# PreVisRE: Novel computational pipeline leveraging integration of AI vision and reasoning models for precision cervical cancer screening and diagnosis in low-resource settings

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## Abstract

PreVisRE is a computational pipeline integrating AI-driven vision and reasoning models to enhance cervical cancer screening and diagnosis in low-resource settings. The pipeline processes Hematoxylin and Eosin (H&E) stained images to evaluate staining intensity, cellular patterns, and malignancy indicators. Optional preprocessing steps, such as noise reduction and color normalization, are incorporated to optimize image quality and ensure accuracy. PreVisRE delivers a versatile solution for histopathological analysis, paving the way for scalable applications in resource-constrained environments.

## Introduction

Cervical cancer remains a major global health challenge, particularly in resource-limited settings where access to trained pathologists is scarce. Screening often relies on protocols with high false positive rates, leading to unnecessary treatments that burden patients physically, psychologically, and financially. Current AI technologies focus on liquid-based cytology or colposcopy applications, leaving histopathology underutilized.

PreVisRE addresses this gap by employing AI vision and reasoning models for cervical cancer histopathology. By leveraging advanced computational tools, including LangGraph for LLM model orchestration, PreVisRE shifts diagnostic responsibility to AI, reducing false positives and overtreatment. This study highlights the pipeline's potential in accurately predicting malignancy, providing a scalable solution for automated analysis.

## Methodology

This study utilizes PreVisRE for automated image analysis through the integration of AI vision and reasoning models to assist in cervical cancer diagnosis. The pipeline processes Hematoxylin and Eosin (H&E) stained images, examining staining intensity, distribution, cellular patterns, and malignancy indicators.

## Methodology

PreVisRE optionally includes preprocessing steps, such as noise reduction and color normalization, to enhance image quality.

The vision analysis employs the Llama 3.2 Vision model for detailed evaluation of tissue morphology and structure. To improve detection accuracy, optional reasoning models like Deepseek-r1 or Llama 3 can be integrated. The pipeline leverages LangGraph, a multi-agent framework, for orchestrating interactions between the large language models (LLMs), ensuring efficient communication and seamless coordination among the models. Implemented in Python, the pipeline also incorporates OpenCV and scikit-image packages, making it adaptable and effective for diverse datasets.

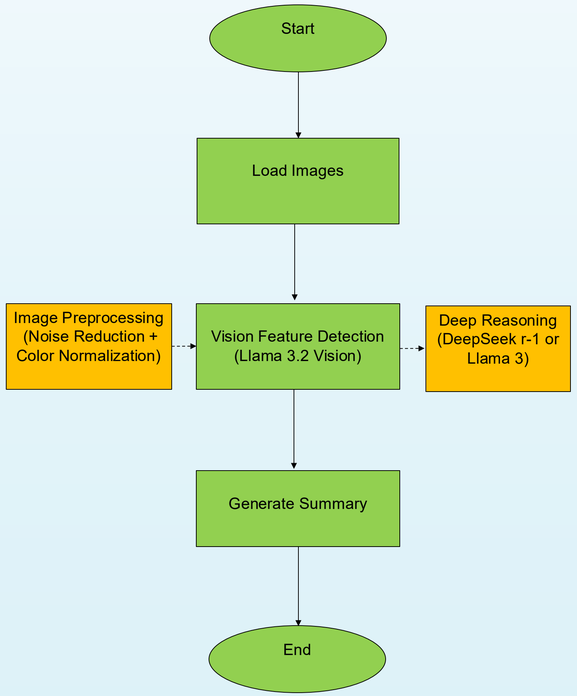
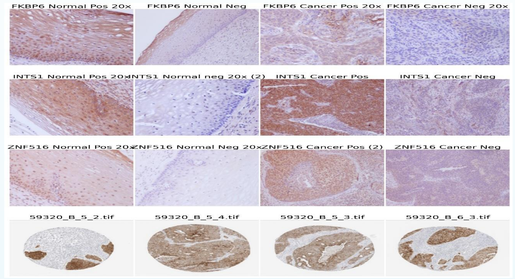



**Figure 1.** PreVisRE for automated image analysis through the integration of AI vision and reasoning models to assist in cervical cancer diagnosis

## Results

PreVisRe was tested on 71 samples: 24 normal cervical mucosa and 47 cervical carcinoma tissue mounted on tissue microarrays (**Figure 2**) stained to identify expression of four proteins: ZNF516; INTS1; FKBP6; and GGTLA4 (**Figure 3**) .

**Figure 2.** Representative image sample set



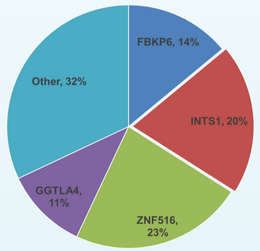




**Figure 3.** Protein marker distribution: ZNF516 (23%); INTS1 20%; FKBP6 (14%); GGTLA4 (11%); Other (32%)

**Table 1.** Accuracy, precision and recall percentages using using vision model pipeline configuration without optional steps.

| Protein | Accuracy | Precision | Recall |
|---|---|---|---|
| FKBP6 | 100% | 100% | 100% |
| INTS1 | 100% | 100% | 100% |
| ZNF516 | 88% | 100% | 75% |
| GGTLA4 | 100% | 100% | 100% |
| Other | 100% | 100% | 100% |
| Total | 97% | 100% | 96% |

Analysis yielded overall accuracy of (97%), precision (100%) and recall (96%) using vision model pipeline configuration without optional steps (**Table 1**). Pipelines containing preprocessing and reasoning steps yielded similar results. Pipelines using image preprocessing required fine tuning color normalization parameters. ZNF516 performance improved slightly using image preprocessing vs. raw images.

## Conclusion

This study focused on predicting cervical tissue malignancy. PreVisRE shifts analytical responsibility to the vision model, offering a model-driven framework for cervical cancer histopathology. This methodology warrants further testing in larger cohorts that include pre-malignant lesions. The processing pipeline does an outstanding job in identifying malignancy features and predicting malignancy diagnosis with high accuracy, precision, and recall. Our results warrant further testing in larger cohorts that include pre-malignant lesions. Further research is needed to determine optimum pipeline configuration to infer protein expression levels. This might require better leveraging of image preprocessing techniques. Additional testing is also recommended with other vision models.

## References

## Acknowledgements

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