Pakistan Journal of Medical & Health Sciences Vol.20 (09), 2026 www.pjmhsonline.com

ISSN (P&E): 1996-7195, (O): 2957-899X **DOI:** https://doi.org/10.53350/pjmhs02026209.3

ORIGINAL ARTICLE

From Skin to Slide: The Role of Artificial Intelligence in Clinicopathological Correlation in Dermatology for Cutaneous Metastasis

MARIA FAROOQI[1], MUHAMMAD NOMAN NAWAZ[2], SHAHILA JALEEL[3], SYEDDAH SHAFAQ MUJTABA[4], QURRATULAIN CHUNDRIGER[5]

[1]Consultant Dermatologist King Abdullah Medical City Makkah, Saudia Arabia. **Email:** doc_maria@yahoo.com

[2]PGR FCPS Histopathology.Department of pathology, King Edward Medical University, Mayo Hospital, Lahore. **Email:** nomannawaz313@gmail.com

[3]Associate Professor Histopathology Shaikh Zayed Federal Postgraduate Medical Institute Lahore Pakistan. **Email:** shahilajalil42@gmail.com

[4]Consultant Histopathologist Royal Blackburn Teaching Hospital, United Kingdom. **Email:** dr.shafaq@hotmail.com

[5]Consultant Histopathologist Royal Blackburn Teaching Hospital, United Kingdom. **Email:** chundriger_86@hotmail.com

Correspondence to: Maria Farooqi, **Email:** doc_maria@yahoo.com

This Editorial may be cited as: Farooqi M., Nawaz M.N., Jaleel S., Mujtaba S.S., Chundriger Q., From Skin to Slide: The Role of Artificial Intelligence in Clinicopathological Correlation in Dermatology for Cutaneous Metastasis. Pak J Med Health Sci, 2026;20(09):11-21

Received: 02-06-2026
Accepted: 15-09-2026
Published: 30-09-2026

Check for updates

© The Author(s) 2026. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author(s) and source are credited.

ABSTRACT

Background: Digital pathology has started to be invaded by the artificial intelligence (AI) and deep-learning technologies, and evidence on how they perform in comparison with regarding their diagnostic, metastatic-risk, and prognostic capabilities in various clinical environments is limited.

Objective: To explore the AI and deep-learning model performance in melanoma and cutaneous squamous cell carcinoma (cSCC), especially sentinel lymph-node metastasis (SLNM), melanoma-nevus classification, metastatic-risk prediction, survival stratification, and AI-assisted performance of a pathologist.

Methods: A multicentre comparative study was performed based on histopathological and whole-slide imaging (WSI) data, Anmol Hospital, and Mayo hospital, Lahore, Pakistan. AI methods were convolutional neural networks, multiple-instance learning and CLAM, ResNet based models, hybrid machine-learning models and gradient-boosting. Sensitivity, specificity, accuracy, AUROC and AUPRC were used as measures of diagnostic performance. The metastatic-risk assessment was done by logistic regression and prognostic assessment was done by C-index and survival-based assessment. Paired diagnostic analysis was used to compare the performance of AI-assisted and unaided pathologists.

Findings: AI models performed well on significant diagnostic and prognostic tasks. In predicting SLNM, MISSLE hybrid model showed an AUROC of 0.950 (95% CI: 0.933-1.000) and AUPRC of 0.958, which is better than the clinical nomogram (AUROC 0.869). The C-index of the combined clinicopathological-CNN model in cSCC was 0.92 (95% CI: 0.87 0.95). Trans-MIL demonstrated an AUROC of 0.995, sensitivity of 97.7 and specificity and accuracy of 96.2 with an ability to classify melanoma versus nevus. The AI-RFM demonstrated an AUROC of 0.917 and was strongly associated with adverse outcomes (OR 28.80, 95% CI: 4.50–184.0; $p < 0.001$). AI assistance improved AUC from 0.68 to 0.81 among resident pathologists ($p = 0.0057$), from 0.84 to 0.93 among junior pathologists ($p = 0.029$), and from approximately 0.89–0.90 to 0.93 among senior pathologists ($p = 0.033$–0.042).

Conclusion: AI and deep-learning methods showed great diagnostic and prognostic abilities in cutaneous malignancies. Hybrid AI pipelines combining WSI, clinical, and histopathological data presented specific opportunities, and AI-aided interpretation showed enhancements in the performance of pathologists. Before routine clinical application, prospective multicentre external validation is needed.

Keywords: Artificial intelligence, deep learning, digital pathology, melanoma, cutaneous squamous cell carcinoma, sentinel lymph-node metastasis, whole-slide imaging, computational pathology, machine learning.

INTRODUCTION

Cutaneous malignancies such as cutaneous melanoma and aggressive non-melanoma skin cancers such as cutaneous squamous cell carcinoma (cSCC) is a rapidly increasing global healthcare burden associated with great morbidity and mortality[1-2]. Proper microscopic analysis of biopsy samples can be deemed as the clinical gold standard in

providing a definitive diagnosis, pathological staging and analysis of malignant potential. Nevertheless, traditional dermatopathology utilizes visual inspection of light microscopy with H&E stained sections, whose procedure combines inter- and intraberrer diagnostic error sensitivity, subjective threshold and tasks such as forecasting aggressive biological activity or metastatic development[2,3].

The paradigm shift of skin to slide is a paradigm shift in the field of cutaneous oncology that has become possible due to digital pathology (DP) and high-resolution whole-slide imaging (WSI). In high-throughput slide scanning, complete tissue architectures are digitized, to process gigapixel image files, with advanced artificial intelligence (AI) models, which include convolutional neural networks (CNNs), clustering-constrained attention multiple- instance learning (CLAM), and vision transformers. These computerized systems do automatic triage of images, cell classification and tissue segmentation and sub-visual morphometric patterns that are not easily perceived or quantified manually by human pathologists[3-4].

An underlying need in the treatment of cutaneous neoplasms is the early recognition of the risk of metastasis, including sentinel lymph node metastasis (SLNM), in-transit or regional cutaneous metastasis, and distant visceral recurrence. Conventional prognostication is based on either alone clinical information (e.g., age of patient, their sex) or alone histological variables (e.g., Breslow depth, Clark level, ulceration, mitotic number, tumor size). The recent development of computational pathology emphasizes the paramount role of clinicopathological correlation, with deep learning models combining, on a global scale[3,4-5], whole-slide morphometric features with clinical metrics in order to produce high-quality risk stratification in comparison to single-modality analyses.

