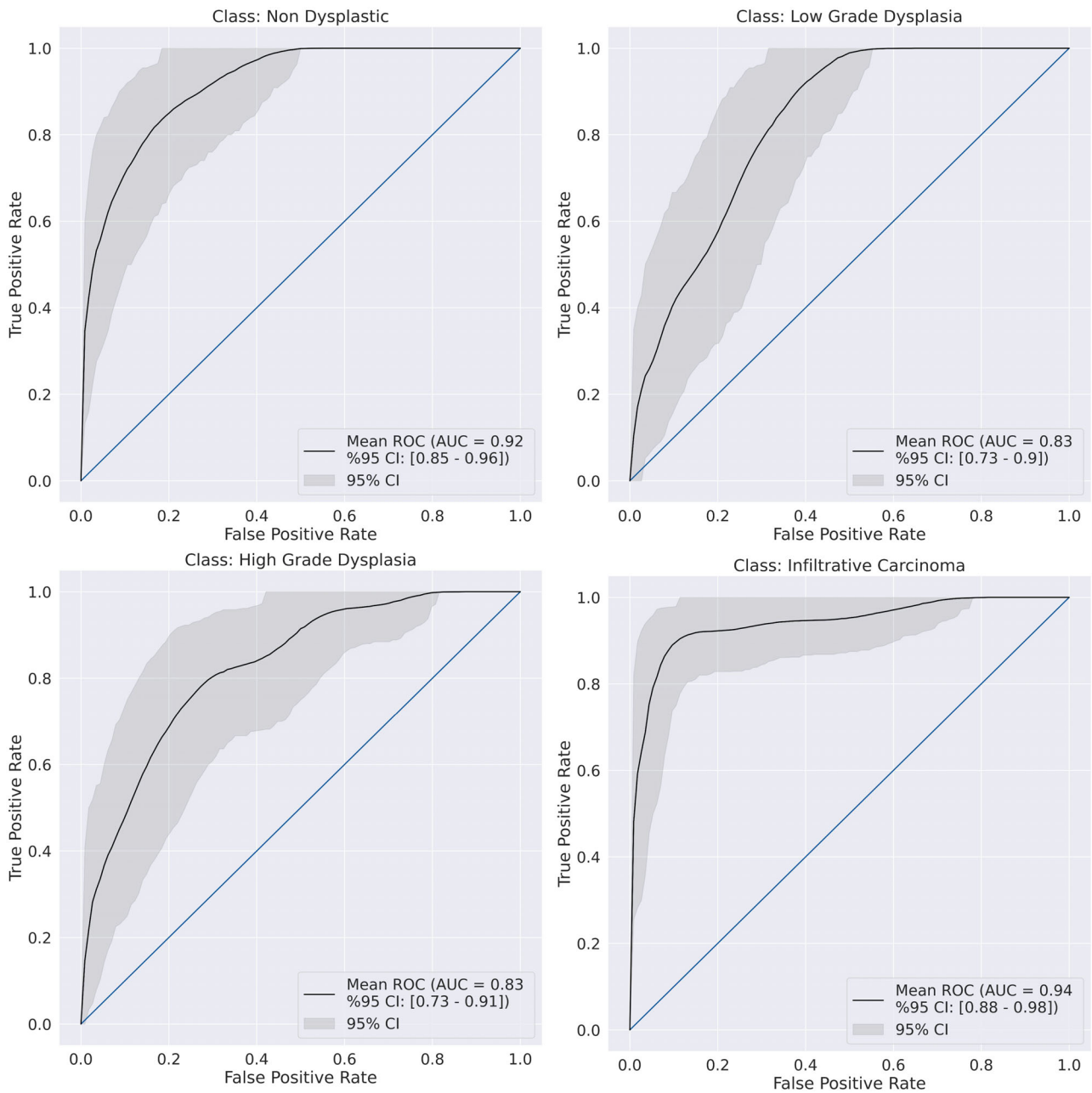


Figure 2. AUC ROC for each class on the reviewed reference standard test set: ROC curves were obtained by bootstrapping of the AI model predictions (10,000 bootstrap samples). They were computed for each class in a One vs Rest manner using consensus labels as a ground truth. ROC AUC of the Carcinoma class is better than for the other classes, certainly because the diagnosis of this class is often less ambiguous than for the other grades. Thus, the training data contains less noise on this class, as well as the test data. Misclassification on Carcinoma class concerned microinvasive lesions. AUC, area under the curve; ROC, receiver operator characteristic.

