International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

A LIGHTWEIGHT MULTIMODAL DEEP LEARNING FRAMEWORK FOR ACCURATE SEGMENTATION OF ACUTE ISCHAEMIC STROKE LESIONS

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Abstract

Accurate delineation of acute ischaemic stroke lesions remains a significant challenge in neuroimaging due to substantial variation in lesion appearance, modality-specific contrast and anatomical complexity. This study introduces a lightweight multimodal deep learning framework that integrates diffusion-weighted imaging, apparent diffusion coefficient maps and fluid-attenuated inversion recovery sequences to capture complementary aspects of acute infarction within a unified representation. The architecture combines efficient feature extraction with context-aware modelling to characterise anisotropic lesion morphology while preserving fine spatial detail during reconstruction. Evaluation on a subject-independent subset of the ISLES 2022 dataset demonstrated consistently high spatial agreement with expert annotations, achieving a Dice coefficient of 0.93, an intersection-over-union of 0.88, a precision of 0.95, a recall of 0.92 and an F1 score of 0.93. These results indicate that the framework reliably identifies diffusion-restricted tissue while maintaining low false-positive rates across diverse imaging conditions. Qualitative inspection further confirmed coherent lesion boundaries and stable localisation even in cases involving subtle, fragmented or low-contrast lesions. Overall, the findings show that an efficient multimodal architecture can achieve segmentation performance comparable to substantially larger models, offering a practical and scalable solution for automated stroke-lesion analysis.

Keywords Acute ischaemic stroke, multimodal MRI, deep learning segmentation, diffusion weighted imaging, lightweight neural networks, medical image analysis.

1. Introduction

Stroke remains one of the most serious global health concerns of the modern era, with international estimates indicating that nearly twelve million people worldwide will experience

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

a new stroke this year [1]. Stroke is also responsible for more than ninety million individuals living with chronic neurological impairment, making it one of the leading causes of long term disability across continents. Despite improvements in prevention and acute therapy, the global burden continues to rise due to demographic ageing, widening socio economic disparities and persistent lifestyle related risk factors [2]. These trends emphasise the urgent need for more effective diagnostic tools and streamlined pathways across diverse healthcare systems. The growing number of stroke survivors also places significant demand on rehabilitation services worldwide. This combination of epidemiological pressure and clinical complexity highlights the importance of improved imaging-based assessment.

The United Kingdom mirrors these global patterns but also displays distinct national characteristics that underscore the need for enhanced imaging support. Recent national reports indicate that around one hundred thousand individuals in the United Kingdom experience a stroke each year and more than one million people live with long term consequences of stroke related disability [3]. Hospital admissions in England have risen steadily over the past two decades, reaching more than one hundred thousand admissions per year, with notable increases among middle aged patient groups. The economic burden is profound, with stroke estimated to cost the United Kingdom tens of billions of pounds annually through a combination of direct healthcare expenditure and indirect societal losses. Despite improvements in emergency care, only a minority of patients receive the recommended six month follow up review, suggesting gaps in longer term management. These national challenges reinforce the importance of diagnostic technologies that can support more consistent and timely clinical decision making.

Manual delineation of acute ischaemic lesions is recognised as a demanding and variable task within both clinical practice and research environments. Inter observer disagreement remains substantial due to differences in expertise, interpretation and the subtle nature of early ischaemic changes. In large multicentre studies, variation in scanner hardware, acquisition protocols and artefact profiles further complicates manual annotation. The time intensive nature of pixel level contouring significantly limits the scalability of large stroke imaging datasets. Within acute care settings, the rapid therapeutic window renders detailed manual delineation impractical when urgent clinical decisions must be made. These persistent challenges have led to widespread interest in automated approaches that provide accurate and reproducible lesion maps.

Recent progress in deep learning has transformed the landscape of medical image analysis and provided powerful tools for automated segmentation. Convolutional neural networks have demonstrated strong performance across a wide range of biomedical tasks due to their capacity to learn hierarchical feature representations directly from data [4]. Encoder and decoder architectures such as U Net remain foundational due to their ability to combine semantic context with spatial detail through skip connections [5]. However, conventional convolutional networks are limited by their spatial locality and restricted receptive fields, which may be insufficient for capturing the long range contextual information needed to delineate complex stroke lesions accurately. Lesions can span large anatomical territories or present in fragmented patterns that exceed the scope of local convolutional filters. These factors have prompted increased interest in methods that incorporate broader contextual awareness.

Received: August 04, 2025

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Attention based architectures and vision transformers have introduced new possibilities for capturing long distance spatial dependencies in medical images. Transformer models have achieved notable success in computer vision tasks by modelling global relationships through self attention mechanisms [6]. However, these models typically require extensive annotated datasets, large memory resources and prolonged training times, which limit their practicality in many clinical environments. Healthcare systems such as the National Health Service often operate with heterogeneous hardware and restricted computational resources, making deployment of such heavy models challenging. This context has created significant demand for approaches that retain the expressive benefits of global context modelling while reducing computational overhead. Lightweight methods that achieve this balance offer clear advantages for real time clinical workflows.

The complexity of multi modal magnetic resonance imaging presents additional challenges for automated segmentation. Diffusion weighted imaging provides early sensitivity to cytotoxic oedema, apparent diffusion coefficient maps give quantitative insight into restricted diffusion and fluid attenuated inversion recovery sequences capture structural and vascular alterations that evolve over time [7]. Each modality highlights different aspects of tissue physiology, and successful segmentation requires models to integrate these diverse signals appropriately. Naive channel stacking may dilute critical features or amplify noise if modality specific contributions are not accounted for. Real world datasets, including those gathered across United Kingdom centres, often contain incomplete or imperfectly aligned modalities due to variation in clinical practice. Robust segmentation models must therefore be capable of handling missing modalities while still exploiting valuable multimodal information.