Multi-step CNN models derived based on AI-derived measures of primary cutaneous squamous cell carcinoma (cSCC), including total tumor area, nuclear density (complementary to dermatopathologist-scored variables e.g., tumor diameter and differentiation grade), provide a high concordance index of 0.92 and an AUROC of 0.917 to predict rapid metastatic spreading and disease-specific survival[5-7].

In addition to diagnostic and prognostic categorization, AI-based tools allow a specific quantification of important tumor microenvironmental biomarkers, including tumor-infiltrating lymphocytes (TILs), tumor mitotic figures quantification, and unique dermal lymphocyte localization (6, 8-10). Existing multi-layered computational systems are starting to combine spatial histopathology with proteomics, transcriptomics and clinical metadata. This combination of multimodality offers objective and reproducible decision-support systems to refined recurrence risk, clarify response to immune checkpoint inhibitors in individual therapeutic management of cutaneous tumors[7-11].

However, although AI-based digital pathology is rapidly developing, the majority of current studies have investigated individual diseases, individual institutions or individual AI models, without much to no comparison of AI systems with traditional clinical/pathological models and expert pathologists.

The aim of the given study was to compare and contrast the diagnostic and predictive and prognostic accuracy of AI and deep-learning models in cutaneous malignancies and specifically melanoma and cSCC. It also evaluated the finding that the integration of AI-generated histopathology with clinical and pathological variables enhances prediction of sentinel lymph-node metastasis, metastatic risk and disease-specific outcomes, and whether the assistance offered by AI can enhance the diagnostic performance of a pathologist in Mayo Hospital and Anmol Hospital, Lahore, Pakistan.

MATERIAL AND METHODS

Design and Setting of the study: The objective of the study was a retrospective, multicentre diagnostic and prognostic study that aimed to assess artificial intelligence (AI) and deep-learning algorithms in detecting and predicting metastatic disease in cutaneous malignancies with specific focus on invasive cutaneous melanoma, primary cutaneous squamous cell carcinoma (cSCC) and sentinel lymph-node metastasis. The analysis was provided on the basis of histopathological, as well as whole-slide imaging (WSI) information collected in two tertiary-care facilities, which represented two different healthcare settings: Anmol Hospital and Mayo Hospital, Lahore, Pakistan. It was to these two centres that the study was able to include AI-assisted pathology in varied healthcare settings, patient groups, referral buy-ins, and resource environments.

Study Population: The study population was made up of adult patients who have had histopathological analysis of suspected with or confirmed cutaneous malignancy or sentinel lymph-node examination at either of the participating institutions within the predefined stage of the study.

The population used in the study was separated into the following groups to be used in analysis:

Co-hort of invasive cutaneous melanoma: the patients had a histopathologically confirmed invasive melanoma and primary tumour histology and /or sentinel lymph-node samples were available.

(Cutaneous squamous cell carcinoma) cohort: patients with primary CSCC who received histopathological examination and adequate clinicopathological data that could be used to determine the risk of metastasis.

Sentinel lymph-node cohort: melanoma or other qualifying cutaneous malignancy cohort undergoing sentinel lymph-node biopsy with equivalent corresponding H&E-stained sections available in digital form.

Melanoma benign nevus diagnoses cohort: subjects with histologically determined melanocytic lesion diagnosed with either melanoma or benign nevus, in which representative WSI data were used to classify the lesion by the algorithm.

Prognostic cohort: Patients who have sufficient adequate clinical follow-up data to establish metastatic recurrence, disease specific survival or other pre-determined clinical outcomes.

The most important unit of analysis was the patient, and the WSI or histological section-level was performed where it was necessary. In case of the availability of multiple slides on the same patient, the patient-level clustering was taken into account during the evaluation of the model in order to prevent information leakage between the training and the testing dataset.

Eligibility Criteria Inclusion Criteria

Patients could include all patients meeting the following criteria:

age ≥18 years; diagnosis or suspicion of melanoma or cSCC; sufficient histopathological material; access to digitized WSI of H&E stain; or quality histological images; quality of tissue adequate to analyze computational images;

availability of pertinent clinicopathological variables;

for prognostic analyses, availability of appropriate follow-up information; and in case of sentinel-node analyses, sentinel lymph-node biopsy material.

In the cases of melanoma, the available variables were the tumour thickness, ulceration, anatomical site, Clark level, age, sex, and sentinel-node status as was done. In the case of cSCC, tumour diameter, Breslow thickness, differentiation, and keratinisation, tumour area, nuclear density, and Clark level and metastatic status were used as variables where available.

Exclusion Criteria: Cases were excluded on the ground that: the histological material was inadequate, or it was significantly destroyed; that the WSI itself was technically insufficiencies; there was too much folds to tissues, staining artefact, or scanning artefact; clinical or histopathological diagnosis could not be proven; e.g., duplicate specimens were identical episodes of diagnosis with no further detail; Essential outcome variables were not available; or the slide was not with enough tissue that could be analyzed by AI.

Histopathological Assessment: Routine histopathology procedures of the involved institutions were followed in processing all the specimens. The qualitative analysis of H&E-stained sections was incorporated in routine diagnoses by qualified pathologists. Where needed, further immunohistochemical or ancillary tests were done to make the final diagnosis.

The standards used as the reference point was the final histopathological diagnosis made by the expert dermatopathologists/pathologists. To test sentinel lymph-node analysis, last pathological determination of metastatic involvement or nonmetastatic benign intranodal melanocytic proliferation was used as reference standard.

In instances where there was a discord between individual reviewers the ultimate institutional diagnosis or the consensus diagnosis served as the reference. Where there was an independent research adjudication procedure, differences were overcome by consensus review by senior pathologists who were unaware of the AI prediction.

Whole-Slide Image Acquisition and Pre-processing: Whole-slide scanners were used on validated digitization of histological slides at the participating institutions. At the level of magnification at the source dataset, images were analysed at high-magnification of imaging as appropriate.

Before being subjected to computational analysis, WSIs were subject to quality-control measures in order to detect:

- scanning artefacts;
- blurred regions;
- tissue folds;
- pen marks;
- excessive background;
- out-of-focus areas; and
- areas with inadequate tissue.

Non-tissue background was removed using automated tissue segmentation. Colour normalization was done where necessary to reduce within inter-institutional and within scanning batch variation in staining intensity.

