



# Artificial Intelligence in Medical Imaging: A Critical Review of Methods, Applications, and Clinical Implementation

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## Abstract

Artificial intelligence (AI) has rapidly advanced the analysis of medical images, opening up new ways to find, diagnose, and make clinical decisions about diseases. This study offers a comprehensive critical review of AI-driven methodologies in medical imaging, focusing on their clinical significance and practical applicability. Using Citation Network Analysis (CNA), a systematic literature search was set up that found five main thematic clusters: oncology, neurodiagnostics, Alzheimer's disease, Multiple Sclerosis, and advanced segmentation techniques. The analysis demonstrates that deep learning methodologies, such as Convolutional Neural Networks and U-Net architectures, have markedly enhanced the precision of tumor detection and segmentation by incorporating high-resolution contextual and spatial features. Machine learning models have shown great promise in neurological imaging for finding problems and keeping an eye on the progress of lesions, especially in Alzheimer's disease and Multiple Sclerosis. Even with these improvements, there are still problems with dataset diversity, ethical issues, and real-world clinical validation. The results show that AI systems need to be integrated into routine clinical practice successfully, which requires collaboration between different fields, fair datasets, and strong regulatory validation.

**Index Terms:** Artificial Intelligence; Medical Applications; Critical Review; Clinical Relevance; Citation Network Analysis; Deep Learning; Healthcare AI; Translational ML.

## 1. Introduction

Artificial intelligence (AI) is a catalyst for innovation across diverse sectors, with medicine being a prominent example. The escalating application of AI within healthcare has, in turn, generated a substantial body of research, a considerable portion of which is still largely theoretical. This review seeks to bridge this divide by examining the existing literature, concentrating on the practical deployment of AI systems, their compliance with established medical protocols, and logistical factors like operational efficiency. To organize this review, we employed Citation Network Analysis (CNA) to categorize the extant studies into thematic clusters, determined by their citation relationships.

A methodological limitation of our approach using CNA is the exclusion of recently published papers that have not yet been cited. This results in the omission of emerging and potentially impactful studies. To address this, we briefly synthesized abstracts from several recently published papers outside the citation network. Article [1]

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demonstrated the value of explainable AI by applying Local Interpretable Model-agnostic Explanations (LIME) and Gradient-weighted Class Activation Mapping (Grad-CAM) to enhance interpretability in deep learning-based medical image classification. Article [2] suggested utilizing classification neural networks for segmentation purposes, generating heatmaps that approximate segmentation results. This approach, employing GuidedBackprop, serves as a low-annotation solution within privacy-constrained environments. Subsequently, [3] presented an architecture that substantially enhanced segmentation accuracy while simultaneously decreasing computational expenses across multi-modal MRI datasets. These investigations underscore the continuous advancements in transparency, efficiency, and scalability.

Rest of the paper is organized as follows; Section outlines the CNA-based methodology, followed by cluster findings and ethical issues in Section 3, and conclusions in Section 4.

