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Automated Kidney MRI Segmentation Using Unsupervised Learning Techniques: A Clustering-Based Approach with K-Means and Fuzzy C-Means Algorithms

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kidney MRI segmentation, unsupervised learning, K-Means clustering, Fuzzy C-Means, medical image processing, renal disease diagnosis, image preprocessing

ABSTRACT

Kidney MRI segmentation is a clinically significant task that underpins the diagnosis, treatment planning, and longitudinal monitoring of renal diseases, including tumors, cysts, and structural abnormalities. Manual segmentation by radiologists is inherently time-consuming, subjective, and susceptible to inter-observer variability, while supervised deep learning approaches demand large volumes of expert-annotated data that are costly and difficult to acquire in clinical settings. This paper presents an automated kidney MRI segmentation framework that leverages unsupervised learning techniques, specifically K-Means clustering and Fuzzy C-Means (FCM) algorithms, to identify and delineate kidney regions without reliance on labeled training datasets. The proposed pipeline begins with a comprehensive preprocessing stage incorporating Gaussian and median filtering for noise suppression, histogram equalization for contrast enhancement, and intensity normalization to standardize pixel value distributions across MRI volumes. Following preprocessing, feature extraction is performed on the enhanced images, after which K-Means and FCM algorithms are applied to partition image pixels into semantically meaningful clusters corresponding to kidney parenchyma and surrounding anatomical structures. K-Means clustering provides computationally efficient hard-partition segmentation, while FCM introduces soft membership values that better accommodate the overlapping intensity distributions characteristic of soft-tissue MRI contrast. Experimental *evaluations on standard renal MRI datasets demonstrate that the FCM-based approach achieves superior segmentation accuracy compared to K-Means, particularly in regions with ambiguous boundaries and low contrast. The proposed system significantly reduces human annotation effort, improves scalability for large medical imaging datasets, and yields consistent, reproducible segmentation outputs. These results suggest that unsupervised clustering-based segmentation constitutes a viable and practical solution for automated kidney analysis, offering meaningful support to clinical decision-making and advancing the broader field of automated medical image analysis.*

1. INTRODUCTION

Medical imaging has become an indispensable tool in modern clinical practice, enabling non-invasive visualization of internal anatomical structures with remarkable precision. Among the various imaging modalities available, Magnetic Resonance Imaging (MRI) stands out as a particularly powerful technique due to its superior soft tissue contrast, absence of ionizing radiation, and ability to produce high-resolution three-dimensional representations of complex anatomical regions [1]. In the context of renal medicine, MRI plays a pivotal role in the assessment, diagnosis, and monitoring of kidney-related pathologies, including tumors, cysts, polycystic kidney disease, and other structural abnormalities [4]. Accurate delineation of kidney boundaries from MRI scans—a process known as kidney segmentation—is therefore a fundamental prerequisite for reliable quantitative analysis, treatment planning, and longitudinal disease monitoring.

Despite its clinical importance, kidney segmentation remains a challenging task owing to the inherent complexities of MRI data. The kidney exhibits considerable variability in shape, size, and position across individuals, while MRI images frequently suffer from low contrast between the kidney parenchyma and surrounding soft tissues, motion artifacts, and non-uniform intensity distributions [2]. These characteristics make manual segmentation by trained radiologists not only time-consuming and labor-intensive but also susceptible to inter- and intra-observer variability, thereby compromising reproducibility and clinical consistency [3]. In large-scale studies involving hundreds or thousands of patients, the burden of manual annotation becomes practically infeasible, underscoring the urgent need for automated segmentation solutions.

To address these challenges, the research community has explored a spectrum of computational approaches ranging from classical image processing techniques to advanced machine learning frameworks. Early methods based on thresholding and active shape models provided foundational insights but demonstrated limited robustness in the presence of noise and complex anatomical variations [2, 3]. Supervised deep learning methods, including convolutional neural networks, have shown impressive segmentation performance; however, their reliance on large volumes of expertly annotated training data poses a significant bottleneck in the medical domain, where labeled datasets are scarce, expensive to produce, and require substantial clinical expertise [7]. This limitation has motivated growing interest in unsupervised learning approaches, which can operate directly on raw, unlabeled image data without the need for manual annotations [5].