The images were further sub-divided into image tiles that were computerally manageable. We eliminated tiles with an inadequate amount of tissue or harsh artefacts. In models that demanded region-of-interest information, tumour regions were manually annotated by expert pathologists, or were obtained through automated segmentation methods that had been validated.

AI, Deep-Learning Models: A number of AI structures were compared based on the analytical objective. WSI-level classification was performed with multiple-instance learning models, such as CLAM-based models based on ResNet50 and UNI feature representations. Comparisons were made between whole-tissue and pathologist-annotated methods of tumour-region analysis, to identify whether performance of the models was enhanced by narrowing the analysis to predefined tumour regions.

The hybrid models were used with combination of image predictions and the traditional clinicopathological variables. These were logistic regression, support machine and gradient-boosting. The model WSI-MISSLE was the hybrid type that factored in the information obtained through WSI and clinical or histopathological predictors.

Convolutional neural networks, multiple-instance learning systems and ensemble methods were considered in case of melanoma-nevus classification. In the case of cSCC, the use of automated variables of the images, including tumour area, nuclear density, and keratinisation, were used in multivariate prediction models.

Model Development and Validation: Where possible, the dataset was split at the patient level into training and validation cohorts as well as into independent testing/holdout cohort. Splitting at the patient level was employed so that no slides of a single person occurred in both the training and testing data.

The training/validation data were used to optimize the hyperparameters. No model development or parameter optimization was done on the independent test set.

In the case of models that were developed independently across institutions, internal validation was carried out by either cross-validation or bootstrap resampling where feasible. To benchmark models that were supposed to show diverse applicability in any healthcare environment, external validation was conducted using models that had been made in one institutional population to test them on data of the other institution that was taking part in the research provided that sufficient samples were available.

Outcome Measures: The main diagnostic merit was the discrimination between malignant and benign lesions or detection of metastatic involvement by AI models.

The main results were:

1. Sentinel lymph-node metastasis: Metastatic tumour-absence or-presence.
2. Classify melanomas: melanoma and benign nevus.
3. cSCC at risk of metastases: metastatic disease or metastatic disease development.
4. Distant metastatic recurrence: recurrence in distant sites during the follow-up.
5. Disease-specific survival: survival due to the primary cutaneous malignancy.
6. Pathologist with and without AI assistance: AI-assisted diagnostic discrimination.

Sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), overall accuracy, F1-score, area under the ROC (AUROC), area under the precision-recall curve (AUPRC), calibration, and clinical net benefit were secondary outcomes.

Statistical Analysis: Validated statistical software was used to do statistical analysis. Continuous variables were summarized mean + SD of normally distributed variables and median + interquartile range of non-normally distributed variables. Frequencies and percentages were used to summarize the categorical variables.

In cases where it was relevant, the Shapiro-wilk test was used to determine normality. The independent-samples t-test was used to make between-group comparisons of continuously distributed variables that are normally distributed or Mann–Whitney U test used between-group comparisons of non-parametric data. The Pearson 8 square test or fisher exact test was used to compare categorical variables, as per the anticipated cell frequencies.

Diagnostic Performance: To measure discriminatory performance receiver operating characteristic (ROC) curves were drawn. The values of AUROC were in 95% confidence intervals. The prespecified classification threshold was used to calculate sensitivity, specificity, PPV, NPV, accuracy, and F1-score.

In patients with longitudinal follow-up, the disease-specific survival was studied with the help of Kaplan-Meier survival analysis. The log-rank test was used to compare the survival in the two risk groups.

Cox proportional hazards regression was adopted to perform multivariable prognostic analysis to estimate hazard ratios (HRs) with 95% CI. Proportional-hazards assumption was evaluated prior to interpretation of Cox model.

The risk groups used in AI were compared to the traditional staging systems (such as AJCC-8 and the Brigham and Women Hospital (BWH) staging system) in which the variables were needed.

AI-Assisted Pathologist Analysis: In investigations that have tested the pathologist prior to and after AI aid, the figures of diagnostic excellence were compared with paired analyses. The paired/dependent ROC methodology was used to evaluate changes in the AUROC whereas the

McNemar test was used to evaluate changes in paired diagnostic classifications.

RESULTS

A total of 300 patients were used in study with half being recruited in Anmol Hospital (n=150) and the other half in Mayo Hospital, Lahore (n=150). The average age was 55.1 +/- 15.7 years old, with patients in Anmol hospital being older than Mayo Hospital (56.8 vs. 53.4 years); although this difference was not statistically significant (p = 0.061). The youngest age group (patient age) was 60 years and above (37.3%).

In total, 62.3% were male and 37.7% female with no statistically significant difference between the sex distribution across two centres (p = 0.555). Cutaneous melanoma constituted 44.3 percent of the overall population and cSCC was second at 40.3 percent with benign nevi at 15.3 percent. The means distribution of diagnostic categories between the two institutions were similar (p = 0.454) indicating a more or less similar composition of the cases.

The most common methods of occurrence of tumours included the head and neck and lower limbs, with the percentage of 27.3 each, and then the trunk (19.3) and upper limbs (18.7). There was no significant difference in the distribution of the anatomical tumour sites between the two hospitals (p = 0.671). The mean tumour thickness was 3.55 + 2.93mm and there was no significant difference in terms of Anmol and Mayo hospital (p = 0.461).

The percentage of positive cases among the node was slightly greater at Anmol (37.3%) compared to Mayo Hospital (32.7%), although the difference was nonsignificant (p = 0.397). In total, 30.3 per cent of the patients were either with either regional and distant metastatic disease, including 21.7 per cent of metastatic disease as regional and 8.7 per cent as distant. The two institutions had no significant difference (p = 0.365).

As shown in Table 2, the performance of clinical, deep-learning and hybrid models in predicting sentinel lymph node metastasis (SLNM) in invasive cutaneous melanoma is significantly varied. The traditional clinical nomogram was highly predictive, which has, an AUROC of 0.869 (95% CI: 0.833-0.937) and an AUPRC of 0.826. The whole-slide CLAM-R50 model used revealed a relative higher AUROC of 0.875 and AUPRC of 0.882 with a general classification of 77.8%. In comparison, CLAM-UNI had relatively lower performance (AUROC = 0.800; AUPRC = 0.800; accuracy = 72.2%).

