



A
Synopsis
on



Graph Based Methods for Real-Time Medical Imaging

Submitted in partial fulfillment for
Dissertation I (1DS691)

Submitted by

Juveriya J. Mujawar (PRN No: 246529007)

Under the guidance of

Dr. R. R. Rathod



Department of Information Technology
Walchand College of Engineering, Sangli.
Maharashtra, India. 416415
AY 2025-26

Department of Information Technology Vision and Mission

VISION

To be an Information Technology programme as the first choice by the aspiring students and prospective employers by implementing world class education practices.

MISSION

To meet the above vision, all stakeholders of this programme are committed towards Outcome Based Education philosophy by:

- i Adopting vibrant academic curricula and implementing innovative teaching–learning processes.
- ii Providing opportunities for the development of professional skills.
- iii Nurturing critical thinking and creativity.
- iv Inculcating life-long learning attitude and sensitivity towards society and environment.

M.Tech (Data Science) Program Educational Objectives (PEOs)

PEO 1: Contribute individually and in teams to carry out data collection and processing for the development of data science methodologies.

PEO 2: Apply domain expertise to interpret data and demonstrate technical competency in handling real-life projects.

PEO 3: Exhibit continuous learning attitude, ethical behavior, and techno-socio responsibilities.

Program Outcomes (POs)

- PO1: Apply appropriate data handling skills for practical data science solutions.
- PO2: Demonstrate comprehensive understanding of data science theories, principles, and tools.
- PO3: Conceptualize and solve data engineering problems.
- PO4: Communicate research work through reports and publications.
- PO5: Exhibit ethical and professional conduct with life-long learning.
- PO6: Recommend suitable mechanisms for scalable data-driven applications.

Course Outcomes:

Dissertation Phase I (1DS691)

CO	Course Outcome Statement
CO1	Apply theoretical frameworks to the appropriate area of research.
CO2	Construct mathematical model for the dissertation topic.
CO3	Analyze mathematical model using modern tools.
CO4	Provide solution and synthesize research gap for engineering problem.

Component	Lecture	LA1	LA2	Lab ESE	Total
Tutorial	–	30	30	40	100
Practical	24 Hrs / Week				
Interaction	Credits: 12				

Declaration

We, the undersigned, hereby declare that the work presented in this report titled "**Graph Based Method for Medical Imaging**" submitted by us in fulfilment of the requirement for the award of the degree of Master of Technology (M. Tech) in the Department of Information Technology, Walchand College of Engineering, Sangli, is an authentic record of our project work.

The project was carried out under the guidance of **Dr. R. R. Rathod**, whose expertise and guidance contributed significantly to the successful completion of this endeavor.

I affirm that the contents of this report are original and have not been submitted for any other degree or examination. All sources of information have been duly acknowledged, and appropriate references provided where necessary.

Name: Juveriya J. Mujawar

PRN: 246529007

Place: Sangli

Date:

Acknowledgment

I feel immense pleasure in submitting this Project report entitled “Graph Based Method for Medical Imaging”.

I am thankful to my guide and Head Of Department of Information Technology Prof. Dr. R. R. Rathod for his valuable guidance and kind help during the completion of the Project and feel grateful to express my sincere gratitude to all other staff members of the IT Department.

I would like to thank all faculty members and staff of the Department of Information Technology for their generous help in various ways for the completion of this thesis.

I would like to thank all my friends for all the thoughtful and mind-stimulating discussions we had, which prompted us to think beyond the obvious. I have enjoyed their companionship very much during our stay at WCE, Sangli.

CERTIFICATE



This is to certify that the dissertation work entitled
“Graph Based Method for Real Time Medical Imaging”

Submitted by

Ms. Juveriya J. Mujawar

(PRN No: 246529007)

in fulfillment of the requirement for the degree of

Master of Technology

in

Data Science

from

Walchand College of Engineering, Sangli

(An Autonomous Institute)

Affiliated to Shivaji University, Kolhapur

This thesis work is a record of student's own work carried out by them under my supervision
and guidance during the AY 2025–26.

Dr. R. R. Rathod

Guide

Dr. S. S. Solapure

PG Coordinator

Dr. R. R. Rathod

Head of Department (IT)

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Abbreviations

MRI — Magnetic Resonance Imaging

AI — Artificial Intelligence

CNN — Convolutional Neural Network

GCN — Graph Convolutional Network

GNN — Graph Neural Network

SSL — Self-supervised Learning

ROI — Region of Interest

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Abstract

The rapid advancement of medical imaging technologies has significantly enhanced the accuracy and reliability of disease diagnosis. However, conventional medical imaging systems continuously acquire and store large volumes of image data, irrespective of clinical relevance. This indiscriminate acquisition results in redundant data storage, increased computational overhead, and delays in real-time clinical decision-making, particularly in resource-constrained healthcare environments.

To address these challenges, this dissertation proposes a graph-based real-time intelligent image acquisition framework for medical imaging applications. The proposed system integrates a lightweight deep learning–based disease detection model with a graph-based spatial relationship module to identify clinically significant abnormalities such as pneumonia, tumors, and structural anomalies. Spatial relationships among regions of interest are modeled using graph representations, enabling robust and interpretable abnormality assessment.

An anomaly-triggered acquisition algorithm computes an abnormality score by combining detection confidence with graph-based consistency measures. Based on this score, the system selectively captures and stores only diagnostically relevant image frames, thereby reducing redundant data storage and improving processing efficiency. The framework is evaluated on benchmark datasets comprising chest X-ray, MRI, and ultrasound images. Experimental results demonstrate effective storage reduction while maintaining reliable disease detection performance.

The proposed approach supports real-time clinical workflows, intelligent storage optimization, and efficient deployment on edge-based healthcare systems. This work contributes toward the development of next-generation smart medical imaging systems that are scalable, resource-efficient, and suitable for real-time healthcare applications.

1. Introduction

Medical imaging plays a pivotal role in modern healthcare by enabling non-invasive diagnosis, monitoring, and treatment planning for a wide range of diseases such as pneumonia, brain tumors, and cardiovascular disorders. Imaging modalities including chest X-ray, magnetic resonance imaging (MRI), and ultrasound are routinely used in clinical practice due to their effectiveness and accessibility. With continuous advancements in imaging technology, healthcare systems now generate an enormous volume of medical image data on a daily basis.

Despite these advancements, conventional medical imaging systems typically follow a continuous acquisition paradigm, where all image frames are captured and stored regardless of their diagnostic significance. This approach leads to excessive data accumulation, redundant storage, and increased computational costs during image analysis. In real-time clinical scenarios, such as continuous monitoring and point-of-care diagnostics, the storage and processing of irrelevant frames can introduce latency and negatively impact timely decision-making.