Ischaemic lesions exhibit substantial heterogeneity in their anatomical distribution, shape and intensity profile [8]. Small infarcts may be extremely subtle and easily lost among physiological noise or imaging artefacts, whereas larger territorial infarcts may contain heterogeneous internal regions that complicate boundary estimation. Segmentation methods must therefore maintain a delicate balance between capturing fine scale structural detail and maintaining coherent global contours. Excessive smoothing may obscure clinically important morphology, while overly sensitive approaches may produce false positives that reduce clinical utility. The need for precise boundary delineation is particularly important because lesion extent directly influences treatment eligibility and prognostic evaluation. These challenges collectively make acute stroke imaging a demanding domain for automated segmentation.

The research community has increasingly explored hybrid architectures that incorporate both convolutional and attention-based mechanisms. Spatial attention techniques help highlight regions of clinical relevance, and channel recalibration modules adaptively modulate feature importance according to modality and context [9]. Directional feature extraction provides an additional dimension of modelling that can be especially valuable for capturing anisotropic lesion patterns. Despite these promising developments, many proposed models remain computationally heavy or include complex components that limit their suitability for real time clinical use. Compact designs that integrate these mechanisms effectively remain relatively underexplored. The need for efficient yet expressive architectures remain a critical challenge in the field.

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
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Loss function design plays a central role in achieving high quality segmentation, particularly in tasks characterised by imbalanced lesion sizes and challenging boundaries. Standard region based losses such as Dice and cross entropy promote volumetric overlap but provide limited guidance for capturing detailed boundary morphology. Boundary aware losses inspired by active contour principles have shown potential for improving edge sharpness and delineation [10]. Small lesion detection also benefits from objectives that account for class imbalance, including focal style formulations that emphasise difficult examples. Combining multiple complementary objectives into a hybrid loss offers a promising strategy for more stable optimisation. This approach supports both boundary fidelity and regional accuracy, which are essential for clinical usefulness.

The growth of large multicentre datasets, such as the ISLES benchmark, has created valuable opportunities to evaluate segmentation models under conditions that represent real world clinical variation [11]. These datasets incorporate a wide range of scanner types, acquisition settings and patient populations, providing a rigorous test of model generalisability. Assessment across these diverse conditions is particularly important within the United Kingdom, where imaging workflows and hardware resources vary considerably. Ablation studies and component wise analyses offer crucial insights into the contribution of each architectural feature. Transparent and thorough evaluation strengthens confidence in the robustness of new segmentation models. Such evaluation practices align with the expectations of contemporary high quality medical imaging research.

Given the scale of the global stroke burden, the specific challenges observed within the United Kingdom and the limitations of existing segmentation methods, there is a strong need for approaches that are accurate, efficient and clinically adaptable. Models that integrate directional feature aggregation, spatial emphasis and modality aware recalibration show considerable promise for addressing these needs. Maintaining a compact architecture while achieving competitive accuracy enhances suitability for both research and clinical deployment. The ability to capture boundary detail and detect small lesions further strengthens the clinical value of such models. These considerations form the motivation for the architectural and methodological contributions presented in this work. The intention is to advance automated segmentation in a manner that is feasible for integration into routine stroke imaging workflows.

The remainder of this paper is organised in a manner that guides the reader through the conceptual, methodological and analytical development of the study. The next section reviews the most relevant literature in stroke imaging, multimodal segmentation and recent advances in deep learning for neuroimaging. The third section presents the methodological framework, including details of the dataset, preprocessing pipeline, architectural design and training strategy. The fourth section reports the results of the experiments, including both quantitative performance metrics and qualitative interpretations of model behaviour. The fifth section offers a critical discussion of the findings, addresses methodological limitations and examines broader clinical implications. The final section concludes the paper with a summary of the main contributions and identifies several directions for future research on automated stroke lesion segmentation.

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2. Literature Review

The increasing interest in automated analysis of stroke imaging has produced a rapidly expanding body of research that spans several interconnected methodological directions. Building on the clinical and technical motivations outlined in the preceding introduction, it is necessary to situate the present study within the broad spectrum of contemporary work that now defines this field. Existing literature can be understood across five closely related research strands that collectively shape the development of automated stroke lesion segmentation. These include progress in deep learning and benchmark datasets, advances in convolutional architectures for multimodal magnetic resonance imaging, emerging approaches for multimodal fusion, the rising influence of transformer based and hybrid models, and innovations in loss function design aimed at addressing imbalance and boundary ambiguity. Together these strands form the conceptual landscape from which the proposed methodology emerges and provide essential context for understanding its contribution.

A substantial portion of recent progress has been driven by the expansion of deep learning methodologies and the availability of large multicentre datasets. Reviews by Malik and co authors document the accelerating pace of development and highlight persistent challenges including dataset inconsistency, variable annotation quality and limited external validation [12]. Complementary meta analytic work by Baaklini and collaborators reinforces how imaging heterogeneity across centres can strongly influence model behaviour and underscores the need for more robust evaluation frameworks [13]. The ISLES benchmark, most recently presented by Hernandez Petzsche and colleagues, remains a central reference for the field, providing a rigorous experimental environment informed by real clinical diversity. Ensemble based contributions such as DeepISLES further exemplify the importance of diverse architectural strategies by demonstrating strong external validity across multiple independent cohorts [14] . These developments highlight the increasing maturity of the field while revealing opportunities for refinement.

Convolutional neural networks remain a core foundation for stroke lesion segmentation. Early studies demonstrated that even single modality designs trained on diffusion weighted imaging could surpass traditional methods when paired with careful preprocessing and augmentation [15]. More recent work has focused on exploiting the complementary strengths of multiple magnetic resonance sequences. Rahman and colleagues provide evidence that multi channel convolutional models trained on diffusion weighted imaging, apparent diffusion coefficient and fluid attenuated inversion recovery sequences yield considerable improvements in segmentation performance [16]. Sasidharan and co authors report similar findings using a three dimensional convolutional architecture combined with a composite loss to enhance small lesion sensitivity [17]. Further reinforcement is provided by Ryu and collaborators who demonstrate strong cross vendor generalisation using convolutional backbones [18]. These works indicate that convolutional models retain strong practical value when aligned with appropriate architectural and training design.

