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Research Article

Performance Evaluation of YOLOv10 and YOLOv11 on Blood Cell Object Detection Dataset

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Abstract:
Background of study: Blood cell analysis is vital for diagnosing medical conditions, but traditional manual methods are laborious and error-prone. Deep learning, especially YOLO models, offers automated solutions for medical image analysis. However, the real-world effectiveness of the latest YOLOv11 in blood cell detection is not thoroughly investigated, as general object detection improvements may not translate to biomedical images due to their unique characteristics.
Aims and scope of paper: This study systematically compares YOLOv10 and YOLOv11 on a public blood cell detection dataset to assess if YOLOv11's advancements provide tangible benefits for blood cell classification. The goal is to identify the most effective model for accurate and efficient detection in microscopic images, guiding AI-driven diagnostic tool selection.
Methods Both models were trained and tested under identical conditions using the Kaggle Blood Cell Detection Dataset (RBCs, WBCs, Platelets). Images were resized to 640x640 pixels. Performance metrics included mAP (mAP@50 and mAP@50–95), Precision, Recall, F1-score, speed, model complexity, and training time.
Result: YOLOv11n consistently showed higher accuracy (mAP50: 0.9279 vs. 0.9120; mAP50-95: 0.6524 vs. 0.6347), particularly for RBCs and WBCs. However, YOLOv11n had longer inference (11.35 ms/image) and postprocessing times (8.64 ms/image) compared to YOLOv10n (7.00 ms/image and 0.90 ms/image). YOLOv11n trained faster (0.311 hours vs. 0.375 hours), with a smaller model size (5.5 MB vs. 5.8 MB), fewer parameters, and reduced computational complexity.
Conclusion: YOLOv11n offers superior accuracy and improved training efficiency, making it suitable for medical image object detection where precision is paramount. The increased inference and postprocessing times indicate a performance-speed trade-off. Model selection should balance these factors based on deployment context.

Keywords: Blood Cell Detection, Mean Average Precision, Medical Imaging, Object Detection.

1. INTRODUCTION

Blood cell analysis plays a fundamental role in the early detection and diagnosis of various medical conditions, including infections, anaemia, and haematological malignancies such as leukaemia (Sankar & Villa, 2021). Traditionally, this process involves manually examining stained blood smears under a microscope, where trained professionals identify and classify different types of blood cells. While well-established, this method is labour-intensive, time-consuming, and prone to human error and observer variability. These limitations highlight the urgent need for more efficient, consistent, and scalable solutions to assist or replace manual inspection, especially in high-throughput clinical environments and regions with limited access to expert haematologists (Han et al., 2025).

In recent years, medical image analysis has significantly shifted toward automation, powered by deep learning and computer vision advances (Elyan et al., 2022). In particular, object detection models have become critical tools for tasks that require identifying and localizing specific components within complex images, such as detecting various blood cell types (Fanous et al., 2022).

Among these models, the YOLO (You Only Look Once) series has gained considerable attention for real-time applications due to its remarkable speed and accuracy (Sapkota et al., 2025). Earlier versions, such as YOLOv3 and YOLOv4, were widely adopted in biomedical imaging due to their reasonable trade-off between performance and computational cost (Sembiring et al., 2024). Recent iterations, including YOLOv5 through YOLOv10, introduced architectural improvements such as CSPDarknet and PANet, alongside enhanced training techniques like auto-learning bounding box anchors and label smoothing.

These advancements have continually pushed the boundary of real-time object detection capabilities (Tanzib Hosain et al., 2024) (Ali & Zhang, 2024).

Ultralytics' YOLOv11, released in September 2024, represents the YOLO family's latest and most advanced version. This model is considered a significant leap forward due to its comprehensive integration of state-of-the-art computer vision techniques (Khanam et al., 2025). It incorporates several architectural and training improvements over its predecessor, YOLOv10, including adaptive feature fusion, which intelligently combines features from different layers to enhance object representation; refined loss functions that more accurately penalize prediction errors; better attention mechanisms that allow the model to focus on more relevant parts of the image; and model pruning techniques that reduce model complexity without sacrificing performance, thereby enhancing both precision and inference speed (Jegham et al., 2025) (Gao et al., 2025). However, while YOLOv11 has shown promising results on standard benchmarks such as COCO and PASCAL VOC, its real-world efficacy in specialized domains, particularly biomedical image analysis, has not been thoroughly investigated.

