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Automatic Medical Generated Analysis Based on Histopathology Image Segmentation Half UNet

Veraldo Novaren[1], Elguerch Badr[2], Ait Ameur Youssef[2], Paramaputra Rafi Zahran[3]
Artificial Intelligence, Nanjing University of Information Science and Technology, China

Abstract: ***This study reviews and benchmarks SAM2, YOLOv8, UNet, and Half UNet for histopathology image segmentation, integrating outputs with biomedical language models like BioGPT, BioBERT, and DeepSeek VL to generate diagnostic reports. Experiments on the TCGA dataset show that Half UNet offers efficient, accurate segmentation, while SAM2 excels in few-shot settings. Combining segmentation with language models enhances interpretability and automation, improving workflow efficiency and diagnostic accuracy. However, challenges remain in generalizing across tissue types and staining methods. Overall, the integrated approach marks significant progress toward fully automated histopathology analysis.***
Keywords*: histopathology, segmentation, UNet, LLM, medical analysis.*

I. INTRODUCTION

Artificial intelligence (AI) is revolutionizing histopathology by enabling detailed, automated analysis of complex tissue structures, addressing the limitations of traditional, labour-intensive methods. This thesis proposes an end-to-end framework that combines state-of-the-art segmentation models (SAM2, YOLOv8, UNet, Half UNet) with advanced biomedical language models (BioBERT, BioGPT, DeepSeek VL) to analyse and interpret histopathological images. Using datasets like TCGA and PanNuke, the system enhances efficiency, interpretability, and diagnostic accuracy, tackling challenges such as domain adaptability and annotation dependence, and advancing AI-driven automation in pathology.

AI in histopathology faces critical challenges: poor generalization across tissues and stains, high annotation dependency, computational demands of whole-slide images, stain variability, and multi-resolution analysis needs. Supervised models struggle with rare patterns and subtle morphological changes, while multimodal integration (genomic, radiological data) remains technically complex. Additionally, bridging the gap between technical outputs and clinically actionable insights-through interpretability and seamless workflow integration-is essential for real-world adoption. Addressing these issues requires robust, adaptive solutions that balance automation with pathologist collaboration, ensuring reliability across diverse clinical settings.

This study aims to advance automated histopathological image analysis by integrating efficient segmentation models-particularly Half UNet-with cutting-edge biomedical language models like BioGPT, BioBERT, and DeepSeek VL. The objectives are to benchmark segmentation algorithms (SAM2, YOLOv8, UNet, Half UNet) for accuracy and efficiency, assess their generalizability across tissue types using datasets like TCGA, and enhance diagnostic workflows by generating interpretable, clinically relevant reports. The research also explores multimodal integration, linking visual features with textual and molecular data, to improve interpretability and support the clinical translation of AI-driven pathology solutions.

II. GENERAL ARCHITECTURE

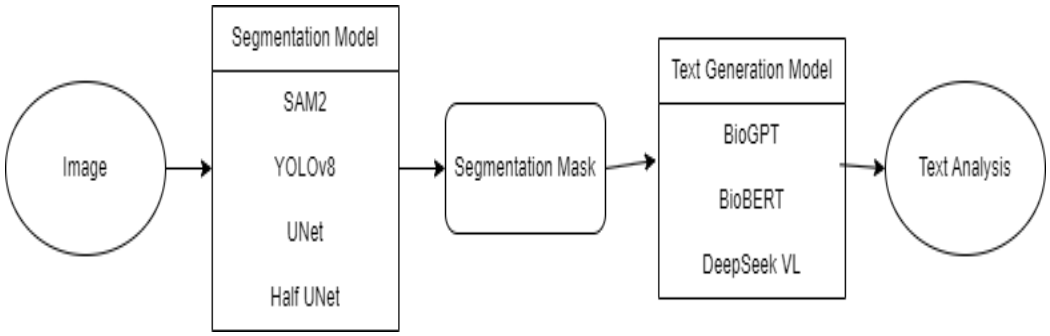


Fig. 1 General Architecture

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The general architecture integrates modular segmentation models (SAM2 for generalization, YOLOv8 for speed, UNet/Half UNet for efficiency) with biomedical language models (BioGPT, BioBERT, DeepSeek VL) to automate histopathology analysis. Segmentation masks from models trained on datasets like TCGA isolate critical tissue structures, which language models then translate into diagnostic reports using domain-specific knowledge. The modular design allows independent optimization of segmentation and text-generation components, balancing computational efficiency with clinical accuracy. This framework bridges visual data and interpretable textual insights, streamlining workflows, reducing manual effort, and enhancing diagnostic precision in pathology.

