

# **Performance Evaluation of Object Detection Algorithms for Brain Tumor Detection in Medical Image Analysis**

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SRM University AP, Andhra Pradesh  
for the partial fulfillment of the requirements to award the degree of

**Bachelor of Technology  
in  
Computer Science & Engineering  
School of Engineering & Sciences**

submitted by

**Sai Monika P - AP20110010637**

**Suprada M - AP20110010657**

**Sandhya N - AP20110010684**

**Venkatesh K - AP20110010144**

Under the Guidance of

**Prof. Anusha Nalajala**



**Department of Computer Science & Engineering**

SRM University-AP

Neerukonda, Mangalgiri, Guntur

Andhra Pradesh - 522 240

May 2024

## DECLARATION

I undersigned hereby declare that the project report **Performance Evaluation of Object Detection Algorithms for Brain Tumor Detection in Medical Image Analysis** submitted for partial fulfillment of the requirements for the award of degree of Bachelor of Technology in the Computer Science & Engineering, SRM University-AP, is a bonafide work done by me under supervision of Prof. Anusha Nalajala. This submission represents my ideas in my own words and where ideas or words of others have been included, I have adequately and accurately cited and referenced the original sources. I also declare that I have adhered to ethics of academic honesty and integrity and have not misrepresented or fabricated any data or idea or fact or source in my submission. I understand that any violation of the above will be a cause for disciplinary action by the institute and/or the University and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been obtained. This report has not been previously formed the basis for the award of any degree of any other University.

Place	:	Date	: May 14, 2024
Name of student	: Sai Monika P	Signature	: .....
Name of student	: Suprada M	Signature	: .....
Name of student	: Sandhya N	Signature	: .....
Name of student	: Venkatesh K	Signature	: .....

**DEPARTMENT OF COMPUTER SCIENCE &  
ENGINEERING  
SRM University-AP  
Neerukonda, Mangalgiri, Guntur  
Andhra Pradesh - 522 240**



**CERTIFICATE**

This is to certify that the report entitled **Performance Evaluation of Object Detection Algorithms for Brain Tumor Detection in Medical Image Analysis** submitted by **Sai Monika, Suprada, Sandhya, Venkatesh** to the SRM University-AP in partial fulfillment of the requirements for the award of the Degree of Master of Technology in a bonafide record of the project work carried out under my/our guidance and supervision. This report in any form has not been submitted to any other University or Institute for any purpose.

Project Guide

Name: Prof. Anusha Nalajala

Signature: .....

Head of Department

Name: Prof. Niraj Upadhayaya

Signature: .....

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Sai Monika P, Suprada M, Sandhya N, Venkatesh K  
(Reg. No. AP20110010637, AP20110010657, AP20110010684,  
AP20110010144)

B. Tech.

Department of Computer Science & Engineering  
SRM University-AP

## ABSTRACT

Accurately detecting and segmenting brain tumors are pivotal aspects of medical diagnosis and treatment strategizing. This study provides an indepth assessment of both two-stage and one-stage object detection algorithms, employing annotated datasets to detect brain tumors effectively. We employed Convolutional Neural Networks (CNN) as representative of two-stage approaches and You Only Look Once (YOLO) as a one-stage detection method. Our dataset consists of annotated brain tumor images, providing ground truth for training and evaluation. The evaluation of each algorithm's effectiveness involved measuring various metrics including precision, recall, and intersection over union (IoU). Through extensive experimentation, we investigated the effectiveness of both algorithms in accurately identifying brain tumor regions within MRI images. Additionally, we analyzed the computational efficiency and speed of each algorithm to assess their practical viability in real-world medical applications. Our results illustrate that both CNN-driven two-stage object detection and YOLO-based one-stage object detection show encouraging potential in precisely identifying brain tumors. However, we observed variations in performance metrics and computational efficiency between the two approaches. These findings contribute to a better understanding of the strengths and limitations of each algorithm In the field of analyzing medical images. This research offers significant insights into how object detection algorithms can be applied to detect brain tumors, laying a foundation for further research and development in medical imaging technology.