A review of existing literature reveals that although numerous studies apply YOLO-based models to medical imaging, including cell detection, cancer classification, and organ segmentation, very few have systematically compared successive YOLO versions on the same biomedical dataset (Ragab et al., 2024) (Debsarkar et al., 2025). Moreover, even fewer studies have focused explicitly on blood cell detection using the most recent YOLO models. Given that blood cell images differ substantially from natural scene images in texture, scale, and contrast, improvements in general-purpose object detection benchmarks are not guaranteed to translate into meaningful gains in this specific medical context (Li et al., 2023). This emphasis on the lack of systematic comparison between the latest versions of YOLO on biomedical datasets is a strong justification for this study.

Therefore, this study proposes a comparative evaluation of YOLOv10 and YOLOv11 on a publicly available blood cell detection dataset. The main objective is to determine whether the architectural improvements and training enhancements introduced in YOLOv11 offer tangible benefits for detecting and classifying blood cells. Both models are trained and tested under identical experimental conditions, using consistent hyperparameters, data preprocessing techniques, and evaluation metrics. Performance is measured using key indicators such as mean Average Precision (mAP), Precision, Recall, and F1-score, which are widely accepted in computer vision and medical imaging communities (Müller et al., 2022).

The rationale for comparing YOLOv10 and YOLOv11 lies in the need to validate whether the generational improvements in YOLOv11 contribute significantly to medical imaging performance, particularly for applications where diagnostic accuracy is paramount. This comparison is not only academically important but also practically valuable for healthcare institutions considering the deployment of AI-driven diagnostic tools (Maleki Varnosfaderani & Forouzanfar, 2024). By establishing a benchmark on blood cell imagery, the findings of this study can guide practitioners in selecting the most suitable YOLO model for clinical applications and inform further research on domain-specific fine-tuning and hybrid model designs. Ultimately, the insights from this study are expected to advance the field of medical image analysis by demonstrating the applicability of state-of-the-art object detection models in hematology and by offering concrete evidence on the trade-offs between speed and accuracy in real-world diagnostic scenarios.

2. MATERIAL AND METHOD

Data Collection

For this study, we utilized the Blood Cell Detection Dataset, publicly available on Kaggle (https://www.kaggle.com/datasets/adhoppin/blood-cell-detection-datatset). This comprehensive dataset comprises labeled microscopic images of human blood cells, meticulously categorized into three primary classes: Red Blood Cells (RBCs), White Blood Cells (WBCs), and Platelets. Each image in the dataset is accompanied by a corresponding annotation file, which provides precise bounding box coordinates for each identified object along with its respective class label (RBC, WBC, or Platelet).

The dataset is specifically designed to simulate the variability seen in real-world diagnostic conditions, making it highly suitable for robust model training. This inherent variability encompasses several key aspects, including diverse cell shapes and sizes, which naturally occur due to biological differences and preparation methods. Furthermore, the dataset accounts for varying cell distributions, mimicking both sparse and dense areas of blood smears. Crucially, it incorporates images with different lighting conditions, varying stain intensities, and the presence of common artifacts or noise often encountered in clinical microscopy. This deliberate inclusion of diverse conditions helps in training models that are more resilient and generalizable to practical clinical scenarios.

To ensure consistency and compatibility with the YOLO model architecture, all images were uniformly resized to a resolution of 640x640 pixels. This standardized resolution is a common and recommended practice for YOLO-based models, optimizing both processing efficiency and model performance. Figure 1 visually represents example images from the Blood Cell Detection Dataset used in these experiments.