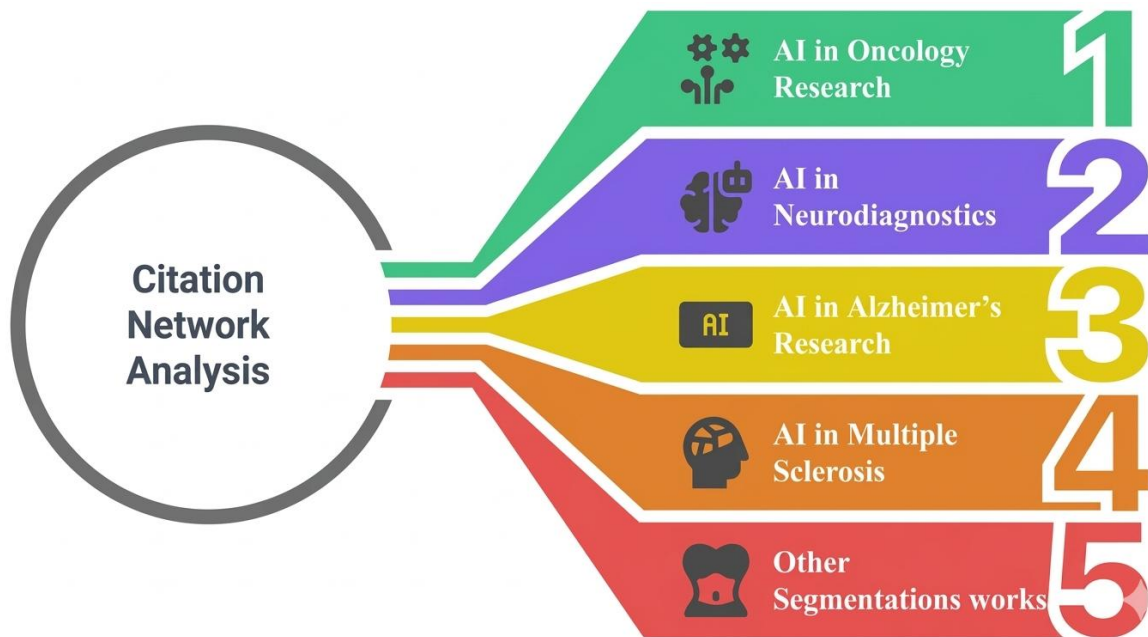
## 2. METHODOLOGY: CITATION NETWORK ANALYSIS

To gather the literature for this review, we used CNA by sourcing academic papers from the Web of Science (WOS). The search used the keywords: "brain image" OR "automatic segmentation" AND "artificial intelligence" OR "machine learning" AND "public health" AND "disease prediction", streamlining the selection to papers focused on brain imaging. We built the citation network using Search Path Link Count (SPLC), which measures how often a connection appears across search paths to highlight influential knowledge flows between papers. The global main path was then derived by linking the highest-weighted connections from seminal to recent studies and visualized using Gephi. An overview of the CNA process is shown in Figure 1.



**Figure 1:** Overview of the Citation Network Analysis (CNA) steps used in this study.

Through main path analysis, we identified five thematic clusters: oncology, neurodiagnostics, Alzheimer’s disease, multiple sclerosis, and advanced segmentation techniques. These clusters are visualized in Figure 2. Modularity-based clustering grouped 500 nodes by theme, and Pajek graphing software visualized the relationships and highlighted significant contributions. We also included segmentation papers not tied to specific pathologies to emphasize broader technical relevance. CNA offers a systematic, data-driven way to review the evolution of AI in medical imaging. By focusing on brain-related studies, we identified key trends, algorithms, and influential work. The combined use of main path analysis and Pajek visualizations clarified how AI-assisted brain diagnostics have progressed in both clinical and technical domains.



**Figure 2:** The thematic clusters derived from Citation Network Analysis.

### 2.1. AI in Oncology Research

This section examines AI methods in oncological research, including tumor detection, surveillance through lymph node metastases assessment, morphological and molecular subtyping, and classification. AI technologies can support both diagnosis and treatment planning by identifying tumors and assessing severity. Shapey et al. in [4] devised a technique for the detection and quantification of vestibular schwannomas (VS) via contrast-enhanced T1- and T2-weighted magnetic resonance imaging (MRI). Given the slow growth rate of these neoplasms, precise monitoring is crucial. A 2.5D convolutional neural network (CNN) was employed, integrating in-plane and through-plane resolutions to enhance segmentation accuracy. Their model demonstrated a 93.68% Dice Similarity Coefficient (DSC) when compared to ground truth annotations, thereby providing a computationally efficient alternative to complete 3D segmentation. The incorporation of adjacent slices facilitates longitudinal observation; however, imaging variability continues to constrain wider implementation.