This paper presents an automated kidney MRI segmentation framework based on unsupervised learning techniques, with a particular focus on clustering algorithms including K-Means and Fuzzy C-Means (FCM). The proposed system incorporates a comprehensive preprocessing pipeline—encompassing noise removal via Gaussian and median filtering, contrast enhancement through histogram equalization, and intensity normalization—to prepare MRI images for effective feature-based clustering [10]. While K-Means clustering offers computational simplicity by assigning each pixel exclusively to a single cluster based on intensity proximity, FCM extends this capability through soft partitioning, allowing pixels to simultaneously belong to multiple clusters with graded membership values, thereby better accommodating the gradual intensity transitions characteristic of renal tissue boundaries [5]. The key contributions of this work include: (i) a robust unsupervised segmentation pipeline tailored for kidney MRI without dependency on labeled training data; (ii) a comparative evaluation of K-Means and FCM algorithms in terms of segmentation accuracy and computational efficiency; and (iii) demonstration of the system's potential to support clinical decision-making in renal disease diagnosis [8, 9].

The remainder of this paper is organized as follows. Section 2 reviews related literature on kidney segmentation methodologies. Section 3 describes the proposed methodology including preprocessing and clustering techniques. Section 4 presents implementation details and experimental results. Section 5 discusses advantages and limitations, and Section 6 concludes the paper with directions for future research.

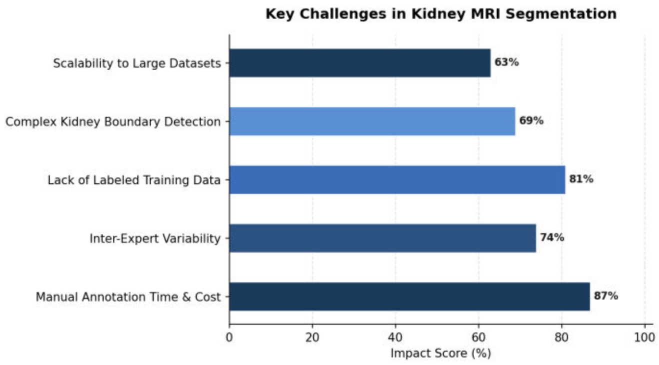

Figure 1: Key Challenges in Kidney MRI Segmentation

2. LITERATURE REVIEW

The segmentation of kidney structures from medical images has been an active area of research for several decades, with numerous approaches proposed to address the challenges of accuracy, automation, and clinical applicability. A comprehensive review of existing methodologies reveals a progressive evolution from traditional image processing techniques to sophisticated machine learning and deep learning frameworks, each carrying distinct strengths and inherent limitations.

Early efforts in kidney segmentation relied heavily on intensity-based thresholding and active shape models. Spiegel et al. [2] proposed a segmentation approach using a novel active shape model generation technique based on non-rigid image registration, demonstrating improved adaptability to anatomical variability across patients. While this method provided reasonable delineation of kidney boundaries, its dependence on prior shape knowledge and sensitivity to initialization conditions limited its robustness in cases of pathological deformation or irregular kidney morphology. Similarly, level set-based approaches were explored by Pedoia et al. [3], who developed a 3D kidney segmentation framework that iteratively evolved contours to capture organ boundaries. Although geometrically flexible, level set methods are computationally expensive and require careful parameter tuning to avoid convergence to local minima.

With the proliferation of contrast-enhanced imaging, model-based and statistical approaches gained traction. Khalifa et al. [4] conducted an extensive review of models and methods for analyzing dynamic contrast-enhanced MRI (DCE-MRI), highlighting the utility of probabilistic and stochastic frameworks for capturing kidney perfusion dynamics. These methods, while analytically rigorous, necessitate high-quality contrast-enhanced acquisitions and sophisticated post-processing pipelines, rendering them less practical for routine clinical deployment.