noise and enhancing classification. Comparison of the classification performances of the independent reviewer (initial labels) and the model demonstrate a negligible difference in accuracy (<0.02) and CIs that significantly overlap, showing that the model performs similarly to an independent reviewer. Table 3

and Figure 3 summarize classification performance and confusion matrices, respectively. Comparison to standard training with cross-entropy loss is presented in Table S5. Analysis of attention heatmaps verified the model's capability to focus on significant regions of the slide (Figure 4).

Table 3. Classification performances: For each class, all the metrics are computed in a “one vs rest” manner: slides from the class are considered positives and slides from other classes are considered negatives

	AUC (95% CI)	NPV (95% CI)	PPV (precision) (95% CI)	Sensitivity (95% CI)	Accuracy (95% CI)	Specificity (95% CI)	AUC (precision/recall) (95% CI)
AI vs consensus labels (reference standard set)	0.878 (0.801–0.937)	0.883 (0.811–0.945)	0.624 (0.439–0.795)	0.621 (0.452–0.788)	0.822 (0.748–0.887)	0.883 (0.815–0.944)	0.708 (0.543–0.844)
Normal (0)	0.916 (0.854–0.962)	0.911 (0.851–0.966)	0.68 (0.48–0.864)	0.68 (0.517–0.862)	0.861 (0.791–0.922)	0.911 (0.849–0.965)	0.78 (0.612–0.903)
Low Grade (1)	0.827 (0.735–0.898)	0.882 (0.802–0.95)	0.4 (0.219–0.572)	0.545 (0.323–0.75)	0.757 (0.67–0.835)	0.806 (0.725–0.882)	0.504 (0.29–0.706)
High Grade (2)	0.827 (0.731–0.905)	0.819 (0.736–0.892)	0.571 (0.333–0.8)	0.414 (0.24–0.593)	0.774 (0.696–0.844)	0.895 (0.829–0.956)	0.633 (0.441–0.795)
Carcinoma (3)	0.942 (0.884–0.982)	0.921 (0.857–0.973)	0.846 (0.722–0.946)	0.846 (0.727–0.946)	0.896 (0.835–0.948)	0.921 (0.855–0.974)	0.914 (0.827–0.973)
Dysplasia (1 + 2)	0.869 (0.8–0.927)	0.797 (0.697–0.889)	0.745 (0.619–0.86)	0.745 (0.615–0.863)	0.774 (0.696–0.844)	0.797 (0.692–0.887)	0.849 (0.754–0.922)
Initial labels vs consensus labels (reference standard set)	0.796 (0.707–0.882)	0.906 (0.841–0.962)	0.682 (0.517–0.839)	0.686 (0.519–0.847)	0.857 (0.791–0.913)	0.907 (0.843–0.962)	0.721 (0.587–0.833)
Normal (0)	0.856 (0.764–0.935)	0.943 (0.889–0.988)	0.714 (0.542–0.879)	0.8 (0.625–0.95)	0.887 (0.826–0.939)	0.911 (0.848–0.966)	0.779 (0.646–0.887)
Low Grade (1)	0.64 (0.532–0.756)	0.862 (0.787–0.929)	0.429 (0.222–0.65)	0.409 (0.207–0.632)	0.783 (0.704–0.852)	0.871 (0.8–0.935)	0.477 (0.287–0.649)
High Grade (2)	0.787 (0.695–0.877)	0.894 (0.826–0.954)	0.667 (0.486–0.829)	0.69 (0.519–0.857)	0.835 (0.765–0.896)	0.884 (0.811–0.946)	0.719 (0.579–0.832)
Carcinoma (3)	0.903 (0.839–0.961)	0.924 (0.861–0.976)	0.917 (0.816–1)	0.846 (0.727–0.95)	0.922 (0.87–0.965)	0.961 (0.912–1)	0.908 (0.836–0.963)
Dysplasia (1 + 2)	0.806 (0.731–0.877)	0.828 (0.73–0.918)	0.784 (0.667–0.894)	0.784 (0.667–0.894)	0.809 (0.739–0.878)	0.828 (0.732–0.918)	0.832 (0.75–0.9)

