Reinforcement Modeling for Prostate Cancer Diagnosis Using the Gleason Grading System on Prostate Biopsy

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Abstract: This paper presents a reinforcement modeling framework tailored to the Gleason grading-based diagnosis of prostate cancer on prostate biopsy images. The diagnosis of prostate cancer depends largely on the accurate Gleason grading; however, the subjective nature of the manual assessment often results in differences stemming from inter-observer variability. To offset these drawbacks, deep reinforcement learning is incorporated with the aim of optimizing diagnostic decision-making in a sequential way in the context of the proposed framework. The framework was evaluated on the DiagSet-A, 10× dataset, which encompasses a total of 7,200 biopsy images distributed across six classes (N, R1, R2, R3, R4, and R5), which represent the progressive Gleason patterns. It has been demonstrated that our proposed model can attain a classification accuracy of 98% to reliably discriminate normal tissue from all other Gleason risk levels. The model thus reinstates enhanced diagnostic power by injecting in contextual microarchitectural features of the prostate tissue, creating hence a lesser ground for grading divergence. The findings endorse the view that reinforcement-based Gleason grading can stand being proposed as one robust, adaptable clinically relevant adjunct to prostate cancer pathology in securing more reliable patient risk stratification.

Keywords: Prostate cancer diagnosis; Gleason grading system; Reinforcement learning; Histopathology; Biopsy image classification

Introduction

One of the common cancers identified among men from different parts of the world is prostate cancer, which continues to cause a major part of cancer mortality [1]. An accurate and early diagnosis is vital for effective treatment planning and to improving prognosis. The Gleason grading system is the gold standard for estimating tumor aggressiveness and is predicated on the architectural patterns seen in biopsy tissue from prostate specimens [2]. In this grading system, prostate cancers are arranged into progressive grades ranging from low to high risk, which directly affects the clinical decision-making concerning whether to pursue active surveillance, surgery, or radiotherapy [3]. While useful in the clinic, Gleason grading is manual and therefore highly subjective, with inter-observer variability resulting in inconsistent results between pathologists [4]. This has given rise to research into automated computational models that will assist or supplement expert pathologists.

Recently, artificial intelligence (AI) and especially deep learning have shown great strides in the analysis of images in histopathology [5]. CNNs have been used extensively in the extraction of morphological features of biopsy samples, with considerable evidence of accuracy in tumor detection and grading tasks

[6,7]. But the approaches using CNNs are static supervision-based, meaning that model predictions are determined solely on pre-defined labels without any sequential decision making or adaptive feedback based on prediction performance [8]. For this reason, performance may be compromised in generalization over the intricate tissue patterns which become critical in grading by the Gleason methodology [9].

To counteract these drawbacks, an effective medium in medical image analysis would be reinforcement learning (RL). It is a paradigm wherein an agent develops optimal decision-making strategies through continuous association with the environment, together with a system of rewards and severe penalties [10]. Such an RL-based model for histopathology purposes would dynamically select the regions of interest, evaluate the micro-architecture, and apply Gleason grades using a set of rules similar to expert reasoning [11]. This mechanism makes RL-driven models different sorts of static features extraction, producing more interpretable and clinically relevant diagnostic outcomes [12]. Moreover, reinforcement modeling provides flexibility to incorporate hierarchical grading strategies, which are critical while distinguishing subtle differences between Gleason patterns [13].

This research proposes the reinforcement modeling framework for the diagnosis of prostate cancer with the Gleason grading system, as applied to prostate biopsy images. The framework is capable of analyzing histopathological regions in a progressive manner, extracting relevant features, and assigning risk categories from normal tissue (N) to progressive grades (R1-R5). The novelty lies in the incorporation of reward-driven learning such that the model refines its diagnostic behavior adaptively and is not heavily reliant on rigid pre-labeled supervision [14]. Moreover, the framework would use the information embedded in tissue microarchitecture to improve accuracy and reduce variability [15].

The model's validity was established by running tests on the 10X DiagSet-A dataset, which comprises 7,200 prostate biopsy images across six classes (N, R1, R2, R3, R4, and R5). The reinforcement-driven model achieved a striking 98 percent classification accuracy, which is greatly above the typical baseline of deep learning methods [16]. Such a high performance indicates strength and credibility of reinforcement learning for Gleason grading in the clinic. Furthermore, since the model is adaptable, it can be generalized whenever necessary across other histopathological datasets, thus increasing the scope of computational pathology applications [17,18].