Stangerup in [5] observed the unpredictable nature of vestibular schwannoma (VS) progression, thereby endorsing a wait-and-scan approach. This observation underscores the necessity of precise monitoring, such as Shapey’s model; although effective on standardized datasets, it necessitates more extensive training to accommodate clinical variability. Likewise, Khawaldeh et al. [6] devised a convolutional neural network (CNN) for glioma classification via MRI. Their algorithm stratified brain images into a three-tier classification system (no tumor, low-grade, high-

grade), which diverges from the TNM staging system, a tool that informs prognosis and treatment decisions in clinical settings.

Brain tumors are often graded 1–4 based on growth rate, metastatic potential, and structural changes, requiring longitudinal analysis to account for heterogeneity. Built on a Krizhevsky-inspired structure in DL4J, the model used contrast-enhanced, normalized, and down-sampled  $160 \times 160$  images to reduce computational load while preserving features. Seo et al. [7] proposed a CT-based liver and tumor segmentation model using a modified U-Net (mU-Net). Liver segmentation is challenging due to the organ's deformable shape and neighboring structures [8]. In the context of radiotherapy, the ability to differentiate neoplasms from surrounding healthy tissue is of paramount importance to mitigate unnecessary radiation exposure. Seo's mU-Net demonstrated enhanced localization capabilities by leveraging edge features and object-aware upsampling techniques, thereby circumventing the patient-specific constraints inherent in atlas-based models. While these results are encouraging, further validation within a wider clinical setting is essential.

The model was trained slice-by-slice, but volumetric learning could better capture 3D morphology. According to Oliva et al. [9], the liver is second only to lymph nodes as a site of metastasis. Seo's model accounts for anatomical variability, deformability, and tumor location. Smaller tumors can be missed in physical exams due to ribcage coverage, a challenge addressed by contrast-enhanced imaging, which improves tissue differentiation. This modality was also used by Shapey and by Hamamci et al. [10], who developed a seeded segmentation model for brain tumors using cellular automata (CA) and contrast-enhanced T1 MRI. Validated on synthetic and clinical data, the model achieved 80–90% overlap with expert annotations. The method demonstrated efficiency and resilience in the face of variable initialization and tumor heterogeneity. Narayanan et al. [11] employed multichannel fuzzy c-means (MFCM) clustering, integrated with particle swarm and bacterial foraging optimization (PSO-BFOA), to segment tumors. This approach effectively tackled difficulties in boundary detection, particularly in the presence of edema and invasion. However, multichannel MRI can introduce bias field inhomogeneity, thereby complicating the segmentation process. Consequently, their PSBFO-MFCM algorithm could be further optimized to accommodate such conditions. Selvapandian and Manivannan [12] utilized a fusion method for glioma detection, incorporating NSCT to enhance image clarity and an Adaptive Neuro-Fuzzy Inference System (ANFIS) for classification purposes.

Their method showed high sensitivity, specificity, and accuracy, highlighting the benefits of combining enhancement with pattern recognition. The clinical implementation of such models is limited by cancer variability, anatomical complexity, and behavioral differences. The studies reviewed show how imaging modality, tumor heterogeneity, and dataset quality influence performance. Scaling these systems for clinical use requires validation, robust datasets, and alignment with frameworks like those of the World Health Organisation (WHO) to ensure standardization and applicability.

## 2.2. AI in Neuro-diagnostics

This section examines Pathological Brain Detection (PBD), a clinical method used to identify conditions like Alzheimer's disease (AD), mild cognitive impairment (MCI), autism spectrum disorder (ASD), multiple sclerosis (MS), microbleeds, and hearing loss. PBD usually uses supervised learning to classify brain scans as either 'pathological' or 'non-pathological', based on their texture, structure, and activity. AI models identify these pathologies by analyzing datasets such as the Whole Brain Atlas (TWBA), focusing on differences in brain features.