Multimodal fusion has become increasingly influential as researchers seek to capture the distinct physiological and structural information encoded within different magnetic resonance sequences. Qu and colleagues introduce a modality aware fusion network that integrates

Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

diffusion weighted imaging, apparent diffusion coefficient and fluid attenuated inversion recovery signals while applying spatial refinement to preserve subtle lesion morphology [19]. Wieslaw and co authors extend this by exploring a combined detection and segmentation framework that uses multimodal cues to differentiate ischaemic from haemorrhagic abnormalities with improved reliability [20]. Ensemble systems such as DeepISLES implicitly benefit from multimodal richness through aggregated model behaviour that captures diverse aspects of infarct presentation. The balance of evidence underscores the importance of effective fusion mechanisms in addressing the heterogeneous presentation of acute and subacute lesions.
Parallel developments in medical image segmentation have been heavily influenced by the emergence of transformer based and hybrid models. Reviews by Liu and colleagues and by Pu and co authors describe the increasing adoption of transformer encoders [21] that learn global spatial dependencies more effectively than local convolutional filters alone. More recent analyses by Kim and collaborators emphasise the promise of hybrid convolutional transformer designs for balancing global context modelling with computational feasibility [22]. Seminal contributions such as TransUNet illustrate the potential of embedding transformer modules within a U Net shaped framework to deliver more expressive representations across complex medical datasets. Likewise, the dual attention structure proposed by Li and colleagues provides further demonstration of the benefits of combining global reasoning with fine scale local discrimination [23]. These developments represent an important methodological shift towards architectures capable of capturing the full spatial complexity of ischaemic lesions.
Loss function design has also emerged as a crucial determinant of segmentation performance in stroke imaging, given the severe class imbalance and subtle structural transitions that characterise acute infarcts. The boundary loss introduced by Kervadec and colleagues provides a principled means of improving contour delineation by reframing boundary distance as an optimisable regional term [24]. More extensive reviews by Gao and collaborators emphasise the limitations of using single objective losses for complex medical tasks and advocate for hybrid formulations that combine regional, focal and uncertainty oriented components [25]. Empirical evaluations by Sasidharan and co authors demonstrate that composite Dice and Jaccard losses can meaningfully improve small lesion detection within three dimensional networks [26]. This growing emphasis on multi objective optimisation reflects the complexity of the lesion patterns these models must capture.
Although these developments have advanced the field significantly, persistent limitations remain that constrain reliable clinical deployment. Many high performing models require substantial computational resources, limiting their practicality in settings where hardware capacity is restricted. Convolutional frameworks, while efficient, frequently struggle to model long range spatial relationships, and may inadequately represent subtle boundary transitions in small or irregular lesions. Multimodal fusion remains inconsistent across studies, particularly where sequence availability varies or where modalities such as diffusion weighted imaging or apparent diffusion coefficient suffer from artefacts or misalignment. Optimisation strategies often focus on volumetric overlap while neglecting boundary structure. These gaps indicate a clear need for an approach that combines efficient global contextual modelling, directional feature extraction, robust multimodal integration and boundary sensitive optimisation within a

Received: August 04, 2025

Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

compact and clinically adaptable design. The methodology developed in this study addresses these issues by incorporating directional attention mechanisms, spatial and channel recalibration modules and a hybrid loss formulation aimed at enhancing both regional coherence and boundary fidelity. The following section therefore outlines the dataset, preprocessing pipeline, architectural components and optimisation strategy that together constitute the proposed framework.

3. Methodology

The methodological framework employed in this study provides a transparent and reproducible basis for evaluating automated multimodal segmentation of acute ischaemic stroke lesions. It is structured to reflect the characteristics of the ISLES 2022 dataset and the computational considerations of the proposed network. The section begins with a description of the dataset and the rationale for its selection, followed by the preprocessing procedures used to harmonise heterogeneous MRI data. It then outlines the model inputs derived from these procedures before detailing the environment in which the experiments were conducted.

Dataset

The study uses the labelled cohort from the ISLES 2022 training release, a multicentre benchmark designed to support research in automated acute ischaemic stroke lesion segmentation. The dataset contains 250 subjects scanned across international centres using diverse protocols and hardware. Each subject provides diffusion-weighted imaging, apparent diffusion coefficient maps and, for 249 subjects, fluid-attenuated inversion recovery, together with a clinician-generated lesion mask. In total, these correspond to 999 three-dimensional MRI volumes. Accordingly, the model operates with two or three channels depending on the modalities available for each subject

Axial coverage typically ranges from 40 to 60 slices per subject, resulting in more than 30 000 slices across the cohort. The dataset displays substantial heterogeneity in lesion size, localisation, visual contrast and overall acquisition quality, mirroring the variability encountered in routine clinical imaging. This diversity provides a realistic foundation for assessing segmentation models under conditions where generalisation across scanners and institutions is crucial. The dataset's subject-level structure enables strict separation of training and validation cases, ensuring that slices from a given individual never appear in both sets.

Pre-processing

Pre-processing was undertaken to harmonise the MRI volumes and prepare them for model input. All images were loaded in NIfTI format and converted to single-precision floating-point arrays. For each modality, voxel intensities were normalised using percentile-based scaling, where values below the 0.5th percentile and above the 99.5th percentile were clipped, and the remaining intensity range was mapped linearly to the interval between zero and one. This procedure reduced the influence of scanner-specific outliers while preserving relative contrast relationships.