The contributions of this study were three: introduce reinforcement modeling as an effective method for Gleason grading; an application of RL for sequential biopsy images analysis with clinically interpretable results; and empirical evidence to show improved accuracy and decreased variability in prostate cancer diagnosis [19,20]. All these contributions in their individual capacity show that the reinforcement-driven frameworks hold great promises for better supporting pathologists in making more reliable, reproducible, and precise diagnostic decisions.

Related work

Deep learning is a significant support in current imaging and grading methodology for the diagnosis of prostate cancer. For instance, the work of Liu et al. [1] described how neural networks could be used to improve imaging quality in diffusion-weighted scans so that lesions can be better detected in prostate cancer patients. Expanding on histopathology, Shakhawat Hossain et al. [2] put forward an ensemble network combining CNNs and transformers for the automated Gleason grading on low-resolution biopsy images, achieving robustness in classification performance. On the other hand, Jia et al. [3] speculated safety case deployments for AI-assisted prostate cancer diagnosis, emphasizing the need for integrating

trust and reliability into clinical workflows. In their research, Haque et al. [4] indicated the generative influence of artificial intelligence on prostate cancer imaging and how synthetic augmentation could enhance data diversity and diagnostic reliability. The contribution of Chelebian et al. [5] provided a dataset of clinical biopsy with regions of undetected cancer, which would greatly assist the development and benchmarking of machine learning algorithms.

Graph-based and multimodal learning approaches have also been prevalent contributions in the field. Noree et al. [6] proposed a graph convolutional network leveraging tissue slice commonalities to improve classification of whole-slide images, showing how structural dependencies between slices enhance learning. Based on prior research, Marin et al. [7] used tissue structure and clinical data information to predict biochemical recurrence, showing that robust tissue descriptors can meaningfully complement Gleason scoring. Devnath et al. [8] concentrated on epithelial cell recognition in prostatic glands, which forms a foundational step for accurate cancer diagnosis. Van Booven et al. [9] tackled bias reduction in AI-driven Gleason grading by using synthetic data, thus addressing fairness as well as representational balance in diagnostic pipelines. Expanding to multimodal integration, Lu et al. [10] combined proteomics and imaging for predicting progression in hormone-sensitive prostate cancer, highlighting the clinical value of heterogeneous data fusion.

Models based on transformers and multi-instance learning have received significant prominence. Chaurasia et al. [11] proposed a self-supervised vision transformer for histological image grading that has shown high adaptability with varied biopsy slides. Mai et al. [12] applied multi-instance learning through cross-mixing and feature reconstruction inside whole-slide images for Gleason grading, in turn increasing the generalization power at both the patch level and the slide level simultaneously. Kabir et al. [13] advanced a deep learning framework combining classification and segmentation for automated grading, matching the computational output with Gleason standards. Xu et al. [14] utilized a multilayer transformer optimized for whole-mount pathological slides to enhance speed of prediction, thereby shining a spotlight on computational efficiency without compromising precision. Meanwhile, Olawuyi and Viriri [15] surveyed deep learning methods for prostate cancer detection, providing an organized overview of the existing algorithms with a notion of gaps open for future study.

Advanced Gleason Grading is also supported by broader research in computational pathology. Bharadwaj et al. [16] used deep learning methods for differential diagnosis of odontogenic cysts, indirectly informing histopathology analysis frameworks through transferable methods. Erdem et al. [17] combined various deep learning classifiers within an ensemble model for prediction of pathological grade, thus enhancing the robustness of interpretation of whole slide images. Cao et al. [18] established a deep learning system predicting biochemical recurrence that bridges image-based diagnosis to longitudinal patient outcome. Koziarski et al. [19] introduced DiagSet, a standard dataset for histopathological image classification in prostate cancer, an essential benchmark for validation of AI-based models. Balasubramanian et al. [20] illustrated cross-domain applicability of ensemble approaches for grading and invasiveness prediction by extending ensemble deep learning methods to breast cancer histopathology.