Table 3. (Continued)

	AUC (95% CI)	NPV (95% CI)	PPV (precision) (95% CI)	Sensitivity (95% CI)	Accuracy (95% CI)	Specificity (95% CI)	AUC (precision/recall) (95% CI)
AI vs initial labels (reference standard set)							
Average (4 classes)	0.817 (0.734–0.888)	0.853 (0.777–0.922)	0.522 (0.353–0.692)	0.523 (0.361–0.686)	0.774 (0.698–0.848)	0.852 (0.777–0.919)	0.6 (0.457–0.733)
Normal (0)	0.91 (0.851–0.962)	0.889 (0.822–0.954)	0.72 (0.531–0.886)	0.643 (0.48–0.826)	0.852 (0.783–0.922)	0.92 (0.857–0.967)	0.76 (0.582–0.901)
Low Grade (1)	0.707 (0.595–0.798)	0.847 (0.767–0.92)	0.267 (0.12–0.445)	0.381 (0.176–0.589)	0.696 (0.617–0.774)	0.766 (0.675–0.848)	0.291 (0.161–0.457)
High Grade (2)	0.716 (0.615–0.812)	0.755 (0.667–0.839)	0.333 (0.12–0.538)	0.233 (0.088–0.391)	0.678 (0.591–0.765)	0.835 (0.759–0.908)	0.458 (0.292–0.617)
Carcinoma (3)	0.932 (0.873–0.978)	0.921 (0.853–0.974)	0.769 (0.639–0.9)	0.833 (0.7–0.939)	0.87 (0.8–0.93)	0.886 (0.817–0.951)	0.892 (0.794–0.959)
Dysplasia (1 + 2)	0.829 (0.748–0.899)	0.766 (0.656–0.864)	0.706 (0.566–0.84)	0.706 (0.571–0.83)	0.739 (0.652–0.826)	0.766 (0.667–0.871)	0.804 (0.693–0.892)
Average (4 classes) (external set)							
Average (4 classes)	0.886 (0.813–0.947)	0.883 (0.814–0.943)	0.655 (0.432–0.863)	0.629 (0.464–0.786)	0.822 (0.741–0.897)	0.878 (0.796–0.946)	0.722 (0.543–0.873)
Normal (0)	0.89 (0.815–0.948)	0.833 (0.747–0.916)	0.6 (0.333–0.857)	0.429 (0.217–0.647)	0.793 (0.701–0.885)	0.909 (0.836–0.971)	0.65 (0.427–0.842)
Low Grade (1)	0.799 (0.7–0.887)	0.818 (0.705–0.909)	0.5 (0.324–0.667)	0.615 (0.407–0.792)	0.701 (0.598–0.793)	0.738 (0.618–0.843)	0.58 (0.381–0.791)
High Grade (2)	0.863 (0.755–0.951)	0.882 (0.805–0.947)	0.727 (0.444–1)	0.471 (0.231–0.706)	0.862 (0.793–0.931)	0.957 (0.9–1)	0.674 (0.423–0.859)
Carcinoma (3)	0.994 (0.981–1)	1 (1–1)	0.793 (0.625–0.929)	1 (1–1)	0.931 (0.874–0.977)	0.906 (0.83–0.971)	0.983 (0.94–1)
Dysplasia (1 + 2)	0.831 (0.74–0.908)	0.727 (0.581–0.854)	0.721 (0.587–0.848)	0.721 (0.581–0.842)	0.724 (0.621–0.816)	0.727 (0.58–0.854)	0.82 (0.702–0.911)

The average corresponds to the average over the four classes. Confusion matrices are shown in Figure 3. Confidence intervals are computed with bootstrapping (10,000 bootstraps). NPV corresponds to the negative predictive value. PPV corresponds to the positive predictive value. Bold values in this table is to highlight the main values to look at (the average over the 4 classes).