However, most PBD systems remain limited to binary classification volume loss as a key marker by tracking degeneration in AD and MCI patients over 6–12 months. due to sparse annotations, class imbalance, and overlapping characteristics across neurological conditions. Article [13] TWBA datasets present significant class imbalance, requiring correction during training. Zhang et al. addressed this by applying SMOTE to balance healthy and pathological brain samples [14]. Their approach combined Wavelet Packet Tsallis Entropy for texture analysis,

Extreme Learning Machines (ELM) for real-time classification, and the Jaya Algorithm for optimization, yielding high diagnostic accuracy. Similarly, Talo et al. in [15] used transfer learning to distinguish normal from abnormal scans with strong results, though still affected by dataset imbalance. TWBA's detailed diagnostic data holds strong potential for machine learning models to move beyond binary classification. Expanding annotated datasets will be essential to enhance interpretability and facilitate clinical deployment.

### 2.3. AI in Alzheimer's research

Alzheimer's disease (AD), a progressive neurodegenerative condition, is the primary cause of dementia. Early identification is crucial for both effective treatment and the management of the disease. The integration of neuroimaging with machine learning (ML) has emerged as a potent method for detecting and classifying AD, leveraging brain structure and function.

This section examines significant research employing machine learning within clinical Alzheimer's disease (AD) datasets, revealing three principal applications: AD investigations concentrate on (1) binary classification (e.g., differentiating AD from healthy individuals), (2) multi-class staging (encompassing MCI-to-AD progression), and (3) the analysis of brain anatomical progression. These methodologies utilize imaging data to extract structural and functional biomarkers, such as brain atrophy and hyperintensities, to facilitate diagnostic classification. Ledig et al. [16] performed segmentation of MRIs into 138 brain regions to assess alterations over a 12–24 month period in patients with AD and MCI. Notably, the hippocampus and amygdala exhibited considerable atrophy and demonstrated substantial discriminatory capability.

Their study used machine learning, support vector machines, and random forest models to assess biomarker utility in predicting disease progression. Recent literature is dominated by two clusters: (1) deployment of deep learning (DL) models for diagnosis, and (2) prediction of MCI-to-AD progression. Ding et al. [17] proposed a deep learning model using 18F- FDG PET (fluorodeoxyglucose positron emission tomography) scans and a pre-trained Inception V3 convolutional neural network (CNN). Fine-tuned with ADNI data using Adam optimization and cross-entropy loss, the model predicted Alzheimer's disease (AD) onset up to 75.8 months in advance with high accuracy. [18] employed a Siamese CNN for multi-class classification, utilizing the Clinical Dementia Rating (CDR) scale, and attained an accuracy of 99.05% across four distinct dementia stages. Nevertheless, the Clinical Dementia Rating scale is more frequently utilized in clinical trials than in practical applications [19]. Ding's model exhibited diminished performance in the context of Mild Cognitive Impairment (MCI), a consequence of the limited interpretability of the biomarkers. Although Mehmood's architecture demonstrated accuracy, it is contingent upon deep networks and Monte Carlo simulations, which raises potential scalability concerns. Schuff et al.

Gupta et al. in [20] reinforced hippocampal and Lin et al. [22] employed CNNs and Extreme Learning Machines (ELM), utilizing features extracted via FreeSurfer, to classify AD, MCI variants, and healthy individuals based on hippocampal and cortical characteristics derived from NRCD. Their model attained a precision of 79.9% in predicting the conversion from MCI to AD, as demonstrated using ADNI data. Furthermore, Altaf et al. [23] introduced a hybrid model that integrated texture-based MRI features with clinical data, achieving high accuracy across both binary and multi-class classification tasks within the ADNI dataset. Consequently, the classification of AD/MCI is supported by CNNs, structural features, and hybrid models. However, clinical translation necessitates the implementation of pruning techniques, interpretability, efficient architectural designs, and validation across a range of real-world datasets.