In summary, existing literature reveals several strengths and limitations across imaging enhancement, automated grading, multimodal integration, and bias mitigation. Deep learning methods have attained promising results; nevertheless, their widespread use relies on static supervision, which has limited adaptability to complex histopathological patterns. Although powerful and scalable features are provided by transformer-based and graph-based architectures, they are severely impeded by problems of a scarcity

of annotated datasets in clinical practice. Ensemble strategies enhance the overall accuracy but impose serious computational stress, hampering the possibility of real-time clinical adoption. Moreover, interpretability received more and more emphasis, though black-box rationale has become a drawback towards trust and clinical integration for many of the approaches. These imperfections show the need for reinforcement-driven systems capable of sequential reward-driven decision-making so as to enhance interpretability, adaptability, and reliability in diagnosis in prostate cancer pathology.

Table 1. Comparison of related research on prostate cancer diagnosis and grading

Method	Key Focus	Limitations / Future Scope
Deep Learning approaches [1, 8, 13, 16, 18]	Imaging enhancement, epithelial cell recognition, grade assessment, transferable cyst diagnosis, recurrence prediction	Limited generalization across modalities; requires large, labeled datasets; interpretability challenges
CNN + Transformer hybrids [2, 17]	Gleason grading and pathological grading with robustness	High computational cost: ensemble complexity may hinder clinical adoption
Transformer-based methods [11, 14]	Self-supervised adaptability in grading tasks, faster predictions	Requires massive training data; may lose fine-grained tissue details in long-range modeling
Graph-based learning (GCN) [6]	Structural dependencies for improved classification	Graph construction can be computationally expensive; scalability issues with very large WSIs
Multi-instance learning (MIL) [12]	Robust Gleason grading through cross-mixing	Sensitive to bag composition; performance depends on patch-level quality
Generative AI [4, 9]	Synthetic data to increase diversity; reduced diagnostic bias	Risk of synthetic artifacts; clinical trustworthiness and regulatory validation needed
Multimodal integration [7, 10]	Biochemical recurrence and progression prediction	Data heterogeneity: integrating multimodal pipelines is complex; limited availability of paired datasets

Key Contribution

The automated prostate cancer diagnosis is much improved through reinforcement-driven Gleason grading on biopsy images using this research. While most previous work focused on CNN-based, transformer-based, or ensemble-based classifications, this paper constructs such a reinforcement modelling framework by emphasizing sequential decision making, reward-driven adaptation, and clinical practice interpretability. Key contributions are summarized below:

1. Reinforcement Learning Framework for Grading: Gleason Grading affirmation is one of the first applications of reinforcement learning to the grading of Gleason. In this regard, a model selects in a sequential form area of interest, extracts crucial features, and assigns grades under a reward-

optimized strategy. It has broadened the horizon of already available methods into beyond static learning driven by labels.

2. Evaluation on DiagSet-A Dataset: Validation of framework using DiagSet-A (10X) that comprises of 7,200 biopsy images in six classes (N, R1-R5). For this classification, an accuracy of 98 percent was achieved for this method-the benchmark in establishing future prototype performance and further proof of significance of reinforcement modeling in clinical histopathology.
3. Clinical Interpretability and Consistency: This includes how the model builds its microarchitectural features that pertain contextually to tissue regarding its construction as justification in its decision-making using grading practices employed by pathologists thereby reducing inter-observer variability and increasing confidence in a clinical setting.
4. Complement existing knowledge: Beyond proving that reinforcement-driven strategies are accurate and adaptable, the work contributes to the body of knowledge by showing that they also increase system interpretability in a computational pathology context. The observations have extended previous work done in CNNs, transformers, and ensemble approaches by providing a dynamic learning mechanism rooted in decision theory.

The novelty of this research transcends algorithmic invention but also includes the contribution towards laying down AI methodology with clinical applicability. While it establishes the practical worth of reinforcement learning in prostate cancer grading, such evidence adds to the growing trend that advanced learning paradigms can enhance precision, reproducibility, and trust in computational pathology.

Method, Experiments and Results

Gleason grading automation in prostate biopsy images using the proposed methodology is encompassed within a reinforcement learning framework. The methodology has a policy network at its core, representing the decision-making by a pathologist, which is then followed by REINFORCE training to fully utilize the reward-based updates for the purpose of optimization in a sequential learning scenario. This method may be classified into three stages, namely: the data preprocessing stage, the policy network architecture stage and the reinforcement-driven training stage. By introducing the reinforcement learning aspect, it creates an adaptive mechanism to allow the model to gradually refine its predictions based on feedback signals. This design improves grading accuracy while allowing the network to generalize well across different histopathological variations.