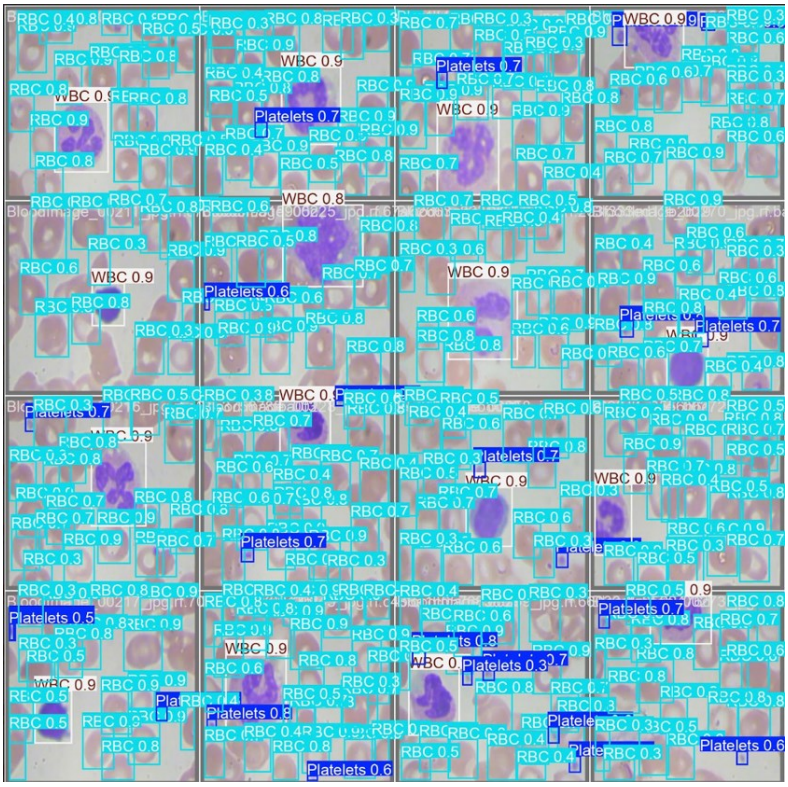

Figure 1. Sample of Blood Cell images 640x640 pixels

Model Selection

This study compared two YOLO object detection model versions, YOLOv10 and YOLOv11. YOLOv10 is a well-established version known for balancing speed and accuracy, making it a popular choice for real-time object detection tasks (Wang et al., 2025). It combines convolutional layers and anchors to predict bounding boxes and class labels. On the other hand, YOLOv11 introduces significant improvements in both model efficiency and detection accuracy (Luo et al., 2025).

YOLOv11 integrates several new architectural enhancements, including improved backbone networks and optimisation techniques, allowing it to perform better on small and large object detection tasks. Given that YOLOv11 is the latest iteration, it was selected to evaluate whether the architectural advancements in this version translate into better performance on the blood cell detection task compared to YOLOv10. Both models were chosen based on their proven capabilities in object detection tasks and their relevance to real-time applications in medical imaging. The comparison aims to identify the most effective model for accurate and efficient blood cell detection in microscopic images. Figure 2 shows the Key architectural modules in YOLOv11.

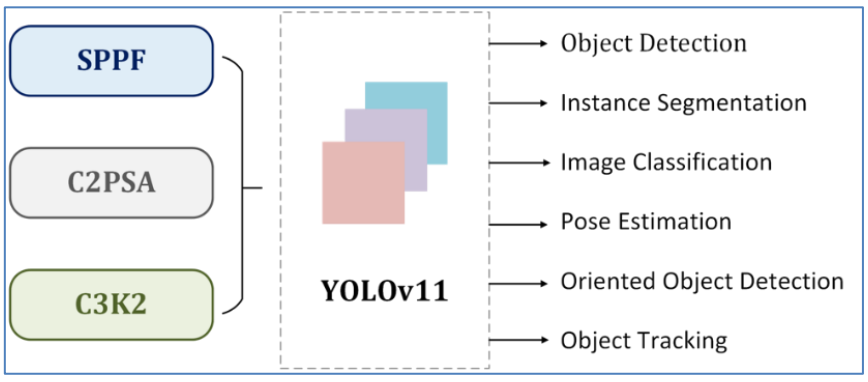

Figure 2. Key architectural modules in YOLOv11(Khanam & Hussain, 2024)

Figure 2 illustrates key architectural modules within YOLOv11. Modules such as SPPF, C2PSA, and C3K2 are components designed to enhance YOLOv11's ability to extract features from images, integrate information across various scales, and focus attention on relevant regions, ultimately contributing to improved object detection accuracy and efficiency (Sorour et al., 2025). In essence, these modules are the refinements behind YOLOv11's superior performance.