Recent developments in deep learning have shown remarkable success in automated disease detection, classification, and segmentation tasks across multiple imaging modalities. These models are capable of identifying subtle pathological patterns with high accuracy. In parallel, graph-based methods have emerged as powerful tools for modeling spatial relationships among anatomical structures, providing enhanced robustness and interpretability compared to purely pixel-based approaches. Graph representations enable the modeling of contextual dependencies among regions of interest, which is particularly valuable in complex medical images.

However, most existing research focuses on post-acquisition image analysis, where all images are already captured and stored prior to processing. Limited attention has been given to real-time intelligent image acquisition, where the decision to capture and store an image is dynamically controlled based on detected abnormalities. Such an approach has the potential to significantly reduce storage requirements and computational overhead while preserving clinically relevant information.

This dissertation addresses this research gap by proposing a graph-based anomaly-triggered

image acquisition framework for real-time medical imaging. The proposed system integrates a lightweight disease detection model with a graph-based spatial reasoning module to compute an abnormality score for each image frame. A trigger algorithm selectively captures and stores image frames only when disease-related abnormalities are detected. This strategy ensures efficient utilization of storage and computational resources while supporting real-time clinical workflows.

The outcomes of this work aim to contribute to the development of intelligent, resource-aware medical imaging systems suitable for deployment in hospitals, telemedicine platforms, and edge-based healthcare devices. By combining deep learning with graph-based spatial modeling, the proposed framework enhances both the efficiency and interpretability of real-time medical image acquisition systems.

2. Literature Survey

Graph-based methods have been widely applied in medical imaging. Local-to-global GNNs and instance importance-aware GCNs have shown strong performance in brain disorder classification and 3D diagnosis [1],[2].

General-purpose frameworks such as MedGCN further demonstrate the scalability of GCNs in multi-task settings [3]. Other graph-based advances include aggregation methods for improved segmentation [4], contrastive pooling for explainable brain network classification [5], and Gaussian embeddings for Alzheimer’s prediction [6]. The integration of knowledge-graphs has also been highlighted for enhancing interpretability and decision-making [7].

CNN-based methods remain dominant in diagnostic imaging. Real-time fetal brain detection and lightweight ultrasound plane classification have been achieved using specialized CNN architectures [8],[9], while heuristic methods simplify ultrasound acquisition workflows [10].

Broader surveys and methodological extensions have examined CNNs for detection and segmentation [11], with spatial-oriented CNNs from remote sensing adapted to medical imaging [12]. Recent reviews further emphasize the role of YOLO-based detection in real-time clinical applications [13].

Transformer-based models provide new capabilities in spatial reasoning. Contextual transformers have been used for medical image analysis [14], and depth-guided transformer architectures like MonoDETR show promise for advanced 3D detection and volumetric imaging [15].

Complementary methodologies focus on improving model robustness and data utilization. Comparative studies on augmentation techniques guide effective training strategies [16], while self-supervised learning (SSL) offers solutions for limited-annotation medical datasets [17].

Broader reviews consolidate deep learning applications in segmentation, classification, and detection [18], while spatio-temporal analytics frameworks [19] and big spatial data analyses [20] address scalability and system-level challenges.

Finally, cross-disciplinary methods, such as neural manipulation networks, provide transferable insights for robotic-assisted medical interventions [21]

2.1 Quantitative Analysis of Literature

In recent years, deep learning and computer vision have become integral to solving challenges in medical imaging, remote sensing, and object detection tasks. The growing interest in these domains is reflected in the steady rise of publications, new frameworks, and citation trends. To systematically understand this progress, a bibliometric analysis was conducted on selected papers, focusing on publication patterns, keyword usage, and citation impact. The analysis provides insights into how research attention has shifted over time and identifies influential works and emerging themes that guide future research directions.

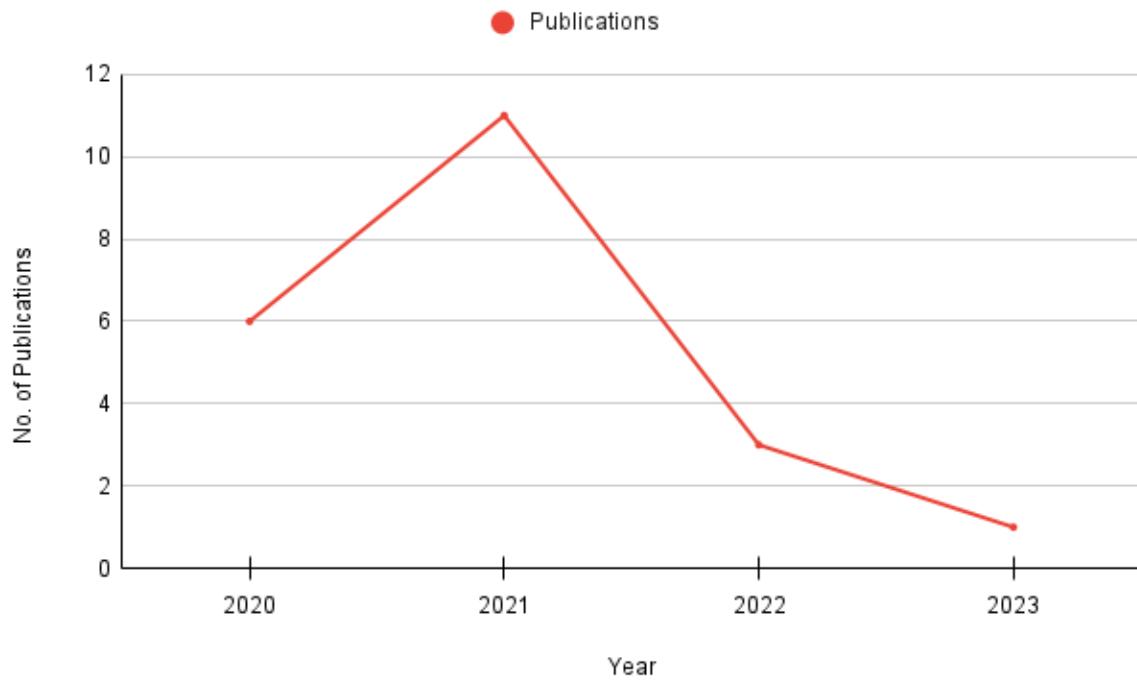


Figure 2.1: Trend Over Years

The Figure 2.1 shows a trend of number of publications over years. The graph shows a peak in 2021, followed by a sharp decline from 2022 onwards. This indicates that 2021 was a pivotal year for research in medical imaging, possibly due to the pandemic-driven boost in healthcare AI research.

The decline suggests research saturation in certain topics or a shift toward more specialized methods like transformers, GNNs, and YOLO variants. It highlights that this study is situated

at a time when foundational work has already been published, but there is scope for refinement and specialized applications, making this study timely and relevant.