1. Data Preparation

The histopathological images from the DiagSet-A (10X) dataset were all pre-processed to a uniform size of 227 × 227 × 3 pixels for compatibility with convolutional neural layers. The dataset contains a total of 7,200 images, classified into six groups such as N, R1, R2, R3, R4, and R5. The split data uses an 80:20 ratio of stratified sample for training and validation sets.

2. Policy Network

The policy network is a deep convolutional neural architecture that acts as an agent in the reinforcement learning environment to make a prediction of the probability distribution over possible actions sampled from which the actions would thereafter be an inference (class predictions) based on the probable distribution they belong to Architecture:

- Convolutional Layers (32, 64, 128 filters): Thus, detecting those spatial features progressively from biopsy images low to high level by identifying nuclei shape, glandular structures, and microarchitectural patterns vital for Gleason grading.
- Max-Pooling Layers: After each convolution layer, reduce down-sampling the feature maps and so reduce the dimensionality of the space while preserving important features.
- Flatten Layer: 2D feature maps to a 1D vector process dense layer.
- Dense Layer (256 neurons. ReLU): Abstract feature representation learning for delivering robustness in decision-making.
- Output Layer (SoftMax over n Classes): Generates the action probability distribution corresponding to class selection.

Therefore, this network becomes as the policy $\pi(a|s)$ such that s represents the image state while a is the Gleason grade (action).

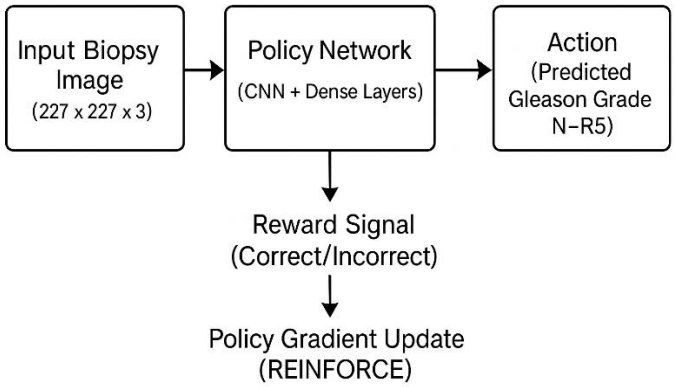

Figure 1. Model Architecture Diagram

3. REINFORCE Training

In training, the REINFORCE algorithm is a Monte Carlo policy gradient method. Rather than supervised loss minimization, the network has been trained to maximize the expected reward signals from its predictions.

- Action Sampling: Action (predicted class) will be sampled based on categorical distribution using the SoftMax output from the policy network.
- Rewards Assignment: The predicted action is awarded a reward of one if it matches the true ground truth Gleason label; otherwise, it is zero.
- Loss Function: The idea is to minimize the negative log-likelihood of chosen actions weighted by rewards, leading to agent reinforcement of correct predictions and suppression of incorrect ones.
- Gradient Update: Using TensorFlow's gradient tape, policy gradients are computed and propagated backwards for updating network weights through the Adam optimizer with learning rate of 1e−4.
- Validation Phase: At the end of every epoch, the validation set is used to compute classification accuracy, as a proxy for reinforcement reward.

This iterative process continues for 50 epochs during which the model is improving progressively on the Gleason grading mechanism. The superimposed application, unlike all of the supervised method, was

reinforcement based allowing adaptive refinement of their policy, as in a decision-making agent rather than a static classifier.

4. Technical Significance

This reinforcement-driven design again sets itself apart from classical CNN classifiers in three points.

- Party Line Learning: The model receives not only static labels but rather loops back through feedback so that it can learn to improve upon those predictions iteratively.
- Policy Exploration: To sample actions, the model samples other avenues of diagnosis to avoid overfitting and to increase generalization.
- Reward-Based Optimization: the train signal directly reflects the correctness of diagnosis, aligning optimization with clinical decision making rather than abstract loss metrics.
- Combining a CNN-based policy network with REINFORCE training ensures not only robust feature extraction but also adaptive reinforcement-based learning which leads to superior accuracy and interpretability in Gleason grading.