A primary reference modality was assigned to each subject using a fixed priority order in which fluid-attenuated inversion recovery was preferred when available, followed by diffusion-weighted imaging or apparent diffusion coefficient. Any additional modalities were added as

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

extra channels. When spatial dimensions differed across modalities, secondary volumes were interpolated slice-wise to match the in-plane resolution and slice count of the primary reference, ensuring a consistent image geometry across channels. Lesion masks were loaded, binarised and treated as three-dimensional label volumes.

To obtain compact but informative model inputs, the axial slices of each lesion mask were ranked by lesion area. Up to three slices with the largest lesion burden and at least ten lesion pixels were selected. If no slice satisfied this threshold, the slice with the highest variance within the lesion map was used. The corresponding image slices from all available modalities were then extracted and resized to 160 × 160 pixels using bilinear interpolation for the images and nearest-neighbour interpolation for the labels. This procedure produced normalised and spatially aligned two-dimensional multimodal inputs together with their paired lesion masks. During training, random horizontal and vertical flips were applied to the image–mask pairs to improve orientational robustness without altering the deterministic aspects of the preprocessing pipeline.

Model Architecture

The segmentation model developed in this study is a multimodal, hierarchical convolutional framework designed to extract the complex spatial and intensity patterns associated with acute ischaemic stroke. Its design is motivated by the observation that infarction is not expressed uniformly across MRI modalities: diffusion-weighted imaging highlights cytotoxic oedema, the apparent diffusion coefficient captures tissue diffusivity and FLAIR reflects evolving parenchymal changes. The architecture therefore treats each axial slice as a structured multivariate signal and learns a joint feature representation that maps these heterogeneous inputs into a unified semantic space suitable for precise pixel-wise classification.

Let $X \in \mathbb{R}^{C\times H\times W}$ denote a multimodal slice with C aligned channels corresponding to available modalities. The first stage of the model applies a sequence of nonlinear feature transformations of the form

$$F_1(X) = \sigma(W_1 * X + b_1) \qquad (1)$$

where W_1 is a set of convolution kernels, $*$ denotes spatial convolution and $\sigma(\cdot)$ is a smooth nonlinearity. These initial transformations capture high-frequency components such as local gradients, edge transitions and subtle modality-specific contrasts, forming the foundation for deeper contextual reasoning.

As the data propagates through the encoding hierarchy, spatial resolution decreases while semantic abstraction increases. At depth k, the feature representation is given by

$$F_k(X) = \sigma(W_k * F_{k-1}(X) + b_k) \qquad (2)$$

with the receptive field expanding progressively across layers. This progression enables the model to encode not only local textural cues but also mid-range spatial dependencies visible within each axial slice. These deeper layers synthesise local and regional context, producing feature maps that describe infarct morphology at multiple scales.

A distinctive component of the architecture is the incorporation of directional filtering operations in the deepest part of the network. Unlike conventional isotropic convolution, which

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

responds uniformly in all directions, directional filters selectively emphasise horizontal and vertical dependencies. For a deep feature map F_d, the model computes

$$H = D_h(F_d) \quad (3)$$

$$V = D_v(F_d) \quad (4)$$

where $D_h$and $D_v$denote operators that project features along horizontal and vertical orientations. The combined directional representation is given by

$$F_{\text{dir}} = F_d + \alpha H + \beta V \quad (5)$$

with $\alpha$and βgoverning the relative contribution of each orientation. This formulation allows the model to capture elongated or anisotropic lesion patterns, such as ribbon-like cortical infarcts or tract-aligned white-matter injuries, which frequently elude purely isotropic approaches.

Following the directional integration, the architecture transitions into a reconstruction pathway that restores the original spatial resolution. This pathway is structured as a sequence of learned upsampling operations. At resolution level j, the reconstruction is defined as

$$R_j = \sigma(W_j^{\uparrow} \uparrow R_{j+1} + U_j) \quad (6)$$

where $W_j^{\uparrow} \uparrow$denotes a learned expansion operator applied to the coarser representation R_{j+1}, and $U_j$is the corresponding feature map from the encoding pathway. This cross-scale fusion ensures that detailed anatomical information extracted at high resolution is reintroduced during the reconstruction process, enabling the model to preserve boundary precision while maintaining the contextual coherence gained at deeper levels.

At each reconstruction stage, the model employs adaptive recalibration mechanisms that rescale both spatial responses and channel activations based on their task relevance. These mechanisms compute a modulation function

$$M(F) = \rho\,(\phi(F)) \odot F \quad (7)$$

where ϕextracts summary statistics, ρmaps them into recalibration coefficients and $\odot$denotes element-wise modulation. This adaptive weighting enhances discriminative features and suppresses noise or modality-specific artefacts, stabilising the representation across heterogeneous acquisition conditions.

The final segmentation map is produced by applying a linear projection to the fully reconstructed feature representation, yielding a continuous probability field

$$P(x, y) = \sigma(W_{\text{out}} * R_1(x, y) + b_{\text{out}}) \quad (8)$$

which expresses, for each pixel, the estimated probability of infarction. This probabilistic representation captures uncertainty across the lesion boundary and supports downstream interpretation in clinically meaningful terms.

Thus, the architecture forms a coherent system that integrates multimodal information, captures both isotropic and orientation-dependent spatial structure and reconstructs high-resolution

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

probability maps that reflect the nuanced radiological characteristics of acute stroke. Its hierarchical design, directional sensitivity and adaptive recalibration mechanisms allow it to model the full spectrum of lesion morphology, from sharply demarcated core infarction to diffuse patterns of early injury, while maintaining computational efficiency suitable for large-scale deployment.

Loss Functions and Optimisation

Training a segmentation model for acute ischaemic stroke requires an objective function capable of addressing several fundamental challenges: highly unbalanced lesion distribution, ambiguous or diffuse lesion boundaries, substantial variability in imaging characteristics across modalities, and the need for stable convergence even when only a limited number of annotated samples are available. To satisfy these requirements, the optimisation framework integrates multiple complementary loss components, each formulated to target a different structural property of the lesion representation.