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## **Chapter 1**

### **INTRODUCTION TO THE PROJECT**

The conventional method for recognizing objects in 3D medical images involves utilizing segmentation models to produce voxel-based annotations for objects of importance. Although this procedure improves the accuracy of the model, it has some disadvantages. Producing precise voxel markers for medical images is a time-intensive task that demands the involvement of numerous experts to uphold label quality. Due to inter-individual heterogeneity, accurate segmentation of organs or lesions may be hindered by undefined structural boundaries that include or exclude relevant information from adjacent tissues. Even with high-quality labels, segmentation models struggle to precisely outline regions within the target structure, often requiring post-processing to address missing volumes and correct false identifications. In general, this makes the training cost of segmentation models too high and may reduce the predictive capability of diagnostic or classification models. Object detection models are another way to avoid these problems for tasks that do not require voxel precision. However, Limited choices exist for object detection in 3D medical images. Utilizing 2D object detection models designed for images, like YOLO [1], can offer bounding box accuracy and segmentation precision. However, 2D models require an output-based modification process to reconstruct the input and predictions using the underlying 3D features, to determine compatibility between the model and the 3D data..



The conversion process also discards three-dimensional spatial information, which is crucial for identifying complex structures. To overcome this drawback, we propose a specialized 3D object detection framework for medical images. Named MedYOLO, this framework is developed based on the Ultralytics YOLOv5 detection model [2], boasting high accuracy, especially for medium and large structures. Furthermore, MedYOLO is designed to seamlessly work with NIfTI images. Our results suggest that the single-shot approach is adept at handling structures in proximity to a patch or sliding window, similar to the challenges encountered in nnDetection [3]

## **Chapter 2**

### **MOTIVATION**

In the realm of healthcare, the stakes couldn't be higher, and the need for precise and efficient tools in medical imaging is paramount. Our project is born out of a profound understanding of the challenges faced by medical professionals every day. From the intricacies of diagnosing illnesses to the delicate planning of surgeries, the accuracy and speed of object localization in 3-D medical imaging can make all the difference in patient care.

We're driven by a shared vision to transform these challenges into opportunities for innovation. By embracing cutting-edge computational techniques, we aim to revolutionize the landscape of medical image analysis. Our motivation stems from the belief that every advancement in this field brings us closer to a future where healthcare is not only more precise but also more accessible and cost-effective for all.

Through our project, we're not just seeking to improve existing methodologies; we're striving to redefine what's possible in medical imaging. By developing tailored object detection models for 3-D medical data, we're breaking down barriers and opening new avenues for diagnosis and treatment.

At the heart of our endeavor lies a commitment to impact. We recognize that the fruits of our labor will directly benefit patients, enabling faster and more accurate diagnoses, personalized treatment plans, and ultimately, better outcomes. By pushing the boundaries of what's achievable in medical imaging, we're not just advancing science; we're improving lives.

Join us in our mission to harness the power of technology for the betterment of healthcare. Together, let's pave the way for a future where innovation knows no bounds and where every patient receives the care they deserve.

## Chapter 3

### LITERATURE SURVEY

Introducing YOLO9000, an advanced real-time object detection system that can identify over 9000 categories of objects. First, we consider the latest improvements to the YOLO search method and the many improvements that have resulted from previous work. YOLOv2, an enhanced model, introduces a novel approach for typical search tasks like PASCAL VOC and COCO. It achieves 76.8 mAP on VOC 2007 at 67 frames per second (FPS), and 78.6 mAP at 40 FPS. However, faster-performing methods such as ResNet and Faster RCNN surpass YOLOv2's speed using SSD. We present an approach for concurrently training object detection and classification, where YOLO9000 is trained on both the COCO detection dataset and the ImageNet classification dataset. This combined training enables YOLO9000 to make detection predictions for various object classes without label detection data. Our approach is validated for ImageNet search performance. Despite having detection data for only 44 out of 200 classes, YOLO9000 achieves a mean average precision (mAP) of the ImageNet detection validation set, YOLO9000 achieves a score of 19.7. In 156 classes outside of COCO, it achieves a mean average precision (mAP) of 16.0. However, YOLO finds over 200 classes. Predict findings for over 9000 different object categories. And it continues to flow in time..