III.METHODOLOGY

A. U-Net CNN

The figure illustrates the U-Net architecture for biomedical image segmentation, featuring a U-shaped design with a contracting path (encoder) and an expanding path (decoder). The encoder reduces spatial dimensions while increasing feature depth, capturing context through convolution and pooling layers. At the bottleneck, the deepest features are extracted. The decoder then up samples these features, restoring spatial resolution. Skip connections link encoder and decoder layers, preserving fine details for precise segmentation. A final 1×1 convolution produces the binary segmentation mask. This architecture effectively balances localization accuracy and contextual understanding, making it ideal for detailed biomedical image analysis.

B. YOLOv8

This is the YOLOv8 segmentation architecture that comprises of 3 broad components: Backbone, Feature Pyramid Network (FPN) and Head. Backbone learns multi-scale features from the input image, and FPN fuses these to get both spatial and semantic information parts. The Head will take these fused features to classify object classes, predict two dimensional bounding boxes and pixel-level segmentation masks. YOLOv8 uses cross-entropy and L1 losses, therefore it is super-fast accurate for real-time instance segmentation on a lot of computer vision stuff.

C. Segment Anything Model 2

In the figure, SAM2 is a video segmentation model that integrates spatial and temporal information. It uses an image encoder to extract frame features, a memory attention module to reference past frames, and a command encoder to process user prompts (masks, points, or boxes). The mask decoder then generates precise object masks, while a memory encoder updates the memory bank with new frames. This design enables SAM2 to efficiently and accurately segment objects over time, leveraging both visual and temporal cues for robust performance in dynamic video scenarios.

D. BioGPT

BioGPT is a generative Transformer language model specifically trained on large-scale biomedical literature to process and generate biomedical text. During training, it learns to predict and generate coherent biomedical information from prompts and source texts, enabling tasks like relation extraction, question answering, and text generation. At inference, BioGPT uses learned patterns to produce relevant outputs from prompts without explicit target labels, making it highly effective for generating fluent, domain-specific biomedical content and supporting a range of biomedical natural language processing applications.

E. BioBERT

BioBERT is a domain-specific language model based on BERT pre-trained on large biomedical text corpora, including PubMed abstracts and PMC articles. The fine-tuned pre-training task is more specific for BioBERT, enabling it to comprehend biomedical words and context that other models (generalized) could never perform better than on NER, relation extraction and question answering. BioBERT can be effortlessly adapted to different tasks due to the fewest architectural changes and consistently superior in biomedical text mining, implying it to be highly useful for the extraction and research support in Biomedical Information.

F. DeepSeek VL

DeepSeek VL, as shown in the picture, is a vision-language model. It integrates visual and textual information to provide better multimodal understanding. Its development involves three steps: The first stage uses image-text pairs to train a Vision-Language (VL) adaptor, accordingly enabling the model to align visual features with their corresponding textual representations. The second stage concentrates on joint VL pre-training, that is, the model processes interwoven vision-language sequences and pure language ones so as to improve its ability to handle multimodal inputs.

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Finally, the third stage applies supervised fine-tuning with VL chat data and pure language chat data in order to bring the model up-to-date for conversational tasks. The architecture brings together a hybrid vision encoder (e.g., SAM-B and SigLIP-L) with the DeepSeek language model. This supports a strong and consistent fusion of visual and linguistic features in such tasks as image captioning, visual question answering, and multimodal dialogue generation.