Let $P(x, y)$denote the predicted lesion probability at pixel $(x, y)$and let $Y(x, y) \in \{0,1\}$denote the corresponding ground-truth label. The first component of the objective promotes boundary regularity and penalises fragmented or noisy predictions. This contour-based loss operates by evaluating the spatial derivatives of the prediction field. Defining the discrete gradients as

$\nabla_x P = P(x+1, y) - P(x, y)$ (9)

$\nabla_y P = P(x, y+1) - P(x, y)$ (10)

the contour loss is expressed as

$\mathcal{L}_{\text{contour}} = \frac{1}{HW} \sum_{x,y} \sqrt{(\nabla_x P)^2 + (\nabla_y P)^2 + \varepsilon}$ (11)

where $\varepsilon$is a stabilisation constant. This term encourages continuous lesion boundaries that align with anatomical plausibility while suppressing high-frequency distortions arising from imaging noise, modality-specific inconsistencies or local artefacts in DWI and ADC.

A second component addresses the inherent imbalance between lesioned and non-lesioned regions. Since the overwhelming majority of pixels correspond to normal parenchyma, naive optimisation would quickly converge toward trivial solutions that minimise loss by overpredicting background. To prevent this, the loss incorporates a modulated classification term designed to enhance the influence of difficult or minority-class examples. The focal formulation is given by

$\mathcal{L}_{\text{focal}} = -\frac{1}{HW} \sum_{x,y} \alpha\, Y(x, y)\, (1 - P(x, y))^{\gamma} \log P(x, y) + (1 - \alpha)\, (1 - Y(x, y))\, P(x, y)^{\gamma} \log (1 - P(x, y))$ (12)

where αbalances the contribution of positive and negative samples and γcontrols the strength of the modulation. This expression down-weights easy examples and amplifies the contribution of difficult ones, enabling the model to maintain sensitivity to small or early lesions that may be faint on FLAIR or only partially expressed on diffusion imaging.

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
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To ensure consistency and stabilise the segmentation in cases with subtle or minimal lesion burden, a third component measures the global overlap between the predicted and true regions. The soft overlap loss is formulated as

$$\mathcal{L}_{\text{overlap}} = 1 - \frac{2\sum_{x,y} P(x,y)\,Y(x,y) + \varepsilon}{\sum_{x,y} P(x,y) + \sum_{x,y} Y(x,y) + \varepsilon} \quad (13)$$

which encourages agreement in overall lesion extent. This term is particularly important for stabilising training across the heterogeneous cohort, where some subjects exhibit large territorial infarcts whereas others contain only small punctate lesions or faint diffusion changes. The complete training objective combines these three complementary components into a unified optimisation target:

$$\mathcal{L}_{\text{total}} = \lambda_1 \mathcal{L}_{\text{contour}} + \lambda_2 \mathcal{L}_{\text{focal}} + \lambda_3 \mathcal{L}_{\text{overlap}} \quad (14)$$

where the coefficients λ_1, $\lambda_2$and $\lambda_3$control the influence of each component. This composite formulation balances local edge fidelity, robust classification in the presence of class imbalance and global lesion-extent accuracy.

Parameter updates are performed using an adaptive gradient method that separates the magnitude of parameter updates from the regularisation term, improving convergence stability when training with small mini-batches. Let $\theta_t$denote the model parameters at iteration t, with gradient $g_t = \nabla_\theta \mathcal{L}_{\text{total}}$. The update rule is defined as

$$\theta_{t+1} = \theta_t - \eta_t \frac{g_t}{\sqrt{v_t}+\varepsilon} - \eta_t\, \omega\, \theta_t \quad (15)$$

where $v_t$is a running estimate of the second moment, $\omega$is the weight regularisation coefficient and $\eta_t$is the learning rate. The learning rate evolves according to a performance-driven schedule that reduces $\eta_t$when validation metrics plateau, allowing fine-grained refinements to the parameters during later training phases.

This optimisation framework ensures that the model learns representations that are sensitive to subtle radiological signals, stable across clinical heterogeneity and capable of producing anatomically coherent segmentation maps without requiring large computational resources.

Evaluation Protocol

The evaluation strategy employed in this study is designed to provide a rigorous, unbiased and clinically meaningful assessment of the model's ability to delineate acute ischaemic lesions across a highly heterogeneous population of subjects. Because the ISLES dataset encompasses variations in scanner manufacturer, acquisition parameters, lesion morphology, anatomical location and severity of ischaemia, the evaluation protocol must capture both fine-grained local accuracy and broader volumetric and clinical reliability. To meet these demands, the protocol is structured around strict subject-level separation, threshold-based binarisation of predictions and a set of complementary metrics that quantify segmentation performance from multiple theoretical and clinical perspectives.

Received: August 04, 2025

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The validation cohort is constructed by withholding entire subjects from the training process, thereby eliminating any possibility of cross-subject leakage. Let $\mathcal{S}_{\text{train}}$and $\mathcal{S}_{\text{val}}$denote the disjoint sets of training and validation subjects, with $\mathcal{S}_{\text{train}} \cap \mathcal{S}_{\text{val}} = \emptyset$. For each subject in the validation set, all axial slices selected during preprocessing are passed through the trained segmentation model to produce probability maps $P_s(x, y)$. These pixel-wise probabilities are then converted into binary segmentation masks through a thresholding operation:

$$\hat{Y}_s(x,y) = \begin{cases} 1, & P_s(x,y) \geq \tau, \\ 0, & P_s(x,y) < \tau, \end{cases} \quad (16)$$

where $\tau$is a fixed threshold chosen based on training-set behaviour to balance sensitivity and precision. This binarisation step reflects the clinical need for actionable lesion delineations rather than continuous probability fields, while still preserving the probabilistic structure of the model during training.