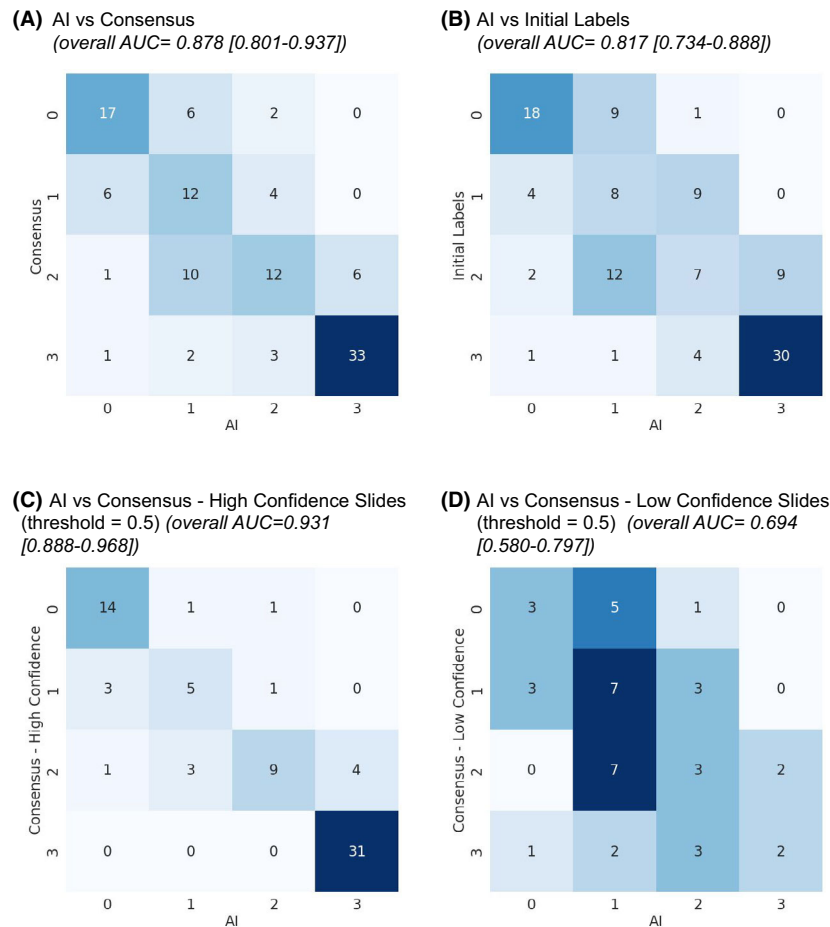


Figure 3. Confusion matrices: AI model's performances are evaluated on the reference standard test set on the reviewed labels (A) and the initial labels (from patient's records) (B). Numbers 0, 1, 2, 3 correspond respectively to classes nondysplastic, low-grade, high-grade, and carcinoma. Classification performances are superior when using reviewed labels, indicating that the review helped reduce noise in the labels. Confusion matrices show that the model is more confused on the Low Grade (1) and High Grade (2) classes, rather than the Carcinoma class (3), for instance, which is justified by the ambiguity carried by these classes, on which even pathologists can struggle. Matrix C corresponds to the confusion matrix on the high confident slides at threshold = 0.5, matrix D corresponds to the low confident slides. Matrix C is almost diagonal, and the overall AUC on the confident slides subset is higher by more than 10% than on the unconfident subset. Additionally, we see that most of the Carcinoma slides are considered confident by the model. Confusion matrix on the external test set can be found in Appendix S1.

CONFIDENCE SCORE ASSESSMENT

For accurate predictions, the average confidence score was 0.846 ± 0.153 , compared to 0.288 ± 0.150 for incorrect predictions. With a 0.5 confidence threshold, 42 slides (36.5%) were marked as uncertain on the reference standard test set, mostly being low-grade dysplasias. For the remaining slides, the invasive carcinoma AUC was 0.977 [0.940–1.000], with the model missing no carcinoma slides (negative predictive value of 1.000 [1.000–1.000]). The overall AUC improved by 5.3% (0.931 [0.888–0.968]) when removing slides with low confidence. Conversely, the overall AUC computed on the uncertain slides was equal to 0.694

[0.580–0.797] (–18.4% compared to the overall AUC on the full test set). Figure 3 shows confusion matrices for confident and nonconfidence slides. Figure S1 suggests the model's confidence level correlates with the likelihood of reviewer disagreement.