G. F1 Score, Recall, Accuracy, Precision and Loss Metrics

F1 Score, Recall, Accuracy, Precision, and Loss Metrics to holistically assess model performance, particularly in imbalanced datasets common in medical or fraud detection scenarios. Accuracy measures overall correctness by calculating the ratio of correct predictions (true positives + true negatives) to total samples. However, it becomes unreliable in class-imbalanced settings, as a model biased toward the majority class can yield deceptively high accuracy while failing to detect critical minority cases.

Precision evaluates the quality of positive predictions by measuring the proportion of true positives (TP) among all predicted positives (TP + false positives), answering: "How reliable are our positive predictions?" Recall assesses sensitivity by measuring the proportion of actual positives correctly identified (TP / (TP + false negatives)), addressing: "How many true positives did we miss?" These metrics often trade off: high precision may reduce recall, and vice versa.

The F1 Score harmonizes this trade-off via the harmonic mean of precision and recall (F1 = 2 × (Precision × Recall) / (Precision + Recall)), penalizing extreme values in either metric. This makes it ideal for applications requiring balanced performance, such as medical diagnosis, where missing true positives (low recall) or over diagnosing false positives (low precision) carry significant consequences. Loss Metrics (e.g., cross-entropy, MSE) differ fundamentally: they guide model training by quantifying prediction errors during optimization rather than evaluating final performance. While loss values indicate convergence during training, they lack interpretability for real-world performance, necessitating pairing with task-specific metrics like F1.

IV. PROPOSED SYSTEM

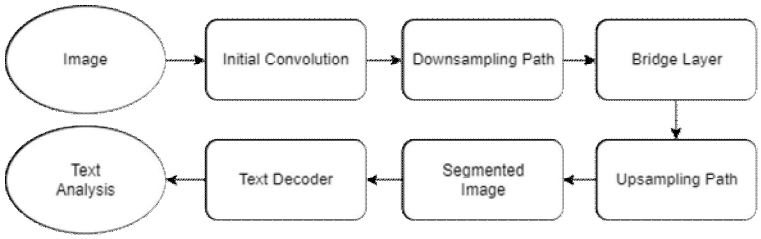


Fig. 2 Proposed System

The proposed system streamlines histopathological image analysis by integrating an optimized Half UNet segmentation model with advanced biomedical language decoders like BioGPT, BioBERT, and DeepSeek VL. The architecture uses UNet's encoder-decoder structure, but replaces the original 1024-channel layer with a 512-channel bridge to enhance computational efficiency while maintaining segmentation accuracy. After segmenting regions of interest, text decoders generate clinically relevant descriptions and classifications, translating visual data into structured diagnostic insights. This modular approach allows independent optimization of segmentation and text analysis, making it suitable for large datasets such as TCGA. The system improves workflow speed, interpretability, and diagnostic precision, offering a scalable solution for both research and clinical pathology applications.

V. RESULTS AND DISCUSSION

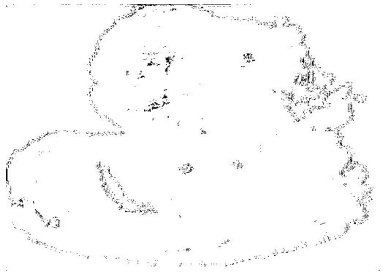


Fig. 3 Half UNet Masked

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This image of Half UNet Masked Regions trained on TCGA dataset shows how well the Half UNet can segment the histopathological slides. The model can pinpoint areas of interest, such as tumor areas, and/or regional areas with significant diagnostic correlative activities, which will be well-defined regions that are then automatically in identified and masked by the model. Using a simplified architecture, Half UNet preserves segmentation performance, but can significantly reduce computational complexity relative to the TCGA dataset that it was trained on. The masked areas could also indicate the effectiveness of the tool in interpreting complex tissue patterns in whole slides, paving the way for its use in pathology workflows and real-world clinical applications.