The primary objective of this update is to present a straightforward YOLOv5 segmentation workflow, akin to current object detection models. The introduction of the new v7.0 YOLOv5-seg model marks just the initial phase, as we plan to enhance

it further in conjunction with our detection and classification models. Your feedback and contributions to this endeavor are greatly valued!

Object localization and classification in medical images is of great clinical importance because diagnostic decisions often depend on object class. For this work, vulnerability and the transformative process of cultural creation is the main area of research. Recently, nnU-Net has effectively addressed the challenge of image segmentation tasks. Building upon the principles of nnU-Net, our paper focuses on streamlining and automating the composition process to identify medical materials. Introducing the selforganizing technique, nnDetection, achieves equal or better results than the state of the art when adapting to medical detection problems without manual intervention. We showcase nnDetection's efficiency through its application on two widely recognized benchmarks, ADAM and LUNA16. Additionally, we suggest evaluating its performance on 11 other public datasets related to drug discovery for a thorough assessment.

The 2021 BraTS Challenge is celebrating its 10th anniversary of the Brain Tumor Segmentation (BraTS) challenge is a collaborative effort between the Radiological Society of North America (RSNA), the American Society for Neuroradiology (ASNR), and the Society for Informatics in Medical Imaging and Computer-Assisted Interventions (MICCAI). Since its inception, BraTS has aimed to establish a standardized diagnostic platform for glioma segmentation alterations using multi-parametric magnetic resonance imaging (mpMRI) data. Glioma, the primary malignant tumor of the central nervous system, exhibits varying degrees of severity and prognosis. The RSNA-ASNR-MICCAI BraTS 2021 challenge seeks to assess software algorithms that analyze tumor segmentation and underlying tumor molecular characteristics using preoperative mpMRI data from 2,040 patients.

BraTS 2021 aims to achieve two primary goals: firstly, segmenting brain tumor regions, and secondly, classifying the O[6]-methylguanine-DNA methyltransferase (MGMT) promoter methylation status of tumors. The evaluation of all algorithms involved in BraTS 2021 will be conducted using the Sage Bionetworks Synapse platform for Task 1 and the Kaggle platform for Task 7 2. The top-performing participant will be awarded a prize of \$60,000

In this paper, we report the setup and results Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) organized in conjunction with the 2012 and 2013 MICCAI tumor conferences submitted to a set of 65 multicontrast MR scans (manually graded by four technicians) for patients with gliomas of low and high grade and 65 comparative scans created using stomach. photo Simulation software. Quantitative evaluation revealed significant differences between human carriers in distinguishing different tumor subregions (from 74% to 85%), showing the difficulty of this task. We find that different algorithms perform better in different subregions (achieving performance consistent with inter-individual variability). However, no single algorithm excels in all subdomains simultaneously. Combining good algorithms using majority voting produces results that are superior to all individual algorithms, indicating the remaining ways to improve the methods. BRATS image and manuscript data are still publicly available through an online review system as a reference resource.

Gliomas, a group of tumors within the central nervous system, comprise various subtypes. Precisely labeling these subregions in radiology is crucial for both clinical and computational research, including radiology and radiogenomic analysis. To address this need, Cancer Imaging is releasing segmented labels and radiographic

features for all preoperative magnetic resonance imaging (MRI) scans (totaling 243) from a multicenter collection of gliomas in the Cancer Genome Atlas (TCGA) Archives (TCIA). Initial symptoms were identified in a subgroup of glioblastomas (TCGA-GBM, totaling 135) and small gliomas (TCGA-LGG, totaling 108) through radiological evaluation. Regional glioma labels were generated using sophisticated automated techniques and then refined by certified neuroradiologists. These refined labels and feature sets are intended to: i) facilitate reproducible and comparative quantitative studies using the TCGA/TCIA glioma collection, leading to novel prognostic and diagnostic assessments, and ii) evaluate the performance of computer-aided segmentation methods, comparing them to conventional manual approaches.