ANALYSIS OF MISCLASSIFIED SLIDES

Most misclassifications were low-grade dysplasias, labeled as nondysplastic. Notably, these slides were initially labeled in the clinical record as “nondysplastic”, showcasing the established ambiguity between these two classes. Four carcinoma slides were misclassified but had low confidence scores, falling beneath

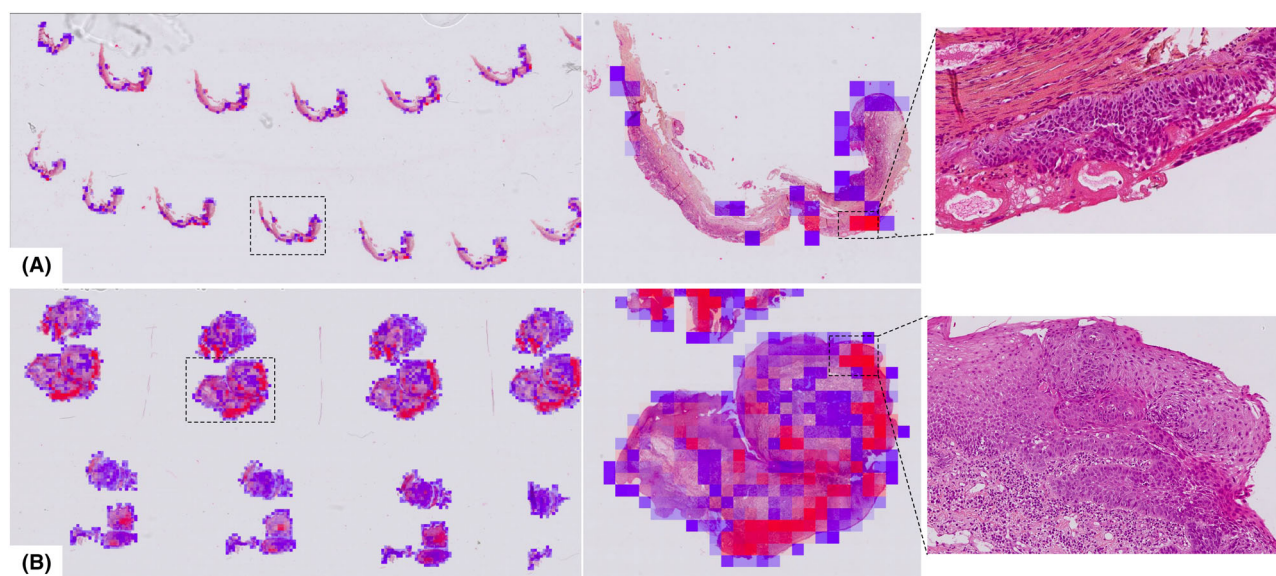


Figure 4. Visualization of Attention Heatmaps: The graphic represents attention scores from the MIL model, overlaid onto WSIs. The colour-coding system ranges from 0 (blue) to 1 (red), signifying attention scores, while a lack of colour indicates a score of 0.5. The figure shows the heatmaps of two well-predicted slides. The areas with the higher attention scores are displayed on the right under 10× magnification. The slide A (slide_1937) accurately predicted as High Grade Dysplasia, presents a confidence score of 0.43, whereas the slide B (slide_2117), accurately identified as Carcinoma, demonstrates a confidence score of 0.47. The highlighted regions correspond to the regions with marked atypia in the epithelium. Interestingly, heatmaps appeared to be fairly selective, highlighting only relevant patterns while displaying low attention scores on normal tissue. Notably, Slide B was discerned by pathologists as containing Micro-Invasive Carcinoma in the initial grading (patient report), and as high-grade dysplasia by a reviewer during the dual blind review, marking a challenging diagnosis.

the filtering threshold. Three of them had significant artefacts. The other showed carcinoma under a non-dysplastic epithelium, which could be more difficult for the model to identify because of the rarity of this presentation. Misclassified slides associated with high-confidence scores were typically upgraded by one class. Table S4 present a summary of the misclassified slides and their associated confidence scores. Figure 5A shows one high-grade dysplasia with a high-confidence score and misclassified as carcinoma. The high-attention tiles displayed severe atypia in the lower epithelium (highlighted by the attention heatmaps). Similarly, Figure 5B shows a low-grade dysplasia classified as high-grade. The two pathologists reviewed the high attention tiles and agreed that these aspects are challenging to interpret.