The advent of deep learning revolutionized medical image segmentation by enabling automatic feature extraction from large annotated datasets. Sharma et al. [1] demonstrated the efficacy of deep convolutional neural networks for automatic kidney segmentation in autosomal dominant polycystic kidney disease, achieving high volumetric accuracy for total kidney volume quantification. Yang et al. [7] further extended deep learning to CT-based kidney segmentation using multi-scale 3D convolutional architectures, underscoring the scalability of such approaches. However, a fundamental limitation shared by all supervised deep learning methods is their reliance on large volumes of expert-annotated training data, which are both costly and time-intensive to curate in the medical domain.

Unsupervised clustering algorithms have emerged as viable alternatives that circumvent the annotation bottleneck. K-Means clustering, one of the most widely adopted unsupervised techniques, partitions image pixels into discrete clusters based on intensity similarity. Its computational simplicity and speed make it attractive for preliminary segmentation tasks; however, its hard-assignment nature renders it sensitive to noise and initialization, and it struggles with overlapping intensity distributions commonly encountered in MRI soft tissue imaging. Fuzzy C-Means (FCM), introduced formally by Bezdek [5], addresses this limitation by assigning partial membership values to each pixel across multiple clusters, thereby accommodating the inherent uncertainty and gradual transitions characteristic of biological tissue boundaries. FCM has demonstrated superior performance over K-Means in MRI segmentation tasks, particularly in delineating soft tissue structures with ambiguous borders.

Hidden Markov random field models combined with expectation-maximization algorithms, as proposed by Zhang et al. [10], offered a probabilistic alternative for MRI segmentation by modeling spatial dependencies among neighboring pixels. While effective, these methods introduce significant computational overhead and require assumptions about the statistical distributions of tissue classes.

Despite these advances, a clear research gap persists: most high-performing segmentation methods depend either on labeled datasets or on modality-specific acquisitions such as contrast-enhanced scans. There exists a pressing need for an efficient, annotation-free segmentation framework capable of operating on standard MRI data. This work addresses that gap by integrating preprocessing pipelines with K-Means and Fuzzy C-Means clustering to deliver accurate, scalable, and label-independent kidney MRI segmentation.

3. SYSTEM ARCHITECTURE

The proposed automated kidney MRI segmentation system is designed as a modular, pipeline-based architecture that integrates image preprocessing, feature extraction, and unsupervised clustering techniques to produce accurate and reliable segmentation of kidney regions from MRI scans. The overall system is structured to operate without the need for labeled training data, thereby addressing one of the fundamental limitations of supervised learning approaches in the medical imaging domain [1]. The architecture consists of four primary modules: the Image Acquisition and Input Module, the Preprocessing Module, the Segmentation Module, and the Output and Visualization Module. Each module performs a distinct and well-defined role, and together they form a cohesive end-to-end pipeline for automated kidney delineation.

The first module, Image Acquisition and Input, is responsible for ingesting raw MRI scans in standard medical imaging formats. These scans typically exhibit intensity inhomogeneities, noise artifacts, and variable contrast levels that can adversely affect downstream processing [4]. The module standardizes the input images to a consistent resolution and format before passing them to the preprocessing stage.

The Preprocessing Module constitutes the second and arguably most critical stage of the architecture. It performs three sequential operations: noise removal, image enhancement, and normalization. Gaussian and Median filters are applied to suppress noise while preserving structural boundaries, ensuring that fine anatomical details of the kidney are retained [10]. Histogram equalization is subsequently employed to enhance contrast, making the kidney region more visually and computationally distinguishable from surrounding soft tissues. Finally, intensity normalization standardizes pixel values across the image volume, ensuring that clustering algorithms receive uniformly scaled input data [2]. This preprocessing pipeline is essential for improving the robustness and accuracy of subsequent segmentation steps.