Training and Evaluation

The training process for both YOLOv10 and YOLOv11 was carried out using the Kaggle environment, with the models being trained on the Blood Cell Detection Dataset. The training was performed over 100 epochs with a batch size and image size set to 640×640 pixels, the standard input size for YOLO models. The models were trained using the PyTorch framework integrated with the Ultralytics implementation of YOLO. During training, both models utilised a single GPU for accelerated processing.

This study employs four widely recognised evaluation metrics to objectively assess and compare the performance of YOLOv10 and YOLOv11 in detecting and classifying blood cells: mean Average Precision (mAP), Precision, Recall, and F1-score. These metrics are essential in determining the effectiveness of object detection models, particularly in high-stakes domains like medical imaging, where both false positives and false negatives carry profound implications. Additionally, the speed comparison processing, model complexity, and training comparison are compared and discussed.

1. Mean Average Precision (mAP) is a critical evaluation metric in object detection tasks because it considers the predicted bounding boxes' classification accuracy and localisation quality (Vo & Jo, 2022). In blood cell detection, mAP helps assess how well the model can identify and precisely locate the correct cell type within the image. Two common variants of mAP used in modern object detection benchmarks are mAP@50 and mAP@50–95, and both are employed in this study to give a comprehensive performance assessment:
    a. mAP@50 (or mAP50): This metric calculates the mean Average Precision at an Intersection over Union (IoU) threshold of 0.50. IoU measures the overlap between the predicted bounding box and the ground truth box. A prediction is correct if its IoU with the ground truth is greater than or equal to 50%. mAP@50 is a relatively lenient metric that helps evaluate whether the model detects objects approximately in the correct location. In biomedical imaging, mAP@50 can indicate the model's basic capability to identify and roughly localise cells.
    b. mAP@50–95 (or mAP50–95): This is a more stringent and comprehensive metric. It averages the mAP scores across multiple IoU thresholds, ranging from 0.50 to 0.95 in steps of 0.05 (i.e., 0.50, 0.55, ..., 0.95). This metric penalises the model for minor localisation errors and better reflects real-world precision. A higher mAP@50–95 indicates that the model identifies cells correctly and places bounding boxes with high spatial accuracy. In clinical applications, where precise measurements of cell morphology might be needed for diagnosis, mAP@50 95 is a more relevant indicator of model reliability.
2. Precision: Precision measures the proportion of true positive detections out of all optimistic predictions made by the model. In other words, it answers the question: Of all the cells the model said were, for instance, neutrophils, how many were neutrophils? High precision is critical in medical diagnostics, where false positives (e.g., incorrectly identifying a healthy cell as abnormal) can lead to unnecessary follow-up procedures, anxiety, or misdiagnosis.
3. Recall: Recall measures the proportion of true positives detected out of all positive instances in the dataset. It reflects the model's ability to detect all relevant instances of a given class. In blood cell detection, a high recall score ensures that the model does not miss any critical cell types, such as abnormal or rare cells that may indicate severe medical conditions like leukaemia. Low recall would imply the model fails to identify significant portions of target cells, potentially overlooking key diagnostic indicators.
4. F1-Score: The F1-score is the harmonic mean of Precision and Recall, providing a single metric that balances the trade-off between them. This is especially useful in imbalanced datasets, where one class (e.g., normal red blood cells) may dominate, and simply achieving high precision or high recall alone is insufficient. The F1-score ensures that both over-detection and under-detection are penalised, promoting a more reliable performance measure in complex biomedical scenarios.

Using these four metrics, the study can evaluate each YOLO model's ability to detect and classify blood cells. The comparative analysis will highlight the absolute performance of YOLOv10 and YOLOv11 and reveal their strengths and weaknesses under identical experimental conditions. This level of detailed metric analysis is critical to ensure that any observed performance improvement in YOLOv11 is statistically significant and clinically meaningful.

3. RESULT AND DISCUSSION

3.1 Results

The performance of the BERT and LSTM models for sentiment analysis of hotel reviews, without applying under-sampling to address class imbalance, is as follows.

Both models were thoroughly evaluated based on several key performance metrics: precision, recall, F1-score, and overall accuracy. Table 1 and Figure 3 show the performance comparison results of the approaches.