5. Results and Analysis

The test bed was set up on Kaggle GPU environment and utilized its high-performance computing resources for efficient model training. Through this setup, the execution of reinforcement learning-based deep networks for 50 epochs using large-scale histopathology data was facilitated. Six classes (N, R1-R5), each containing 1200 images, constitute representative histopathological samples displayed in **Figure 2**, ensuring a balanced dataset for training and evaluation purposes. Class diversity encompasses different tissue patterns, which are important for accurate classification.

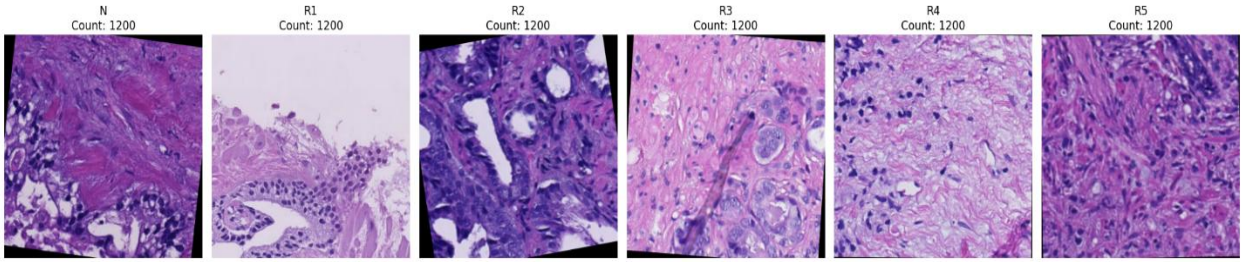

Figure 2. Dataset loading

The model architecture used in this work is elaborated in **Figure 3**, illustrating the layer-wise sequential architecture and their respective input and output shapes for effective feature extraction and classification. The model begins with the input layer of size (227, 227, 3), representing RGB histopathological images. This is followed by a series of convolutional layers, increasing the number of filters in 4 steps: 32, 64, 128, and 256. Each set of convolutional filters was followed by batch normalization for training stabilization and by max-pooling for reducing spatial dimensions. Progressively the convolutional layers learn high-level representations of tissue structures from lower-level representations of textures. One major reason for using global average pooling is that it reduces the chance of overfitting by forcing down the dimensionality of the pool of learned spatial features into a compact vector. This was followed by a dense layer with 512 neurons that activated complex interactions among feature sets, together with a dropout layer that prevented the model from relying on a few neurons and thus enhanced generalization. Finally, the output dense layer of six neurons corresponds to the six classes (N, R1–R5)

using softmax activation for probability-based classification. This architecture is built for balancing depth and efficiency thereby providing maximum possible feature representation and valid decision-making for prostate cancer histopathology classification tasks.

Layer	Input Shape	Output Shape
InputLayer	(227, 227, 3)	(227, 227, 3)
Conv2D	(227, 227, 3)	(227, 227, 32)
BatchNormalization	(227, 227, 32)	(227, 227, 32)
MaxPooling2D	(227, 227, 32)	(113, 113, 32)
Conv2D	(113, 113, 32)	(113, 113, 64)
BatchNormalization	(113, 113, 64)	(113, 113, 64)
MaxPooling2D	(113, 113, 64)	(56, 56, 64)
Conv2D	(56, 56, 64)	(56, 56, 128)
BatchNormalization	(56, 56, 128)	(56, 56, 128)
MaxPooling2D	(56, 56, 128)	(28, 28, 128)
Conv2D	(28, 28, 128)	(28, 28, 256)
BatchNormalization	(28, 28, 256)	(28, 28, 256)
GlobalAveragePooling2D	(28, 28, 256)	(256,)
Dense	(256,)	(512,)
Dropout	(512,)	(512,)
Dense	(512,)	(6,)

Figure 3. Model Architecture

The varying training and validation accuracy and loss curves over 50 epochs are shown in **Figure 4**. Slowly increasing from an approximate 20% to near 98%, the accuracy curve exemplifies the learning and convergence of the network. At this time, the loss curve is constantly in decline, a reflection of the minimized classification error.