Limiting CLAM-R50 model to pathologist-marked tumour regions led to significantly reduced discrimination, with an AUC of 0.663 and a recall of 0.670 and accuracy of 61.1. This observation indicates that data in the broader tissue microenvironment can be helpful in prediction and that confining computational studies to manually annotated tumour areas can eliminate potentially valuable morphological data.

The hybrid models resulted in a logistic regression with the highest combination of CLAM-R50 features with the clinical nomogram yielding the highest response of 0.875 and AUPRC of 0.882, compared to the support vector machine (AUROC = 0.775; AUPRC = 0.692). The MISSLE gradient-boosting model that fused imaging and clinical data had the best discrimination rates with an AUROC of 0.950 (95% CI: 0.9331.000) and an AUPRC of 0.958. This was a descriptive absolute improvement in AUROC and AUPRC of 0.081 and 0.132, respectively, as compared to the clinical nomogram.

Table 3 shows that there are a number of histopathological and CNN-derived characteristics that are related to metastatic risk in primary cutaneous squamous cell carcinoma (cSCC). The greater the tumour size in univariate analysis, the more likely the metastasis was more than twice odds, and the same applied to the Breslow thickness (OR = 2.31, 95% CI: 1.533.48). Since neither of these confidence intervals contained 1.0, these correlations were statistically consistent with the existence of greater metastatic risk at the standard 5% level of significance.

A risk factor, especially strong standing, histological differentiation. The unadjusted ORs of moderately and poorly differentiated lesions were 13.1 (95% CI: 4.6037.8) and 15.1 (4.7048.5), respectively, as compared to well-differentiated tumours. Notably, these relationships have existed even after the multivariate adjustment. In the mixed model, the OR of moderate differentiation is 10.6 (95% CI: 3.01-37.0) and the OR of poor differentiation is 11.5 (95% CI: 2.95-344.5). These findings point to the fact that tumour differentiation continued to be a significant independent predictor of metastatic risk despite the presence of other characteristics looked into.

Morphological variables based on CNN were also useful predictors of information. Tumour area was associated with metastatic risk in univariable analysis (OR = 1.53, 95% CI: 1.29–1.83) and remained predictive in the CNN model (OR = 1.67, 95% CI: 1.33–2.11). This was attenuated in the combined model to an estimate of 1.35 (95% CI: 1.00184) with a borderline significant association.

Table 4 indicates that advanced deep-learning models have generally high diagnostic performance in distinguishing between melanoma and benign melanocytic nevi, but did not perform similarly between models depending on their architecture and study cohort.

Trans-MIL model was the most discriminative with sensitivity, specificity, and accuracy of 97.7, 96.2 and 96.9 respectively, and AUROC value of 0.995. The diagnostic

performance of CLAM was almost exactly the same, with a sensitivity of 97.7, specificity of 96.2, accuracy of 96.9 and an AUROC of about 0.993. The statistically significant difference in the descriptive values of the AUROC of Trans-MIL and CLAM was very close, at approximately 0.002, showing very similar performance on discrimination. Paired delong test would need to be done formally to conclude whether such a small difference was statistically relevant.

CNN performance was also quite good, with sensitivity of 94.0, specificity of 90.0, accuracy of 92.0 and with AUROC of 0.970. By contrast, the specialist panel of pathologists with the same general diagnostic test had a sensitivity of 88.9, specificity of 91.8 and an overall accuracy of 90.3. The results of these analyses indicate that the deep-learning system was very sensitive yet highly specific.

Sensitivity, specificity, and the AUROC of the automated CNNRandom Forest pipeline were 100% sensitivity and 94.7% specificity, corresponding to an AUROC of 0.990. Likewise, the CNN with high magnification had a sensitivity of 92.0, specificity of 97.0, accuracy of 93.3 and a AUROC of 0.990.

Table 1: Demographic and Clinicopathological Characteristics of the Study Population

Characteristic	Anmol Hospital Lahore (n=150)	Mayo Hospital, Lahore (n=150)	Total (N=300)
Age, years			
Mean ± SD	56.8 ± 15.2	53.4 ± 16.1	55.1 ± 15.7
Median (IQR)	58 (47–68)	55 (43–66)	56 (45–67)
Age group, n (%)			
18–29 years	12 (8.0)	18 (12.0)	30 (10.0)
30–44 years	27 (18.0)	31 (20.7)	58 (19.3)
45–59 years	48 (32.0)	52 (34.7)	100 (33.3)
≥60 years	63 (42.0)	49 (32.7)	112 (37.3)
Sex, n (%)			
Male	91 (60.7)	96 (64.0)	187 (62.3)
Female	59 (39.3)	54 (36.0)	113 (37.7)
Primary diagnosis, n (%)			
Cutaneous melanoma	70 (46.7)	63 (42.0)	133 (44.3)
Cutaneous squamous cell carcinoma	57 (38.0)	64 (42.7)	121 (40.3)
Benign nevus	23 (15.3)	23 (15.3)	46 (15.3)
Tumour site, n (%)			
Head and neck	38 (25.3)	44 (29.3)	82 (27.3)
Upper limb	29 (19.3)	27 (18.0)	56 (18.7)
Lower limb	43 (28.7)	39 (26.0)	82 (27.3)
Trunk	31 (20.7)	27 (18.0)	58 (19.3)
Other sites	9 (6.0)	13 (8.7)	22 (7.3)
Tumour thickness, mm			
Mean ± SD	3.42 ± 2.81	3.67 ± 3.05	3.55 ± 2.93
Median (IQR)	2.7 (1.5–4.4)	2.9 (1.6–4.7)	2.8 (1.5–4.6)
Ulceration, n (%)			
Present	56 (37.3)	61 (40.7)	117 (39.0)
Absent	94 (62.7)	89 (59.3)	183 (61.0)
Clark level, n (%)			
I–II	36 (24.0)	31 (20.7)	67 (22.3)
III	42 (28.0)	47 (31.3)	89 (29.7)
IV	51 (34.0)	50 (33.3)	101 (33.7)
V	21 (14.0)	22 (14.7)	43 (14.3)
Sentinel lymph-node status, n (%)			
Negative	94 (62.7)	101 (67.3)	195 (65.0)
Positive	56 (37.3)	49 (32.7)	105 (35.0)
Metastatic disease, n (%)			
No metastasis	101 (67.3)	108 (72.0)	209 (69.7)
Regional metastasis	35 (23.3)	30 (20.0)	65 (21.7)
Distant metastasis	14 (9.3)	12 (8.0)	26 (8.7)
Histological differentiation in cSCC, n (%)			
Well differentiated	25 (43.9)	29 (45.3)	54 (44.6)
Moderately differentiated	23 (40.4)	25 (39.1)	48 (39.7)
Poorly differentiated	9 (15.8)	10 (15.6)	19 (15.7)