Table 1. Performance Comparison Approaches

Approaches	Class	Precision	Recall	mAP50	mAP50-95
YOLOv10n	Platelets	0.813	0.829	0.874	0.469
	RBC	0.737	0.862	0.874	0.619
	WBC	0.959	0.980	0.988	0.816
YOLOv11n	Platelets	0.781	0.846	0.896	0.518
	RBC	0.787	0.853	0.903	0.653
	WBC	0.973	0.989	0.983	0.787

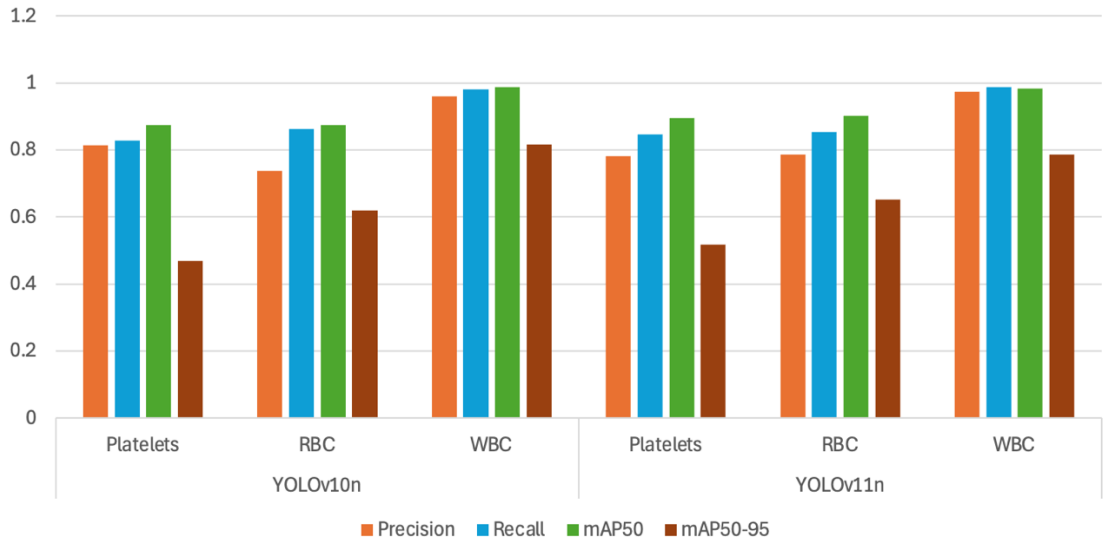

Figure 3. Performance Comparison Approaches in Graphs

Table 1 and Figure 3 show that the study has great promise for automated blood cell detection in medical imaging tasks. YOLOv11's enhanced accuracy makes it an ideal choice for medical diagnostics where high precision is required, especially for smaller cell types like Platelets. However, YOLOv10 offers a faster inference speed, making it suitable for real-time applications where speed is a priority, such as automated blood sample analysis during medical procedures.

Table 2 and Figure 4 show the Comparison of speech between YOLOv10 and YOLOv11.

Table 2. Speed Comparison Between YOLOv10 and YOLOv11

Approaches	Preprocessing	Inference	Postprocessing
YOLOv10n (Ms/image)	4.27	7.00	0.90
YOLOv11n (Ms/image)	4.18	11.35	8.64

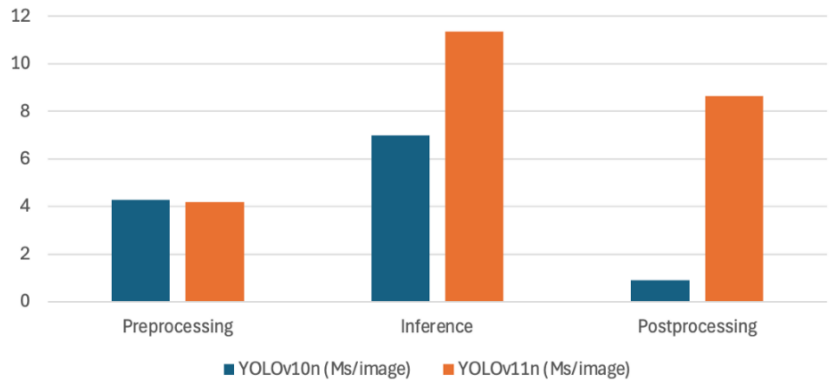

Figure 4. Speed Comparison Between YOLOv10 and YOLOv11

Regarding computational efficiency, Table 2 and Figure 4 illustrate the time taken per image during the preprocessing, inference, and postprocessing stages for YOLOv10 and YOLOv11. The preprocessing times are relatively comparable, with YOLOv10 requiring 4.27 Ms/image and YOLOv11 slightly faster at 4.18

ms/image. However, a significant difference is observed in the inference and postprocessing stages.