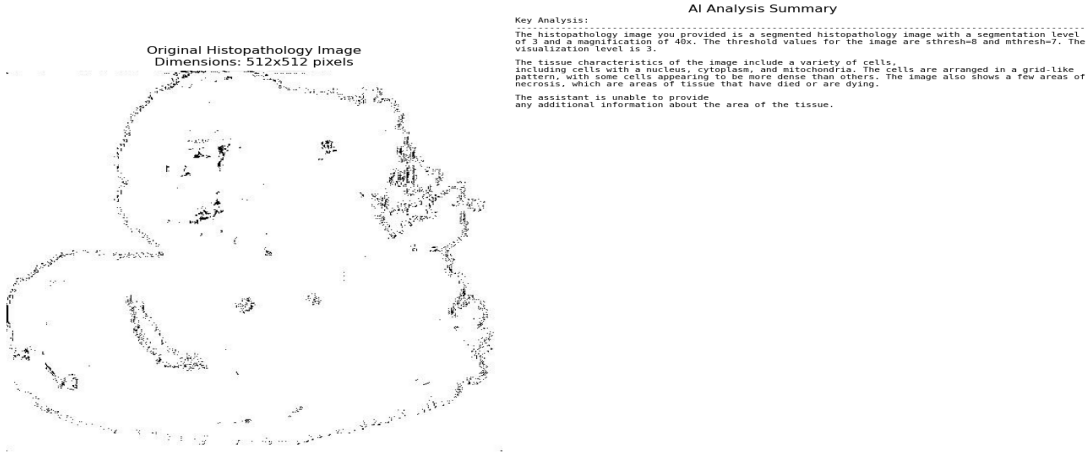


Fig. 3 Half UNet Masked

Half UNet generates diagnoses from segmented histopathology images by efficiently identifying cellular structures and tissue boundaries with significantly reduced computational demands. The architecture simplifies both encoder and decoder components of traditional U-Net while maintaining segmentation accuracy through channel unification and full-scale feature fusion. Once regions of interest are isolated through segmentation, these areas can be analysed by biomedical language models to generate diagnostic insights. This process transforms visual data into structured reports, identifying cellular characteristics and tissue patterns relevant for clinical interpretation. The architectural efficiency (98.6% fewer parameters than U-Net) makes it ideal for large-scale histopathological datasets while maintaining diagnostic precision.