## **Chapter 4**

### **DESIGN AND METHODOLOGY**

#### **4.1 EXISTING SYSTEM**

The typical method for object recognition in 3D medical images involves employing segmentation models are utilized to generate voxel-based annotations for objects of interest, enhancing the model's precision. However, this method comes with certain drawbacks. Generating accurate voxel markers for medical images is time- consuming and requires many experts to ensure the quality of the labels. Dueto interindividual variability, precise segmentation of organs or lesions can be problematic with undefined structural boundaries that may or may not include relevant information from adjacent tissues. Even when provided with high-quality labels, segmentation models face difficulties in precisely delineating target structural areas and frequently need post-processing to address missing volumes and eliminate falsely identified ones. In general, this makes the training cost of segmentation modelstoo high and may reduce the predictive capabilities of diagnostic or classification models.

#### **4.2 PROPOSED SYSTEM**

We evaluated MedYOLO using four categories of medical images. These include: 1) FLAIR scans from the BRaTS 2021 Task 1 dataset, consisting of 1000 training scans and 251 validations, utilizing full-mask unit partitioning to generate connected boxes. 2) LIDC lung nodule dataset, comprising 689 training scans and 173 validations, with two distinct label sets. One method



applies bounding boxes around individual nodes, whereas the alternative approach utilizes a single bounding box that contains all nodes. In each scan. These datasets were employed to evaluate the model's ability to detect small objects with diverse structures. Additionally, the Tumor Organ Segmentation Database (with 60 training scans and 15 validations) was utilized. This database involved creating junction boxes for various organs, including the organs include the left kidney, right kidney, spleen, pancreas, diaphragm, bladder, uterus, prostate, aorta, spinal cord, stomach, and liver. A previous method was utilized to generate the inverse training model for this dataset. Training images were rotated horizontally using five specific angles predetermined beforehand ( $0, \pm 8, \pm 17$  degrees) for each sample, with a random increment of  $\pm 3$  degrees. The same rotation is performed on the separator mask for each shape, and then bounding box labels are created for the rotated patterns. To reduce spurious signals from the interpolation algorithm used for transformation, the original untransformed samples were included in the training set. In total, 360 training samples were generated for the unit dataset.

4) Attempted to predict clinical diagnosis and randomization performed on the study utilized a collection of computed tomography (CT) data, comprising 648 scans for training and 163 for verification, with a particular emphasis on bandages around the heart and thoracic aorta. To maintain data integrity, these datasets were partitioned at the individual patient level, preventing any overlap between the training and validation sets.

## Chapter 5

### SYSTEM REQUIREMENT

#### HARDWARE REQUIREMENTS

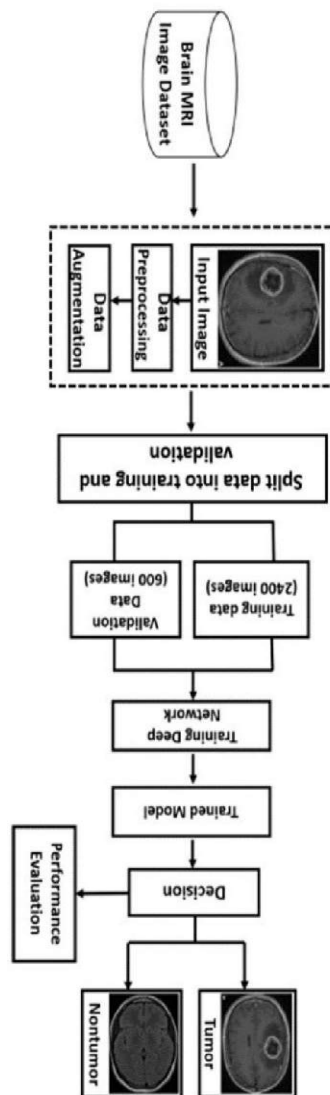
- Processor - i3(min)
- RAM - 2GB (min)
- Hard Disk - 25GB

#### SOFTWARE REQUIREMENTS

- Operating System : Windows/Linux
- Modules : Python  
Matplotlib  
NumPy  
Urllib  
Pandas  
Seaborn
- Language : Python