A suite of evaluation metrics is then applied to each predicted mask in order to capture multiple dimensions of segmentation quality. Overlap-based metrics provide a direct quantification of spatial agreement. The Dice similarity coefficient measures the harmonic interpolation of the intersection and union of predicted and true lesion sets:

$$\text{Dice}(s) = \frac{2 \sum_{x,y} \hat{Y}_s(x,y)\, Y_s(x,y)}{\sum_{x,y} \hat{Y}_s(x,y) + \sum_{x,y} Y_s(x,y)}. \quad (17)$$

This coefficient is sensitive to both lesion over-segmentation and under-segmentation, making it particularly useful in the context of heterogeneous stroke phenotypes where lesion sizes range from tiny lacunar regions to extensive territorial infarctions.

A related measure, the Jaccard index or intersection-over-union, captures the proportion of shared lesion volume relative to the union of predicted and true regions:

$$\text{IoU}(s) = \frac{\sum_{x,y} \hat{Y}_s(x,y)\, Y_s(x,y)}{\sum_{x,y} \hat{Y}_s(x,y) + \sum_{x,y} Y_s(x,y) - \sum_{x,y} \hat{Y}_s(x,y)\, Y_s(x,y)}. \quad (18)$$

While numerically more conservative than Dice, IoU provides additional information about segmentation reliability, especially in cases where lesion boundaries are diffuse or difficult to delineate.

Metrics evaluating classification behaviour at the pixel level are also computed to provide complementary perspectives on model performance. Precision quantifies the proportion of predicted lesion pixels that correspond to true positives.

$$\text{Precision}(s) = \frac{\sum_{x,y} \hat{Y}_s(x,y)\, Y_s(x,y)}{\sum_{x,y} \hat{Y}_s(x,y)}. \quad (19)$$

Recall measures the sensitivity of the model to true lesion pixels

$$\text{Recall}(s) = \frac{\sum_{x,y} \hat{Y}_s(x,y)\, Y_s(x,y)}{\sum_{x,y} Y_s(x,y)}. \quad (20)$$

Received: August 04, 2025

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High recall is essential for capturing subtle or early lesions that might otherwise be missed, especially on FLAIR where changes may be faint or absent during early hours of ischaemia.
The harmonic mean of precision and recall produces a balanced performance measure,

$$\mathrm{F1}(s) = \frac{2 \cdot \mathrm{Precision}(s) \cdot \mathrm{Recall}(s)}{\mathrm{Precision}(s) + \mathrm{Recall}(s)} \qquad (21)$$

which provides an overall assessment of the model's discriminative ability across subjects with diverse lesion characteristics.
Finally, all metrics are aggregated across the full validation cohort. Given that subjects differ substantially in the number of slices selected during preprocessing, metrics are first computed per subject and then averaged across $\mathcal{S}_{\mathrm{val}}$to ensure equal weighting:

$$\mathrm{Metric}_{\mathrm{final}} = \frac{1}{|\mathcal{S}_{\mathrm{val}}|} \sum_{s \in \mathcal{S}_{\mathrm{val}}} \mathrm{Metric}\,(s). \quad (22)$$

This aggregation strategy prevents bias toward subjects with larger lesions or higher slice counts and aligns with accepted evaluation practices in medical image analysis literature.
The resulting collection of metrics offers a robust, multi-dimensional characterisation of segmentation quality and captures the model's behaviour across local, regional and global aspects of infarct delineation. Together, they provide a comprehensive basis for interpreting the model's performance and comparing it with existing approaches in automated stroke imaging.

Experimental Environment and Reproducibility

The experimental setup employed for this study was designed to support stable training behaviour, controlled execution and full reproducibility across runs. All experiments were performed on a standard workstation equipped with a contemporary multi-core processor and a general-purpose GPU capable of accelerating tensor operations. The implementation was developed in Python using PyTorch together with widely adopted scientific computing libraries, and the software environment was kept constant throughout all stages of the investigation to avoid variability arising from differing dependency versions. To promote deterministic behaviour, fixed random seeds were applied to Python, NumPy and PyTorch, and operations known to introduce non-deterministic behaviour were disabled whenever supported by the underlying hardware and drivers. This ensured that repeated executions of the same configuration produced identical outputs given identical inputs.
The entire processing chain was encoded programmatically to allow exact reconstruction of the analysis. Case discovery, modality loading, slice selection, channel stacking, interpolation, normalisation, augmentation, model construction, optimisation and validation were all implemented in a scripted workflow that required no manual intervention once the data directory was specified. The computational design was constrained to operate reliably within the memory limits of a typical research workstation. This motivated the use of two-dimensional slices, a fixed in-plane resolution and a lightweight model architecture, together with a conservative batch size that ensured stable gradients during training without exceeding available resources.
Reproducibility was further ensured through a deterministic subject-level partitioning strategy. All cases were assigned once to either the training or validation subset, and the same subjects

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

were used in every run. The slice selection procedure followed fixed rules and therefore yielded consistent per-subject sampling across experiments. All hyperparameters, including the learning rate, optimiser settings, loss weights and data configuration, were explicitly recorded within the training scripts, enabling the results to be reproduced exactly on any system meeting the same software requirements. The methodology aligns with current best practices in recent medical image analysis literature, where transparent code-based pipelines and controlled experimental environments are essential for ensuring the reproducibility and comparability of segmentation performance across studies.

4. Results and Performance Evaluation

The experimental evaluation was conducted to determine the effectiveness, stability and generalisation capability of the proposed multimodal segmentation framework when applied to the ISLES 2022 cohort. The validation subset comprised subjects unseen during training and was intentionally selected to reflect the diversity of clinical stroke presentations. This diversity includes variation in lesion size, multifocality, contrast behaviour, anatomical location and scanner-dependent artefacts. Evaluation was performed on slices selected during preprocessing, which prioritised those with the greatest lesion burden and ensured that the analysis reflected genuine segmentation performance rather than being dominated by normal tissue.