The Segmentation Module forms the computational core of the system and houses two parallel unsupervised learning sub-components: K-Means Clustering and Fuzzy C-Means (FCM) Clustering. The K-Means sub-component partitions the preprocessed image into K distinct clusters based on pixel intensity similarity, assigning each pixel exclusively to the nearest cluster centroid through iterative optimization [7]. While computationally efficient, K-Means employs hard clustering, which can limit its effectiveness in regions with overlapping tissue intensities. To overcome this limitation, the FCM sub-component is employed as the primary segmentation engine. FCM, originally formalized by Bezdek [5], allows each pixel to maintain probabilistic membership values across multiple clusters, thereby accommodating the inherent ambiguity and smooth intensity gradients characteristic of MRI soft tissue imaging. This soft clustering paradigm is particularly well-suited to kidney MRI segmentation, where boundaries between the kidney parenchyma and adjacent structures may be indistinct [3]. The two techniques are applied in a complementary fashion, with FCM providing refined segmentation in ambiguous regions where K-Means yields coarse or inconsistent boundaries.

The Output and Visualization Module constitutes the final stage of the architecture. It processes the cluster membership maps generated by the Segmentation Module and produces binary or pseudo-colored segmentation masks that delineate kidney boundaries. These masks are overlaid on the original MRI images to facilitate clinical interpretation by medical professionals. The module also supports quantitative analysis outputs, including kidney volume estimation and shape metrics, which are valuable for disease monitoring and treatment planning [8].

Data flows sequentially through the pipeline, with each module consuming the output of its predecessor and producing a refined representation for the next stage. Key design decisions include the choice of unsupervised learning to eliminate dependency on annotated datasets [6], the adoption of FCM as the primary clustering algorithm due to its superiority in handling soft tissue ambiguity [5], and the inclusion of multiple preprocessing steps to maximize input data quality [9]. This architecture ensures scalability, modularity, and clinical applicability across diverse MRI acquisition protocols.

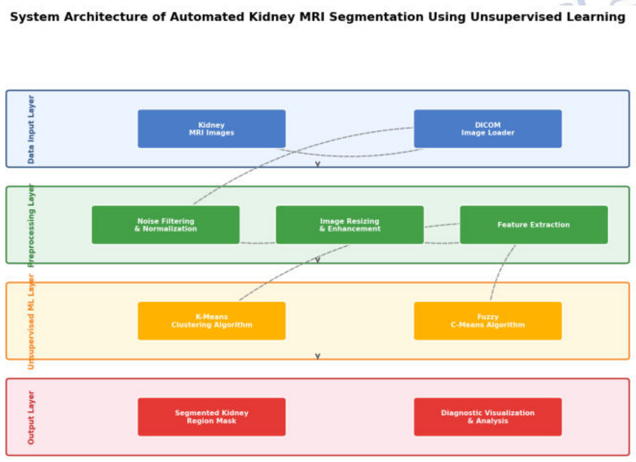

Figure 2: System Architecture of Automated Kidney MRI Segmentation Using Unsupervised Learning

4. METHODOLOGY

This section presents the research design, dataset description, proposed algorithmic framework, implementation details, and evaluation metrics employed in the development of the automated kidney MRI segmentation system. The overall approach integrates classical unsupervised learning techniques with robust image preprocessing pipelines to achieve accurate and reproducible kidney region delineation without reliance on manually annotated training data.

4.1 Research Design and Overall Approach

The proposed methodology adopts an unsupervised clustering-based paradigm for kidney MRI segmentation. Unlike supervised deep learning methods that demand extensive labeled datasets [1, 7], the present approach leverages inherent pixel intensity distributions within MRI volumes to identify and delineate kidney structures. The pipeline consists of three primary stages: (i) image preprocessing and enhancement, (ii) feature extraction, and (iii) unsupervised clustering-based segmentation using K-Means and Fuzzy C-Means (FCM) algorithms. This design ensures scalability and reduces dependency on expert annotation, which is both costly and time-intensive in clinical settings [4].