## Chapter 6

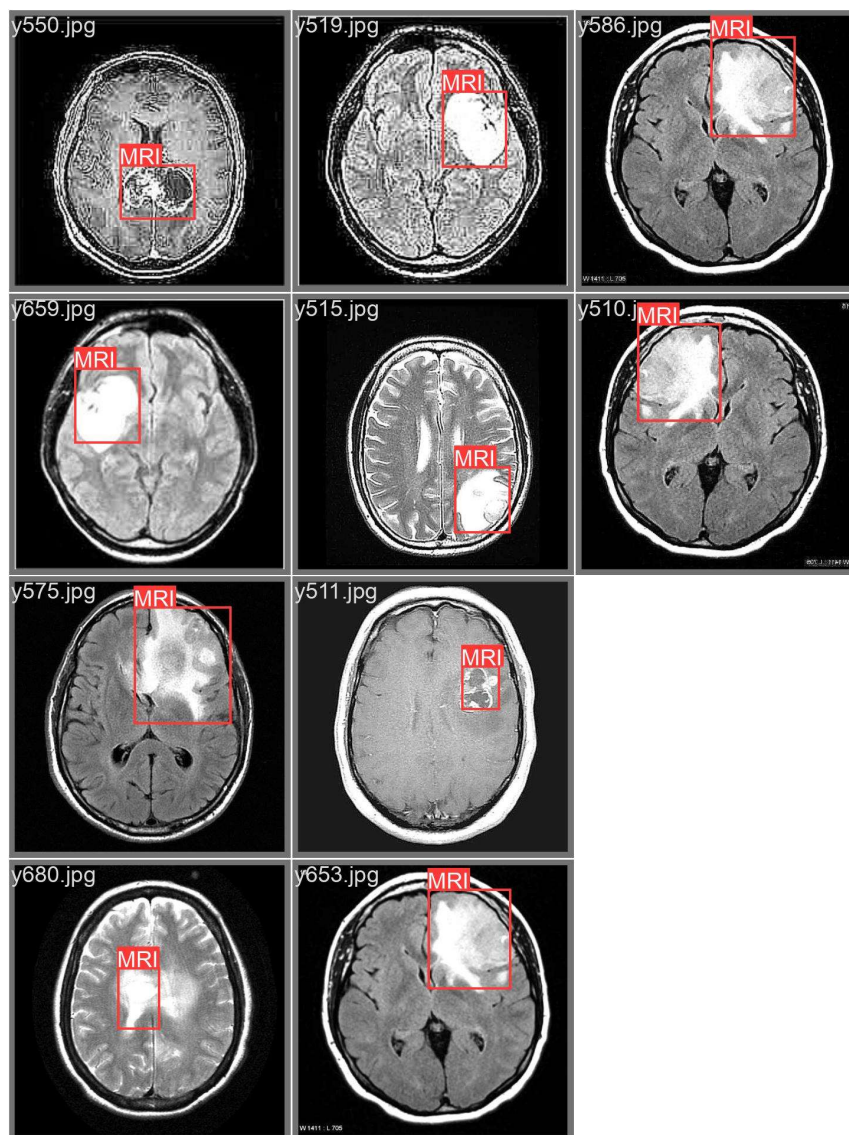
### SYSTEM ARCHITECTURE



## Chapter 7

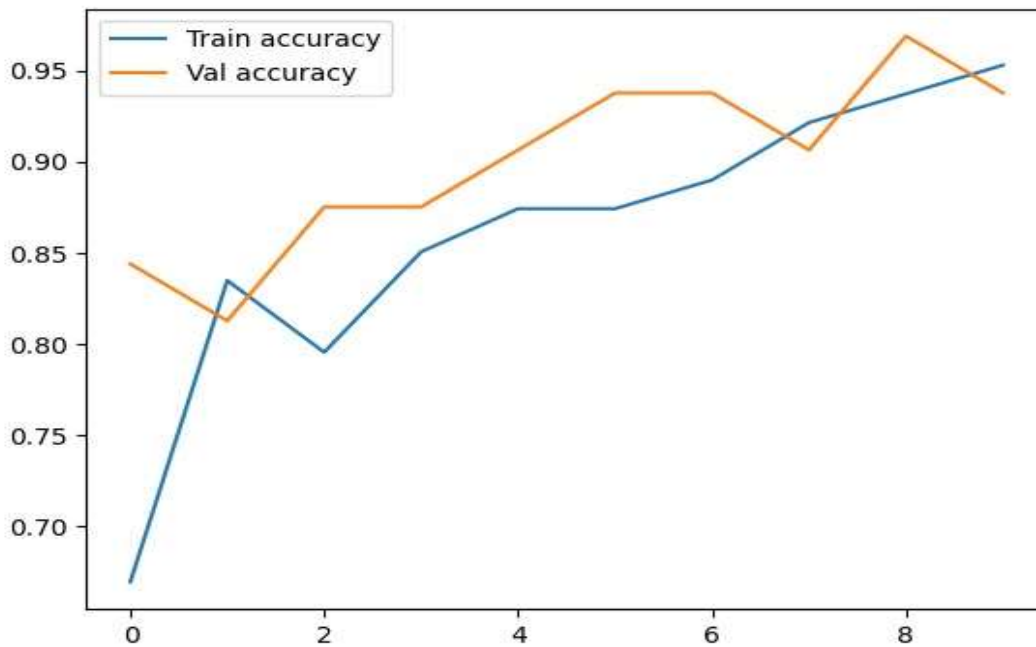