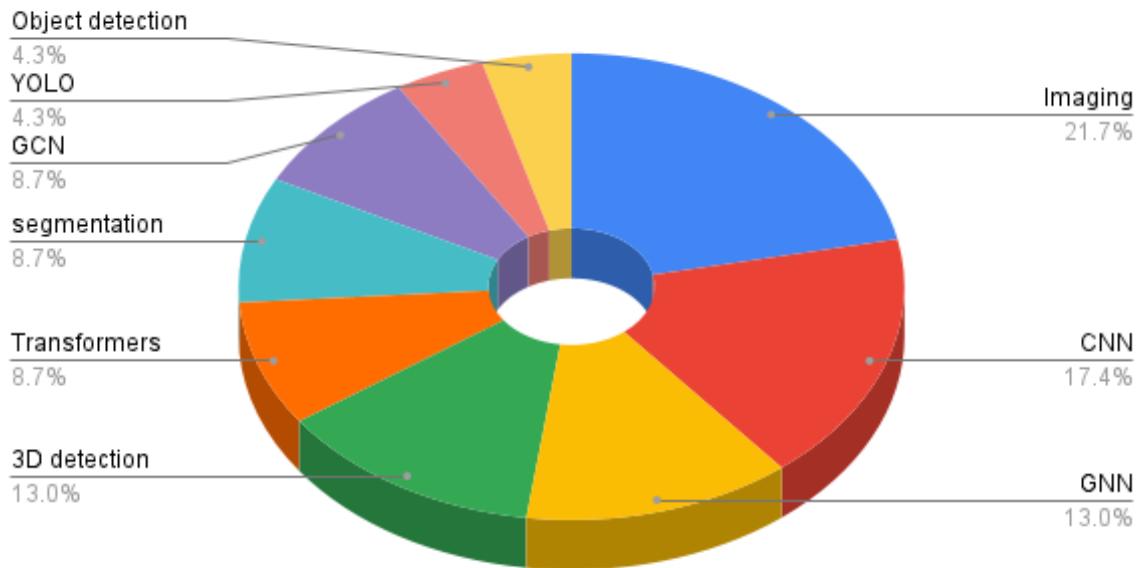


Figure 2.2: Keyword Analysis

The Figure 2.2 depicts the keyword distribution of literature studied. The dominance of terms like Imaging, CNN, GNN, and 3D detection shows the core techniques driving the field.

The presence of GCN, YOLO, and segmentation indicates a shift towards more complex, structured, and multimodal problems. However, this study aims to address less explored domains like YOLO in medical imaging with high impact domain like GCN.

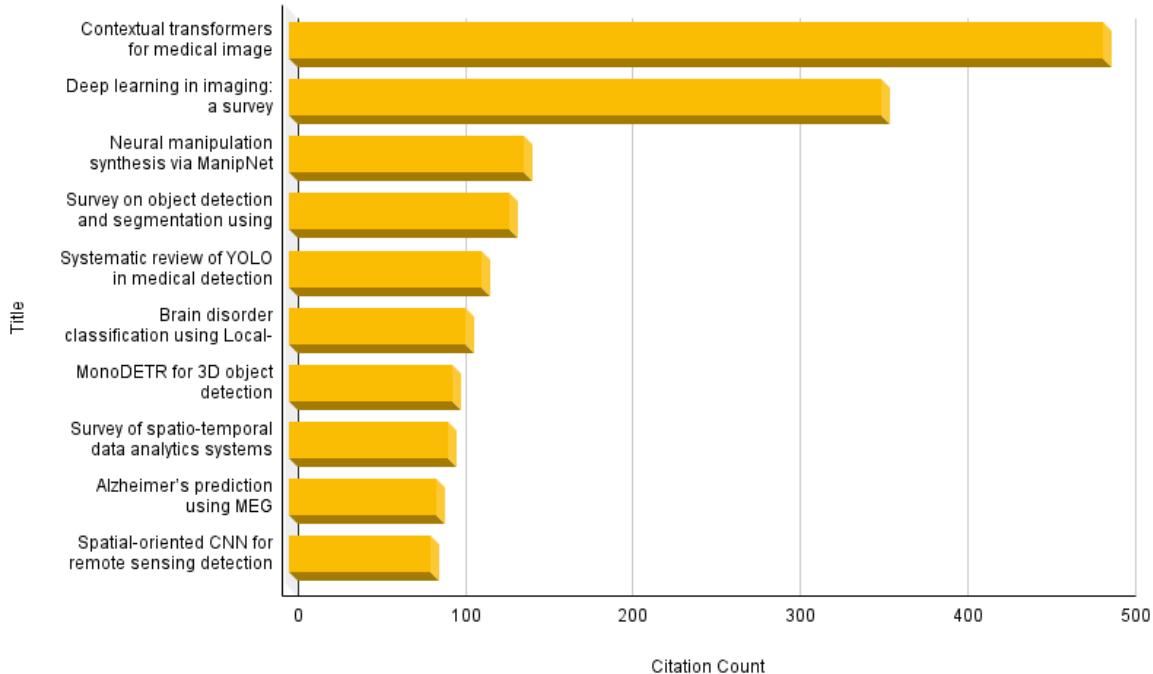


Figure 2.3: Highly Cited Papers

Figure 2.3 shows top 10 cited research. Papers on contextual transformers, imaging surveys, YOLO reviews, and spatio-temporal analytics dominate citations, reflecting community recognition.

This shows that transformers and YOLO-based architectures are at the research forefront, while CNNs remain strong but are gradually being complemented by newer paradigms. Thus, citing and building upon these highly influential works strengthens this study foundation, and developing real-time detection gives novelty to this study.

3. Scope of Work

The scope of the present study is focused on the design and development of an intelligent, graph-based framework for real-time medical image acquisition aimed at reducing redundant data storage and improving diagnostic efficiency. The work addresses the limitations of conventional medical imaging systems that capture and store all image frames without considering their clinical relevance.

The proposed research primarily focuses on integrating a lightweight disease detection model with graph-based spatial relationship analysis to identify abnormalities in medical images. Spatial relationships among regions of interest are modeled using graph representations to incorporate anatomical context, which is often ignored in traditional pixel-based detection methods. This enables more robust and interpretable abnormality detection in modalities such as MRI.

The scope includes the development of an anomaly-triggered capture mechanism that computes an abnormality score based on detection confidence and graph-consistency measures. This mechanism selectively captures and stores only those image frames that exhibit disease-related abnormalities, thereby reducing redundant storage and improving computational and network resource utilization.

The study involves experimental evaluation using benchmark medical imaging datasets to analyze performance in terms of detection accuracy, storage reduction, and processing efficiency. The framework is designed with an emphasis on real-time applicability and suitability for deployment in resource-constrained environments such as edge devices and point-of-care systems.