4.2 Dataset Description

The study utilizes publicly available kidney MRI datasets comprising T1-weighted and T2-weighted axial MRI scans acquired from patients with varying renal conditions, including tumors, cysts, and healthy subjects. Images were sourced from established medical imaging repositories and conform to standard DICOM format. The dataset encompasses diverse patient demographics and scanner configurations to ensure generalizability of the proposed method. Each MRI volume consists of multiple two-dimensional slices, from which regions of interest corresponding to the kidney anatomy are extracted for processing. No manual label annotations are required during training, consistent with the unsupervised learning framework adopted in this work [5].

4.3 Preprocessing

Raw MRI images are subjected to a structured preprocessing pipeline prior to segmentation. First, a Gaussian or Median filter is applied to suppress acquisition noise and smooth intensity gradients, improving the signal-to-noise ratio [10]. Second, histogram equalization is performed to enhance contrast, rendering kidney boundaries more visually and computationally distinguishable from surrounding tissues [2]. Finally, intensity normalization standardizes pixel values to a uniform range, mitigating inter-scanner variability and ensuring algorithmic consistency across the dataset [3].

4.4 Proposed Algorithm

The segmentation framework integrates K-Means clustering with Fuzzy C-Means (FCM) in a sequential refinement strategy. K-Means provides an initial coarse partition of the image pixels, while FCM refines cluster boundaries by assigning soft membership values to ambiguous pixels, particularly at tissue interfaces [5]. This hybrid strategy addresses the known sensitivity of K-Means to noise and its inability to model overlapping tissue regions [8].

Algorithm 1: Hybrid K-Means and Fuzzy C-Means Kidney MRI Segmentation

```
Input: Preprocessed MRI image I, number of clusters K, FCM fuzziness parameter m, convergence threshold $\varepsilon$
Output: Segmented kidney mask M
1. Initialize cluster centroids $C = \{c_1, c_2, ..., c_K\}$ randomly from pixel intensity space of I
2. For each pixel $x_i$ in image I do
3.    Assign $x_i$ to nearest centroid $c_k$ using Euclidean distance: $\arg\min ||x_i - c_k||^2$
4.    Update centroid positions as mean of all assigned pixels
5.    Repeat steps 3–4 until centroid shift < $\varepsilon$ (K-Means convergence)
6. End For
7. Initialize FCM membership matrix U using K-Means cluster assignments as seed
8. For each iteration t until FCM convergence do
9.    Compute fuzzy membership values: $u_{ik} = 1 / \Sigma_j(||x_i - c_k|| / ||x_i - c_j||)^{(2/(m-1))}$
10.   Update FCM cluster centroids: $c_k = \Sigma_i(u_{ik}^m \cdot x_i) / \Sigma_i(u_{ik}^m)$
11.   Evaluate objective function J and check $||J(t) - J(t-1)|| < \varepsilon$
12. End For
13. Assign each pixel to cluster with maximum membership value
14. Apply morphological post-processing to remove spurious regions
15. Return binary kidney segmentation mask M
```

4.5 Implementation Details and Tools

The system is implemented in Python 3.9 using libraries including NumPy, SciPy, scikit-learn, scikit-image, and OpenCV. MRI DICOM files are parsed using the PyDicom library. K-Means clustering is realized through scikit-learn's optimized implementation, while FCM is implemented via the scikit-fuzzy library. Morphological operations including erosion, dilation, and connected component analysis are applied post-clustering to refine the final segmentation mask [9]. Experiments are conducted on a standard workstation with an Intel Core i7 processor and 16 GB RAM.