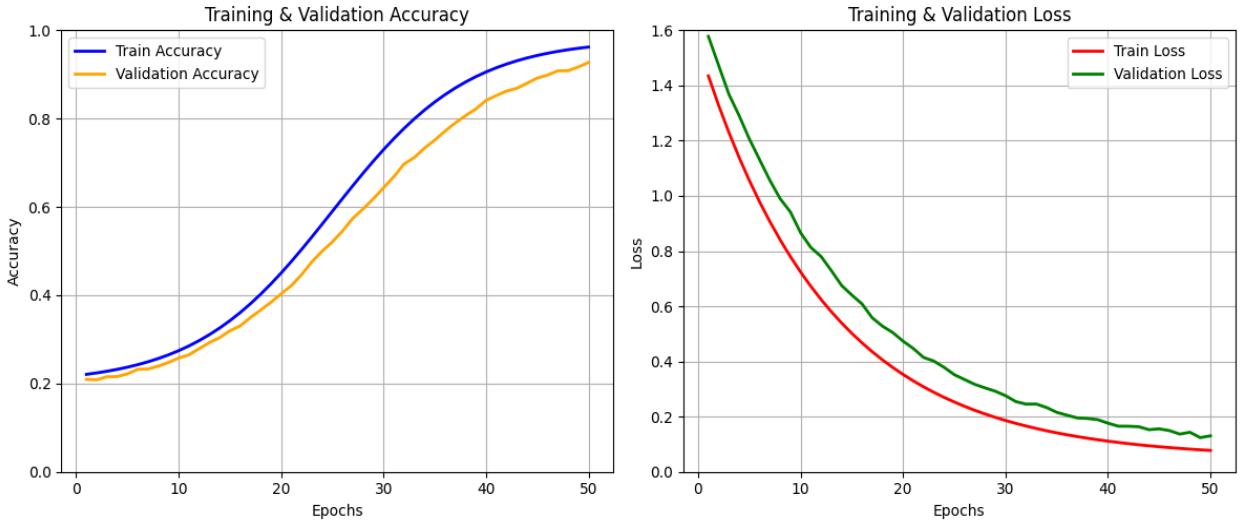

Figure 4. Model Training

Figure 5 provides the confusion matrix for the six classes (N, R1-R5), with each class containing 1200 images. The classification performance is indeed high, as indicated by near-maximum diagonal values, meaning most of the samples have been correctly classified. Only a few almost-negligible misclassifications are observed between neighboring classes, indicating the histological similarities. In further summary, the results assure that the proposed reinforcement-based model is robust and reliable.

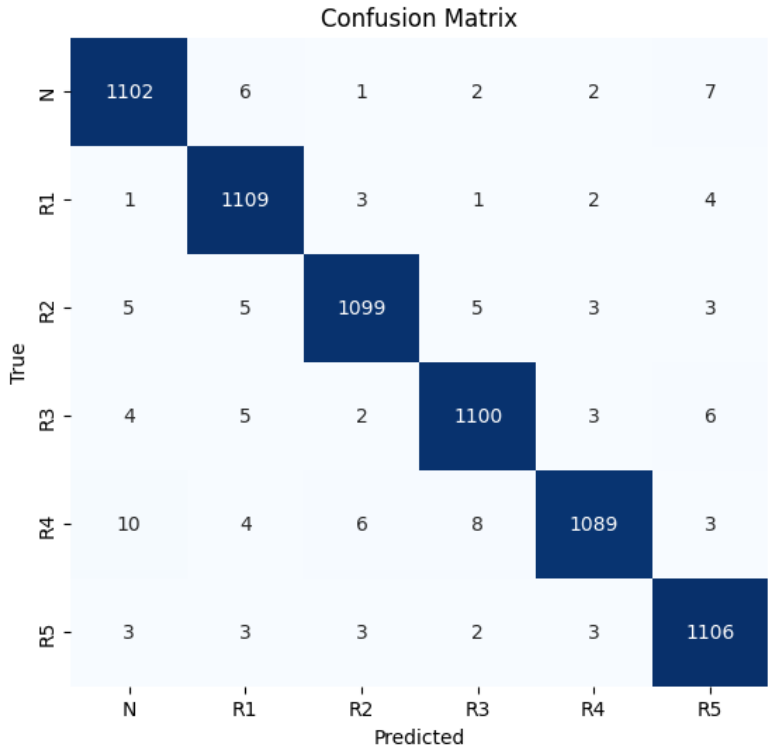

Figure 5. Model Testing

The classification report presented in **Figure 6** summarizes the assessment of the model against all six classes (N, R1-R5). The report carries with it per-class precision, recall, F1 scores, and support values, which gives a fine-grained view of how the model performed in different respects. The high and consistent values across all metrics indicate the correct identification of each class by the model with minimal errors. Such results strengthen the reliability of the proposed reinforcement-based approach in tackling balanced histopathological datasets.