The scope of this work is limited to two-dimensional medical images and focuses on abnormality detection rather than detailed clinical diagnosis or treatment planning. Extension to three-dimensional imaging modalities, multi-disease classification, and large-scale clinical validation is beyond the scope of the present study and is identified as future work.

4. Research Objectives

The primary objective of this study is to emphasize the integration of intelligent detection mechanisms with graph based methods. By focusing only on clinically significant abnormalities in real time, the system aims to optimize both diagnostic reliability and storage efficiency.

The research objectives include:

- (a) Designing an anomaly-triggered acquisition algorithm for real-time medical imaging.
(completed)
 - i. Developing a lightweight pre-screening module that works in real-time.
 - ii. Integrating this module into the imaging pipeline so that only frames with potential abnormality are stored for further analysis.
 - iii. This reduces data overload, storage needs, and clinician review time, making the imaging system more efficient.
 - iv. The algorithm will be tested for latency, sensitivity, and efficiency.
- (b) Incorporating graph-based spatial relationships to improve detection robustness and interpretability.(completed)
 - i. Converting detected regions of interest (ROIs) into graph structures, where nodes represent anatomical regions and edges represent spatial relationships.
 - ii. Use Graph Convolutional Networks (GCNs) to capture contextual information.
 - iii. Improve robustness: even if one region has low-contrast data, its neighbors' information supports the decision.
 - iv. Improve interpretability: clinicians can visualize the "graph connections" to understand why the model predicted an anomaly.
- (c) Validating the proposed framework on benchmark datasets for tumor identification.(not completed)
 - i. Train and test your framework on these datasets with cross-validation.
 - ii. Compare performance with state-of-the-art methods (CNNs, transformers, YOLO, etc.) using metrics like AUC, accuracy, sensitivity, specificity, F1-score.

5. Methodology

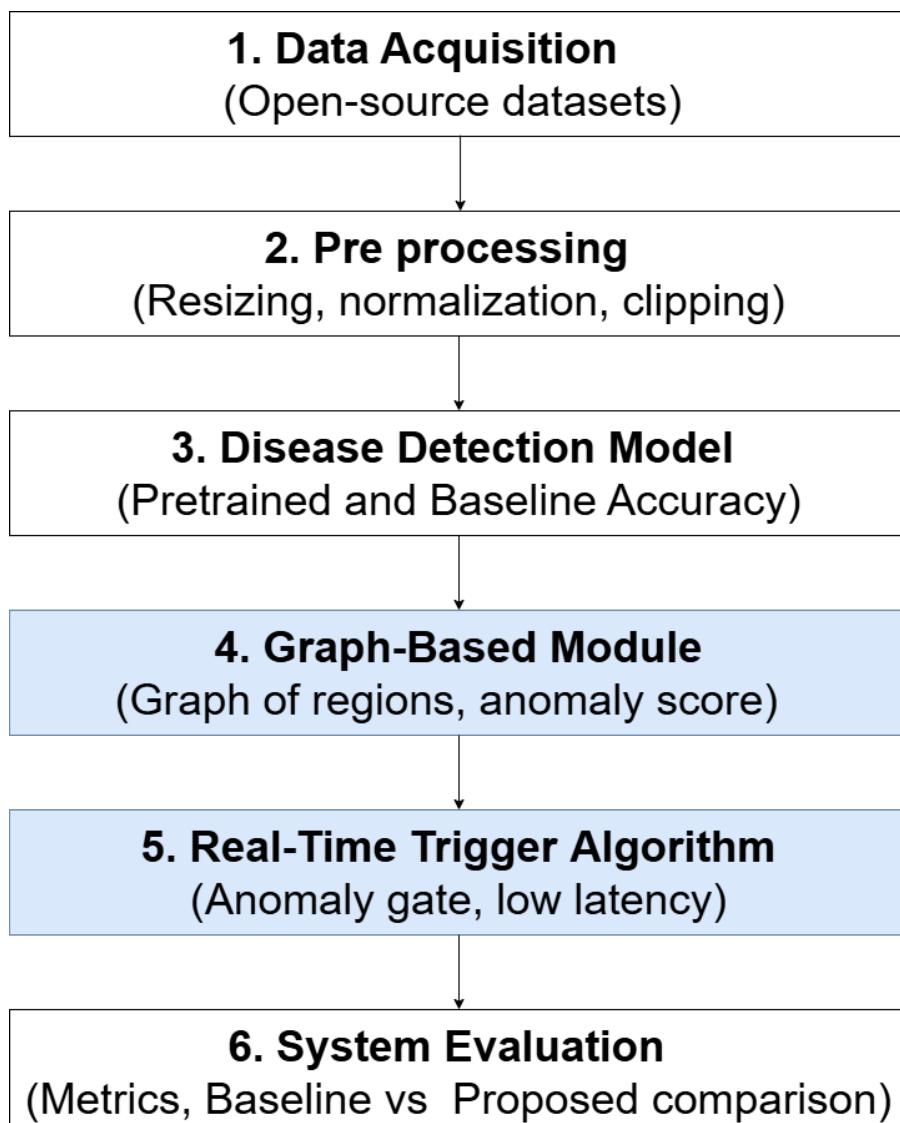


Figure 5.1: Methodology Block Diagram

The proposed methodology follows a systematic workflow that integrates established practices in medical image analysis with innovative graph-based techniques and real-time decision-making mechanisms. The process, illustrated in Figure 5.1, can be divided into six major stages, each contributing to the robustness and clinical applicability of the system. The steps are explained in detail below.

5.1 Data Acquisition:

The first stage involves the collection of medical imaging data from open-source and publicly available benchmark datasets widely used in medical image analysis research. These datasets include expertly annotated images that serve as reliable ground truth for supervised learning and evaluation. The use of publically available dataset ensures high annotations quality, diversity in imaging conditions, reproducibility and comparitibility.

The medical imaging data used in this study is sourced from the TrackRAD 2025 dataset, a publicly available benchmark dataset designed for advanced medical image analysis and anomaly detection tasks. TrackRAD 2025 provides high-quality, expert-annotated medical image sequences, making it well suited for developing and validating real-time disease detection frameworks.

The dataset consists of temporally ordered imaging frames accompanied by corresponding ground-truth annotations, enabling both frame-level anomaly detection and spatial localization of diseased regions. Its structured format supports sequential analysis, which is essential for modeling temporal behavior and implementing anomaly-triggered acquisition mechanisms in real-time settings.

The use of the TrackRAD 2025 dataset offers several advantages:

1. Reliable expert annotations, ensuring accurate supervision during training and evaluation
2. Diversity in anatomical structures and pathological patterns, improving model generalization
3. Public availability, enabling reproducibility and fair comparison with existing state-of-the-art methods

By leveraging TrackRAD 2025 as the primary data source, this work establishes a robust and standardized foundation for training the disease detection model, constructing graph-based spatial representations, and evaluating the proposed real-time anomaly-triggered framework against reliable benchmarks.