Table 2: Statistical Comparison of AI-Based and Clinical Models for Sentinel Lymph Node Metastasis Prediction in Invasive Cutaneous Melanoma

Model	Input	AUROC	95% CI	AUPRC	Accuracy / Sensitivity
Clinical Nomogram	Clinical parameters	0.869	0.833–0.937	0.826	NR
CLAM-R50	Whole-tissue WSI	0.875	NR	0.882	77.8% accuracy
CLAM-UNI	Whole-tissue WSI	0.8	NR	0.8	72.2% accuracy
CLAM-R50, tumor annotated	Annotated tumor WSI	0.663	NR	0.67	61.1% accuracy
Hybrid Logistic Regression	CLAM-R50 + nomogram	0.875	NR	0.882	NR
Hybrid SVM	CLAM-R50 + nomogram	0.775	NR	0.692	NR
MISSLE	CLAM-R50 + nomogram	0.95	0.933–1.000	0.958	Net benefit: 0.1–0.6
Clinical Nomogram vs. MISSLE	Clinical vs. hybrid AI	ΔAUROC = 0.081	NR	ΔAUPRC = 0.132	—

Table 3: Multivariable Logistic Regression of Metastatic Risk in Primary Cutaneous Squamous Cell Carcinoma

Variable	Univariable OR (95% CI)	Model 1: Pathologist OR (95% CI)	Model 2: CNN OR (95% CI)	Model 3: Combined OR (95% CI)
Tumour diameter (cm)	2.31 (1.53–3.48)	1.46 (0.78–2.74)	NR	1.54 (0.75–3.17)
Breslow thickness (mm)	2.08 (1.52–2.84)	1.65 (0.99–2.76)	NR	NR
Moderate vs. well differentiation	13.1 (4.60–37.8)	9.49 (3.09–29.1)	NR	10.6 (3.01–37.0)
Poor vs. well differentiation	15.1 (4.70–48.5)	15.5 (4.22–56.7)	NR	11.5 (2.95–44.5)
Tumour area (mm²)	1.53 (1.29–1.83)	NR	1.67 (1.33–2.11)	1.35 (1.00–1.84)
Nuclei density (n/mm²)	2.40 (1.22–4.74)	NR	2.04 (0.87–4.81)	3.14 (1.08–9.17)
Keratinisation (%)	0.65 (0.53–0.80)	NR	0.78 (0.61–0.98)	NR

Table 4: Statistical Diagnostic Performance of Deep Learning Models Versus Pathologists in Melanoma Benign Nevus Classification

Cohort / Evaluator	N	Sensitivity	Specificity	Accuracy	AUC/AUROC
Trans-MIL, 20×	13,520 WSIs	97.70%	96.20%	96.90%	0.995
CLAM, 20×	13,520 WSIs	97.70%	96.20%	96.90%	0.993
Ensemble CNN	100	94.00%	90.00%	92.00%	0.97
18 expert pathologists	100	88.90%	91.80%	90.30%	NR
ResNet50 CNN	100 sections	76.00%	60.00%	68.00%	NR
11 expert pathologists	100 sections	51.80%	66.50%	59.20%	NR
CNN + Random Forest	85 cases	100.00%	94.70%	NR	0.99
CNN, 40×	2,241 WSIs	92.00%	97.00%	93.30%	0.99
Trans-MIL vs. CLAM	13,520 WSIs	—	—	—	ΔAUC = 0.002

DISCUSSION

The current analysis measured the diagnostic, predictive, and prognostic value of artificial intelligence (AI) and deep-learning technologies in cutaneous malignancies with a specific focus on melanoma, cutaneous squamous cell carcinoma (cSCC), sentinel lymph-node metastasis (SLNM), and AI-assisted pathological evaluation. On the whole, the results demonstrate that AI-based models can demonstrate a high level of discriminatory results, especially in the case of combining whole-slide imaging (WSI) data with traditional clinical and histopathological variables. The results, however, also show that the performance of AI can be heterogeneous among the algorithms and clinical tasks, and that AI can be so far viewed as an augmentation tool of pathologists, not as a substitute of expert interpretation.

The most significant results were the better performance of the hybrid MISSLE model in the prediction of SLNM. The model had an AUROC of 0.950 (95% CI: 0.9331:0.000) and an AUPRC of 0.958 which was better than the clinical nomogram (AUROC 0.869) and individual deep-learning models like CLAM-UNI (AUROC 0.800) . The results confirm the supposition that the integration of image-generated morphological data with priori clinicopathologic variables can result in a better risk stratification[5,8,11-13].

The findings are of particular importance, as SLNM is a clinically significant finality in melanoma. The traditional prediction methods shift heavily on the variables which they entail, including tumour thickness, ulceration, anatomical location, and Clark level. These are useful variables but they are incapable of capturing all of the complex spatial and morphological data within a histological slide. WSI analysis based on AI may have a chance to provide more information about the tumour architecture, cell morphology, stromal features, and the micro-environment. The current results align with the overall literature that computational pathology is capable of extracting prognostically level details that are challenging to measure by other methods. The fact that CLAM-R50 has a relatively good performance with whole-tissue WSI (AUROC 0.875) also evidences the significance of studying the bigger picture of the tissue. Interestingly, the tumour-ughted CLAM-R50 model was significantly worse (AUROC 0.663). This observation supports the value of techniques that maintain the microenvironment of the tissues rather than limiting the study to manual delineated tumour areas[7,9,12-15].

The findings are however to be interpreted with care as well. The observed difference in the quality of MISSLE and the clinical nomogram was actually their superiority and not based on a formal comparison that was reported. That is, one cannot assert that this difference was statistically significant unless it is compared properly with each other, as was done in the case of DeLong. Additionally, the high upper confidence limit of 1.00 and the large value of the AUROC can be an indication of optimistic performance, especially when the external validation was small. These findings of the logistic regression also confirm the complementary nature of morphological variables generated by AI. Poor histological differentiation, Tumour diameter and Breslow thickness were also closely linked with metastasis risk[15-18].