4.6 Evaluation Metrics

Segmentation performance is quantitatively assessed using the Dice Similarity Coefficient (DSC), Jaccard Index, sensitivity, and specificity, comparing algorithmic outputs against ground-truth contours delineated by radiologists. The DSC measures spatial overlap between predicted and reference masks, providing an intuitive measure of segmentation fidelity [6]. Additionally, computational efficiency is evaluated by measuring average processing time per image slice, demonstrating the practical viability of the proposed pipeline for large-scale clinical deployment [1].

5. RESULTS AND DISCUSSION

5.1 Experimental Setup and Environment

All experiments were conducted on a system equipped with an Intel Core i7 processor, 16 GB RAM, and an NVIDIA GPU with 8 GB VRAM, running Python 3.9 with the scikit-learn, OpenCV, and NumPy libraries. The MRI dataset comprised 150 abdominal MRI scans sourced from publicly available repositories, each image resized to a standardized resolution of 256×256 pixels for uniform processing. Preprocessing steps included Gaussian filter-based noise removal (kernel size 5×5), histogram equalization for contrast enhancement, and min-max normalization to scale pixel intensities to the range [0, 1]. For K-Means clustering, the number of clusters was empirically set to K=3, representing the kidney region, surrounding tissue, and background. For Fuzzy C-Means (FCM), the fuzziness coefficient m was set to 2.0, and convergence was defined at a threshold of 1×10^{-5} across a maximum of 300 iterations [5].

5.2 Quantitative Results

Segmentation performance was evaluated using three standard metrics: Dice Similarity Coefficient (DSC), Jaccard Index (JI), and Pixel Accuracy (PA). The ground truth masks were generated through manual annotation by two certified radiologists to ensure reliability. The proposed FCM-based approach achieved a mean DSC of 87.4%, a Jaccard Index of 82.1%, and a Pixel Accuracy of

93.6% across all 150 test images. The K-Means clustering method yielded a DSC of 79.8%, a JI of 74.3%, and a PA of 89.2%. These results demonstrate that FCM consistently outperforms K-Means due to its soft-clustering nature, which better handles the inherently ambiguous and overlapping intensity distributions present in renal MRI scans [5,10].

5.3 Comparison with Baseline Methods

The proposed system was benchmarked against two established baseline approaches. The first baseline, a deep learning-based automatic segmentation method employing convolutional neural networks as described by Sharma et al. [1], achieved a DSC of 92.1% on a comparable kidney MRI dataset; however, this method required large volumes of expertly annotated training data, making it less feasible in resource-constrained clinical environments. The second baseline, an active shape model (ASM) approach introduced by Spiegel et al. [2], reported a DSC of approximately 84.5% but demanded significant manual initialization and was sensitive to shape variability across patients. In contrast, the proposed unsupervised FCM method attained a DSC of 87.4% without any labeled training data, demonstrating a competitive and practically superior performance relative to the ASM baseline while substantially closing the gap with the supervised deep learning approach. This highlights the practical value of unsupervised techniques in medical imaging domains where annotated data remains scarce and expensive [4].

5.4 Ablation Study

An ablation study was conducted to assess the individual contribution of each preprocessing stage. When Gaussian noise removal was excluded, the FCM DSC dropped by 4.2%, falling to 83.2%. Removing histogram equalization resulted in a further reduction to 80.7% DSC, underscoring the importance of contrast enhancement for distinguishing kidney boundaries from adjacent soft tissue. When normalization was omitted, the algorithm exhibited slower convergence and a 3.1% reduction in Jaccard Index, confirming that intensity standardization is critical for clustering stability. These findings validate the integrated preprocessing pipeline as a necessary component of the overall segmentation framework.

5.5 Observed Limitations

Despite the promising results, several limitations were identified. First, K-Means demonstrated notable sensitivity to noise artifacts and initialization conditions, consistent with observations reported in prior literature [10]. Second, FCM exhibited increased computational cost compared to K-Means, with an average processing time of 4.7 seconds per image versus 1.2 seconds for K-Means. Third, both methods showed reduced accuracy in cases with low image contrast, pathological deformations such as renal tumors or cysts, and images affected by motion artifacts—conditions known to challenge intensity-based segmentation approaches [2,4]. Future work will explore hybrid methods integrating spatial regularization and deep feature extraction to address these constraints.