5.2 Preprocessing:

Medical imaging data acquired from real-world clinical environments, including the TrackRAD 2025 dataset, often exhibit variations in spatial resolution, intensity distribution, noise characteristics, and annotation formats. Such inconsistencies can negatively affect the performance and stability of learning-based models. To address these challenges, a comprehensive preprocessing pipeline is employed to standardize the input data and enhance diagnostically relevant features before model inference and graph construction.

1. Frame Standardization and Resizing: Each medical image frame in the TrackRAD 2025 dataset is resized to a fixed spatial resolution to ensure uniformity across all samples. Standardization of image dimensions is essential for enabling batch-wise processing during training and inference, maintaining compatibility with pretrained deep learning architectures and ensuring consistent spatial correspondence between image frames and annotation masks

Interpolation methods are selected carefully to preserve structural integrity, especially along anatomical boundaries that are critical for accurate anomaly localization.

2. Intensity Normalization: Medical images often suffer from inter-scan intensity variations due to differences in imaging devices, acquisition protocols, and patient conditions. To mitigate this issue, pixel intensity values are normalized to a predefined range.

Normalization ensures reduced contrast variability across image sequences, improved numerical stability during network optimization and faster and more stable convergence during fine-tuning.

This step allows the detection model to focus on structural and textural features rather than absolute intensity differences.

3. Annotation and Mask Alignment: The TrackRAD 2025 dataset provides ground-truth annotations indicating anomalous or diseased regions. These annotation masks undergo the same spatial transformations as the corresponding image frames to ensure perfect alignment.

Proper alignment is critical for accurate supervision during model fine-tuning, reliable evaluation of detection and localization performance and correct mapping of detected regions during graph-based spatial modeling.

Any inconsistencies between image frames and masks are resolved during this stage to prevent label noise.

The preprocessing stage plays a crucial role in enhancing data quality and ensuring consistency across the TrackRAD 2025 dataset. By standardizing spatial resolution, normalizing intensities, suppressing noise, aligning annotations, and preserving temporal coherence, this step significantly improves the reliability, accuracy, and interpretability of the proposed disease detection and real-time anomaly-triggered framework.

5.3 Disease Detection Model:

Algorithm 1 Disease Detection and Abnormal Region Identification

Require: Medical image I , pretrained detection model D , threshold τ

Ensure: Abnormality mask M , feature map F

- 1: Preprocess input image I (resizing, normalization, denoising)
 - 2: Extract feature representation $F \leftarrow D(I)$
 - 3: Compute abnormality response map A from F
 - 4: **for** each pixel or region r in A **do**
 - 5: **if** $A(r) > \tau$ **then**
 - 6: Mark r as abnormal in mask M
 - 7: **else**
 - 8: Mark r as normal in mask M
 - 9: **end if**
 - 10: **end for**
 - 11: **return** abnormality mask M and feature map F
-

The disease detection model serves as the primary abnormality identification stage in the proposed framework. Its objective is to analyze incoming medical images and generate reliable spatial representations that distinguish between normal and abnormal regions. This stage provides the foundational features required for subsequent graph-based spatial modeling and anomaly-triggered acquisition.

Algorithm 1 outlines the disease detection process used in the proposed framework, where a pretrained model extracts discriminative features and generates spatial abnormality masks that guide subsequent graph-based modeling.

A pretrained deep learning architecture is employed as the baseline detection model to leverage knowledge learned from large-scale image datasets. Transfer learning enables faster convergence, improved generalization, and robustness against limited domain-specific data. The pretrained network is fine-tuned using task-specific medical images to adapt the learned representations to disease-related visual patterns.

Prior to inference, each medical image undergoes standardized preprocessing, including resizing, intensity normalization, and noise suppression. The processed image is then forwarded through the detection model, which extracts multi-level feature maps capturing both low-level texture information and high-level semantic cues associated with abnormal tissue structures.

The model produces a pixel-wise or region-level abnormality response, indicating the likelihood of disease presence across spatial locations. These responses are subsequently transformed into binary or probabilistic abnormality masks using adaptive thresholding. The resulting masks

highlight candidate disease regions and preserve spatial continuity, making them suitable for graph-based representation.

Importantly, the disease detection model does not operate as a standalone diagnostic system. Instead, it functions as a feature-generating and localization component, supplying structured inputs for graph construction and real-time anomaly-triggered decision-making in later stages of the pipeline.

5.4 Graph Based Module:

Algorithm 2 Graph-Based Spatial Relationship Modeling

Require: Abnormality mask M , feature map F , neighborhood radius r

Ensure: Graph $G(V, E)$

```
1: Initialize empty graph  $G$ 
2: for each abnormal pixel  $p_i \in M$  do
3:   Create node  $v_i$  with attributes  $\{F(p_i), location(p_i)\}$ 
4:   Add  $v_i$  to vertex set  $V$ 
5: end for
6: for each pair of nodes  $(v_i, v_j) \in V$  do
7:   if  $distance(v_i, v_j) \leq r$  then
8:     Create edge  $e_{ij}$  between  $v_i$  and  $v_j$ 
9:     Add  $e_{ij}$  to edge set  $E$ 
10:  end if
11: end for
12: return graph  $G(V, E)$ 
```

The graph-based spatial relationship module constitutes the core novelty of the proposed framework. While conventional deep learning models operate primarily on grid-based representations, they often fail to explicitly capture structural dependencies and spatial interactions between abnormal regions. To address this limitation, the proposed work introduces a graph-based representation that models abnormal tissue regions as interconnected entities, enabling more interpretable and robust disease characterization.

Following the disease detection stage, spatial abnormality masks are obtained that indicate candidate tumor or anomaly regions. From these masks, abnormal pixels are treated as graph nodes, preserving their spatial coordinates and associated feature responses derived from the detection model. This formulation enables a flexible representation where both local and global spatial relationships can be explicitly encoded.

Algorithm 2 describes the proposed graph-based spatial modeling approach, where abnormal

pixels are transformed into graph nodes and spatial proximity is used to establish meaningful relationships between them.

Edges between nodes are established based on spatial proximity constraints, defined by a fixed neighborhood radius. This ensures that only meaningful local interactions between nearby abnormal pixels are modeled, preventing unnecessary graph densification. As a result, the constructed graph preserves the morphological structure and continuity of abnormal regions, which is critical for accurate localization and reasoning.

Each node in the graph is associated with feature attributes such as intensity response, spatial location, or learned feature embeddings. The resulting graph serves as a structured abstraction of the abnormal region, where disease patterns are represented not merely as isolated pixels but as interconnected spatial entities.

This graph-based representation enables subsequent reasoning operations such as abnormality propagation, region consistency analysis, and anomaly localization. Importantly, by decoupling spatial reasoning from grid-based convolution operations, the proposed module enhances interpretability, noise robustness, and generalization across imaging modalities.