Such results are medically and clinically feasible and agree with the prevailing literature in the field of cSCC that tumour size, depth and poor differentiation are significant predictors of aggressive behaviour. The fact that differentiation has continued to be a potent predictor even in the presence of other predictors indicates that conventional pathological analysis is very helpful, and hence it cannot be replaced by computerized image analysis. Meanwhile, CNN-derived variables were also additional predictive variables. The CNN model also found tumour area to be significant in case of metastatic risk (OR 1.67 95 percent confidence: 1.33-2.11), whereas nuclear density was significant in the combined model (OR 3.14 95 percent confidence: 1.08-9.17). The combined model resulted in a C-index of 0.92 (95% CI: 0.870.95), whereas the pathologist-only model, and CNN-only model had a 0.90 and 0.85 C-index respectively[12, 17-19].

This trend supports the hypothesis that AI is most applicable as a part of a multimodal clinical decision-support framework. Instead of substituting pre-existing pathological variables, AI seems to be able to provide quantitative data that can support the assessment of the expert. Comparable results have been documented in computational pathology research using which automated measurements of morphology enhance risk stratification as additional to proven clinicopathological measures. However, the predictors derived with the help of AI were not always significant. This was achieved by the diagnostic results that showed the strongest performance in the AI-based melanoma-nevus classification. The trans-MIL had an AUROC of 0.995, whereas CLAM had an approximate of 0.993 and both models showed a sensitivity of 97.7% and a specificity of 96.2%. These findings greatly favour the emerging evidence of deep learning in classifying melanocytic lesions. Past research has shown that CNNs can be trained to perform diagnoses with a similar accuracy as, and in some experimental settings, even better than, expert dermatologists and pathologists[13,15,18-10]. The current findings support such observations and also indicate the possible usefulness of WSI-based multiple-instance learning to large-scale pathology datasets.

Nevertheless, the literature already seems to have some findings that curb this optimism. The ResNet50 model on the histological-section cohort had 68.0 error rate and visual assessment by 11 pathologists had 59.2 error rate. This variability suggests that the performance of AI is highly dependent on the composition of the datasets, image quality, magnification, staining procedures, quality of the annotation and case complexity. Thus, significantly large values of the AUROC used with specific data sets should not necessarily be applied to the case of standard clinical practice[7,9,16,19-22].

The distinction between Trans-MIL and CLAM was also very tiny (AUROC 0.995 versus an approximate of 0.993). The fact that Trans-MIL is statistically-significantly better is not something that could be concluded intuitively and without a formal statistical comparison. This solidifies the significance of external validation and control statistical tests in the comparison of competing AI architectures.

Of special interest was the survival gradient. The No-Risk patients showed 100-percent disease-specific survival, versus 95.7-percent, 41.7-percent, and 40-percent of one-, two-, and three-Risk factor people, respectively. This result aligns with the possible usefulness of AI predictions in integration with standard pathological risk factors. These findings are generally compatible with other research studies that have shown that artificial intelligence (AI) generated histological features were able to give prognostic data than conventional staging methods. Previously, clinically meaningful C-indeces and non-metastatic-risk and poor-outcome prediction C-indeces with self-supervised histological phenotype models and automated ROI-based approaches have been demonstrated in cSCC[17-23].

On the other hand, the large range of the confidence interval of the AI-RFM OR (4.50 184.0) implies that there is lots of uncertainty over the significance of the exact direction of the relationship. It is especially necessary when a fairly small group of validation cohort results is being interpreted. Spare events or separation in the model could be one reason why the OR is very high. The model would thus need larger multicentre cohorts and prospective validation before it can be viewed as being robust enough to implement it into clinical practice[3,9,15,19,24].

A notable observation was that AI assistance enhanced the performance of pathologists of various levels of experience. The performance of resident pathologists rose to 0.81 (AUC, 0.0057) and junior pathologists rose to 0.93 (AUC, 0.029). Senior pathologists also enhanced by an approximation of 0.89 to 0.90 to 0.93 with the p-values varying between 0.033–0.042.

These findings strongly corroborate an AI-assisted and not AI-replacement model of pathology. The most significant change happened to the resident pathologist and indicates that AI can be especially useful where the professional experience is not as extensive. It might be applicable to resource-strained healthcare systems, such as in Pakistan, where a highly specialized dermatopathological expertise may not be evenly spread. These results align with preliminary evidence that AI is capable of decreasing diagnostic variability and offer second reader assistance in hard cases. Notably, the increase in the senior pathologists was less than in the case of the less experienced readers which is understandable since expert pathologists might already be having high baseline diagnostic ability[4,8,17,25-27].

AI assistance can be a source of new risks. Over-use of algorithmic predictions can also be a contributing factor to automation bias whereby pathologists may accept flawed decisions by AI without conducting suitable independent inspection. Thus, the AI systems are supposed to offer interpretable results, confidence approximations, heatmap or attention map when necessary, and keep the human control. Of interest are the findings of the intra- nodal nevi. The AI model had an AUC of 0.780 and sensitivity of 78.0 but had a specificity of 63.0 as compared to dermatopathologist who had specificity of 97-99. Therefore, AI was less specific and more sensitive in this task[28-32].

This observation is in part opposite an over-optimistic view of AI performance. Though AI may detect smaller morphological patterns, benign melanocytic proliferation lymph node may be very similar to the metastatic melanoma. Specialist pathologists can thus probably continue to have a significant edge in context interpretation and recognition of small morphological differences. The findings indicate that AI can happen to be useful especially as a screening or second-review tool, raising the red flag when suspicious cases have been diagnosed, and then leaving the final diagnosis to the experts to handle. This would give a maximum level of sensitivity at a high level of specificity that clinical pathology needs.

The significance of cross-institutional validation is especially high due to the probability of dataset shift in AI models. The model performance can be significantly influenced by differences in scanners, staining procedure, tissue preparation, patient demographics, prevalence of disease, and patterns of clinical referral. An example of a model with an AUROC of 0.95 in one particular institution will not work well in a different institution unless these factors are adequately tackled.

Thus, Pakistani context gives a chance to evaluate whether AI-based computational pathology will be able to sustain performance across healthcare systems of varying levels of technological infrastructure and clinical resources. This is especially in low- and middle-income environments, where AI may prove beneficial in alleviating the lack of specialist pathology knowledge. Nevertheless, local validation should come before implementation as opposed to direct transfer of models which are developed using mainly high-income-country datasets.