### 2.4. Multiple Sclerosis

Multiple Sclerosis (MS) is a neurological autoimmune disease marked by inflammation and demyelination of the central nervous system (CNS). Magnetic resonance imaging is the standard imaging modality for identifying MS lesions, detecting inflammation, loss of myelin, and scar tissue in the brain and spinal cord. Manual segmentation is labor-intensive and inconsistent; AI methods address challenges like irregular shapes, low contrast, inter- and intra-observer variability, and anatomical variability. Moeskops et al. in [24] proposed a cascade of two 3D patch-

wise CNNs to segment white matter hyperintensities (WMH), a common MS indicator. Their patch-based method localized subtle lesion features effectively and demonstrated strong performance in segmenting WM lesions. Valverde et al. [25] introduced a two-stage 3D CNN. The first network detected lesion voxels, while the second reduced false positives. This cascade approach achieved high Dice Similarity Coefficient (DSC) and Positive Predictive Value (PPV) scores and performed well on small datasets, making it suitable where manual annotations are limited. Van Leemput et al. in [26] developed a stochastic segmentation model treating MS lesions as statistical outliers. The method employed intensity-based tissue classification, MR field inhomogeneity correction, and a Markov random field for spatial consistency. While lesion volume correlation was strong, voxel-level precision was limited by the model's assumption of a single tissue type per voxel. Gao et al. [27] used multichannel MRI (T1, T2, FLAIR ((Fluid-Attenuated Inversion Recovery))) with a nonlocal means regularization technique to suppress noise and improve boundary clarity. The model demonstrated almost perfect specificity across multiple metrics, although it encountered difficulties in distinguishing between white and gray matter within FLAIR sequences. These investigations collectively highlight the diverse array of AI methodologies employed for MS lesion segmentation, each characterized by distinct advantages and disadvantages. Valverde's model is particularly effective in data-scarce environments, yet it may exhibit sensitivity to variations in MRI data. Van Leemput's statistical approach offers adaptability, but it is limited by its voxel-level precision. Gao's regularization technique improves segmentation accuracy, but it requires enhanced tissue discrimination capabilities. Adaptive networks and hybrid models, which integrate clinical and imaging data, could be essential for improving the segmentation of MS lesions. Training these models on individual patient data might mitigate overfitting and enhance their applicability across diverse patient populations. Furthermore, autoencoders present a promising avenue for increasing resilience to noise, particularly when dealing with scans that are heterogeneous or lack standardization. Longitudinal models that incorporate both spatial and temporal segmentation could facilitate more accurate tracking of disease progression. These prospective strategies are crucial for the creation of AI systems that are both robust and adaptable, thereby enabling their routine clinical use and ultimately improving the precision and efficiency of MS treatment.

### *2.5. Other Segmentation Works*

Automated medical image segmentation has seen considerable progress across a wide array of anatomical targets, encompassing both substantial organs like the heart and liver, and more specialized areas such as infant brain segmentation. Dou et al. [28], for instance, developed a 3D Deep Supervised Network (DSN) to segment organs within volumetric space. This model utilized deep supervision at various stages, which in turn enhanced both the precision of the segmentation and the speed of the learning process.

Although proficient in defining intricate anatomical formations, its substantial computational requirements could impede its prompt integration into clinical practice. Infant brain segmentation is particularly challenging, stemming from the developmental characteristics of brain tissue and the diminished contrast between white matter (WM) and gray matter (GM). Approximately six months postnatally, WM and GM frequently exhibit isotense properties on MRIs, thereby hindering boundary identification during this developmental phase.