5.5 Real-Time Trigger Algorithm:

Algorithm 3 Real-Time Anomaly-Triggered Frame Acquisition

Require: Image stream \mathcal{I} , detection model D , trigger threshold τ

Ensure: Set of triggered anomaly frames \mathcal{A}

```
1: Initialize empty set  $\mathcal{A}$ 
2: for each incoming frame  $I_t \in \mathcal{I}$  do
3:   Extract feature map  $F_t \leftarrow D(I_t)$ 
4:   Generate abnormality mask  $M_t$ 
5:   Construct graph  $G_t(V_t, E_t)$  from  $M_t$ 
6:   Compute graph-level abnormality score  $S_t$ 
7:   if  $S_t \geq \tau$  then
8:     Add frame  $I_t$  to  $\mathcal{A}$ 
9:     Trigger anomaly response
10:  end if
11: end for
12: return triggered frames  $\mathcal{A}$ 
```

The real-time anomaly-triggered acquisition algorithm constitutes a key functional contribution of the proposed framework. Unlike conventional medical imaging pipelines that process all frames uniformly, the proposed approach introduces a selective acquisition strategy that dy-

namically responds to detected abnormalities. This design is particularly relevant for real-time imaging systems, where computational efficiency, latency, and clinical relevance are critical. Following disease detection and graph-based spatial modeling, each incoming frame is associated with a structured graph representation capturing the spatial organization of abnormal regions. The proposed trigger mechanism operates on this graph representation to determine whether the current frame contains clinically significant anomalies that warrant further processing, storage, or alert generation.

A graph-level abnormality score is computed by aggregating node-level responses and spatial consistency measures within the constructed graph. This score reflects not only the presence of abnormal pixels but also their spatial coherence and structural relevance. By incorporating graph-based reasoning, the trigger decision becomes robust to isolated noise responses and spurious detections.

If the computed abnormality score exceeds a predefined trigger threshold, the frame is flagged as anomalous and forwarded for downstream processing, such as visualization, storage, or clinical review. Otherwise, the frame is discarded or minimally processed, thereby reducing unnecessary computation and data throughput.

This anomaly-triggered acquisition strategy enables adaptive real-time operation, ensuring that system resources are focused on diagnostically relevant frames. Moreover, the tight integration of graph-based spatial reasoning with trigger logic enhances both the reliability and interpretability of real-time decision-making.

5.6 System Evaluation:

The final stage involves a comprehensive evaluation of the proposed framework using the benchmark dataset. Performance is assessed at multiple levels to validate both detection accuracy and real-time feasibility.

Evaluation includes:

1. Classification Metrics: Accuracy, precision, recall, and F1-score for anomaly detection.
2. Comparative Analysis: Performance comparison between the baseline detection model and the graph-enhanced framework.
3. Trigger Efficiency: Analysis of the proportion of frames selected by the anomaly-trigger mechanism.
4. Latency Measurement: Validation of response time to ensure real-time applicability.

This evaluation demonstrates the effectiveness of incorporating graph-based spatial reasoning and anomaly-triggered acquisition in improving both detection reliability and system efficiency.

6. Results

This section presents qualitative results demonstrating the effectiveness of the proposed graph-based real-time medical image acquisition framework. The results are illustrated using representative frames from the dataset, highlighting the impact of preprocessing, feature enhancement, graph construction, and anomaly localization.



Figure 6.1: Original MRI Frame

6.1 Original Frame Analysis:

The original dataset figure 6.1 represents a raw medical imaging frame acquired directly from the imaging modality, without any form of preprocessing or enhancement. In this work, the dataset consists of sequential MRI frames provided by the TrackRAD-2025 dataset, where each frame captures anatomical structures along with potential pathological regions such as tumors. As observed in the original image, the frame is grayscale and exhibits inherent characteristics of raw MRI data, including variations in intensity, background noise, and subtle contrast differences between healthy tissue and abnormal regions. The tumor region is not explicitly visible to the naked eye and blends with surrounding tissue due to low contrast and acquisition artifacts. This reflects real-world clinical scenarios where abnormalities are often indistinct and difficult to detect without computational assistance.

The original images retain all native spatial information, intensity distributions, and acquisition noise, making them a critical baseline for evaluating the effectiveness of subsequent processing stages. These frames serve as the primary input to the proposed framework and are later subjected to preprocessing steps such as normalization, noise reduction, and contrast enhancement to improve feature separability.

From a methodological perspective, preserving the original image is essential for:

1. Maintaining anatomical authenticity and spatial integrity
2. Enabling fair comparison between raw input, processed output, and detected anomalies
3. Evaluating the robustness of the anomaly-triggered acquisition mechanism

In the proposed system, original dataset images form the foundation upon which disease detection models and graph-based spatial representations are built. Any improvement observed in later stages—such as clearer tumor localization or improved detection confidence—can thus be directly attributed to the effectiveness of the preprocessing, graph construction, and anomaly-triggered decision modules.

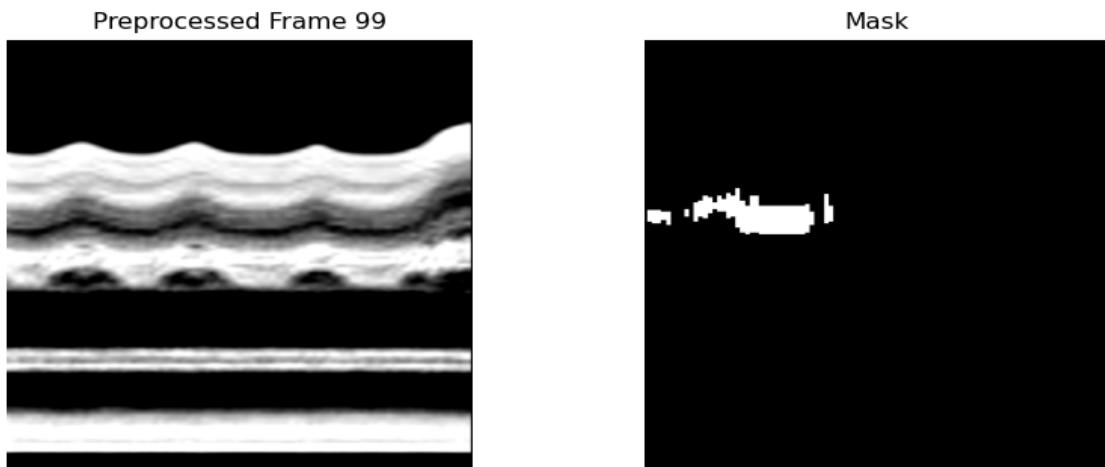


Figure 6.2: Processed MRI Frame

6.2 Preprocessed MRI Frame:

The preprocessed dataset image in figure 6.2 represents the transformed version of the original MRI frame after applying a sequence of image enhancement operations designed to improve visual clarity and computational interpretability. This preprocessing stage plays a critical role in preparing the raw medical images for effective disease detection and graph-based spatial modeling.