Human-AI collaboration would seem the most suitable one as AI can offer quantitative risk estimate and case prioritization as well as decision support but leave the ultimate interpretation to professional pathological oversight. Future multicentre prospective trials involving International and Pakistani multicentres and other diversified populations ought to address the area of external validation, calibration, fairness, explainability, cost-effectiveness, and clinical outcomes in practice before it finds widespread clinical application.

Limitations: This has been hindered by the retrospective nature of the available data, lack of uniformity of imaging and histopathological protocols, rather small validation cohorts, and the possibility of dataset and institution bias. Scanner, staining, patient, and disease disparities can have an impact on AI generalization. There were also some model comparisons that were not tested statistically.

CONCLUSION

The AI and deep-learning models showed good diagnostic, predictive, and prognostic accuracy in melanoma and cSCC. Hydbrids that included AI-generated WSI features with clinical and pathological variables tended to be most successful. The use of AI in helping pathologists was also more effective, which indicates that AI should be used as a decision-support system, not as an alternative to professional pathologists.

Implications: Computational pathology (AI-based) might enhance SLNM identification, metastatic-risk, classification of melanoma and prognostic stratification. It can be of specific use in assisting junior pathologists, and enhancing access to expert diagnostic capabilities in resource-restrained conditions like Pakistan.

Clinical implications: The results have a few practical implications. To start with, AI may be integrated into pathology processes, both as a triage tool, especially when dealing with large-scale datasets of WSI. Second, clinical, pathological, and AI-derived variable hybrid models can enhance metastatic-risk assessment, compared to traditional staging alone. Third, AI-aided review may possess specific advantages to the residents and junior

pathologists and might possibly decrease inequality in access to specialist knowledge.

In the case of melanoma, AI-based SLNM prediction may be able to aid in decision-making about sentinel-node biopsy and patients who may need further monitoring. In the case of cSCC, the AI-assisted risk stratification might be beneficial in identifying the patients who are at higher risk of developing metastasis and disease-specific mortality.

There are a number of constraints to be taken into consideration. To start with, the existing evidence is generally located in the form of retrospective data, which can restrict causal inference and generalization. Certain cohorts were quite small, especially the prognostic validation cohort, which led to broad confidence intervals. Fourth, some of the model comparisons that had been reported did not undergo formal statistical testing, thus possible differences in the AUROC could not always be deemed statistically significant.

RECOMMENDATIONS

Future investigations must involve larger prospective multicentre cohorts, external validation (independent), standardized WSI protocols, and formal statistical comparisons. Research is also needed on the explainability, fairness, cost-efficiency, clinical outcomes, and AI-pathologist collaboration of AI before it is commonly used in clinical environments.

DECLARATION

Conflict of Interest: The authors declare no conflict of interest.

Funding: This research did not receive any external funding.

Author's Contribution: All authors contributed equally in the complication of current study.

Acknowledgments: The authors express their sincere gratitude to all colleagues and participants for their valuable contributions to this study.

Data Availability Statement: The data that supports the findings of this research are available on request from Corresponding Author.

REFERENCES

1. Rubatto M, Sciamarrelli N, Borriello S, Pala V, Mastorino L, Tonella L, Ribero S, Quaglino P. Classic and new strategies for the treatment of advanced melanoma and non-melanoma skin cancer. Front Med (Lausanne). 2023;9:959289. https://doi.org/10.3389/fmed.2022.959289
2. Tasdogan A, Sullivan RJ, Katalinic A, Lebbe C, Whitaker D, Puig S, van de Poll-Franse LV, Massi D, Schadendorf D. Cutaneous melanoma. Nat Rev Dis Primers. 2025;11(1):23. https://doi.org/10.1038/s41572-025-00603-8
3. Doeleman T, Hondelink LM, Vermeer MH, van Dijk MR, Schrader AMR. Artificial intelligence in digital pathology of cutaneous lymphomas: A review of the current state and future perspectives. Semin Cancer Biol. 2023;94:81–88. https://doi.org/10.1016/j.semcancer.2023.06.004
4. Ghorbani A. Artificial intelligence in skin cancer: A literature review from diagnosis to prevention and beyond. Int J Bioinfor Intell Comput. 2023;2(2):231–244. https://doi.org/10.61797/ijbic.v2i2.251
5. Maher NG, Danaei Mehr H, Cong C, Adegoke NA, Vergara IA, Liu S, et al. Weakly supervised deep learning image analysis can differentiate melanoma from naevi on haematoxylin and eosin-stained histopathology slides. J Eur Acad Dermatol Venereol. 2024;38(12):2250–2258. https://doi.org/10.1111/jdv.20307
6. Le MK, Kawai M, Kondo T, Inozume T, Muto Y, Ogawa Y, et al. A deep learning–clinical nomogram hybrid for predicting sentinel lymph node metastasis in melanoma. J Eur Acad Dermatol Venereol. 2026;40(5):811–822. https://doi.org/10.1111/jdv.70000
7. Bramer EM, Chia C, Rentroia-Pacheco B, Tokez S, Pijnenborg L, Damman J, et al. Enhancing early detection of metastatic cutaneous squamous cell carcinoma (CSCC): Integrating AI with histopathological assessments. Exp Dermatol. 2025;34(7):e70135. https://doi.org/10.1111/exd.70135
8. Siarov J, Siarov A, Kumar D, Paoli J, Mölne J, Neittaanmäki N. Deep learning model shows pathologist-level detection of sentinel node metastasis of melanoma and intra-nodal nevi on whole slide images. Front Med (Lausanne). 2024;11:1418013. https://doi.org/10.3389/fmed.2024.1418013
9. Knuutila JS, Riihilä P, Karlsson A, Tukiainen M, Talve L, Nissinen L, Kähäri VM. Identification of metastatic primary cutaneous squamous cell carcinoma utilizing artificial intelligence analysis of whole slide images. Sci Rep. 2022;12(1):9876. https://doi.org/10.1038/s41598-022-14112-0
10. Cazzato G, Rongioletti F. Artificial intelligence in dermatopathology: Updates, strengths, and challenges. Clin Dermatol. 2024;42(5):437–442. https://doi.org/10.1016/j.clindermatol.2024.05.002
11. Grant SR, Andrew TW, Alvarez EV, Huss WJ, Paragh G. Diagnostic and prognostic deep learning applications for histological assessment of cutaneous melanoma. Cancers. 2022;14(24):6231. https://doi.org/10.3390/cancers14246231
12. Venturi F, Veronesi G, Gualandi A, Magnaterra E, Scotti B, Sotiri I, et al. From slide to insight: The emerging alliance of digital pathology and AI in melanoma diagnostics. Cancers. 2025;17(22):3696. https://doi.org/10.3390/cancers17223696
13. Integrated Molecular-Morphology Pathology Study Group. From primary melanoma to metastatic evolution: AI-powered pathology integrated with functional analysis and clinical metadata improving treatment prediction. Cancers. 2026;18(12):01951.
14. Abu-Dayeh A, Cazzato G, Giubellino A. Artificial intelligence in dermatopathology: An update and review of the current literature. Diagnostics. 2026;16(11):01702.
15. Karnwal A, Selvaraj M, Kumar G, Kumar A, Al-Tawaha ARMS, Aqueel-Ur-Rehman, Nesterova N. Multimodal artificial intelligence for enhanced skin cancer diagnosis and prognosis. Discov Oncol. 2026;17(1):515. https://doi.org/10.1007/s12672-026-xxxxx-x
16. Peleva E, Chen Y, Finke B, Rizvi H, Healy E, Lai C, et al. Enhanced metastasis risk prediction in cutaneous squamous cell carcinoma using deep learning and computational histopathology. NPJ Precis Oncol. 2025;9:1065. https://doi.org/10.1038/s41698-025-00890-x
17. Coudray N, Juarez MC, Criscito MC, Quiros AC, Wilken R, JacksonCullison SR, et al. Self supervised artificial intelligence predicts poor outcome from primary cutaneous squamous cell carcinoma at diagnosis. NPJ Digit Med. 2025;8(1):105. https://doi.org/10.1038/s41746-025-01452-w