The MICCAI Grand Challenge on infant segmentation spurred the development of diverse methodologies aimed at overcoming these constraints. Wang et al. [29] benchmarked 21 algorithms on a shared dataset of six-month-old brain scans, identifying key failure regions and emphasizing the value of selective data usage and feature granularity in low-contrast zones. Nie et al. [30] introduced a 3D multimodal fully convolutional network (FCN) that utilized both T1- and T2-weighted MRIs to augment texture information. Their architecture integrated coarse and dense feature maps to segment white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF), with batch normalization contributing to training stability. This multiresolution approach effectively mitigated early tissue ambiguity, thereby illustrating the advantages of multimodal integration. Dou's DSN for large-organ segmentation, along with the infant-specific models developed by Nie and Wang, underscores the versatility of

artificial intelligence across diverse segmentation tasks. Furthermore, refinements such as model pruning and memory optimization will be crucial for clinical implementation. Together, these advances support the growing role of AI-driven segmentation in tailored diagnostics and treatment planning.

### **3. Ethical Considerations**

#### *3.1. Patient Privacy and Data Use*

The development of AI models for medical imaging depends a lot on large clinical datasets that have private patient information. There are ethical issues with how this kind of data is gathered, stored, processed, and used again for things like training and testing algorithms. In numerous instances, datasets utilized for AI development were initially gathered for clinical care rather than for research or algorithmic modeling. Even though people often use de-identification and anonymization methods, recent research has shown that medical imaging data can still be linked back to the original person when combined with other datasets or metadata. This risk is especially important for high-dimensional imaging techniques like MRI or CT scans that may show unique patterns in the body.

To deal with these worries, strong data governance frameworks must be put in place that make sure strict access control, encryption, and secure storage rules are followed throughout the data lifecycle. Federated learning, differential privacy, and secure multi-party computation are some examples of privacy-preserving machine learning methods that have also shown promise as ways to allow AI development to happen without sharing data in a central location. Also, using data ethically means having clear ways for patients to give their consent, where they are told how their data might be used to make algorithms, including possible secondary uses. Institutions should also set clear rules for data stewardship, auditability, and accountability to make sure that AI-driven healthcare systems use data responsibly.

#### *3.2. Bias and Fairness in Model Performance*

Bias in AI systems poses a considerable ethical and clinical issue, especially when models are developed using datasets that lack geographical, demographic, or clinical representativeness. Medical imaging datasets frequently derive from a restricted number of institutions or regions, potentially leading to models that excel with the training population yet falter with underrepresented groups. These kinds of biases can cause differences in how accurate diagnoses are for different groups of patients based on their age, gender, ethnicity, socioeconomic status, or other health problems.

AI systems trained on limited or nondiverse datasets may underperform on underrepresented groups, leading to inconsistent outputs across variables such as age, gender, or ethnicity. To mitigate this, models must be developed and validated using diverse datasets to identify and address demographic bias. For instance, a model predominantly trained on data from a particular demographic group may not generalize effectively to patients exhibiting diverse anatomical variations or disease manifestations. In clinical practice, this could lead to delayed diagnosis, improper risk stratification, or unequal treatment recommendations. To deal with this problem, we need to find and fix bias before and during the development and validation of models. Stratified performance evaluation, fairness-aware training algorithms, and domain adaptation methods are some of the ways to find and fix differences in model outputs based on demographics.

Furthermore, the establishment of extensive, multi-institutional datasets that accurately reflect diverse populations is crucial for enhancing model generalizability. Ethical AI development should also include regular checks on how well algorithms work for different groups of people and clear reporting of any possible biases. These practices help make sure that AI systems help make healthcare more fair instead of making the gaps that already exist worse.

#### *3.3. Clinical Accountability and Decision Authority*

AI systems should function as assistive tools that augment, but not replace clinical judgment. Clinicians must retain diagnostic authority and remain responsible for interpreting AI outputs and making final decisions. To

maintain clear accountability structures, healthcare organizations should set rules for how AI systems should be used in clinical workflows. These rules should make it clear that licensed clinicians are still responsible for making the final decisions about diagnosis and treatment. AI systems should also have ways to estimate uncertainty or give confidence scores so that doctors can better judge how reliable model predictions are. Healthcare systems can make sure that AI helps, not hurts, professional clinical judgment by keeping human-in-the-loop decision frameworks.