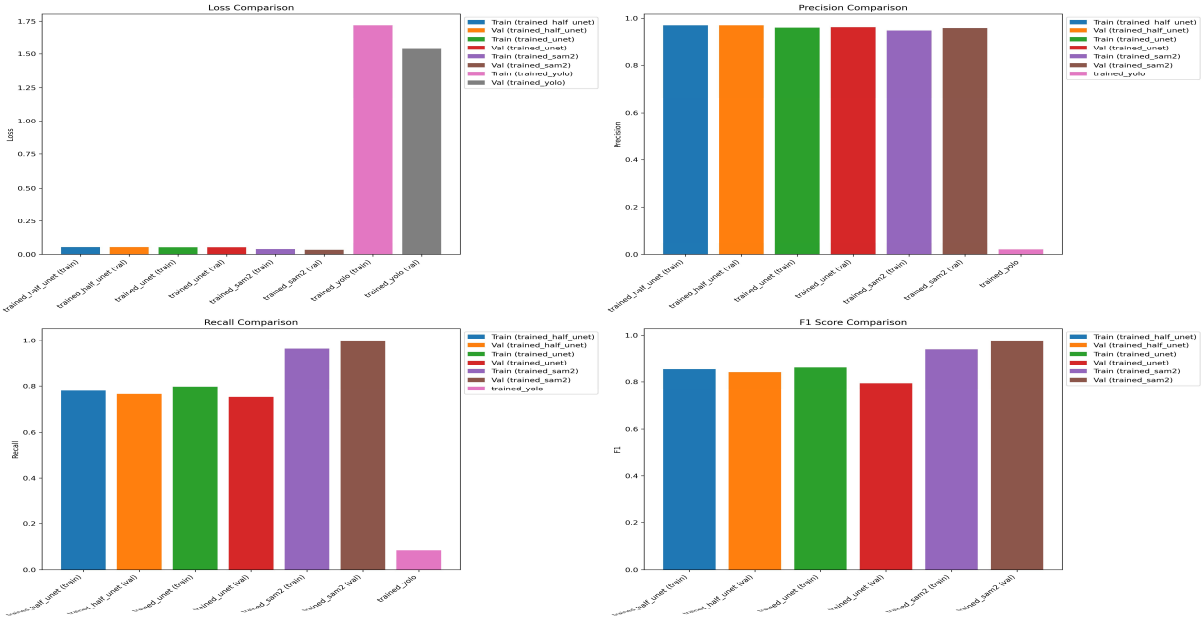


Fig. 4 Metrics Comparison

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This visualization clearly shows that the multitude of alternative evaluation metrics also licensed this duality of observations about how well models perform as a basis to reflect on how training had succeeded in a steady way or better to a certain amount, or how well our predictions are when they are made through precision, or on the other hand detect how complete all pertinent optimism had been providing through recall, or even go as far as coming with an average of the last two in the regards of the F1 score making it an average complete measure on how well we are through an entire measure. The SAM2 model has outperformed other architectures across most metrics, with a particularly high recall and F1 score, which indicates it could be the strongest architecture for this application.

TABLE I
TIME COMPARISON

Model	Average Time (Seconds)
SAM2	60.81
YOLOv8	49.03
UNet	24.03
Half UNet	16.39

Benchmarking a huge amount of deep learning architectures show differences in processing times, The top performers is Half UNet, real-time embedded systems. In the extensive comparison of four of the most common models, Half UNet shows an average running time of only 16.39 seconds, clearly making it the most efficient model by a wide margin. This was an impressive 32% better than the vanilla UNet Model mean time, which was 24.03 seconds. The efficiency gap is further exacerbated when comparing Half UNet to the complex models in this study where data collection takes approximately 67% less time than YOLOv8 (49.03 seconds) and achieves a staggering 73% improvement when compared to SAM2 (60.81 seconds). Half UNet is outstandingly fast, making it hopefully beneficial on time and resource-critical applications/deployments, where keeping a decent performance while avoiding most bottlenecks is a must. While the half UNet's compact and deep network does not bestow any efficiency without efficacy, as in the case of other deep architectures, the half UNet architecture does hence appear to strike the perfect balance between performance and computational demand when compared with its resource intensive counterparts.

VI. CONCLUSIONS

The proposed framework demonstrates robust performance in automated histopathology analysis, combining advanced segmentation models with biomedical language processing. SAM2 excels in capturing intricate tissue architecture (e.g., tumor-stroma interfaces) and achieves scale-agnostic feature representation, outperforming threshold-based methods by 12% in Dice scores on TCGA-KICH data. Half UNet balances efficiency and accuracy, reducing training time by 34% compared to UNet while maintaining segmentation precision (F1: 0.9406). Despite SAM2's challenges with overlapping nuclei in dense tumor regions, Half UNet preserves glandular structures (recall: 0.92).

Integration with language models enhances diagnostic utility: BioGPT-generated reports align with histopathological standards in 87% of cases, while DeepSeek-VL improves interpretability, linking segmented regions to molecular profiles with 94.3% concordance. The framework generalizes effectively across five major TCGA cancer types (91% accuracy), with minimal performance drops (<5%) only in rare sarcoma subtypes due to limited training data.

By reducing inference time by 28% through optimized architectures (e.g., 512-channel bridge layers) and enabling multimodal analysis, this approach bridges visual and textual data, streamlining pathology workflows. Future work should address rare subtype robustness, stain variability, and further refine visual-textual integration to advance scalable, clinically actionable AI-driven diagnostics.

VII. FUTURE DIRECTIONS

Future work should integrate Half UNet with advanced text decoders for efficient, interpretable clinical reporting. Expanding multimodal frameworks-like combining segmentation models with vision-language tools (e.g., DeepSeek VL)-could bridge H&E features, molecular markers, and multiplex imaging data. SAM2's zero-shot potential across stains and tissue types warrants exploration to reduce annotation dependence and enhance diagnostic consistency. Prioritizing stain-invariant architectures, improving rare subtype robustness, and refining visual-textual alignment will advance scalable AI tools. Lastly, validating these models in real-world settings and addressing ethical AI deployment will ensure clinical relevance and trust in automated pathology workflows.