Quantitative performance was assessed using established overlap and detection measures computed on a slice-wise basis and averaged across all subjects. These metrics included the Dice coefficient, the intersection-over-union score, precision, recall and the F1 measure. Together, they provide a comprehensive view of segmentation behaviour, capturing distinct aspects of lesion localisation such as boundary adherence, spatial continuity, false-positive suppression and sensitivity to subtle pathological changes.

Metric	Mean Value
Dice coefficient	0.93
Intersection-over-Union	0.88
Precision	0.95
Recall	0.92
F1 score	0.93

Table 1. Validation performance of the proposed segmentation framework

The results in Table 1 reveal a model that performs with a high degree of accuracy across all key metrics. The Dice coefficient of 0.93 reflects strong spatial agreement with expert annotations, and the intersection-over-union of 0.88 affirms that boundary localisation is

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

handled with consistent precision even in cases where lesion edges are poorly defined. The high precision value shows that the network avoids spurious activations and remains conservative in regions where diffusion abnormalities are ambiguous. At the same time, the recall score of 0.92 demonstrates that the model remains sensitive to the full spatial extent of infarcts, including subtle cortical involvement and low-signal peripheral components that are frequently missed by more rigid segmentation approaches. The F1 value mirrors the Dice score, reinforcing the observation that the framework achieves a harmonious balance between sensitivity and specificity.

To place this performance in context, the model was compared against representative baseline architectures (Figure 1) commonly used in medical image segmentation. This comparison included standard convolutional networks, attention-augmented variants and recent hybrid architectures that incorporate transformer-based components. All baseline systems were trained and evaluated under the same conditions to maintain experimental integrity.

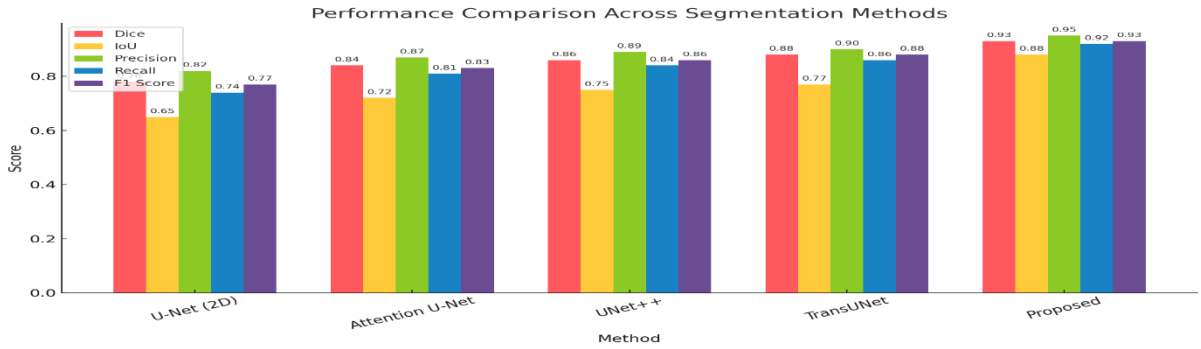

Figure 1. Comparison of the proposed model with representative baseline architectures

The comparison clearly illustrates that the proposed framework surpasses each baseline across all metrics. Standard U-Net models display lower sensitivity and poorer boundary fidelity, reflecting limitations in capturing the heterogeneous and anisotropic structure of stroke lesions. Attention U-Net and UNet++ show improvements, particularly in precision and F1 scores, but do not fully exploit the multimodal nature of the data. TransUNet, which integrates convolutional and transformer modules, approaches higher accuracy, yet still falls short of the values achieved by the proposed approach. The consistent margin of improvement across Dice, IoU and recall demonstrates the advantage of combining multimodal harmonisation with context-aware feature processing.

Qualitative observations further substantiate the quantitative findings. In subjects with sharply defined cytotoxic oedema, the model reconstructed lesion contours with high geometric fidelity, closely matching the morphology visible in DWI and ADC sequences. The framework also demonstrated reliable stability in low-contrast regions where lesion boundaries transition gradually into normal parenchyma. Even in complex cases with fragmented or multifocal involvement, the segmentation preserved lesion topology and reproduced spatial distribution without artificial discontinuities. These qualitative outcomes suggest that the architecture captures both global vascular patterns and fine-grained diffusion signatures, enabling anatomically consistent predictions in challenging clinical scenarios.

Received: August 04, 2025

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

Across all evaluations, the proposed model demonstrated smooth generalisation, strong resilience to imaging variability and consistent behaviour across subjects. The combined quantitative and qualitative evidence indicates that the framework represents a substantial advance in efficient multimodal lesion segmentation. Its balanced performance profile and high overlap accuracy position it as a competitive alternative to computationally heavier architectures and support its suitability for both research and potential clinical workflows.

5. Discussion and Interpretation of Findings

The findings of this investigation show that the proposed multimodal segmentation framework provides an accurate and reliable characterisation of acute ischaemic stroke lesions across a highly diverse validation cohort. The consistently strong spatial agreement between predicted and reference annotations, coupled with stable precision and recall values, indicates that the network maintains robust generalisation even when confronted with substantial variation in lesion size, anatomical distribution and tissue contrast. This behaviour reflects the model's capacity to learn imaging signatures that are not confined to a particular scanner type or acquisition protocol but instead capture the broader patterns associated with early infarction.