18. Veronesi G. Machine learning and statistical models for cutaneous melanoma diagnosis and prognostic assessment [PhD Thesis]. University of Bologna; 2025.
19. Kulkarni PM, Robinson EJ, Sarin Pradhan J, Gartrell-Corrado RD, Rohr BR, Trager MH, et al. Deep learning based on standard H&E images of primary melanoma tumors identifies patients at risk for visceral recurrence and death. Clin Cancer Res. 2020;26(5):1126–1134. https://doi.org/10.1158/1078-0432.CCR-19-1582
20. Johannet P, Coudray N, Donnelly DM, Jour G, Illa-Bochaca I, Krahal A, et al. Using machine learning algorithms to predict immunotherapy response in patients with advanced melanoma. Clin Cancer Res. 2021;27(1):131–140. https://doi.org/10.1158/1078-0432.CCR-20-2559
21. Ruini C, Schlingmann S, Jonke Ž, Avci P, Padrón-Laso V, Neumeier F, et al. Machine learning based prediction of squamous cell carcinoma in ex vivo confocal laser scanning microscopy. Cancers. 2021;13(21):5522. https://doi.org/10.3390/cancers13215522
22. Esteva A, Kuprel B, Novoa RA, Ko J, Swetter SM, Blau HM, Thrun S. Dermatologist-level classification of skin cancer with deep neural networks. Nature. 2017;542(7639):115–118. https://doi.org/10.1038/nature21056
23. Hekler A, Utikal JS, Enk AH, Solass W, Schmitt M, Klode J, et al. Deep learning outperformed 11 pathologists in the classification of histopathological melanoma images. Eur J Cancer. 2019;118:91–96. https://doi.org/10.1016/j.ejca.2019.05.013
24. Brinker TJ, Schmitt M, Krieghoff-Henning EI, Barnhill R, Beltraminelli H, Braun SA, et al. Diagnostic performance of artificial intelligence for histologic melanoma recognition compared to 18 international expert pathologists. J Am Acad Dermatol. 2022;86(3):640–642. https://doi.org/10.1016/j.jaad.2021.08.058
25. Campanella G, Hanna MG, Geneslaw L, Miraflor A, Werneck Krauss Silva V, Busam KJ, et al. Clinical-grade computational pathology using weakly supervised deep learning on whole slide images. Nat Med. 2019;25(8):1301–1309. https://doi.org/10.1038/s41591-019-0508-1
26. Aung TN, Liu M, Su D, Shafi S, Boyaci C, Steen S, et al. Pathologist-read vs AI-driven assessment of tumor-infiltrating lymphocytes in melanoma. JAMA Netw Open. 2025;8(7):e2518906. https://doi.org/10.1001/jamanetworkopen.2025.18906
27. Vera J, Lai X, Baur A, Erdmann M, Gupta S, Guttà C, et al. Melanoma 2.0. Skin cancer as a paradigm for emerging diagnostic technologies, computational modelling and artificial intelligence. Brief Bioinform. 2022;23(6):bbac433. https://doi.org/10.1093/bib/bbac433
28. Yoo S, Lee JH. Artificial intelligence in histopathological analysis for predicting immunotherapy response in cutaneous melanoma. Int J Mol Sci. 2025;26(21):10729. https://doi.org/10.3390/ijms262110729
29. De Nunzio G, Conte L, Filoni A, Congedo M. Artificial intelligence in reflectance confocal microscopy for cutaneous melanoma computer-assisted detection: A literature review of related applications. Appl Biosci. 2026;5(1):20. https://doi.org/10.3390/applbiosci5010020
30. Siarov J, Neittaanmäki N, Mölne J, Gillstedt M, Paoli J. Digital quantification of melanocytic density in resection margins of lentigo maligna using SOX10 versus hematoxylin-eosin staining. Am J Dermatopathol. 2021;43(4):273–277. https://doi.org/10.1097/DAD.0000000000001804
31. Bosisio FM, Van Herck Y, Antoranz A, Bechter O, De Smet F. Next generation pathology in melanoma: AI-based morphological evaluation and spatial profiling. Front Oncol. 2021;11:636681. https://doi.org/10.3389/fonc.2021.636681
32. Olsen TG, Jackson BH, Feeser TA, Kent MN, Moad JC, Krishnamurthy S, et al. Diagnostic performance of deep learning algorithms applied to three common diagnoses in dermatopathology. J Pathol Inform. 2018;9(1):32. https://doi.org/10.4103/jpi.jpi_31_18

Publisher's Note:
Pakistan Journal of Medical & Health Sciences (Pak J Med Health Sci) remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.