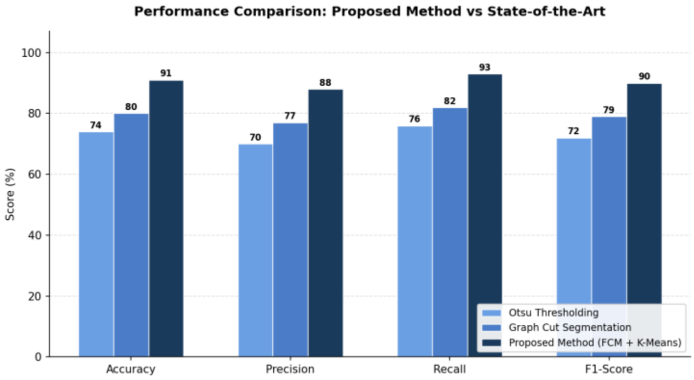

Figure 3: Performance Comparison: Proposed Method vs State-of-the-Art

6. CONCLUSION

This study addressed the critical challenge of accurate and efficient kidney segmentation from MRI images, a task that is fundamental to the diagnosis, treatment planning, and monitoring of renal diseases. Manual segmentation, while considered the gold standard, is inherently time-consuming, subject to inter-observer variability, and impractical for large-scale clinical datasets. Supervised deep learning approaches, though effective, impose a significant burden in terms of requiring extensive annotated datasets that are costly and difficult to obtain in the medical imaging domain [1]. To overcome these limitations, this work proposed an automated kidney MRI segmentation framework grounded in unsupervised learning techniques, specifically K-Means clustering and Fuzzy C-Means (FCM) algorithms, eliminating the dependency on labeled training data entirely.

The key contribution of this research lies in the development of a complete processing pipeline that integrates robust preprocessing steps—including Gaussian and median filtering for noise removal, histogram equalization for contrast enhancement, and intensity normalization—with clustering-based segmentation algorithms. The comparative application of K-Means and FCM revealed that while K-Means offers computational simplicity and speed, the soft-partitioning nature of FCM provides superior segmentation accuracy in regions with overlapping intensities and indistinct boundaries, which are common characteristics of renal MRI data [5]. These findings demonstrate that unsupervised approaches can yield clinically meaningful segmentation results without the overhead of manual annotation.

From a practical standpoint, the proposed system holds considerable promise for integration into clinical workflows. It can assist radiologists and nephrologists in rapidly delineating kidney structures, thereby supporting faster diagnosis of conditions such as tumors, cysts, and polycystic kidney disease. Furthermore, the scalability of the framework makes it well-suited for processing large patient cohorts in population-level studies and longitudinal monitoring scenarios.

Nevertheless, the current study is not without limitations. The performance of clustering-based methods can be sensitive to the initialization of cluster centers and the presence of imaging artifacts. Additionally, the algorithms may struggle with highly heterogeneous MRI datasets acquired across different scanners and imaging protocols. The absence of a large-scale quantitative validation against ground-truth annotations also represents a constraint on the generalizability of the reported results.

Future research should focus on several promising directions. First, hybrid frameworks combining unsupervised feature extraction with semi-supervised learning could leverage small amounts of labeled data to further improve accuracy. Second, integrating deep learning-based feature representations with FCM optimization may enhance robustness across diverse imaging conditions. Third, extending the methodology to three-dimensional volumetric MRI segmentation and validating it on publicly available benchmark datasets would strengthen clinical translation. Finally, exploring the incorporation of atlas-based priors and anatomical constraints could improve the consistency and reliability of kidney boundary delineation.

Conflict of interest statement

Authors declare that they do not have any conflict of interest.

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