## RESULTS

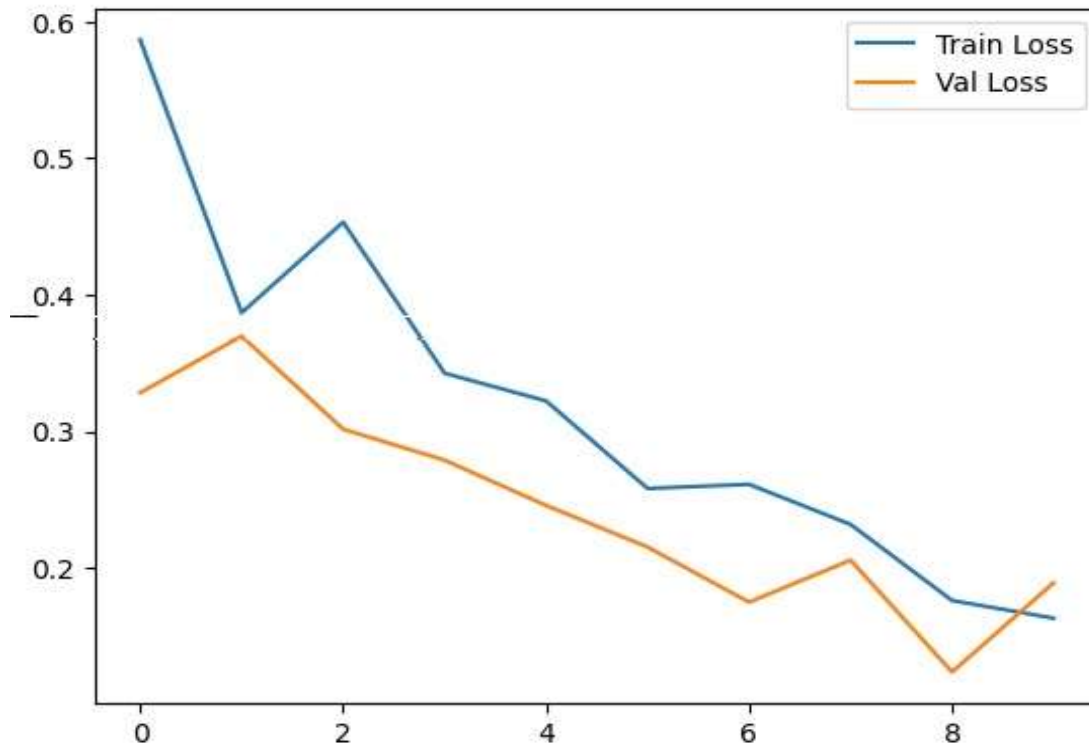
### 6.1 Object Detection for Medical Image Analysis (YOLO)