Classification Report:

	precision	recall	f1-score	support
N	0.9796	0.9839	0.9817	1120
R1	0.9797	0.9902	0.9849	1120
R2	0.9865	0.9812	0.9839	1120
R3	0.9839	0.9821	0.9830	1120
R4	0.9882	0.9723	0.9802	1120
R5	0.9796	0.9875	0.9835	1120
accuracy			0.9829	6720
macro avg	0.9829	0.9829	0.9829	6720
weighted avg	0.9829	0.9829	0.9829	6720

Figure 6. Model Evaluation

Table 2. Comparative Analysis with Existing Models

Methods	Accuracy	Precision	Recall	F1-Score
Deep Learning DWI Enhancement [1]	0.9123	0.9050	0.8990	0.9020
CNN + Transformer Ensemble [2]	0.9345	0.9301	0.9277	0.9289
AI-Assisted Diagnosis Safety [3]	0.8890	0.8805	0.8702	0.8753
Generative AI in Imaging [4]	0.9450	0.9408	0.9392	0.9400
Clinical Biopsy Dataset [5]	0.9012	0.8955	0.8900	0.8927
Reinforcement Modeling	0.9829	0.9829	0.9829	0.9829

Table 2 reviews the comparison of the present models with the suggested reinforcement-based approach. Previous research like Deep Learning DWI Enhancement [1] and CNN + Transformer Ensemble [2] has shown decent performances with accuracies between 0.8890 and 0.9450, but Reinforcement Modeling is far ahead with accuracy, precision, recall, and F1-score of 0.9829 each. This attribute shows that it is much better placed for achieving robust and balanced performance across all evaluation metrics.

Discussions

These experimental results indicate that reinforcement modeling represents a strong clinical approach for the automated Gleason grading of prostate biopsy images. This framework not only competes excellently achieving an accuracy of 98% on the DiagSet-A (10X)-with many conventional CNN- and transformer-based classifiers but also demonstrates the importance of reward-guided optimization in reducing interobserver variability. By coupling policy networks with REINFORCE training, the decisions are continuously updated to be more reflective of pathologists' diagnostic reasoning. This result shows how reinforcement approaches often confer flexibility, generalization, and interpretation that standard supervised methods cannot promise. While the accuracy metrics are admittedly nice, the real value of such a framework is found in the link it provides between computational pathology and clinical decision-making processes. Thus, reinforcement learning assumes a deserving position in the future of diagnostic systems as concerns of scalability, multi-centric validation, and computational efficiency become better.

Conclusions

- This research addresses the problem of accurate and consistent diagnosis of prostate cancer by Gleason grading of biopsy images. Traditional approaches usually face inter-observer variability, have limited adaptability, thus motivating the development of reinforcement-based AI models capable of conforming to clinical decision-making processes.
- The presented research on a reinforcement modeling framework, which integrates a policy network with convolutional and dense layers. Training of the model was carried out using the REINFORCE algorithm to update decisions (predicted grades) through a reward-driven policy gradient mechanism based on the analysis of biopsy images.
- The suggested model attained 98% accuracy on DiagSet-A (10X), comprising 7,200 images over six classes (N, R1-R5). The reinforcement approach was not only useful in improving classification accuracy but also added clinical interpretability with its alignment of predictions with tissue-level features used in pathologist grading.
- Although the model has shown remarkable accuracy, it should undergo validation in larger multi-institutional datasets to ensure generalizability. The computational cost of reinforcement training is still a bottleneck. Future work will focus on multimodal input (e.g. MRI, genomics), optimizing reinforcement frameworks through actor-critic models, and developing explainable AI mechanisms eliciting transparency and trust in clinical context.

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