YOLOv10 demonstrates faster inference with 7.00 ms per image than YOLOv11, which requires 11.35 ms per image. This suggests that YOLOv10 is more efficient in generating predictions. Furthermore, the postprocessing stage of YOLOv11 takes considerably longer at 8.64 ms/image, whereas YOLOv10 completes it in just 0.90 ms/image. The longer postprocessing time in YOLOv11 may be attributed to its more advanced architecture or additional refinement steps introduced in the newer model.

Despite the increased latency, YOLOv11 offers superior accuracy metrics, which may justify the trade-off in applications prioritising precision over speed. YOLOv10 might be a more practical option for real-time or resource-constrained scenarios.

Table 3. Model Complexity and Training Comparison

Approaches	Training Time	Model Size (.pt)	Parameters	FLPOs	No of Layer
YOLOv10n	0.375 hour (~22,5 min)	5.8 MB	2,695,586	8.2	125
YOLOv11n	0.311 hour (~18.7 min)	5.5 MB	2,582,737	6.3	100

Table 3 summarises the training and architectural characteristics of the YOLOv10n and YOLOv11n models. YOLOv11n completed training faster, requiring only 0.311 hours (approximately 18.7 minutes) for 100 epochs, while YOLOv10n took 0.375 hours (approximately 22.5 minutes) under identical conditions on a Tesla P100 GPU.

Both versions are lightweight in terms of model size, with YOLOv11n slightly smaller at 5.5 MB compared to YOLOv10n's 5.8 MB. YOLOv10n has a marginally higher number of parameters (2.69M vs. 2.58M) and computational complexity (8.2 GFLOPs vs. 6.3 GFLOPs), which may explain its slightly longer training time and lower inference speed.

Interestingly, despite YOLOv11n having fewer layers (100 vs. 125), it still outperforms YOLOv10n in training speed and accuracy, suggesting an architectural efficiency improvement in the newer version.

3.2 Discussion

The comparative analysis between YOLOv10n and YOLOv11n reveals notable differences in accuracy, speed, and computational efficiency when applied to the blood cell detection dataset. YOLOv11n consistently outperformed YOLOv10n in accuracy-related metrics, achieving a higher mAP50 (0.9279 vs. 0.9120) and mAP50-95 (0.6524 vs. 0.6347), indicating improved detection performance across all classes of blood cells. This gain is particularly evident in detecting RBCs and WBCs, where YOLOv11n exhibited more balanced precision and recall values than its predecessor.

Despite its superior accuracy, YOLOv11n introduces a trade-off regarding inference and postprocessing time. Specifically, YOLOv11n took 11.35 Ms/image for inference and 8.64 Ms/image for postprocessing, significantly higher than YOLOv10n's 7.00 Ms and 0.90 Ms, respectively. These results suggest that while YOLOv11n brings architectural improvements that enhance accuracy, they come at the cost of increased latency, which may impact real-time deployment scenarios.

From a training perspective, YOLOv11n demonstrated better efficiency, completing 100 epochs in approximately 18.7 minutes compared to YOLOv10n's 22.5 minutes. Furthermore, YOLOv11n maintained a lower model size (5.5 MB vs. 5.8 MB) and reduced computational complexity (6.3 GFLOPs vs. 8.2 GFLOPs), indicating an optimised architectural design despite having fewer layers (100 vs. 125). These factors contribute to YOLOv11n's suitability for deployment in resource-constrained environments where performance and model size are critical.

Overall, YOLOv11n offers a strong balance between detection performance and model compactness, making it an effective model for medical image analysis tasks such as blood cell detection. However, YOLOv10n may still be preferred for time-sensitive applications requiring low latency due to its faster inference and postprocessing speeds. The choice between the two models should, therefore, consider the specific requirements of the deployment environment.