## 6.2 Object Detection for Medical Image Analysis (CNN)

```
Epoch 1/10
4/4 [=====] - 6s 1s/step - loss: 0.5866 - accuracy: 0.6693 - val_loss: 0.3283 - val_accuracy: 0.8438
Epoch 2/10
4/4 [=====] - 5s 1s/step - loss: 0.3868 - accuracy: 0.8346 - val_loss: 0.3696 - val_accuracy: 0.8125
Epoch 3/10
4/4 [=====] - 4s 992ms/step - loss: 0.4531 - accuracy: 0.7953 - val_loss: 0.3015 - val_accuracy: 0.8750
Epoch 4/10
4/4 [=====] - 4s 1s/step - loss: 0.3425 - accuracy: 0.8504 - val_loss: 0.2789 - val_accuracy: 0.8750
Epoch 5/10
4/4 [=====] - 5s 1s/step - loss: 0.3222 - accuracy: 0.8740 - val_loss: 0.2457 - val_accuracy: 0.9062
Epoch 6/10
4/4 [=====] - 4s 971ms/step - loss: 0.2581 - accuracy: 0.8740 - val_loss: 0.2153 - val_accuracy: 0.9375
Epoch 7/10
4/4 [=====] - 4s 968ms/step - loss: 0.2612 - accuracy: 0.8898 - val_loss: 0.1749 - val_accuracy: 0.9375
Epoch 8/10
4/4 [=====] - 5s 1s/step - loss: 0.2318 - accuracy: 0.9213 - val_loss: 0.2056 - val_accuracy: 0.9062
Epoch 9/10
4/4 [=====] - 4s 978ms/step - loss: 0.1761 - accuracy: 0.9370 - val_loss: 0.1238 - val_accuracy: 0.9688
Epoch 10/10
4/4 [=====] - 4s 987ms/step - loss: 0.1631 - accuracy: 0.9528 - val_loss: 0.1890 - val_accuracy: 0.9375
```





YOLOv8 is tailored for real-time object detection and proves optimal for this objective.

While CNNs serve multiple computer vision tasks, they may not match the speed of YOLOv8 in object detection.

Evaluation through performance metrics remains crucial for assessing object detection algorithms.

YOLO v8 consistently stands out as the top performer in this comparison, surpassing CNNs in both precision and processing speed

## Chapter 8

### CONCLUSION

After examining the current landscape of object localization in 3-D medical imaging, it's clear that while segmentation models offer impressive accuracy, they are burdened with challenges like time-intensive annotation processes, variability among annotators, and the need for extensive post-processing. Object detection models offer a promising alternative, but their adaptation to 3-D medical imaging is hindered by the complexities of converting input and output data.

Moving forward, our project underscores the importance of addressing these challenges to advance the field. We propose focusing on three key areas:

1. Developing specialized object detection models tailored for 3-D medical imaging, leveraging the unique characteristics of medical data to enhance efficiency and precision.
2. Investigating methods to seamlessly integrate 3-D data into existing 2-D object detection models, streamlining the workflow and reducing the need for conversion processes.
3. Refining post-processing techniques to ensure compatibility between object detection outputs and downstream tasks in 3-D medical imaging analysis.

By addressing these critical areas, our research aims to unlock the full potential of object detection in 3-D medical imaging. This endeavor contributes to the advancement of medical image analysis, ultimately benefiting healthcare professionals and patients by improving diagnostic accuracy and treatment planning.

## **8.1 SCOPE OF FURTHER WORK**

We present the creation of MedYOLO, an anchor-based object detection framework specifically designed for application in 3D medical imaging. MedYOLO performs as well or better than Detection in general language structure detection without over-the-counter optimization. Areas that need improvement in the pipeline are the addition of improved functionality as better 3D algorithms are developed and the introduction of more sophisticated integration methods to reshape the input data into the desired pipe shape.



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