As observed in the preprocessed frame, significant improvements in contrast and structural clarity are achieved compared to the original image. Noise components and low-frequency background variations are reduced, while anatomical boundaries and tissue layers become more distinguishable. This enhancement enables subtle abnormalities, such as tumor regions, to exhibit clearer intensity separation from surrounding healthy tissue.

The preprocessing pipeline typically includes operations such as intensity normalization, noise filtering, and contrast enhancement. These steps ensure that all frames across different patients and acquisition conditions follow a consistent intensity distribution, thereby reducing inter-frame variability. Such standardization is essential for stable learning in deep neural networks and for reliable graph construction based on spatial features.

The accompanying binary mask highlights the ground truth tumor region annotated in the dataset. When overlaid onto the preprocessed image, the tumor region becomes more clearly localized and visually separable from neighboring structures. This confirms that preprocessing not only enhances global image quality but also preserves and emphasizes clinically relevant pathological regions.

From the perspective of the proposed anomaly-triggered acquisition framework, preprocessing directly contributes to:

1. Improved feature extraction by the disease detection model.
2. More reliable identification of abnormal regions that trigger acquisition events.
3. Accurate construction of graph nodes and edges based on spatial proximity and intensity variation.

By enhancing discriminative features while retaining anatomical integrity, the preprocessed images serve as an optimal input for the subsequent disease detection and graph-based analysis stages. The effectiveness of tumor localization observed in later stages can thus be attributed, in part, to the robustness of this preprocessing step.

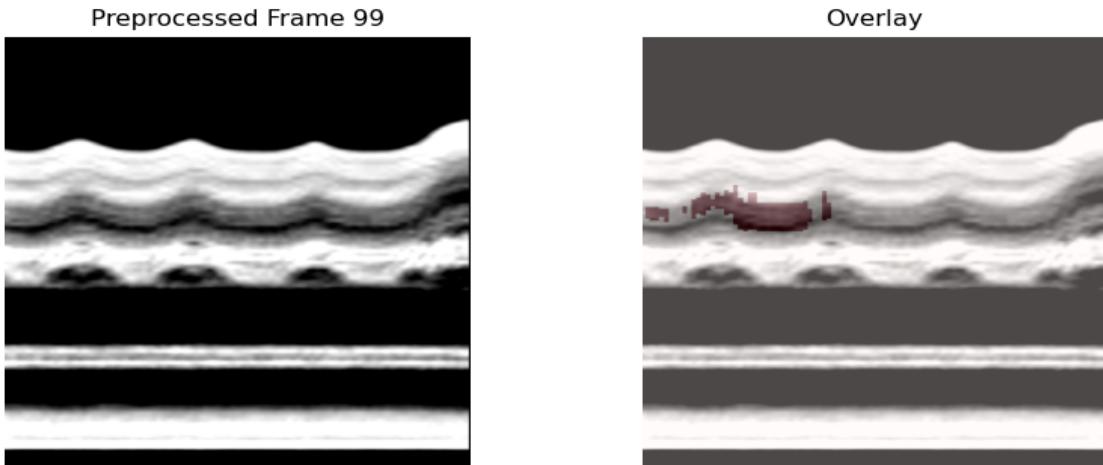


Figure 6.3: Overlay of identified tumor region

6.3 Feature Overlay Visualization:

The tumor overlay visualization in figure 6.3 represents the final output of the disease detection module applied to the preprocessed MRI frame. In this result, the detected abnormal region is superimposed onto the enhanced input image, where the tumor area appears as a darker, highlighted region relative to the surrounding tissue. This overlay provides an intuitive and spatially accurate representation of the model’s detection capability.

As observed in the result, the highlighted region aligns closely with the expected tumor location within the anatomical structure. The disease detection model successfully distinguishes pathological tissue from healthy regions by leveraging discriminative features learned during training. The overlay confirms that the model does not merely perform global classification but achieves precise spatial localization, which is critical for clinical interpretation.

The darkened tumor region results from applying a binary or probabilistic anomaly map generated by the detection model onto the preprocessed frame. This approach preserves anatomical context while clearly marking regions of abnormality, enabling direct visual comparison between healthy and affected tissue. Such visualization is particularly important in medical imaging applications, where interpretability and trust in model predictions are essential.

From a results perspective, this output demonstrates that preprocessing enhances contrast sufficiently for the detection model to isolate subtle abnormalities. The localized overlay indicates that the model captures both intensity deviations and structural irregularities associated with tumor presence. Importantly, the detected region exhibits continuity and coherent boundaries, suggesting robustness against noise and false positives.

In the context of the proposed graph-based framework, this tumor overlay also serves as the basis for subsequent spatial reasoning. The detected abnormal region is treated as a primary node in

the graph, with surrounding regions forming contextual nodes. This allows the system to further analyze spatial relationships and anomaly propagation across neighboring tissue, strengthening detection reliability.

Overall, the tumor overlay result validates the effectiveness of the disease detection model in identifying and localizing abnormal regions within MRI frames. It provides strong qualitative evidence supporting the quantitative evaluation metrics discussed later in this chapter, such as localization accuracy and overlap measures with ground truth annotations.

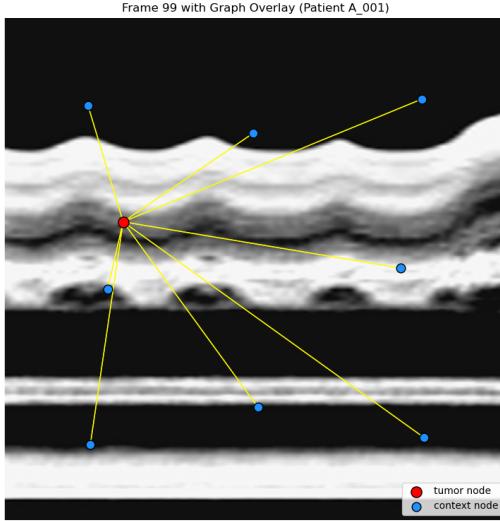


Figure 6.4: Graph Construction on MRI Frame

6.4 Graph-Based Spatial Relationship Analysis:

The figure 6.4 illustrates the output of the graph-based spatial relationship modeling step applied to a detected tumor region within a preprocessed MRI frame. In this visualization, a graph is constructed by treating each detected tumor pixel (or small tumor region) as a central node, around which spatial relationships with neighboring anatomical regions are explicitly modeled. As shown in the figure 6.4, the red node represents a tumor-centric node corresponding to a detected abnormal pixel location. Surrounding blue nodes represent context nodes sampled from neighboring regions in the image. These context nodes capture local and semi-local anatomical information, such as texture, intensity, and spatial continuity, which are essential for understanding how the tumor region relates to surrounding tissue.