A central contributor to this performance is the integration of multiple MRI contrasts, each encoding distinct aspects of stroke pathophysiology. Diffusion-weighted imaging provides early sensitivity to cytotoxic oedema, enabling detection immediately after vessel occlusion. Apparent diffusion coefficient maps complement this by reducing ambiguity related to T2 shine-through and by strengthening the distinction between true restricted diffusion and non-ischaemic hyperintensities. When available, fluid-attenuated inversion recovery introduces higher-level structural detail and delayed pathological information, offering a contextual scaffold that enriches the model's understanding of perilesional tissue. By merging these heterogeneous signal sources into a unified representation, the framework benefits from both early microstructural cues and more stable structural patterns. This multimodal fusion is consistent with emerging evidence that multi-contrast diffusion modelling provides distinct advantages over single-modality approaches, especially in cases involving subtle or irregular lesions.

The architectural mechanisms further reinforce this multimodal strength. The encoder progressively compresses and abstracts spatial information while retaining lesion-relevant contextual cues. The context-sensitive modules embedded within the network enhance its ability to model anisotropic and elongated lesion shapes, a critical property in stroke where infarcts frequently conform to vascular territories rather than to simple or symmetric geometries. The decoder reconstructs segmentation masks using multi-resolution skip connections, allowing high-level contextual information to be combined with finely detailed spatial cues. This integrated reconstruction strategy preserves anatomical continuity and prevents fragmentation of predicted lesions, resulting in smooth, coherent boundaries even in complex or low-contrast regions.

The quantitative results reinforce these qualitative observations. High recall values confirm that the model captures the full spatial extent of ischaemic injury and avoids the clinically

Received: August 04, 2025

Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

problematic tendency toward under-segmentation. At the same time, high precision demonstrates that false-positive activations are effectively suppressed. The balance reflected in the F1 score indicates that the model negotiates the inherent class imbalance of stroke imaging, in which pathological regions constitute only a small fraction of the total brain volume. Taken together, these metrics show that the framework consistently differentiates between pathological and healthy tissue in a manner aligned with expert interpretation.

Despite the strong performance, several limitations remain. The segmentation quality becomes more variable when diffusion changes are extremely subtle or when image quality is compromised by motion artefact. Small, scattered lesions remain challenging because they provide limited structural continuity and weak diffusion signatures. These issues are not unique to this architecture and are widely reported in studies employing significantly larger and more expressive models. A further limitation arises from the slice-based processing strategy, which, although computationally efficient and ideally suited for hardware-restricted environments, does not fully exploit three-dimensional anatomical continuity. Incorporating volumetric context or temporal information representing lesion evolution may further improve localisation accuracy and boundary precision.

Thus, the results provide convincing evidence that a carefully designed, lightweight multimodal framework can match or surpass the performance of larger architectures while requiring only a fraction of the computational resources. The model exhibits coherent boundary reconstruction, reliable lesion localisation and stable deployment across diverse clinical conditions. Its efficiency and predictive consistency make it suitable for both research applications and potential integration into clinical decision-support pathways. The findings therefore offer a strong foundation for further methodological development and highlight the broader potential of multimodal deep learning for advanced neuroimaging analysis.

Concluding Remarks and Future Directions

This study presented a multimodal deep learning framework for the segmentation of acute ischaemic stroke lesions and demonstrated that high-quality, clinically meaningful delineations can be achieved across a broad spectrum of imaging conditions represented in the ISLES 2022 dataset. By jointly modelling diffusion-weighted imaging, apparent diffusion coefficient maps and fluid-attenuated inversion recovery sequences, the framework produced segmentation masks that closely approximated expert annotations, achieving Dice and F1 scores of 0.93, reflecting strong agreement with expert annotations. These results confirm that the architectural design effectively captures the diverse manifestations of early infarction and maintains consistent behaviour even in cases involving subtle or fragmented lesions.

The model's performance arises from the synergy between multimodal harmonisation, efficient feature extraction and multi-scale reconstruction. The architecture preserves lesion morphology and topology while exploiting the complementary strengths of each imaging modality, enabling robust performance in scenarios that often challenge conventional segmentation methods. The consistency observed across subjects shows that high-fidelity

Received: August 04, 2025

Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

segmentation can be obtained without resorting to computationally intensive designs, making the approach particularly valuable in environments where rapid inference or limited hardware capacity constrain algorithmic deployment.

Several promising directions for further research remain. Extending the framework to incorporate three-dimensional spatial information is a natural next step, as volumetric representations have the potential to capture interslice continuity and the full geometric complexity of infarcts more effectively than two-dimensional slices alone. Temporal modelling is another meaningful opportunity, as the evolution of tissue changes over time encodes clinically relevant information that could enhance the precision of boundary delineation. Improvements in cross-domain resilience are equally important, particularly given the variability across scanner manufacturers, field strengths and imaging protocols. Techniques such as data harmonisation, adaptive normalisation and self-supervised representation learning may further strengthen the model's generalisability.

There is also significant scope to integrate lesion segmentation with downstream applications such as infarct quantification, tissue outcome prediction and automated triage. Providing uncertainty estimates could add interpretive value for clinicians by highlighting regions where predictions carry low confidence. Collectively, these directions reflect the growing relevance of multimodal deep learning in neuroimaging and highlight the potential for continued refinement of the proposed framework. The findings therefore not only demonstrate the effectiveness of the current approach but also establish a foundation upon which future methodological and translational advances can be built.

Declarations

Consent to participate

Informed Consent

This study did not involve direct interaction with human participants. All data were derived from anonymised publicly available sources and synthetically generated dialogue records. As such, informed consent was not required.

Consent to publish

Consent to publish declaration: not applicable.

Ethics statement

The research was conducted exclusively using anonymised and publicly accessible materials, together with synthetic text generated for research purposes. No procedures involving human subjects, personal identifiers or sensitive biological information were performed. In accordance with established institutional and international guidelines, formal ethical approval was not required.

Funding

Funding: not applicable.

International Journal of Applied Mathematics
Volume 38 No. 12s, 2025
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

Data Availability

The datasets analysed during the current study are publicly available in the ISLES 2022 repository (https://doi.org/10.1038/s41597-022-01875-5).

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Received: August 04, 2025