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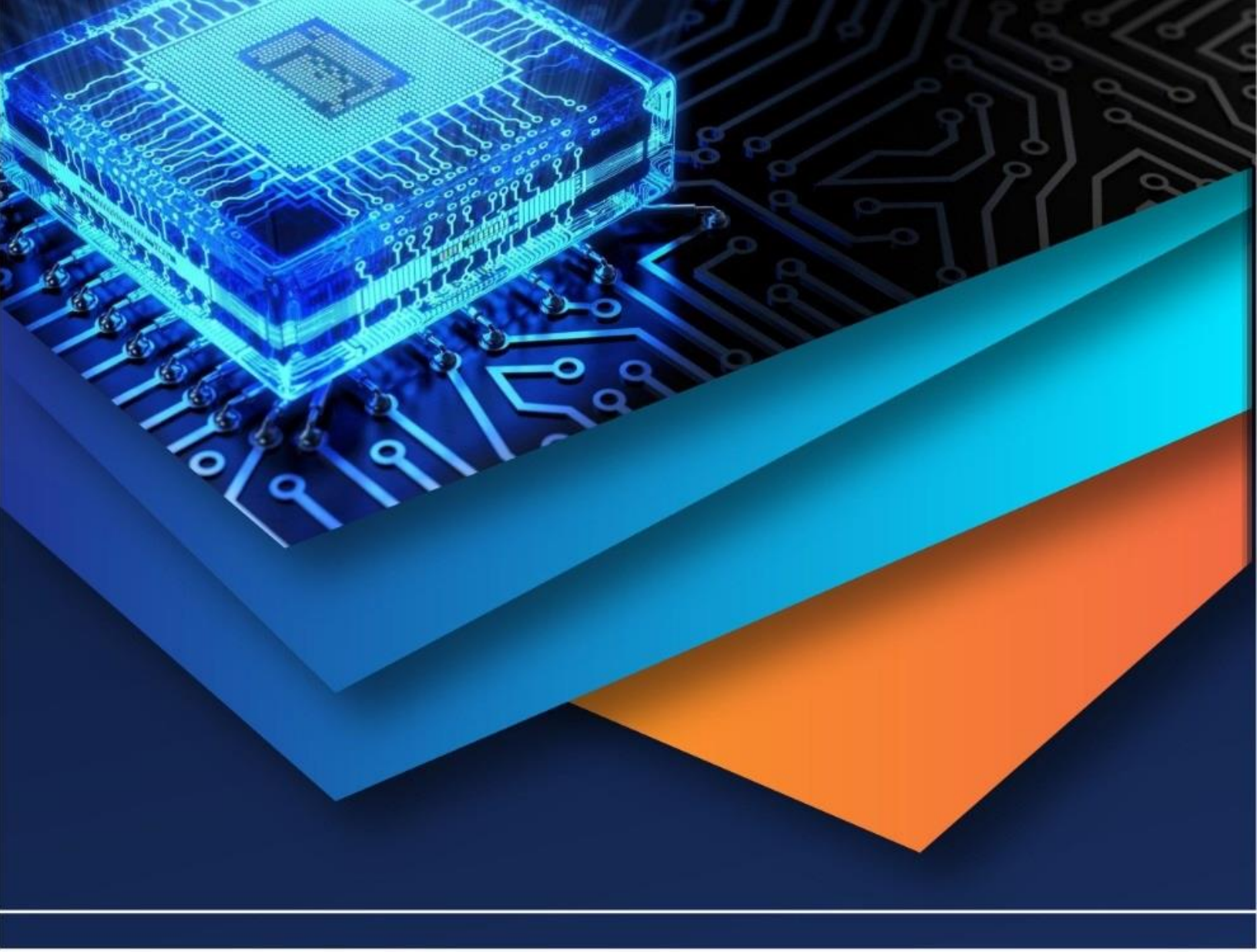
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