3.2.1 Implications

The findings of this comparative study between YOLOv10n and YOLOv11n have significant implications for the field of medical image analysis, particularly in automated blood cell detection. YOLOv11n's superior accuracy, evidenced by higher mAP50 and mAP50-95 scores, positions it as a highly suitable model for medical diagnostics where precision is paramount, especially for subtle or smaller cell types like platelets. While YOLOv11n offers enhanced accuracy and better training efficiency with a more compact model size, its increased inference and postprocessing times suggest a trade-off between performance and speed. This implies that the choice between the two models should be carefully considered based on the specific requirements of the deployment environment, balancing the need for high accuracy in diagnostic applications against the demand for real-time processing in other scenarios.

3.2.2 Research contribution

This study makes a significant research contribution by systematically comparing the performance of YOLOv10 and the latest YOLOv11 on a publicly available blood cell detection dataset under identical experimental conditions. It specifically addresses a gap in existing literature, as very few studies have thoroughly investigated the real-world efficacy of the most recent YOLO models in specialized biomedical domains, especially concerning blood cell detection. By evaluating both models using widely accepted metrics such as mAP, Precision, Recall, and F1-score, and also analyzing speed, model complexity, and training comparisons, this research provides concrete evidence on the trade-offs between speed and accuracy for these state-of-the-art object detection models in a critical medical context. The established benchmark for blood cell imagery can guide practitioners in selecting the most suitable YOLO model for clinical applications and inform future research on domain-specific fine-tuning and hybrid model designs.

3.2.3 Limitations

While this study provides valuable insights into the performance of YOLOv10n and YOLOv11n for blood cell detection, it does have certain limitations. The evaluation was conducted on a single, publicly available blood cell detection dataset. Although this dataset is designed to simulate real-world variability, the generalizability of the findings to other diverse clinical datasets, potentially with different imaging conditions, cell types, or pathologies, might require further validation. The training was also performed using a single GPU, which, while accelerating processing, might not reflect the performance in highly parallelized or distributed computing environments. Furthermore, the study focused on a specific set of hyperparameters; exploring a broader range of hyperparameter configurations could potentially yield different performance characteristics for both models.

3.2.4 Suggestions

Future research could explore several avenues to build upon the findings of this study. One suggestion is to evaluate YOLOv10n and YOLOv11n on a more diverse and larger collection of blood cell image datasets, including those with rare cell types or specific pathological conditions, to further assess their robustness and generalizability in varied clinical scenarios. Investigating the impact of different hyperparameter tuning strategies and data augmentation techniques on the performance of both models could also provide valuable insights. Additionally, exploring hybrid model designs that combine the strengths of YOLOv11n's accuracy with YOLOv10n's faster inference speed could lead to more optimized solutions for real-time diagnostic applications where both precision and low latency are crucial. Finally, further research could delve into the interpretability of the models' predictions, which is essential for building trust and facilitating the adoption of AI-driven tools in critical medical diagnostics.

4. CONCLUSION

This study conducted a performance evaluation of two object detection models, YOLOv10n and the latest YOLOv11n, on a blood cell detection dataset. The results demonstrated that YOLOv11n outperforms YOLOv10n in detection accuracy, achieving higher values across key evaluation metrics such as mAP50 and mAP50-95. YOLOv11n also showed improved model efficiency, with fewer parameters, reduced FLOPs, and a slightly smaller file size.

Regarding training performance, YOLOv11n completed the training process more quickly than YOLOv10n, suggesting architectural optimisations in the newer model. However, the increased inference and postprocessing times of YOLOv11n indicate a trade-off between detection performance and speed, which may impact its applicability in real-time systems.

YOLOv11n is a competent model for medical image object detection tasks like blood cell identification, especially where accuracy is prioritised. Nevertheless, the selection between YOLOv10n and YOLOv11n should consider the specific demands of the deployment context, particularly in balancing inference speed and model performance.

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6. AUTHOR CONTRIBUTION STATEMENT

NB, RH, and F conceived and designed the study. NB and RH performed the experiments and data analysis. All authors contributed to the interpretation of results. NB wrote the initial draft of the manuscript. RH and F reviewed and edited the manuscript. All authors approved the final version of the manuscript.

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