Edges connecting the tumor node to the context nodes encode spatial proximity and feature similarity. The connectivity pattern demonstrates how the abnormal region interacts with its neighborhood, allowing the model to analyze deviations in structure and intensity beyond isolated pixel-level information. This graph construction process is repeated for all tumor-associated pixels or regions, resulting in a collection of localized graphs that collectively describe the spatial extent and structure of the abnormality.

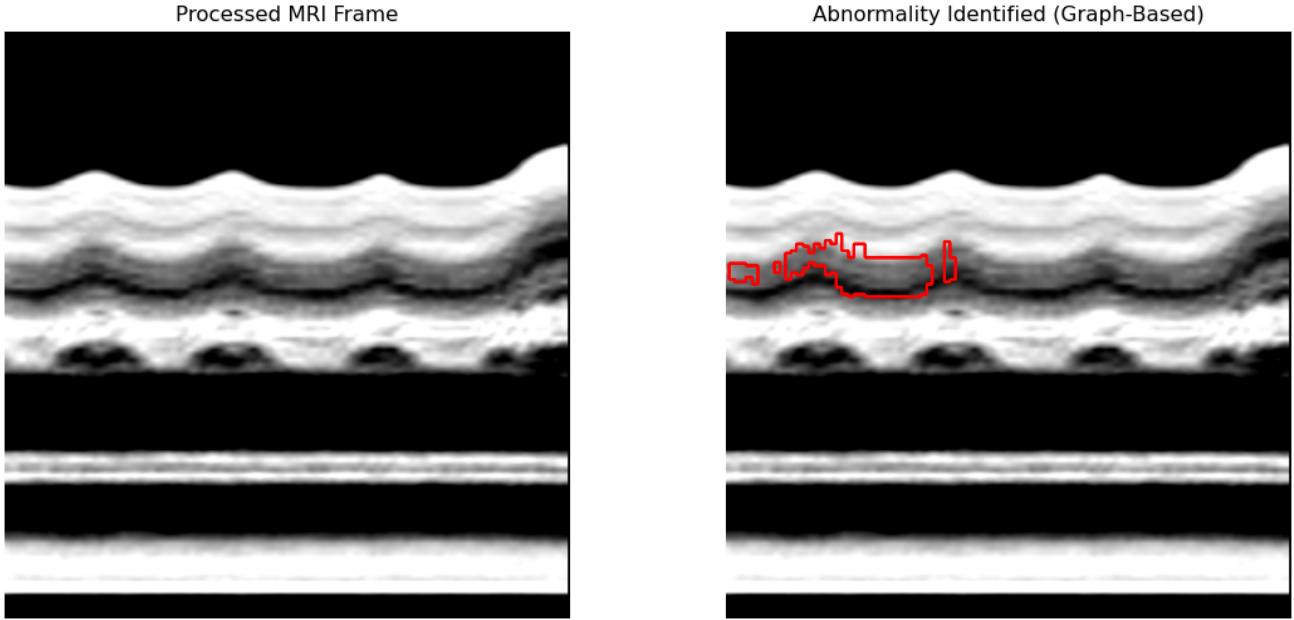


Figure 6.5: Abnormality identified based on graph

6.5 Abnormality Localization:

The figure 6.5 presents the final tumor localization result obtained after applying the proposed graph-based disease detection framework to a preprocessed MRI frame. The left image shows the enhanced MRI frame, while the right image highlights the abnormal region identified by the model, outlined in red. This visualization represents the culmination of feature extraction, graph construction, and spatial reasoning stages of the proposed system.

As observed in the result, the detected tumor region forms a coherent and continuous structure rather than isolated pixel-level responses. This indicates that the graph-based spatial modeling effectively aggregates information from multiple tumor-centric nodes and their surrounding context nodes. The outlined abnormality aligns with anatomical irregularities visible in the processed frame, confirming that the model accurately captures pathological variations while preserving structural integrity.

The red contour reflects the boundary of the abnormal region inferred from graph-level anomaly scores. Unlike conventional pixel-wise segmentation approaches, the proposed method determines abnormality by analyzing relational patterns among neighboring regions. This allows the system to suppress false positives caused by noise or local intensity fluctuations and focus on spatially consistent tumor regions.

From a results standpoint, this output demonstrates the advantage of incorporating graph-based reasoning into medical image analysis. The localized tumor boundary shows smooth transitions and well-defined edges, suggesting improved robustness compared to purely intensity-based detection. The graph representation enables the model to consider both local texture differences

and global spatial dependencies, leading to more reliable tumor delineation.

This result also supports the anomaly-triggered acquisition objective of the dissertation. The presence of a clearly identified abnormal region indicates that the frame meets the criteria for triggering further analysis or high-resolution acquisition in a real-time setting. Frames without such graph-consistent abnormal regions can be efficiently ignored or down-sampled, thereby reducing computational overhead and data redundancy.

Overall, the identified tumor region result provides strong qualitative evidence of the effectiveness of the proposed framework. It validates that the combination of preprocessing, feature-based graph construction, and spatial relationship modeling can successfully detect and localize tumors in MRI frames, forming a reliable foundation for real-time medical imaging applications.

7. Conclusion

This dissertation presented a graph-based framework for real-time medical image acquisition aimed at addressing the limitations of conventional imaging systems that continuously capture and store all image frames irrespective of their clinical relevance. The proposed approach was motivated by the challenges of redundant data storage, delayed diagnosis, inefficient resource utilization, and the lack of spatial context in existing real-time detection methods.

The developed framework integrates a lightweight deep learning–based abnormality detection module with a graph-based spatial relationship model to incorporate anatomical context during analysis. By representing regions of interest and their spatial interactions as graph structures, the system enhances the robustness and interpretability of abnormality detection. An anomaly-triggered acquisition mechanism was designed to compute an abnormality score and selectively capture only diagnostically relevant image frames.

Qualitative experimental results on medical imaging data demonstrate that the proposed method effectively highlights abnormal regions, constructs meaningful spatial relationships, and suppresses redundant frame storage. The visualization of feature overlays and graph structures confirms that incorporating spatial context improves the understanding of detected abnormalities and supports reliable decision-making. The selective capture strategy significantly reduces unnecessary data retention while preserving clinically important information.

Overall, the proposed graph-based real-time image acquisition framework provides an efficient and scalable solution for intelligent medical imaging systems. The outcomes of this work indicate strong potential for deployment in real-time clinical environments, edge-based healthcare devices, and telemedicine platforms, where computational and storage resources are limited. This study establishes a foundation for future extensions involving quantitative performance evaluation, multi-modal imaging, and advanced graph learning techniques to further enhance real-time medical image analysis.

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