EXTERNAL VALIDATION

On the external validation set the model delivered an average AUC of 0.886 (95% CI: [0.813–0.947]) across the four classes. In particular, the AUC on the carcinoma class reached 0.994 (95% CI: [0.981–1]). Similar to the internal test set, classification performances reached AUC > 0.8 for all classes, even

though the performances are slightly lower on the low-grade dysplasia class (class 1), as expected. The confusion matrix is available in Figure S2).

Discussion

Our study proposes the first deep-learning model for grading HN squamous lesions according to the WHO classification system.

Owing to the absence of a publicly accessible annotated HN dysplasia database, we collected a large-scale dataset of HN samples from the HEGP, a prestigious HN diagnosis and healthcare centre in France.

We proposed a rigorous reference standard test set for robust model evaluation. The two-phase protocol enabled the creation of a highly reliable ground truth by promoting consensus and encouraging thorough discussion between the two reviewers. By actively engaging in constructive feedback, potential oversight and subjectivity were mitigated. Furthermore, the exclusion of discordant slides yielded a meticulously curated test set. Additionally, we validated our model on an external dataset sourced from a different hospital. This external dataset consisted of slides sampled

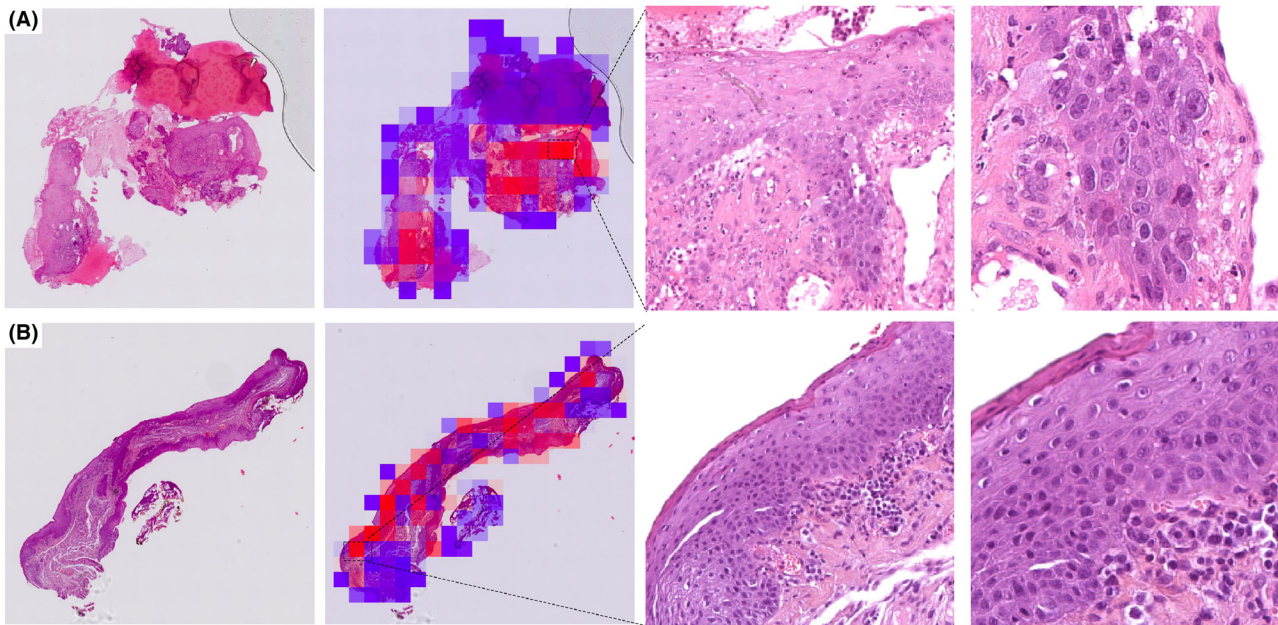


Figure 5. Misclassified slides: attention score analysis. Heatmaps and tiles with high attention scores attributed by the MIL model. First column: one level of a WSI. Second column: WSI overlaid with attention score heatmap. Scores range from 0 (blue) to 1 (red). Third column: 10 \times . Fourth column: 20 \times magnification. (A) slide_237. High-grade dysplasia predicted as invasive carcinoma. The model focused on marked basal atypia and bulky rete ridges. (B) slide_2712. Low-grade dysplasia predicted as high-grade. The model focused on marked basal atypia with a corrugated lamina propria. The two lesions are located in the larynx.

much more recently (2016–2023) than the primary dataset (2000–2013), providing an additional source of heterogeneity in the data. The labels were sourced from the pathological reports, and thus not reviewed. Interestingly, the performances on this external dataset were equivalent if not higher than on the internal reference standard test set. This could be explained by several factors: first, the slides being more recent, the staining quality was more homogenous and less susceptible to deterioration; second, the dysplasia diagnoses (concerning slides from 2017) were made according to the 2017 binary version of the WHO classification, a simpler system that could help the diagnosis being more robust and accurate. Finally, the vast heterogeneity and noise in the training data and the use of self-supervised pretraining contributed to make to model robust and widely applicable.