### *3.4. Transparency and Explainability*

For AI tools to be safely and effectively integrated into clinical workflows, clinicians must understand the rationale behind the outputs. Explainability is critical, as black-box models may be misunderstood or misused if their predictions are not interpretable or justifiable in a clinical context.

For AI to be used safely and ethically in clinical settings, it must be clear and easy to understand. Many state-of-the-art deep learning models, particularly convolutional neural networks used in medical imaging, operate as complex black-box systems whose internal decision-making processes are difficult to interpret. Even though these kinds of models can be very accurate at predicting things, the fact that they can't be understood can make doctors less trusting and slow down their use in the clinic.

Explainable AI (XAI) methods try to solve this problem by giving clear explanations of how models make predictions. Saliency maps, Gradient-weighted Class Activation Mapping (Grad-CAM), SHAP (SHapley Additive exPlanations), and attention mechanisms are all ways to show which parts of an image or which features are most important to the model's decisions. These visualization tools let doctors check to see if the model's predictions are based on patterns that are clinically relevant, not false correlations or artifacts. In addition to improving interpretability, transparency also means keeping detailed records of how models were built, including the training data sets, preprocessing methods, model architecture, and validation procedures. Reporting that is open and honest allows for independent verification and makes it easier to repeat research. In the end, making models easier to understand not only builds trust among clinicians, but it also makes it safer to use AI technologies in real-life diagnostic workflows.

### *3.5. Regulatory Compliance and Real-World Validation*

Many AI models are validated only on benchmark datasets, limiting their generalizability in real-world clinical settings. Ethical deployment requires rigorous testing across diverse clinical environments and adherence to regulatory frameworks, such as the WHO Guidance on Ethics and Governance of Artificial Intelligence for Health [31]. These measures ensure clinical viability and equitable adoption.

AI systems must undergo stringent external validation across various clinical institutions and heterogeneous patient populations to guarantee safe and ethical deployment. To see how strong and reliable an algorithm is, we need to do clinical trials and keep an eye on how it works in the real world. The U.S. Food and Drug Administration (FDA), the European Medicines Agency (EMA), and international health organizations are also working on rules for AI-based medical devices. These frameworks stress the need for clinical validation, risk assessment, openness, and monitoring after deployment.

The World Health Organization and other global groups have also put out guidelines for the ethical use of AI in healthcare. These guidelines stress fairness, openness, responsibility, and long-term viability. To make sure that AI technologies provide safe, effective, and fair healthcare outcomes, it is important to follow these rules and ethical standards. To find performance drift as clinical data distributions change over time, there should also be ongoing monitoring and periodic model re-evaluation.

## **4. Conclusion**

This review highlights the application of machine learning in medical imaging, particularly in oncology for detecting tumors that are delicate, hard to localize, or located in regions with high variability in shape and

placement. Methods such as CNNs and U-Net architectures have improved segmentation accuracy by combining high-resolution and low-level spatial features. Outside of cancer research, machine learning has been used to find brain abnormalities in conditions like Alzheimer's and Multiple Sclerosis. Research has looked into deep learning, hybrid CNNs, NSCT-based enhancement, and pretrained models. In MS, accurate monitoring of lesion progression is especially important for disease management. The Citation Network Analysis (CNA) served as the data-driven foundation for this review. CNA facilitated a structured examination by pinpointing five primary thematic clusters: oncology, neurodiagnostics, Alzheimer's disease, Multiple Sclerosis, and advanced segmentation. This approach provided a concise overview of research trajectories and significant contributions, thereby ensuring comprehensive coverage and emphasizing nascent areas of focus. The effective incorporation of AI systems into clinical practice will necessitate sustained collaboration between clinicians and engineers, the creation of equitable datasets for underrepresented pathologies, and real-world validation via regulatory processes and scalable frameworks.

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#### Conflicts of Interest

The author declares no conflicts of interest.

#### Ethical Approval and Consent to Participate

Not applicable.

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