We designed a weakly supervised deep-learning model for accurate HN dysplasia grading from annotated WSI, providing an assisted diagnosis tool. Our work introduces a novel confidence score, defined as the difference between the top two class probabilities, ranging from 0 (equally likely) to 1 (maximal confidence). This score was previously validated in a separate study,³⁵ highlighting its relevance in grading precancerous lesions.

This confidence score provides pathologists with a more objective grading method and enhances the practicality and acceptance of AI grading models. High-confidence predictions of severe lesions could be prioritized to reduce delays in diagnosis, while low-confidence cases could be addressed for precautionary review. Analysis of false-negative carcinoma samples revealed that technical artefacts causing classification issues also resulted in low confidence scores that would have filtered them out according to our procedure.

In conclusion, our robust deep-learning model effectively classifies HN squamous cell nondysplastic epithelium, dysplastic, and invasive lesions. Amid a shortage of experts to screen samples or give a second read on difficult interpretations, this model could be used as a powerful and reliable tool by pathologists for faster diagnosis and better grading, ultimately benefiting patient care and follow-up.

Acknowledgements

We thank the Keen Eye team for thoughtful discussions and technical support, and Yan Petit for code implementation assistance.

Author contributions

Concept and design: Cécile Badoual, Thomas Walter, and Sylvain Berlemont. Ethical approvals processes: Cécile Badoual, Sylvain Berlemont, and Yaëlle Bellahsen-Harrar. Creation of the clinical and pathology database, slides selection, and labelling: Yaëlle Bellahsen-Harrar. Access to external data: Sarah Atallah and Emmanuelle Vaz. Data management and processing, software implementation, experiments realization, and statistical analysis: Mélanie Lubrano. Choices on experiments: Mélanie Lubrano and Yaëlle Bellahsen-Harrar. Design of AI methods: Mélanie Lubrano and Thomas Walter. Results analysis: Mélanie Lubrano and Yaëlle Bellahsen-Harrar. Discussion of results: Mélanie Lubrano, Yaëlle Bellahsen-Harrar, Thomas Walter, and Cécile Badoual. Article writing and review: all authors. All authors read and approved the final article.

Funding information

ML was supported by a CIFRE PhD Fellowship founded by TRIBUN HEALTH, Paris, France and ANRT (CIFRE 2019/1905). Furthermore, this work was supported by the Ministère de l'Enseignement supérieur, de la Recherche et de l'Innovation under management of Agence Nationale de la Recherche as part of the "Investissements d'avenir" program, reference ANR-19-P3IA-0001 (PRAIRIE 3IA Institute), also, TW acknowledges financial support from ITMO Cancer (20CM107-00).

Conflict of interest

The authors declare no competing interests.

Ethics approval and consent to participate

Our study was approved by the Ethics Committee of Assistance Publique – Hôpitaux de Paris Centre (CER-APHP, Centre – Institutional Review Board registration #00011928). All the patients were informed by a notification letter of the study and the possibility to refuse the use of their medical data, in line with current legislation. The study was performed in accordance with the Declaration of Helsinki.

Posted history

This article was previously posted to bioRxiv: <https://doi.org/10.1101/2022.12.21.521392>.

Data availability statement

The WSI datasets described in the article were subject to hospital regulations and could not be publicly released. Data sharing should be possible with other research teams under formal agreement with Assistance Publique – Hôpitaux de Paris (contact first and last authors for more information).

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Data S1. Supplementary materials.

Table S1. MIL architecture summary.

Table S2. Classification error costs.

Table S3. Consensus meeting results.

Table S4. Misclassified slides.

Table S5. Cost sensitive vs cross entropy.

Figure S1. Confidence level distributions.

Figure S2. Confusion matrix on the external test set.